



Contrasting phylogeographic patterns of a phytophagous insect and its host plants

Neus Marí- Mena, Carlos Lopez-Vaamonde, Horacio Naveira, Marie-Anne Auger-Rozenberg, Marta Vila

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On the maintenance of sex in natural populations (53716)

Tanja Schwander.

University of Lausanne.

The overwhelming success of obligate sexual reproduction among eukaryotes implies that sex generates advantages that fully compensate for its inherent costs relative asexuality. Theoretical approaches have shown that the potential for sex to be advantageous increases in spatially or temporally heterogeneous environments. However, it remains unknown whether environmental heterogeneity contributes to the maintenance of sex in natural populations. I will discuss different competition experiments between sexual and asexual grasshrips in natural habitats and semi-natural mesocosm conditions through which we evaluated whether and how habitat heterogeneity can contribute to the maintenance of sexual lineages when in competition with co-occurring asexuals.

Evolutionary advantage of sexual algal prey exposed to predation (51656)

Hanna Koch, Sophia Wagner, Lutz Becks.

Max Planck Institute for Evolutionary Biology; Plön, Germany.

Here, we present results from an experimental evolution study using a predator-prey system to evaluate theory for the evolution of sexual reproduction. Specifically, we tested whether sex is beneficial when populations are exposed to predation. We used an algal-rotifer system to first show that sex in an algal prey provides a direct fitness benefit by combining different beneficial mutations - for increased growth rates and grazing resistance - into one genome, whereas asexual populations suffer trade-offs in these traits. We also found that sexual prey populations evolved to higher levels of fitness over time compared to asexual prey populations. The results confirm the theory that asexual populations evolve more slowly due to clonal interference and a lack of recombination. We used the same system in a second experimental evolution study to show that the in-situ rate of sex was maintained at high levels in the presence of predation, but not in treatments without predation. Together, these results show that sex not only provides a direct fitness benefit in the presence of predation, but is also maintained which suggests an evolutionary advantage that outweighs the costs of sex within this relevant ecological context.

Invasion of the selfers! Evolutionary ecology and the maintenance of outcrossing. (53322)

Levi Morran.

Emory University.

Outcrossing is inherently costly relative to self-fertilization. Nonetheless, outcrossing is quite prevalent in nature. What prevents the widespread invasion and fixation of alleles permitting self-fertilization in mixed mating and obligately outcrossing populations? Here, I will discuss the results of several experimental evolution studies testing the role of parasites in preventing, slowing, and perhaps even facilitating the spread of self-fertilization in host populations. Additionally, I will discuss the potential limitations of parasites with regards to the maintenance of outcrossing and explore other factors that may impede the spread of self-fertilization.

Session 1 MON GEN C 1

Fitness consequences of parasite-mediated selection on sexual reproduction in a natural population (51671)

Amanda Gibson, Lynda Delph, Curt Lively.

Indiana University.

Sex is costly relative to asexual reproduction, yet it is widespread in nature. What force prevents sex from being out-competed? The Red Queen Hypothesis argues that coevolving parasites select for sex in hosts. Our study tests if parasites are a sufficient force to maintain sex in nature. Sexual lineages of a freshwater snail persist in competition with asexual forms, and a castrating trematode parasite has been indirectly linked to this persistence. We combine field sampling with experimental mesocosms to test if parasite selection alone can confer a fitness advantage to sexual individuals in competition with asexual clones. The Red Queen predicts that the fitness of sexuals relative to clones will be periodically higher in the presence vs. absence of parasites. At present, we find that sexuals are more parasitized than are clones, and that parasites lower the relative fitness of sexuals. Accordingly, long-term field data suggest that the frequency of sexual individuals is declining in the natural population. With multi-year sampling, we further test the Red Queen's prediction that the direction of parasite selection will shift to favor sex as clones increase in frequency. Our work provides a much-needed direct test of the Red Queen in a natural system.

Session 1 MON GEN C 1

Brachionus calyciflorus evolves higher levels of sex with more loci under selection. (51689)

Pepijn Luijckx, Eddie Ho, Madjid Gasim, Connor Yanchus, Suyang Chen, Yuna Kim, Aneil Agrawal.

University of Toronto.

The widespread occurrence of sexual reproduction, despite its well-known costs, has been a long standing problem in evolutionary biology. Although there are numerous theories for why sex is the most common mode of reproduction, critically few assumptions and predictions of these theories have been tested. Using experimental evolution with the facultative sexual rotifer *Brachionus calyciflorus* we tested whether higher levels of sex evolve when more loci are under selection as predicted by Hill-Robertson interference, a popular theory for the maintenance of sex. The number of loci under selection were manipulated by adapting *B. calyciflorus* to either one, two or three abiotic stressors in a full factorial design (i.e. each multi stressor was composed of different combinations of the single stressors). Results from two independent evolution experiments (over one million animals scored) confirmed the hypothesis. *B. calyciflorus* produced more sexual eggs when adapting to more complex environments. Furthermore, common garden experiments confirmed that this change was genetic and as we standardize population size these changes were unlikely due to differences in genetic drift. These findings can explain why sex is the dominant mode of reproduction as natural populations may experience a multitude of selection pressures at any one time.

Session 1 MON GEN B 5

How important are sex-linkage and non-additive genetic variation in the variance structure of sexually dimorphic traits? (52037)

Daphne Fairbairn.

University of California, Riverside.

Selection favoring different trait values in males and females is expected to favor the evolution of both sex-specific patterns of gene expression and sex-linkage. Although genomic and transcriptomic studies suggest that both mechanisms are important, quantitative genetic analyses often fail to find disproportionate effects of sex-linkage for sexually dimorphic traits. Non-additive interactions are also likely to be important for genes involved in sexual dimorphism, but the effects of these on genetic variances have been difficult to estimate independently of sex linkage. This presentation summarizes the results of a breeding experiment designed to estimate additive and non-additive, sex-linked and autosomal variances for 16 morphological traits in an insect with XX/XO sex determination, the water strider, *Aquarius remigis*. The traits range from sex-limited to sexually monomorphic and a subset is subject to strong sexual selection in males. The results reveal major differences in genetic architecture between sexes, often with disproportionate contributions of sex-linked genes and large non-additive effects. As predicted, sex-linkage is associated with lower between-sex genetic correlations. The relationships between genetic architecture, sexual dimorphism and the pattern of selection are broadly consistent with predictions from evolutionary theory, but several anomalies suggest avenues for future research.

Session 1 MON GEN B 5

X-linkage of sex-specific genetic variance revealed using G-matrix analyses and a novel laboratory technique (51959)

Robert Griffin, Holger Schielzeth, Urban Friberg.

Uppsala University; Bielefeld University; Linköping University.

Intralocus sexual conflict can constrain the evolution of sex-specific phenotypic optima via correlated responses to selection. Genetic variance-covariance matrices, G-matrices, can be applied to data to estimate the variance within traits, and covariance between multiple traits, environments, and sexes. Several methods can then be used to describe and compare the characteristics and geometry of G-matrices and component sub-matrices. We use partial-hemiclones, a novel laboratory method using *Drosophila melanogaster*, which allows us to powerfully estimate X-chromosome and autosomal contributions to genetic (co)variance. Two G-matrices were constructed, for the X-chromosome and autosomes separately, containing (co)variance estimates for 3 traits (including longevity) in both sexes. Differences between these G-matrices are tested using multiple analytical methods, including the multivariate breeder's equation. Principally these are used to test for differences in the B-submatrix, which shows the intersexual genetic covariance, between the two types of partial-hemiclone lines. We show that more intersexual genetic covariance is found in the autosomes, suggesting that the X-chromosomes represent a hotspot for sex-specific genetic variance. Major sex chromosomes could therefore play a significant role in the resolution of intralocus sexual conflict.

Session 1 MON GEN B 5

The geography of sex-specific selection, local adaptation, and sexual dimorphism (51691)

Tim Connallon.

Monash University.

Local adaptation and sexual dimorphism follow parallel conceptual threads. Each represents an iconic evolutionary scenario of intra-specific adaptive differentiation in the face of gene flow, and each is associated with a set of influential theoretical predictions within its respective evolutionary context. Here, I merge theories of local adaptation in space, and sex-specific adaptation over time, and show that their confluence yields several unique predictions about the roles of context-specific selection, migration, and genetic correlations, in adaptive diversification. I specifically revisit two influential predictions from classical studies of clinal adaptation and sexual dimorphism: (1) that local adaptation should decrease towards species range margins; and (2) that opposing directional selection between the sexes (sexual antagonism) should accompany the evolution of sexual dimorphism. I show that both predictions often break down under clinally varying selection. The geography of local adaptation can be sexual dimorphic, with locations of relatively high and low local adaptation differing extensively between the sexes. Moreover, the intensity and duration of sexual antagonism is highly variable across the species range. Subpopulations near the range center are hotspots for sexual antagonism. Peripheral subpopulations exhibit a stronger alignment of directional selection within each sex.

TRANSCRIPTOME-WIDE EFFECTS OF MALE SEXUAL SELECTION ON THE FATE OF NEW MUTATIONS (52609)

Julie M. Collet, Mark W. Blows, Katrina McGuigan.

University of Queensland; University of Queensland; University of Queensland.

Traits that determine male mating success are predicted to have widespread effects on sex-specific genetic variation as a consequence of the pleiotropic allelic effects of sexual and non-sexual traits. We manipulated the opportunity for sexual selection on males during 27 generations of mutation accumulation in inbred lines of *Drosophila serrata*. To complement previous analyses of the effects of male sexual selection on male and female phenotypes, we used a microarray platform to investigate the effect of sexual selection on the expression of 2689 genes. Over all genes, mutational variance in gene expression increased by an average 42%, in sexually selected lines, compared to lines that did not evolve under sexual selection. However, there was no significant effect of sexual selection on average gene expression. Our results provide clear evidence that sex-specific selection on males can generate widespread effects across the genome. An increase in mutational variance without a corresponding change in mean is consistent with divergence generated by widespread pleiotropic associations with traits affecting male mating success. Furthermore, a Gene Ontology term enrichment analysis comparing treatments will enable the identification of the functions targeted by male sexual selection.

Red males revealed: a cytochrome P450 gene cluster controls production of derived red ketocarotenoids in the zebra finch bill (52724)

Nick Mundy, Jessica Stapley, Clair Bennison, Terry Burke, Tim Birkhead, Staffan Andersson, Jon Slate.

Department of Zoology, University of Cambridge; Department of Animal and Plant Sciences, University of Sheffield; Department of Zoology, University of Gothenburg.

Red coloration is commonly involved in sexual, social or interspecific colour signalling. Highly chromatic (“bright”) red integument (skin, scales, feathers) in birds is typically caused by ketocarotenoids, such as canthaxanthin, which are metabolically derived from dietary yellow carotenoid precursors. However, this key molecular mechanism underlying sexual dichromatism in birds has remained obscure. Here we investigate the pigmentary, genetic and gene expression basis of the yellowbeak mutation in the zebra finch, an autosomal recessive mutation. Wildtype ketocarotenoids are absent in the beak and tarsus of yellowbeak birds. Using a candidate gene approach in a low resolution QTL analysis we identified a haplotype in the CYP2J2 cluster on chromosome 8 that is perfectly associated with the yellowbeak phenotype. The yellowbeak haplotype has a whole gene deletion of the second locus (CYP2J2B) in the cluster. CYP2J2B is specifically expressed in ketocarotenoid-coloured beak and legs of wildtype zebra finches but not in liver. Our results suggest that CYP2J2B is

essential for the sexually selected red beak of the zebra finch, that it likely encodes a functional C4 ketolase enzyme, and that the conversion is primarily peripheral in this species, i.e. in the ketocarotenoid-pigmented tissues.

Session 1 MON POL A 28

Identifying the causes of natural selection: What have we learned from 25 years of experiments? (53330)

Christina Caruso.

Department of Integrative Biology, University of Guelph.

Phenotypic selection varies in space and time. To understand why there is variation in selection, we need to identify which environmental factors cause traits and fitness to covary. One way to identify these factors was described by Wade and Kalisz (1990): experimentally manipulate the environment and measure selection within each treatment group. If the manipulated environmental factor causes traits and fitness to covary, then selection will differ between treatment groups. Although this experimental approach to identifying the causes of selection was described 25 years ago, the results of these experiments have yet to be reviewed.

I will review what 25 years of ecological experiments have, and have not, taught us about the causes of natural selection. First, I will use a case study of selection on floral traits of the wildflower *Lobelia siphilitica* to illustrate how experimental manipulations can be used to test longstanding assumptions about the causes of selection. Second, I will use a meta-analysis of selection estimates from experimental studies published over the last 25 years to test two hypotheses about the relative importance of different causes of selection. I will conclude by describing priorities for the next 25 years of experimental studies of the causes of selection.

Session 1 MON POL A 28

The fluctuation of selection and its evolutionary consequences in an alpine rodent population. (51725)

Timothée Bonnet, Erik Postma.

Institute of Evolutionary Biology and Environmental Studies .

Temporal variation in the strength and direction of directional selection has important implications for the maintenance of genetic variation and for the prediction of evolutionary change in wild populations. However, empirical estimations of the fluctuation of selection, together with the genetic response, are still scarce and hampered by confounding sampling variance.

Using the long-term monitoring of a wild snow vole (*Chionomys nivalis*) population, we quantify the temporal fluctuation of the selection acting on morphological traits, while

accounting for sampling variance. Climatic factors appear as a possible driver of change in the strength and direction of selection. Moreover, contrasting patterns of fluctuation among viability, fertility, and total selection highlight the importance of considering all fitness components. We then relate the fluctuation of selection to year-by-year genetic changes, using both a candidate gene approach and multivariate quantitative genetic models. This provides a direct test of whether fluctuation can explain evolutionary stasis in this population, and illustrate that the selection patterns observed at the phenotypic level do not necessarily translate into parallel genetic changes.

Session 1 MON POL A 28

Measuring fluctuating phenotypic selection (53320)

Luis-Miguel Chevin, Marcel Visser, Jarle Tufto.

CNRS.

Fluctuating selection caused by randomly changing environments is a ubiquitous feature of natural systems. The magnitude and predictability of these fluctuations are expected to strongly impact the evolution and demography of populations, but few attempts have been made to quantify these parameters and relate them to relevant environmental variables, in a way that connects to theoretical predictions. In this talk, I will first briefly review theoretical results for evolutionary demography in a randomly changing environment affecting the optimum phenotype for a quantitative trait. I will then discuss some of the challenges with measuring fluctuating selection using classical methods such as selection gradients. Finally, I will introduce an approach for estimating patterns of changes in an optimum phenotype, which allows inferring parameters that directly appear in theoretical predictions. This will be illustrated by an application to the breeding time of a population of great tits in the Netherlands, a classic example of evolution in response to climate change.

Session 1 MON POL A 28

The Spatial Scale of Local Adaptation (51756)

Jarrold Hadfield, Albert Phillimore.

University Of Edinburgh; University Of Edinburgh.

The distribution of phenotypes in space will be a compromise between local adaptation increasing the fit of phenotypes to local conditions and gene-flow reducing that fit. Few theoretical models have considered the evolution of quantitative characters on spatially explicit landscapes, and those that have, only consider scenarios where optimum trait values change as a deterministic function of space, such as clines. Here we extend these models to include a stochastic spatially autocorrelated aspect to the environment, and as a consequence the optimal phenotype. We show that under these conditions the regression of phenotype on the environmental variable becomes steeper as the spatial scale on which individuals, or

populations, are sampled becomes larger. Under certain deterministic models - such as smooth clines - the regression is constant. The way in which the regression changes with spatial scale is informative about the degree of phenotypic plasticity, the relative scales of effective gene flow and environmental autocorrelation, and the environmental dependency of selection. Methods to estimate these parameters from spatially replicated data are discussed, and the theory suggests a common scale on which temporal and spatial fluctuations in selection can be compared.

Session 1 MON POL A 28

DETECTING CHANGING SELECTION INTENSITIES FROM TIME-SAMPLED DATA (51758)

Hyunjin Shim, Stefan Laurent, Matthieu Foll, Jeffrey D. Jensen.

Ecole Polytechnique Fédérale de Lausanne (EPFL); Swiss Institute of Bioinformatics (SIB); International Agency for Research on Cancer.

The possibility of fluctuating selection in natural populations was suggested by Wright (1948) during his famous controversy with Fisher regarding the phenotypic dataset of *Panaxia dominula*, and the subject has since been considered in various analyses - ranging from Kimura (1954) to Cain et al. (1990). Until now, the focus of discussion mainly centered on the random fluctuation of selection intensities. Here, we present a novel method to consider nonrandom fluctuation of selection intensities using ABC-based approaches, in order to detect and evaluate the change in selection strength in time-sampled data. The novel method estimates jointly the position of a change point and the strength of both corresponding selection coefficients (as well as dominance for diploid cases) from the allele trajectory. Furthermore, the method is applied on the historical dataset of *Panaxia dominula* to test for a change in selection intensity, as well as on a whole-genome time-serial study of influenza virus in order to identify mutations with changing selection intensities in response to drug treatment.

Session 1 MON POL B 15

The gibbon genome: swinging between evolution, speciation and disease (53396)

Lucia Carbone.

Oregon Health & Science University.

Gibbons are small Asian apes heavily threatened by extinction. They carry many distinctive traits that set them apart from their close relatives, human and the great apes, including brachiation (i.e. locomotion mainly using their upper limbs), pair bonding, and duet singing to advertise their territory. Their most striking trait, however, is the unusually high number of chromosomal rearrangements. There are four gibbon genera (*Nomascus*, *Hoolock*, *Hylobates*,

and *Symphalangus*) that split from each other only 5 million years ago and each of them carries a distinct karyotype with chromosome numbers ranging from 38 to 52. This exceptional accelerated karyotype evolution makes gibbons an ideal model to study chromosome evolution and mechanism of genome instability. Together with geographical changes occurring in their territory, the abundance of chromosomal rearrangements was responsible for an “instantaneous” radiation of the gibbon genera and the higher number of species (n=19) found in the gibbon family. We discovered that a gibbon specific retrotransposon, the LAVA element, inserted in genes involved in chromosome segregation, suggesting that in these species chromosome fragility might have been triggered by mis-segregation during meiosis. This phenomenon has recently been characterized in cancer genomes and embryo development, highlighting an analogy between mechanisms underlying genome instability during species evolution and disease.

Session 1 MON POL B 15

Fitness consequences of inversion polymorphisms in the zebra finch (51889)

Wolfgang Forstmeier, Ulrich Knief, Georg Hemmrich-Stanisak, Michael Wittig, Andre Franke, Simon Griffith, Bart Kempnaers.

Max Planck Institute for Ornithology; Institute of Clinical Molecular Biology; Macquarie University.

Genome-wide scans for signatures of past selection can help identify loci with strong effects on fitness. In the present study, we searched for patterns in the allele frequency spectrum across genomic regions among 23,000,000 SNPs identified from pool-seq data of genomic DNA from 100 wild-caught zebra finches. Using sliding windows of a measure of pooled heterozygosity, we found several genomic regions where the great majority of SNPs showed a minor allele frequency close to 50%. Subsequent genotyping of 3,804 SNPs spread across these regions and the entire genome in 948 wild zebra finches identified these regions as break points of inversion polymorphisms. Altogether, we found that 4 out of 31 covered chromosomes harbored inversion polymorphisms that span between 13 and 60 megabases and cover large proportions of the affected chromosomes with inversion frequencies close to 50%, which is suggestive of balancing selection resulting from heterozygote advantage. Hence, we studied phenotypic effects of these inversions on morphology, relative fitness and embryo mortality in up to 6,000 mostly captive zebra finches to gain an understanding of the selective forces that lead to the maintenance of these remarkable polymorphisms.

Session 1 MON POL B 15

Human Evolution by Segmental Duplication (53374)

Evan Eichler.

University of Washington & HHMI.

Human duplicated sequences show extraordinary sequence complexity and are important sources for gene innovation and rearrangement associated with neurocognitive diseases such as autism and intellectual disability. Evolutionary genomic reconstructions point to a burst of segmental duplications in the common ancestor of human and the apes in contrast to other mutational processes that have slowed at this point in time. I will show that much of the interspersed human duplication architecture is focused around core duplicons corresponding to the expansion of gene families, which show strong signatures of positive selection and which lack orthologs in other mammalian species. I will present an overview of the evolution of human-specific segmental duplications, their copy number variation in diverse human populations and their potential to form neofunctional gene fusions. I will highlight novel genes that have evolved within the human lineage and appear to have contributed to adaptive aspects of human brain function as well as examples where this evolutionary plasticity has been positively selected. Using single-molecule real-time (SMRT) sequencing technology, I will show how such complex regions can be resolved and show how radically these regions of our genome have changed and differ among human populations. Paradoxically, the duplication architecture complexity has led to a high background rate of copy number variation mutations associated with neuropsychiatric and neurodevelopmental disease in the human species suggesting that novel adaptations and increased disease burden are linked.

Session 1 MON POL B 15

Parental investment predicts genetic diversity of animal species (52005)

Jonathan Romiguier, Nicolas Galtier.

University of Lausanne; CNRS.

Genetic diversity is the amount of variation observed between DNA sequences from distinct individuals of a given species. This pivotal concept of population genetics has implications for species health, domestication, management and conservation. Levels of genetic diversity seem to vary greatly in natural populations and species, but the determinants of this variation, and particularly the relative influences of species biology and ecology versus population history, are still largely mysterious. Here we show that the diversity of a species is predictable, and is determined in the first place by its ecological strategy. We investigated the genome-wide diversity of 76 non-model animal species by sequencing the transcriptome of two to ten individuals in each species. The distribution of genetic diversity between species revealed no detectable influence of geographic range or invasive status but was accurately predicted by key species traits related to parental investment: long-lived or low-fecundity species with brooding ability were genetically less diverse than short-lived or highly fecund ones.

Session 1 MON POL B 15

A genomic study of the contribution of DNA methylation to regulatory evolution in primates (52018)

Julien Roux, Irene Hernando-Herraez, Nicholas Banovich, Raquel Garcia-Perez, Jonathan Pritchard, Tomas Marques-Bonet, Yoav Gilad.

University of Lausanne; University of Chicago; Institute of Evolutionary Biology (UPF-CSIC), PRBB, Barcelona; Howard Hughes Medical Institute, Stanford University; Departments of Biology and Genetics, Stanford University.

A long-standing hypothesis is that changes in gene regulation play an important role in adaptive evolution, notably in primates. Yet, in spite of the evidence accumulated in the past decade that regulatory changes contribute to species-specific adaptations, we still know little about the mechanisms of regulatory evolution. In this study we focused on DNA methylation, an epigenetic mechanism whose contribution to the evolution of gene expression remains unclear.

To interrogate the methylation status of the vast majority of cytosines in the genome, we performed whole-genome bisulfite conversion followed by high-throughput sequencing across 4 tissues (heart, kidney, liver and lung) in human, chimpanzee and macaque. In parallel, we collected gene expression profiles using RNA-seq from the same tissue samples, allowing us to perform a high resolution scan for genes and pathways whose regulation evolved under natural selection.

We integrated these datasets to characterize better the genome features whose methylation status leads to expression changes across tissues and species. We discovered that, in contrast to the well-known negative association between gene expression and methylation changes across tissues, the association between these two variables was greatly reduced across species. Our study questions the role of epigenetic modifications as a mechanism causing regulatory changes in primates.

Session 1 MON POL B 15

Recombination and GC-biased gene conversion shape genome evolution in the honeybee (*Apis mellifera*) (52102)

Andreas Wallberg, Sylvain Glémin, Matthew T Webster.

Department of Medical Biochemistry and Microbiology, Science for Life Laboratory, Uppsala University; UMR 5554, Institute of Evolutionary Sciences, University of Montpellier.

Recombination is crucial for sexual reproduction and has pervasive effects on genetic diversity. The eusocial honeybee *Apis mellifera* has among the highest recombination rates observed in any eukaryote (~22 cM/Mb). The reasons for these high rates and their effects on genome evolution are unknown. We have used whole-genome resequencing data from 30 honeybees to build a fine-scale map of recombination from patterns of linkage disequilibrium. We have studied the associations between recombination, DNA methylation, gene expression and the site frequency spectrum to assess how recombination shapes the honeybee genome.

We find that recombination frequencies are not highly variable nor restricted to hotspots, in contrast to many sexual plants, fungi and vertebrates. They are greatly influenced by germline

CpG-methylation, which suppresses recombination. The site frequency spectrum is highly skewed towards the fixation of GC alleles, indicative of a major impact of GC-biased gene conversion (gBGC), which we estimate as 5-50x higher than in humans. The fixation bias specifically favours mutations that generate CpG sites, which occur in excess in honeybees.

Recombination determines levels of genetic variation in honeybees. At such high rates, gBGC strongly interferes with selection, resulting in rapid fixation of deleterious alleles and altered nucleotide composition across the genome.

Session 1 MON POL C 14

Stalking the elusive generalist: Understanding the relationship between the fundamental and realized niches of *Pseudomonas* in the home (53353)

Susanna Remold.

University of Louisville.

Many species of *Pseudomonas* have the ability to use a variety of resources and have been isolated from diverse environments, and as a result, *Pseudomonas* are often characterized as having broad fundamental niches. In culture-based and culture-independent surveys of a broad range of environments found in and around the human home, we assessed the degree to which *Pseudomonas*' realized niches, where they are actually found in nature, are equally broad. We found temporal and spatial variability in recovery of the three species groups of *Pseudomonas* most commonly found in homes: the *P. aeruginosa*, *P. fluorescens* and *P. putida* species groups. In addition, we found that these *Pseudomonas* species groups' distributions also differ from each other. In a series of studies characterizing strains collected in these surveys and individually and in pairwise interactions, we explored biotic and abiotic factors that may cause *Pseudomonas*' realized niches to differ from each other, and to be smaller than their fundamental niches. In my talk I will describe some of these studies and discuss applications of studies linking fundamental to realized niches.

Session 1 MON POL C 14

Sub-inhibitory antibiotic concentrations can radically alter the eco-evolutionary consumer-resource dynamics in microbial communities (51684)

Teppo Hiltunen, Lutz Becks, Matti Jalasvuori, Ville Ojala, Jouni Laakso.

University of Helsinki; Max Planck Institute for Evolutionary Biology; University of Jyväskylä.

Modern medicine relies heavily on the effective use of antibiotics. However, antibiotic resistant pathogens are on the rise. This problem has been often studied in simplified single species setting, but in natural environments bacteria reside in multispecies communities where they interact with other microbes. Yet, virtually nothing is known about community aspects,

such as how predation affects the emergence and spread of antibiotic resistance. Furthermore, recent evidence highlights the importance of sub-inhibitory concentrations of antibiotics on bacteria. In addition to the fact that these low concentrations can alter the bacterial gene expression, communication, and select for antibiotic resistant genotypes, an important question is whether this modifies the community level dynamics. By using experimental evolution methods with a microbial model system consisting of bacterial prey, *Pseudomonas fluorescens* SBW25, parasitic phages and protozoan predators, we found that subinhibitory concentrations of antibiotic streptomycin can radically alter the eco-evolutionary community dynamics. Moreover, the community structure determined the emergence of antibiotic resistant genotypes in the bacterial population. In addition to the phenotypic data, also a massive re-sequencing of the experimental *Pseudomonas* populations is underway. Our results highlight the importance of understanding the eco-evolutionary community aspects when fighting the antibiotic resistance problem.

Session 1 MON POL C 14

Experimental evolution of bacteria in the laboratory and in the wild (53482)

Tom Bell.

Imperial College London.

Understanding how species adapt to novel environments is among the greatest challenges in evolutionary biology. However, experimental studies and theories have focused almost exclusively on simplified systems containing at most a few species. If species interactions in natural communities fundamentally alter evolutionary outcomes, then there is a need to study the adaptive process within the context of entire communities, and to understand the consequences of adaptation for community structure and functioning. I will discuss a series of experiments using bacterial microcosm communities of increasing complexity. When challenged with a novel environment, the evolutionary dynamics of mixtures of a few species differ substantially from those grown as single species, and species interactions evolve over time, resulting in a change in the functioning of the entire community. The outcome appears to depend critically on the diversity of the surrounding community, suggesting a complex interplay between ecological and evolutionary processes.

Session 1 MON POL C 14

Bacterial biodiversity: the role of spatial structure and competition within species (51688)

Anne Leinweber, Rolf Kümmerli.

University of Zurich.

Bacteria often live in multispecies communities, which is difficult to explain, because strongly competitive species should eventually displace weaker counterparts. Spatial structure

has been suggested to stabilize diversity by separating competitors from each other. Alternatively, it has been proposed that strong competitors are more prone to within-species competition, which can relax between-species competition. To test these hypotheses, we use *Pseudomonas aeruginosa* (PA) and *Burkholderia cenocepacia* (BC), two bacterial species naturally co-occurring in soil and human opportunistic infections. However, under standard laboratory conditions PA eradicates BC. We manipulated spatial structure by growing the bacteria in medium with varying viscosities. To manipulate within-species competition, we introduced a PA cheating mutant strain to co-cultures. Under the iron limited conditions of our experiments, this mutant is able to exploit the iron scavenging siderophores secreted by the wildtype PA. Using a mixture of competition assays and experimental evolution, we found that spatial structure consistently inhibited species co-existence. Within-species competition, meanwhile, promoted co-existence in unstructured habitats, because it allowed cheats to efficiently exploit PA, which eased the competitive burden of PA on BC. Thus, we identified within-species competition as an important driver of long-term species coexistence.

Session 1 MON POL C 14

Experimental coevolution and the effects of parasite species co-infection on parasite virulence and fitness (51718)

Suzanne Ford, Kayla King.

University of Oxford.

The simultaneous infection of a single host by multiple parasite strains and species, termed co-infection, is common in nature. Co-infecting parasites that share ecological niches within the host compete for space and resources in numerous ways. This competition is likely to impose selection on interacting parasites and as such could play a role in shaping host-parasite coevolutionary trajectories. Importantly, the degree to which co-infection affects the evolution of key parasite traits such as competitive ability and virulence is uncertain. In this project we experimentally coevolved two bacterial parasites, *Enterococcus faecalis* and *Staphylococcus aureus*, by serially co-infecting them within a non-evolving host organism, *Caenorhabditis elegans*. Firstly, we found that coevolved *S. aureus* gained a significant competitive advantage under co-infection compared to singly evolved controls and became locally adapted in time to its competitor, *E. faecalis*. Secondly, we found that parasite species co-infection significantly altered the evolved level of intrinsic virulence of both species compared to singly evolved controls. Together, our results support the hypothesis that parasite species co-infection could be a selective factor in the evolution of key parasite traits. This further suggests that interspecific interactions between parasites could play a role in shaping coevolutionary interactions between parasites and their hosts.

Session 1 MON POL C 14

Pathogen adaptation to individual and social host defences in ants (51808)

Miriam Stock, Anna V. Grasse, Sylvia Cremer.

IST Austria (Institute of Science and Technology Austria), Austria.

In co-evolving host-pathogen systems, both players undergo continuous adaptations. For social insect hosts, these include individual behavioural and immunological adaptations, and their collectively performed, social disease defences. We performed an evolution experiment testing for pathogen adaptation of an insect-pathogenic fungus to an ant host. A genetically diverse starting population of the pathogen – consisting of a mix of naturally co-occurring fungal strains isolated from the field – was let to adapt to the ants over 10 host passages under two different conditions: (1) a single host treatment, involving only the individual defences of the exposed ant, and (2) a social host treatment, in which the exposed ant was accompanied by nestmates, allowing for additional collective disease defences. Fungal diversity decreased drastically by competitive strain exclusion in both treatments, yet a greater variation remained among replicates in the social host treatment. Testing the evolved fungal lines from both treatments under both single and social rearing conditions revealed an effect of 'evolution history' on pathogen killing rate and transmission stage production, as well as on the induction of host sanitary behaviours. We conclude that the additional collective disease defences in insect societies add selection pressures on coevolving pathogens affecting their ability to adapt to the host at the group level.

Session 1 MON MAX 410 6

The social side of sex: Male/female coevolution and social plasticity affect reproductive patterns (53319)

Suzanne Alonzo.

Department of Ecology and Evolutionary Biology, University of California Santa Cruz.

Extensive empirical and theoretical research has focused on understanding the diversity of reproductive patterns and behavioral interactions observed in nature. I have argued that considering both coevolutionary dynamics and social interactions can improve our ability to explain and predict this striking variation. In my talk, I will discuss why these dynamics are essential for understanding the evolution of male and female reproductive traits. I will first present the results of some general theory examining how social interactions affect evolutionary dynamics and discuss extensions of this theory to our understanding of specific reproductive behaviors. I will then present some data on how interactions between the sexes at mating and fertilization affect sexual selection, potentially driving the evolution of sperm allocation and paternal care in a Mediterranean fish (the ocellated wrasse, *Symphodus ocellatus*). Finally, I will discuss what these and other similar empirical patterns have to say about what theory and data are needed if we wish to improve our understanding of and capacity to predict the diversity of reproductive patterns observed in nature.

Session 1 MON MAX 410 6

Promiscuity modulates the male Bateman gradient in *Drosophila melanogaster* (51636)

Juliano Morimoto, Grant C. McDonald, Tommaso Pizzari, Stuart Wigby.

University of Oxford.

Sexual selection favours genes that increase success in intra-sexual competition. In a classic study, Angus Bateman measured the association between the number of mates and offspring production (the “Bateman gradient”) and found that the gradient was more positive for males than for females, which Bateman interpreted as evidence for stronger intra-sexual competition in males. Although Bateman’s study has had a strong influence on the field of sexual selection – and the Bateman gradient is widely used to measure the strength of sexual selection – Bateman’s principles only address competition for mates (pre-copulatory sexual selection), thus ignoring the effects of differential fertilisation success. Here, we genetically manipulated mating frequency in female *D. melanogaster* and found that in populations with significantly increased promiscuity (i.e. both females and males have more sexual partners), the male Bateman gradient is significantly reduced whereas female Bateman gradients are unaffected (i.e. non-significantly positive). Our study complement Bateman’s paradigm by providing direct empirical evidence of the effects of promiscuity on pre- vs post-copulatory sexual selection in males. In addition, our study corroborates a central expectation in sexual selection field, namely that the main driver of sexual selection in males switches from pre-copulatory to post- copulatory in high promiscuous populations.

Session 1 MON MAX 410 6

Coalescence and genomics with linked selection in systems with bi- and uniparental reproduction: contrasting partial asexuality and selfing (53310)

Aneil Agrawal.

University of Toronto.

Much of evolutionary genomic inference relies on coalescence but most previous theory assumes full sex (or haploidy). We have been integrating partial asexuality in diploids into the coalescent framework to understand how low rates of sex affects coalescence, especially in the presence of background and balancing selection. Low rates of sex greatly enhance background selection, thereby reducing effective population size, via both a recombination effect and a segregation effect. Total background selection tends to be stronger with partial asexuality than with selfing, but linked and unlinked loci contribute differently under these alternative reproductive systems. In contrast to background selection, balancing selection increases the coalescent time for a linked neutral site. With partial asexuality, the effects of balancing selection are increased via a recombination effect but reduced through a segregation effect. In contrast, with selfing, both recombination and segregation effects enhance the consequences of balancing selection. Finally, I will discuss these theoretical results with respect to the (preliminary) interpretation of our new population genomic data from a facultatively sexual plant, the duckweed *Spirodela polyrhiza*.

Genetics of attractiveness and mate choice in *Drosophila melanogaster* (51690)

Devin Arbuthnott, Daniel Promislow.

University of Washington.

The genetic and physiological control of mate choice and mate competition has broad implications for the evolution of sexually selected traits and mating systems. While particular mutations and manipulations of specific metabolic pathways have illustrated important regions of control for attractiveness and mate choice, little is known about the extent and nature of genetic variation for these traits in natural populations. We measured attractiveness and mate choice traits among the *Drosophila* Genetic Reference Panel to quantify variance and genetically map these traits. There was significant and substantial genetic variation in female attractiveness and male choosiness among these inbred lines of *Drosophila melanogaster*. Furthermore, we identified several significant genetic regions explaining this variance, including genes influencing growth and energy metabolism. However, there was no overlap in the regions influencing female attractiveness and male choosiness, nor was there any phenotypic correlation between these traits. Our work sheds light on the genetic control of sexually selected traits, which broadens our understanding of the evolution of sexual traits and its interaction with developmental pathways.

Does sexual selection augment or oppose natural selection? (51715)

Luke Holman.

Australian National University.

Sexual selection has been portrayed as both a friend and a foe of natural selection. The degree of alignment between natural and sexual selection is difficult to measure fully, yet has ramifications for diverse topics including conservation biology, the evolution of sex, and the speed of adaptation. Here, I discuss experiments measuring the effects of sexual selection on adaptation and naturally-selected fitness components in beetles. I first ask whether sexual selection helps to clear radiation-induced mutations that harm survival and fecundity. Next, I use experimental evolution to show that populations founded by polyandrous females are substantially fitter than those founded by singly mated females. Thirdly, I test whether sexual selection impedes or enhances the speed of adaptation to pesticide using experimental evolution. The experiments reaffirm that sexual selection can both help and harm targets of natural selection such as fecundity and survival, and highlight that sexual selection has a role to play in dispersal ecology and the evolution of resistance.

Sexually transmitted infection and the evolution of serial monogamy (51732)

David McLeod, Troy Day.

Queens University.

The selective forces shaping mating systems have long been of interest to biologists. One particular selective pressure that has received comparatively little attention is sexually transmitted infections (STIs). While it has been hypothesized that STIs could drive the evolutionary emergence of monogamy, there is little theoretical support. Here we use an evolutionary invasion analysis to determine what aspects of pathogen virulence and transmission are necessary for serial monogamy to evolve in a promiscuous population. We derive a biologically intuitive invasion condition in terms of population-specific quantities. From this condition, we obtain two main results. First, when pathogen virulence causes mortality rather than sterility, monogamy is more likely to evolve. Second, we find that at intermediate pathogen transmission rates, monogamy is the most selectively advantageous, whereas at high- and low-transmission rates, monogamy is generally selected against. As a result, it is possible for a pathogen to be highly virulent, yet for promiscuity to persist.

Session 1 MON POL D 34

Inversions as barriers to recombination and facilitators of speciation: Studies in *Drosophila pseudoobscura*/ *D. persimilis* (51934)

Mohamed Noor, Katharine Korunes.

Duke University.

Many studies suggest that limiting recombination in species hybrids may facilitate the persistence of the hybridizing species. Chromosomal inversions, thought to have limited recombination/ gene flux in hybrids, exhibit greater nucleotide differentiation between species than uninverted regions, and inversions preferentially harbor factors associated with speciation-related traits. However, the effectiveness of inversions as barriers to gene flux has been inferred primarily from patterns in natural populations. This talk presents results obtained thus far attempting to measure reductions in gene flux associated with inversion heterozygosity directly in laboratory populations, and relates these findings to existing theoretical models on the role of inversions in speciation.

Session 1 MON POL D 34

Genome divergence during early stage speciation with gene flow (51640)

David A. Marques, Laurent Excoffier, Ole Seehausen.

Institute of Ecology & Evolution, University of Berne, Switzerland; Eawag: Swiss Federal Institute of Aquatic Science and Technology, Kastanienbaum, Switzerland; Swiss Institute of Bioinformatics.

The number of speciation studies using population genomics approaches has increased quickly, yet few have compared replicate events of the same process with variation in geographical opportunity for gene flow between incipient species. We studied genome-wide differentiation among threespine stickleback (*Gasterosteus aculeatus*) lake and stream ecotypes that evolved in the last 150 years within the Lake Constance drainage system. We tested predictions of speciation with gene flow theory by comparing genomic differentiation between lake and stream ecotypes breeding in sympatry versus in parapatry. Consistent higher gene flow, we found fewer genomic islands of differentiation and lower genome-wide levels and heterogeneity of differentiation in the sympatric case. However, 15 genomic islands of differentiation resisting gene flow in sympatry showed parallel divergence and are thus candidate regions for adaptive divergence among lake and stream ecotypes. Interestingly, 12 of these islands cluster in a low-recombination region on chromosome VII. Furthermore, islands showed non-random overlap with many known quantitative trait loci, most of them controlling phenotypic traits divergent between Lake Constance ecotypes. The genomic co-localization of parallel differentiation, trait architecture and recombination landscape suggests that both divergent natural selection and the genomic arrangement of heritable traits are important in adaptation and early stage ecological speciation with ongoing gene flow.

Session 1 MON POL D 34

The multifarious histories charting the multifaceted landscapes of genomic differentiation (53342)

Nicolas Bierne.

University of Montpellier.

One of the most striking and consistent results of genome-wide surveys of differentiation is the heterogeneity of differentiation across the genome, including highly differentiated regions, sometimes called “genomic islands of differentiation”. Several theories have been proposed to explain this pattern: (i) speciation with gene flow driven by local adaptation, (ii) background selection and hitchhiking in low recombining regions and (iii) variable persistence after secondary contact of differences accumulated in allopatry. I will first recall that the contrasted spatial structures between island and non-island genomic regions or the argument that adaptation to a new environment is recent, by no way can provide evidence for one or the other hypothesis. The history needs to be reconstructed from gene genealogies, and methods do not cease improving. It has recently become possible to account for genome-wide heterogeneity (GWH) in introgression rates or in effective population size. This has proven to have profound impacts on the biological conclusions drawn from the inference. We have applied these methods to a large RNAseq dataset of 70 pairs of taxa of animals that were not initially chosen to champion one or another model of speciation. We show that the existence of ongoing gene flow is robustly detected but the timing of gene-flow during divergence is difficult to infer, that GWH is widespread and needs to be accounted for, and initiate a

description of the relationship between divergence and genome porosity from this kind of analysis.

Session 1 MON POL D 34

Evolution of genome differentiation across the speciation continuum: From patterns to mechanisms to regions related to species-specific evolution (51805)

Reto Burri, Alexander Nater, Takeshi Kawakami, Carina F. Mugal, Pall I. Olason, Linnea Smeds, Alexander Suh, Dutoit Ludovic, Hans Ellegren.

Uppsala University.

Recent studies have documented distinct and widespread regions of elevated differentiation ('differentiation islands') across genomes, but it remains unclear how the differentiation landscape evolves as speciation advances, which processes drive the evolution of differentiation islands, and ultimately how differentiation islands are related to speciation. Based on 200 re-sequenced genomes from 10 populations of four *Ficedula* flycatcher sister species, we show that differentiation islands evolve in structured populations as the result of background selection and divergent selection in genomic regions of low recombination. The heterogeneous differentiation landscape starts emerging among populations within species, and evolves recurrently among independent lineages. Together with the absence of pervasive gene flow in this model system, this demonstrates that a heterogeneous landscape of differentiation is not a consequence of speciation. We show how accounting for the mechanisms underlying the heterogeneous differentiation landscape using phylogenetic controls enables the identification of genome regions related to species-specific evolution.

Session 1 MON POL D 34

Genome-wide tests for introgression between cactophilic *Drosophila* implicate a role of inversions during speciation (51823)

Konrad Lohse, Magnus Clarke, Michael G. Ritchie, William J. Etges.

University of Edinburgh; University of Sheffield; University of St. Andrews; University of Arkansas.

Models of speciation-with-gene-flow have shown that the reduction in recombination between alternative chromosome arrangements can facilitate the fixation of locally adaptive genes in the face of gene flow and contribute to speciation. However, it has proven frustratingly difficult to show empirically that inversions have reduced gene flow and arose during or shortly after the onset of species divergence. We present an analysis of whole genome data from a pair of cactophilic fruit flies, *Drosophila mojavensis* and *D. arizonae*, which are reproductively isolated in the wild and differ by several large inversions on three chromosomes. We found an increase in divergence at rearranged compared to colinear chromosomes. Using the density of divergent sites in short sequence blocks we fit a series of

explicit models of species divergence in which gene flow is restricted to an initial period after divergence and may differ between colinear and rearranged parts of the genome. These analyses show that *D. mojavensis* and *D. arizonae* have experienced post-divergence gene flow which ceased around 270 KY ago and was significantly reduced in chromosomes with fixed inversions. Moreover, we show that these inversions most likely originated during or after the onset of species divergence as predicted by theoretical models of speciation with gene flow.

Session 1 MON POL D 34

Traversing the micro-evolution to macro-evolution boundary in *Caenorhabditis* nematodes with full-genome population genomics, crosses, and hybrid phenotypes (52010)

Asher Cutter.

University of Toronto.

How do population processes translate into evolutionary divergence in genomes and development between species? We are applying full-genome sequencing of *Caenorhabditis* nematode individuals to characterize the influence of recombination, selection, and selfing vs. outbreeding life history on patterns of population variation and divergence between sister species. In the highly selfing *C. briggsae*, we find that long stretches of genetic linkage interact with selection to severely reduce genetic variation across much of the genome. This selection at linked sites also exerts its influence on genomic patterns of differentiation between divergent populations. Analysis is ongoing for the outbreeding, partially reproductively-isolated sister species *C. remanei* and *C. latens*, which are known to have enormous effective population sizes and extremely high densities of polymorphisms and so may permit exceptionally fine-scale resolution of selection in their genomes. Coupled with classic genetic crosses and recombinant strain libraries within and between species, we have mapped aspects phenotypic divergence and reproductive incompatibility with the goal of integrating this with inferences about contemporary selection pressure and functional mechanism.

Session 1 MON MAX 415 13

Linking patterns and processes across scales: a case study with Neotropical hummingbirds (53334)

Catherine Graham.

A fundamental challenge for ecology and evolution is connecting broad scale biogeographical and macro-evolutionary mechanisms with local scale patterns of diversity. Community phylogenetics attempts to create this link by evaluating patterns of relatedness, and often trait similarity, among co-occurring species at multiple sites to generate hypotheses about the role of different mechanisms governing community assembly. In Neotropical hummingbirds,

biogeographic studies show that closely related species co-occur less frequently than expected when compared to a species pool that considers environmental filtering or predicted species range overlaps. This pattern may result from limiting similarity and competitive exclusion of closely related species. However, traits that should influence these mechanisms are not highly conserved and community level analyses of phylogenetic and trait spacing does not always correspond. As a result, the precise role of limiting similarity and niche conservatism in influencing local assemblages is difficult to infer from biogeographic patterns alone. This is perhaps because competition occurs among individuals in local assemblages and cannot be deduced from broad-scale studies. In contrast, local scale studies often use manipulative experiments to evaluate how competition affects specific ecological processes. However, generalization of local scale studies across different assemblages or to broader geographic extents remains elusive. To address this scale mismatch we present an experiment which evaluates if hypotheses developed at biogeographic scales are consistent with local scale observations of competition in Neotropical hummingbirds. This study provides an initial link between patterns established by broad scale biogeography and mechanisms learned from local scale community ecology.

Session 1 MON MAX 415 13

Using low coverage multispecies genomic data to reconstruct the assembly of a widespread insect community (51821)

Lynsey Bunnefeld, Jack Hearn, Konrad Lohse, Graham N. Stone.

University of Edinburgh.

Whether biologically widespread communities assemble through codispersal of associated lineages (host tracking) or local recruitment (ecological sorting) remains an open question. The answer is central to our understanding of the temporal and spatial scales of multispecies interactions such as coevolution. Sequence data has been used to understand the relationships of populations within species, but inference has usually been limited by the small numbers of loci analysed. While short read sequencing allows generation of data for very large numbers of loci, model-based inference has been limited by a lack of methods suitable for data processing and analysis beyond a handful of model organisms. We have developed an efficient maximum likelihood method that can use de novo low-coverage genome assemblies to fit explicit models of community history. We use our method to assess the evidence for host tracking and ecological sorting models during the assembly of a community of herbivorous gallwasps and parasitoid wasp natural enemies, each sampled from a longitudinal series of Pleistocene glacial refugia spanning the Western Palearctic. Our inference framework is extremely flexible, requires no prior genetic resources and can be extended to assess support for a wide range of demographic histories.

Session 1 MON MAX 415 13

Comparative population genomics for community-scale demographic inferences (53313)

Mike Hickerson.

City University of New York.

The historical dynamics and evolution of natural biological communities is critical for understanding how communities respond to invasions, extinctions and can shift with adaptive evolution associated with ongoing climate change. One approach to understanding how whole communities respond to changes in climate and landscape is to use data and methods from the dynamic and exploding field of population genomics. Inferences from population genomics can make detailed inference about the demographic and evolutionary history of a species and by making community-level inference using aggregated data across taxa, researchers can better understand how changes in climate and landscape can drive or destroy regional patterns of biodiversity as well as ask whether groups of presently co-occurring species tracked each other in space and time through cycles of global climate shifts. To illustrate an application of this approach, I present an inferential hierarchical model of multi-species demographic history that makes use of high density SNP data sampled from co-distributed species. As genomic data becomes routinely collected from non-model taxa, researchers will be able to better test hypotheses about the varied and/or parallel responses to climate and landscape changes that affected whole communities.

Session 1 MON MAX 415 13

Ecological correlation reinforcement facilitates collective community behaviours without group selection (51958)

Daniel A. Power, Richard A. Watson, Eörs Száthmary.

University of Southampton, Electronics & Computer Science; University of Southampton, Institute for Life Sciences/Electronics & Computer Science; The Parmenides Foundation, Center for the Conceptual Foundations of Science.

Ecosystem population dynamics are shaped by evolution and coevolution amongst their component species. Adaptations to biotic and abiotic environments modify interactions between community members, but we currently lack a framework that predicts how evolutionary responses of community members impact ecosystem properties including stability, resilience, susceptibility to invasion and regime shifts. We use Lotka-Volterra simulations to demonstrate how past events shape communities' collective behaviours. We show that ecological character displacement, operating strongest where species interact at highest densities:

- i) Results in systems more resilient to invasion compared with communities with shorter shared histories, and that members of coevolved communities are better able to facilitate one another's invasion into other ecosystems (invasional meltdown).
- ii) Provides systems with the potential to learn underlying environmental structure which, when correctly learned, results in greater system biomass and resilience.
- iii) Enables ecosystems to learn multiple environmental states, and to store a distinct memory of each of these states (alternative stable states).

These complex system-level behaviours are not resultant from group selection processes, but arise only from selective pressures reinforcing correlations between community members.

Crucially, we recognise that this pattern of correlation learning is already well understood in connectionist models of learning, where simple reinforcement of connections produces networks with non-trivial collective behaviours.

Session 1 MON MAX 415 13

Ecological novelty may facilitate homoploid hybrid speciation in cichlid fish (52437)

Oliver Martin Selz, Ole Seehausen.

Department of Fish Ecology and Evolution, Center for Ecology, Evolution and Biogeochemistry, EAWAG,; Aquatic Ecology and Evolution, Institute of Ecology and Evolution, University of Bern.

Because homoploid hybrids are usually occurring within the range of the parental species, a central challenge to the concept of hybrid speciation is understanding how hybrids can persist in sympatry with their parental species. Persistence within the range of the parents is possible if the hybrid species inherit ecological traits that allow them to occupy a novel ecological niche, thereby allowing the lineage to escape competition from both parental species. Here, we investigate experimentally if novel feeding efficiencies can arise in synthetic first-generation hybrids that could make hybrids superior in ecological niches that neither of the parent species is adapted to.

We generated two first-generation hybrid crosses between different species of African cichlid fish. In feeding efficiency experiments we determined the performance of the hybrids and their parental species on food types representing the niches of the parental species and on other “novel” food types that represent niches of other species of cichlids in African lakes. We found that hybridization can result in higher feeding efficiency of the hybrids on novel food types when compared to either parent taxon. These results suggest that hybridization can generate novel phenotypic variation that might allow hybrids to escape competition from the parental species, thereby promoting ecological hybrid speciation.

Session 1 TUE GEN C 3

Beetles, Birds, Snakes & Flies: The Diversity of Sex Chromosomes and their Evolution (53361)

Doris Bachtrog.

In many species with separate sexes, gender is determined by heteromorphic sex chromosomes. Sex chromosomes have evolved independently in both plants and animals from ordinary chromosomes, but little is known about the evolutionary forces driving their differentiation. I will discuss how the study of diverse types of sex chromosomes, ranging

from beetles to birds, snakes and flies, has allowed us to make progress in understanding the diverse mechanisms that drive the evolution of sex chromosomes.

Session 1 TUE GEN C 3

Interactions Between A Master Regulator Of Sex Determination And Haploid Sex Chromosomes In The Evolution Of Dimorphic Sexes (53315)

James Umen, Ayano Miyagi, Takashi Hamaji, Sa Geng.

Donald Danforth Plant Science Center.

Male and female sexes have evolved repeatedly in eukaryotes but the origins of dimorphic sexes and their relationship to mating types in unicellular species are not understood. Volvocine algae include isogamous species such as *Chlamydomonas reinhardtii* and oogamous multicellular species such as *Volvox carteri* with sperm-producing males and egg-producing females. We recently found that a single conserved mating locus (MT) gene in volvocine algae—MID, which encodes a RWP-RK domain transcription factor—evolved from its ancestral role in *Chlamydomonas* as a mating-type specifier, to become a determinant of sperm and egg development in *Volvox*. Transgenic *Volvox* females expressing MID produce functional sperm packets while transgenic male *Volvox* with RNAi-mediated knockdowns of MID produce functional eggs or self-fertile hermaphrodites. Crosses with sex-reversed strains uncouple sex determination from sex chromosome identity and reveal roles for male and female mating locus genes in sexual development, gamete fitness and reproductive success. Together these findings suggest the emergence of antagonistic interactions between genes in the male and female sex chromosomes of *Volvox*. We have begun to elucidate the genetic networks controlled by *Chlamydomonas* MID (CrMID) and *Volvox* MID (VcMID) in order to understand how this transcription factor and its targets evolved in the transition from mating types to sexes.

Session 1 TUE GEN C 3

Baby sex chromosomes in the housefly (51681)

Leo W Beukeboom, Daniel Bopp, Ernst Wimmer, Louis van de Zande, Akash Sharma, Yanli Wu, Martijn Schenkel, Sander Visser, Ljubinka Francuski.

University of Groningen; University of Zurich; University of Goettingen; Univeristy of Novi Sad.

Sex chromosomes carry gender specific sex determining genes. Several stages can be distinguished in the evolution of sex chromosomes, from origin, via molecular evolution as a result of the sex determination function, to degeneration following recombination suppression. We study the dynamic and polymorphic sex determination system of the housefly, *Musca domestica*. The standard system is XX-XY with a male determiner (M) on the Y chromosome, rendering it a male-determining chromosome. However, M-factors can

also be present on any of the five autosomes and as a result modify such chromosomes into neo-sex (Y) chromosomes. In addition, autosome 4 can carry a dominant female determiner (F), modifying it in a female determining sex chromosome, and a ZZ-ZW system. We provide data on the nature of the female and male determining genes. Recent transposition events of male determining genes over the genome has resulted in new sex chromosomes that are in the very initial stages of differentiation (hence “baby” sex chromosomes). Here we present how we use this unique system to test theories about sex chromosome evolution and to investigate the genomic processes that act during the early stages of differentiation into male and female determining sex chromosomes.

Session 1 TUE GEN C 3

Wolbachia bacterial endosymbionts and the evolution of sex determination in the isopod *Armadillidium vulgare* (51902)

Sébastien Leclercq, Julien Thézé, Isabelle Giraud, Mohamed Chebbi, Bouziane Moumen, Lise Ernenwein, Pierre Grève, Clément Gilbert, **Richard Cordaux**.

CNRS / Université de Poitiers.

In the isopod *Armadillidium vulgare*, sex determination (SD) follows female heterogamety (ZZ males and ZW females). However, many *A. vulgare* populations harbor maternally-inherited *Wolbachia* bacterial endosymbionts which can convert genetic males into phenotypic females, leading to populations with female-biased sex ratios. The W sex chromosome has been lost in lines infected by *Wolbachia* and all individuals are genetic males. Female sex is determined by *Wolbachia* infection of the *A. vulgare* individual, thereby shifting from chromosomal to cytoplasmic SD. Surprisingly, some *A. vulgare* lines exhibit sex ratio biases despite the lack of *Wolbachia*. In these lines, female individuals are genetic males carrying an unknown feminizing factor. To elucidate the genetic basis of female SD in these lines, we sequenced the genome of a female. We identified a large piece of the *Wolbachia* genome transferred to the *A. vulgare* nuclear genome. The transferred genomic fragment co-segregates perfectly with female sex in pedigrees. Our results indicate that SD in these *A. vulgare* lines is under control of nuclear gene(s) of bacterial origin. More generally, they emphasize that bacterial endosymbionts are powerful sources of evolutionary novelty, e.g. by driving shifts in SD mechanisms in their animal hosts. Funded by an ERC Grant to RC.

Session 1 TUE GEN C 3

Why are there so many species with Y-autosome fusions? (51913)

Jun Kitano, Matthew Pennell, Mark Kirkpatrick, Sarah Otto, Jana Vamosi, Catherine Peichel.

National Institute of Genetics; University of Idaho; University of Texas, Austin; University of British Columbia; University of Calgary; Fred Hutchinson Cancer Research Center.

Sex chromosomes turn over rapidly in some taxonomic groups. One of the mechanisms causing the turnover of sex chromosome is a chromosomal fusion between a sex chromosome and an autosome. We estimate the rate at which fusions establish between sex chromosomes and autosomes through phylogenetic analyses of fishes and reptiles. Both the incidence among extant species and the establishment rate of Y-autosome fusions is much higher than for X-autosome, Z-autosome, or W-autosome fusions. Our theoretical analysis showed that the excess of Y-autosome fusions can be explained by (i) fixation of deleterious fusion by drift under the conditions of male-biased origination rates or male-biased variance in reproductive success, (ii) sexually antagonistic selection under the conditions of male-biased origination rates, and (iii) female meiotic drive against fusions. Because some of these evolutionary forces would also affect autosome-autosome fusions, further studies on the driving forces of sex chromosome-autosome fusions will give insight into the mechanisms causing not only sex chromosome turnover, but also karyotypic evolution.

Session 1 TUE MAX 410 21

The Evolution of Epigenetic Inheritance (53348)

Eva Jablonka.

The Cohn Institute for the History and Philosophy of Science and Ideas; The Sagol Tel-Aviv University.

Epigenetic inheritance has many direct and indirect evolutionary effects, and it is likely that these are reflected in the evolved mechanisms underlying it. I therefore start with an overview of the effects of epigenetic inheritance on adaptive evolution, speciation, and the major evolutionary transitions. I then present existing models that explore the effects of ontogenetic epigenetic inheritance on evolutionary change, discuss different types of transgenerational epigenetic inheritance (somatic and gametic), and examine ideas about the environmental conditions that can lead to the evolution of trans-generational plasticity. I suggest that the diversity of selection regimes may explain the diversity of epigenetic mechanisms that are involved in trans-generational plasticity and metaplasticity.

Session 1 TUE MAX 410 21

How does plasticity influence adaptive evolution? (53341)

Cameron Ghalambor.

Colorado State University.

A fundamental unresolved question in evolutionary biology is how patterns of plasticity observed within a generation influence evolutionary changes across generations. New environments, such as those encountered during colonization events or those generated by human activities, are likely to induce a range of both adaptive and non-adaptive plastic responses, thus providing an opportunity to test the relationship between initially plastic

responses and subsequent evolutionary change. We experimentally transplanted Trinidadian guppies (*Poecilia reticulata*) adapted to a stream with cichlid predators to cichlid free streams, and tested if plasticity in the source population predicted evolutionary change in the transplanted populations. We measured a suite of traits, including gene expression, body shape, growth rate, and metabolism. We found evidence for both adaptive and non-adaptive plastic responses in the source population and rapid evolution of traits and their plasticity in the experimental population. Traits exhibiting non-adaptive plasticity (i.e. a plastic response in the opposite direction favored by selection) diverged from the source population more rapidly. These results suggest traits exhibiting non-adaptive plasticity in new environments are likely to experience stronger directional selection and evolve more rapidly compared to traits exhibiting adaptive plasticity.

Session 1 TUE MAX 410 21

An evolutionary model of maternal effects (51650)

Rebecca Hoyle, Bram Kuijper.

University of Southampton; UCL.

Theory suggests that maternal effects can have substantial impact on the evolutionary process. However current models typically treat maternal effects as evolutionarily constant parameters. In order to glean insight into how maternal effects themselves are shaped by evolution, we present a quantitative genetics model that captures the interacting evolutionary dynamics of both maternal effects and within-generation phenotypic plasticity. In constant environments, we find that maternal effects evolve to slightly negative values that reduce phenotypic variance in the population. By contrast, in the wake of an extreme environmental shift, they evolve to large positive values over ten to a hundred generations. These transient positive values allow offspring to rapidly adopt beneficial phenotypes that are closer to the new optimum. Once this new optimum has been reached through within-generation plasticity and genetic assimilation, maternal effects drift back towards negative values where they eventually settle. Lastly, in cyclically fluctuating (e.g. seasonal) environments, maternal effects often evolve to positive values when fluctuations are slow, whereas negative maternal effects dominate for faster cycles. We find that cyclical environments favour weak maternal effects unless selection on the overall phenotype is strong and the efficacy of within-generation phenotypic plasticity is constrained through costs or informational timelags.

Session 1 TUE MAX 410 21

Paternal heat exposure causes immediate and inherited epigenetic response in Wild guinea pigs (51721)

Alexandra Weyrich, Dorina Lenz, Marie Jeschek, Tzu Hung Chung, Felix Heeger, Kathrin Rübensam, Frank Goeritz, Katrina Jewgenow, Jorns Fickel.

Leibniz Institute for Zoo and Wildlife Research; Berlin Center for Genomics in Biodiversity Research; Zymoresearch, EpiQuest, Irvine, CA 92614, USA..

Epigenetic modifications, of which DNA methylation is the best studied one, are a mechanism to convey environmental information through generations via parental germ lines. The majority of studies have focused on the maternal transmission of epigenetic information to the offspring, whereas the paternal role in transgenerational transmission has received little attention. Here we show that exposure to a temporally increase in ambient temperature led to changes in DNA methylation patterns in exposed males and were transmitted to their male offspring. Five F0 adult male guinea pigs, a phenotypically and genetically heterogeneous mammal species, were exposed to an increase in ambient temperature for two months. Reduced representation bisulfite sequencing revealed differentially methylated regions (DMRs) in liver samples of F0 fathers before and after heat treatment, as well as in liver and testes of F1 sons sired before and after heat treatment. Since testicular methylation changes imply transmission to the F2 generation, exposure of fathers to increased temperature resulted in rapid and heritable epigenetic modifications that were transmitted paternally. In the context of climate change this mechanism is increasingly relevant for the survival of exposed populations with rising global temperatures.

Session 1 TUE MAX 410 21

Genome methylation patterns across castes and generations in a parasitoid wasp (51740)

Roei Shaham, **Tamar Keasar**, Rachel Ben Shlomo.

University of Haifa - Oranim.

Environmental influences play a crucial role in shaping phenotypes within and across generations. In vertebrates, these influences often involve epigenetic modification of gene expression through DNA methylation. Modifications of methylation patterns also mediate caste and task allocation in eusocial insects. However, the effects of parental environment on DNA methylation in offspring are yet unknown in insects. We looked for within- and between-generation variability in methylation in the polyembryonic parasitoid wasp *Copidosoma koehleri*, which also features a unique simple caste system.

To study within-generation effects, we tested for methylation differences between reproductive and soldier clone-member larvae. To explore between-generation effects, we exposed larvae to either high or low rearing densities. We compared methylation in their offspring at three developmental stages (larvae, pupae and adults). Methylation rates and patterns were characterized using the methylation-sensitive amplified fragments length polymorphism (MS-AFLP) method.

DNA methylation patterns differed significantly between soldier and reproductive larvae, although frequencies of methylated fragments were similar across castes (~20%). Parental rearing density did not affect methylation rates and patterns in their offspring in any of the developmental stages. Thus, DNA methylation is associated with within-generation (caste) phenotypic variation, but we found no evidence for its involvement in trans-generational epigenetic effects.

Region-specific selection on floral signals in a terrestrial orchid (52200)

Karin Gross, Florian P Schiestl.

University of Zürich.

Geographically structured phenotypic selection can lead to adaptive divergence. In flowering plants, the link between selection and trait divergence has been shown for flower morphology, but not yet for floral signals, despite their importance for pollinator attraction. In this study, we measured phenotypic selection on display size, floral color, and floral scent in four lowland and four mountain populations of the nectar-rewarding orchid *Gymnadenia odoratissima*. We also quantified differences in these traits and in pollinator-community composition. Our results show positive selection on display size and positive, negative, or absence of selection on different scent compounds. Selection on the main scent compounds was consistently stronger in the lowlands than the mountains in two years, and lowland plants emitted more of most of these compounds. Pollinator-community also differed among regions. We also found an association between population differences in some scent compounds and the respective differences in selection on them. Moreover, selection on floral scent was more variable than selection on display size, and scent emission was also more variable than display size. Overall, our study is the first to document consistent regional differences in selection on floral scent, and suggests this selection pattern contributes to population divergence in floral chemical signaling.

Selection and real-time evolution of floral traits in plants with different pollinators (52209)

Daniel Gervasi, **Florian P Schiestl**.

University of Zürich.

Selection mediated through pollinators plays a key role in floral adaptation and reproductive isolation in plants. The aim of this study was to investigate pollinator-driven selection by experimentally changing pollinator environments. Specifically we investigate the effects of different pollinators on the evolution of floral traits and plant reproductive success. We use *Brassica rapa* (Wisconsin rapid cycling) as model plant and the bumblebee, *Bombus terrestris*, and the hoverfly, *Episyrphus balteatus* as pollinators. In our study we found that bumblebees and hoverflies differ in the selection they impose on floral traits. The strength of selection on the floral traits also varies significantly between the two pollinators. We observed strong positive selection on plant height and flower number in bumblebees while hoverflies imposed no selection on these traits. In terms of evolutionary response we observed in bumblebee-visited plants an increase in plant height and flower number. Additionally, bumblebee pollinated plants had a significantly higher reproductive success than hoverfly pollinated

plants. After 7 generations hoverfly-pollinated plants showed a significant increase in reproductive success indicating adaptations to this type of pollinators have evolved. This study thus shows for the first time the effects of changing pollinators on plant evolution in an experimental approach over several generations.

Session 1 TUE POL A 28

Over-dominance and adaptive gene duplications (52262)

Pascal Milesi, Mylène Weill, Pierrick Labbé.

Institut des sciences de l'évolution; CNRS; Université de Montpellier.

For 40+ years, organophosphorus insecticides (OPs) have been used to control *Culex pipiens* mosquito populations. A punctual mutation of the *ace-1* gene conferring resistance was rapidly selected for, despite the strong selective cost it induces. As a consequence, selection is environment-dependent: susceptible homozygotes are selected in the untreated areas, whereas resistant homozygotes are selected in the treated ones. Nevertheless, with intermediate selection intensities, e.g. in a fluctuating or structured environment, heterozygotes with intermediate advantage and cost could be the fittest, i.e. marginal over-dominance.

In the last 20 years, gene duplications at the *ace-1* locus invaded *C. pipiens* natural populations. They associate on a same chromosome a susceptible and a resistant copy of *ace-1*, and recent study showed that they confer a phenotype similar to standard heterozygotes. It was thus suggested that these duplications were selected because they alleviate the heterozygote segregation cost, thereby allowing fixation of the over-dominant phenotype.

We tested this over-dominance hypothesis and its relation to insecticide dose, i.e. selective pressure intensity. Our results show that selective pressure heterogeneity can play a key role in the emergence of adaptive gene duplications.

Session 1 TUE POL A 28

Temporal fluctuation in the phenotypic optimum of laying date in a wild Blue tit population (52355)

Pascal Marrot, Dany Garant, Charmantier Anne.

Centre d'Ecologie Fonctionnelle et Evolutive; Université de Sherbrooke.

Understanding the role of temporal fluctuations in natural selection in maintaining phenotypic variance in natural populations is central in evolutionary ecology. Temporal fluctuation of natural selection is generally estimated by comparing annual selection gradients, which represent the slope of the fitness landscape. However, such variation in selection gradients does not necessarily reflect variation in the fitness-trait relationship, but can be caused by changes in the extent of phenotypic variance present under genetic drift. In this context, it

could be more informative to investigate temporal variation in the phenotypic optimum on the fitness landscape rather than in selection gradients. Here, we apply a model recently developed by Chevin & Haller (2014) to explore temporal variation and temporal autocorrelation in the phenotypic optimum for laying date using a 23 year blue tit (*Cyanistes caeruleus*) data set. Our results show that the phenotypic optimum varied between years and followed a negative temporal autocorrelation pattern. This result suggest that selection pressures within a given year cannot be predicted from selection pressures observed during the previous year, which emphasizes the variability of selection pressures across years. Moreover, this model allows us to investigate the relationship between temporal variation in phenotypic optimum and environmental covariables such as spring temperature or precipitation.

Session 1 TUE POL A 28

THERE IS MORE TO POLLINATOR-MEDIATED SELECTION THAN POLLEN LIMITATION: INTERACTION INTENSITY VERSUS FUNCTIONAL SIGNIFICANCE (52367)

Nina Sletvold, Jon Ågren.

Uppsala University.

Spatial variation in pollinator-mediated selection ($\Delta\beta_{\text{poll}}$) is a major driver of floral evolution, but we lack a quantitative understanding of its link to pollen limitation and net selection on floral traits. To determine whether $\Delta\beta_{\text{poll}}$ is positively related to pollen limitation and whether differences in the magnitude of $\Delta\beta_{\text{poll}}$ can explain spatio-temporal variation in net selection, we quantified $\Delta\beta_{\text{poll}}$ on floral traits for 2-5 years in two populations each of two orchid species differing in pollen limitation. In both species, $\Delta\beta_{\text{poll}}$ varied among years and populations, and spatio-temporal variation in $\Delta\beta_{\text{poll}}$ explained much of the variation in net selection. Selection was consistently stronger and the proportion that was pollinator-mediated was higher in the severely pollen-limited deceptive species than in the rewarding species. Within species, variation in pollen limitation could not explain variation in $\Delta\beta_{\text{poll}}$ for any trait, indicating that factors influencing the functional relationship between trait variation and pollination success govern a major part of the observed variation in $\Delta\beta_{\text{poll}}$. Separating the effects of variation in mean interaction intensity and in the functional significance of traits will be necessary to understand spatio-temporal variation in selection exerted by the biotic environment.

Session 1 TUE POL A 28

Local adaptation is prevented along patchy ecological gradients (52510)

Jon Bridle, Roger Butlin.

University of Bristol; University of Sheffield.

Population genetic models of evolution along spatial gradients in selection cannot explain why species have finite geographical distributions and narrow niches. Unless gradients in population density are imposed by locally varying carrying capacity, gene flow helps rather than hinders local adaptation, provided the standing genetic variance it generates does not impose too much of a demographic cost. Continuous evolutionary models therefore either generate extinction or adaptation everywhere, instead of the finite distributions that are ubiquitous in nature and that define biological communities. We use individual-based simulations to explore how non-linear ecological gradients affect local adaptation by varying gene flow and overall carrying capacity along: (1) a steepening ecological gradient and (2) a linear ecological gradient with a flat centre of variable width. We find that adaptation is prevented along non-linear gradients because populations within flat regions escape the demographic load generated by gene flow elsewhere. These flat regions can prevent adaptation even when remarkably narrow relative to mean dispersal. At the same time however, patchy gradients make population establishment easier, and prevent global extinction. We discuss our results in the light of our empirical work on evolutionary responses to climate change in the UK butterfly *Aricia agestis*.

Session 1 TUE POL B 20

Genomics of local adaptation in the face of high gene flow (52868)

Outi Savolainen, Timo Knürr, Sonja Kujala, Jaakko Tyrmi, Katri Kärkkäinen, Tanja Pyhäjärvi.

University of Oulu; Luke Natural Resources Center Finland.

Populations of many species with high gene flow have little differentiation across much of the genome, but can still be highly differentiated for phenotypic traits related to local adaptation. Scots pine and many other forest trees show this kind of patterns of variation. In common garden experiments, northern Scots pine seedlings set bud much earlier than southern ones, an important adaptive difference. Analysing selection in common garden tests at different latitudes, we found a cline in the optima over latitudes, and within individual populations, strong stabilizing selection on the timing of bud set. The strength of selection varied between sites at different latitudes. Further, we examined clines of nucleotide variation across European wide sampling, using limited SNP genotyping and exome sequencing. The results are compared to predictions of models of clinal selection.

Session 1 TUE POL B 20

Variation and selection of genes controlling ecologically important traits in nature (53317)

Thomas Mitchell-Olds, Nadeesha Perera, Julius Mojica, Lauren Carley, C. Olson-Manning, J. Anderson, C-R Lee.

Duke University; University of Chicago; University of Georgia; Gregor Mendel Institute.

Although many studies provide examples of evolutionary processes such as balancing selection or deleterious polymorphism, the relative importance of these processes for phenotypic variation is unclear. To understand the evolutionary forces that influence complex trait variation in a wild relative of *Arabidopsis*, we cloned an ecologically important QTL in natural populations and measured the fitness of alleles in the populations where they evolved. Ecological measurements of selection indicate that this polymorphism is influenced by spatially heterogeneous natural selection, with changes in rank fitness across environments. Next, we examined the relationship between flux and protein polymorphism in this pathway, showing that flux control is focused in the first enzymatic step, encoded by a gene experiencing selective diversification in several related species. Finally, to identify the genes responsible for ecologically important trait variation in nature, we are conducting a Genome-Wide Association Study (GWAS) on a panel of reference genotypes from 500 populations across the species range. For these accessions we combine data from genome-wide resequencing and genotyping by sequencing, as well as trait variation for defensive chemistry, resistance to multiple herbivores, flowering time, and complex traits in lab and field. Implications for ecological genomics will be discussed.

Session 1 TUE POL B 20

Genetic variance associated with overwintering adaptation in a butterfly. (51641)

Peter Pruisscher, Christopher Wheat, Karl Gotthard.

Stockholm University.

Diapause is a pre-programmed state of arrested development in insects that is a crucial part of life cycle regulation. Many species induce diapause depending upon environmental conditions, allowing for either continuous development during optimal conditions (summer) or diapause (overwintering). This adaptation to seasonal stress is primarily triggered by photoperiod and temperature. The propensity of populations to enter diapause in response to a given light/dark regime shows strong adaptive clines along environmental gradients. Diapause is a complex multi-locus trait incorporating cold-tolerance, immunity and growth patterns, suggesting that many loci are likely involved. Here we scan the genome of divergent populations of the Speckled Wood butterfly *Pararge aegeria*, as well as data from F1 and F2 crosses, to investigate the genetic mechanisms underlying diapause. Our analysis identifies a range of high quality candidate loci known to be involved in diapause in other species [e.g. clock genes, heat-shock proteins]. Furthermore, prime candidates, such as the gene *Timeless*, show nonsynonymous substitutions fixed between the divergent populations.

Session 1 TUE POL B 20

Experimental evidence for mitochondrial genomic adaptation to climate (51932)

M. Florencia Camus, Carla M. Sgrò, Jonci N. Wolff, Damian K. Dowling.

Monash University.

Mitochondria are key components of cellular metabolic processing, providing most of the cellular energy required for survival. It was traditionally thought that the mitochondrial genome exhibits very limited capacity to respond adaptively to natural selection. However, thermal sensitivity of mitochondrial functioning, coupled with the observation that mitochondrial haplotype frequencies tend to associate with latitude or altitude, suggests that thermal selection may play a role in shaping the molecular architecture of the mitochondrial DNA. Here, we present experimental support for this contention. We describe two major mitochondrial haplotypes in *Drosophila melanogaster*, which exhibit opposing patterns of clinal variation along the Australian eastern seaboard and are delineated by 15 synonymous SNPs. We extracted each of these haplotypes from two opposing populations and introgressed them into a single isogenic nuclear background. After assaying each population for thermal tolerance we found the northern haplotype confers greater heat resistance. The underlying SNPs involved in this phenotypic response lie unambiguously in the mitochondrial genome, and are hypothesized to affect the level of codon bias. Thus, we have uncovered a new-found role for SNPs that were previously considered to be completely non-functional, inside a genome that was likewise traditionally considered to be devoid of functional segregating allelic variation.

Session 1 TUE POL B 20

Origin, history and local adaptation of the recent polyploid *Capsella bursa-pastoris* (51946)

Martin Lascoux, Amandine Cornille, Adriana Salcedo, Dmytro Kryvokhyzha, Karl Holm, Ulf Lagercrantz, Sylvain Glémin, Stephen Wright.

Uppsala University; University of Toronto.

It took more than 80 years, since George Shull started to use *Capsella bursa-pastoris* as a model species for the study of Mendelian genetics, to decipher the origin of the species. It took as long to start to unravel its demographic history and to estimate the nature and extent of the natural selection it went through as it colonized the world. The analysis of full genomes shows that *Capsella bursa-pastoris* is an allotetraploid of the self-incompatible *C. grandiflora* and the self-compatible *C. orientalis*. It also indicates that polyploidization was accompanied by relaxed selection but rather limited gene loss. As shown by the genotyping of 260 accessions from Europe, the Middle East and Asia, the species is today made up of clearly delineated genetic clusters corresponding to these three areas. The species likely originate in Western Eurasia from which it later on spread eastwards. Clear differences in gene expression were detected among 24 accessions originating from these three clusters but a contrast analysis also suggest that those differences may simply reflect the demographic history of the species and may not be adaptive. Finally, three common garden experiments of the 260 accessions located in Uppsala, Toronto and Guangzhou are currently under analysis.

Session 1 TUE POL B 20

The genomics of avian breeding time – an ecologically relevant trait for adaptation to climate change (51982)

Phillip Gienapp, Mario P.L. Calus, Veronika N. Laine, Kees van Oers, Martien A.M. Groenen, Jon Slate, Marcel E. Visser.

Department of Animal Ecology, Netherlands Institute of Ecology; Animal Breeding and Genomics Centre, Wageningen UR; Department of Animal and Plant Sciences, University of Sheffield.

Climate change has led to selection on phenological traits such as avian seasonal breeding time and hence evolutionary rescue will be necessary to ensure population persistence in the long-term. Numerous quantitative genetic studies in wild populations have shown that avian seasonal breeding time is heritable, yet no study could show the expected evolutionary change. One possible explanation for this ‘evolutionary stasis’ is that heritability estimates are inflated by environmental conditions shared among relatives. A good understanding of the genetics of avian breeding time is thus crucial to predict whether this trait can respond to selection. We here explored the genomic basis of avian seasonal breeding time in a wild bird species, the great tit, using our recently assembled and annotated whole genome sequence and high-density SNP-chip of this bird species. We genotyped 2000 individuals with known egg-laying dates from our long-term study population on a 675k SNP-chip and identified genomic regions related to breeding time using both QTL-mapping and by quantifying locus-specific allele-substitution effects using a genomic-breeding approach.

Session 1 TUE POL C 11

Defence heterogeneity under the double-edged sword of mammalian immunity (53314)

Andrea L. Graham.

Princeton University.

To mitigate the effects of infection on fitness, hosts must minimize the costs of both parasitism and defence. This may entail clearing parasites, but it may be even more important for hosts to repair tissue damage caused by parasites and by immune effectors. Hosts may also need to maintain physiological homeostasis while mitigating energetic costs. Striking an optimal balance amongst these competing physiological demands is a dynamic problem. For example, the optimal strategy may vary with age, condition, risk of parasite exposure and/or availability of resources in the environment. To what extent can mammalian hosts match their defensive stance to environment? Must competing demands be met simultaneously or are sequential solutions possible – e.g., to kill parasites rapidly then shift to a damage- and energy-reduction strategy later, or, conversely, to tolerate parasites up to a threshold and resist them thereafter? Indeed, how much of defence heterogeneity, including varied susceptibility to autoimmune disease, can be understood in light of this multivariate physiology? I will address these questions using immunological, nutritional and histopathological evidence from both wild mammals and human cohorts.

Balancing selection and convergent evolution in an antimicrobial peptide (53316)

Brian P. Lazzaro, Robert L. Unckless, Virginia M. Howick.

Cornell University, USA.

Conventional thinking has been that antibacterial peptides (AMPs) are functionally redundant and evolutionarily dispensable at the individual gene level. In *Drosophila*, this inference has been drawn from observations that antibacterial peptide genes show low rates of amino acid divergence between species and high rates of genomic duplication and deletion, and that genetic variation in individual AMP genes makes little or no contribution to organism-level defense phenotypes. However, we identified a serine/arginine polymorphism in the Diptericin A gene of *Drosophila melanogaster* that is highly predictive of resistance to specific bacterial infections. The same amino acid polymorphism is segregating in the Diptericin A gene of the sister species *D. simulans*, with equivalent phenotypic effect and having arisen convergently by independent mutation of the homologous codon. Examination of the larger *Drosophila* phylogeny reveals that the arginine mutation has arisen independently at least 5 times in the genus. These observations prompted us to revisit the molecular evolution of other antibacterial peptide genes and we find that molecular convergence and shared interspecific polymorphism are surprisingly common. We additionally have found multiple loss-of-function mutations, which cause high susceptibility to infection in *D. melanogaster* and *D. simulans*. We have reevaluated the previously supposed mode of evolution of Diptericin and other antibacterial peptide genes, and now favor the hypothesis that AMP genes evolve under a model where the selection pressure favoring alternative amino acid states fluctuates over time and space. The frequent incidence of loss-of-function alleles in nature suggests that AMP function in immune defense is balanced by deleterious consequences in the absence of infection, and serial pseudogenization and duplication-subfunctionalization may explain the rapid gene family dynamics. Since previous screens for molecular adaptation have explicitly tested for adaptive divergence, these would have failed to detect convergent or balanced mutations.

Genome wide analysis of selection in immune genes within and among butterfly populations (51667)

Naomi Keehnen, Chris Wheat.

Stockholm University.

Insects are one of the most diverse clades of life on earth. Located in nearly every corner of Earth, they are exposed to a wide variety of pathogens. As populations adapt to their local environment some modifications to their immune system are expected to occur. While the genes encoding for immune responses have been identified and studied in several insect

species, little work has focused upon non-model species originating from natural populations. Furthermore, it is unknown which part of the immune defense modules (recognition, signaling, and the effectors) shows most genetic variation within and between species. Here we focus upon the ecological model species, the Green Veined White (*Pieris napi*) and Speckled Wood (*Parage aegeria*). They are common and widespread, with limited gene flow between populations. We have identified many of the immune genes in both butterfly genomes using orthologous blast searches and RNA-Seq analysis of individuals infected with either gram-negative (*E. coli*) or gram positive bacteria (*M. luteus*). Genomic scans of these immune genes indicate signatures of local adaptation and reveal significant differences in diversity among the immune defense modules. These findings could explain the observed variation in immune responses within and between butterfly species.

Session 1 TUE POL C 11

Functional variation at innate immune loci in the Seychelles warbler (51755)

Danielle Gilroy.

University of East Anglia.

Understanding the relative roles of different evolutionary forces in shaping genetic variation within a population is a key focus in evolutionary biology. Moreover, understanding the levels and distribution of functional genetic variation in bottlenecked populations has great importance to conservation. The Seychelles warbler (*Acrocephalus sechellensis*) is an endemic passerine that went through a severe population bottleneck in its recent past and we investigated whether variation has been maintained within two innate gene groups, avian beta-defensins (AvBDs) and toll-like receptor genes (TLRs). We also examine these genes in several other *Acrocephalus* species, revealing very different selection regimes for the two gene groups within the Seychelles warbler and across the genus. All six AvBD loci were monomorphic in the contemporary population of Seychelles warbler and five out of seven TLR loci were polymorphic. By using population genetic statistical tests and simulation studies, we show that founder effects have reduced levels of variation at TLRs, but balancing selection has indeed maintained some functional variation at five of the loci. Furthermore, a cohort analysis of TLR15, examined allele-specific associations with survival and malaria infection that enabled us to better understand whether pathogen-mediated selection could potentially be the underlying balancing selective force in this population.

Session 1 TUE POL C 11

Genetics of natural variation of *Daphnia magna* resistance to a bacterial pathogen (51867)

Gilberto Bento, Jarkko Routtu, Yann Bourgeois, Dieter Ebert.

University of Basel.

Daphnia magna is a model for ecology and evolution, in particular, for host-pathogen coevolution. *D. magna* is infected by the bacterium *Pateuria ramosa* with severe deleterious fitness consequences. We investigate the *D. magna*-*P. ramosa* system for the genetic and molecular basis of natural variation in host resistance. Specificity in genotype-to-genotype interactions was previously reported. In addition, using a *D. magna* F2 panel, it was found that one QTL (locus A) explains variation in host resistance to one *P. ramosa* genotype, C19. We found that one exceptionally large insertion-deletion polymorphism (~50 kb) underlies locus A. Next, we found that variation in locus A is associated to a combination of resistance to *P. ramosa* C1 and susceptibility to C19 throughout a genetically and phenotypically diverse *D. magna* meta-population. Our results are consistent with the *D. magna*-*P. ramosa* relationship evolving by negative frequency dependent selection. We are currently investigating which specific genes located in locus A are responsible for the phenotypes observed. For that we are using a technique of directed genome editing, CRISPR/Cas9, that was recently established for *Daphnia magna*. We expect to knockdown candidate genes, and to establish functional relationship between gene and host resistance.

Session 1 TUE POL C 11

Experimental evolution of host specificity by comparing single and multiple infections (51918)

Rebecca D Schulte, Joy Bose, Michaela H Kloesener.

University Osnabrueck.

Host-parasite coevolution is considered as one of the main drivers of evolution since it requires continuous adaptation and counter-adaptation of both antagonists. However, host-adaptation towards specific parasites often entails a loss of adaptation towards other parasites. Evolution of host defence should thus depend on the parasites they encounter and coevolve with, and should result in diversification between populations. We studied adaptation of the nematode *Caenorhabditis elegans* to its microparasite *Bacillus thuringiensis* using experimental evolution. Specifically, hosts coevolved either with one parasite strain or with a mix of two strains. We found that hosts evolving with one parasite strain evolve defence against it, but loose defence against an unknown parasite strain, i.e. they evolve specificity. Hosts evolving with two strains simultaneously show intermediate levels of survival when encountering only one strain, but survive better with a combination of both strains compared to hosts which evolved with one strain only. This indicates adaptation trade-offs, i.e. hosts cannot be well adapted to two strains at the same time. Our results show that parasites select for diversification between as well as for diversification within host populations depending on the parasite communities they encounter and thus support the role of parasites for diversification and speciation.

Session 1 TUE MAX 415 30

The thin line between conformational freedom and anarchy - negative epistasis and evolvability in TEM-1 beta-lactamase (53309)

Dan Tawfik.

Weizmann Institute of Science.

Epistasis is a key factor in evolution, since it determines which combinations of alleles provide adaptive solutions and which mutational pathways towards these solutions are accessible by natural selection. There is growing evidence for the pervasiveness of sign epistasis, particularly in protein evolution, yet its molecular basis remains poorly understood. I will describe the structural basis of reciprocal sign epistasis between two adaptive mutations in the antibiotic-resistance enzyme TEM-1 β -lactamase, G238S and R164S. Separated by 10Å, these mutations initiate two trajectories towards increased resistance. Both mutations allow the enzyme's active-site to adopt alternative conformations and accommodate the third-generation antibiotic cefotaxime. However, whereas G238S induces discrete conformations, R164S causes local disorder. When combined, the mutations in 238 and 164 induce local disorder whereby nonproductive conformations that perturb the enzyme's catalytic pre-organization dominate. This local disorder is not restored by stabilizing, global suppressor mutations and thus leads to an evolutionary cul-de-sac.

Session 1 TUE MAX 415 30

How do proteins evolve? Simulating evolution with in silico models of protein thermodynamics (53331)

Richard A. Goldstein.

University College London.

As with the blind men and the elephant, researchers with various perspectives have developed different conceptual models for how proteins evolve. Evolutionary biologists motivated by Fisher's geometric model have emphasised how conservative mutations would be more likely to be accepted than more radical changes, just as how adjusting the fine focus of a microscope is more likely to yield an improvement than adjusting the course focus. Scientists with more of a structural biology background describe the match between location in the protein and the suitability of any amino acid for such a location - mutations to more suitable amino acids, including radical changes, should be accepted at a higher rate. There has been a growing understanding that a protein is an integrated system so that many of the selective constraints are properties of the entire protein such as structure, stability, solubility, and resistance to aggregation. In this perspective, the selection acting on one site is always in the context of the amino acids found in other sites. And as with the tangled bank described by Darwin, there will be a complex network of feedback loops; substitutions at one focal position will affect the selection acting on other sites; the corresponding substitutions at these other sites will, in turn, influence the selection acting on the focal position. One aspect of this is the so-called 'Stokes Shift', where the rest of a protein adopts itself to the new amino acid resident at a given site so that, as long as that amino acid remains at the site, it becomes increasingly suitable for that position. These contrasting perspectives suggest different approaches to understanding and interpreting molecular evolution. We can simulate protein evolution in silico over long periods of evolutionary time. We can use these simulations to evaluate how well these

different models capture the evolutionary process, the types of errors that might result from an inappropriate model, and how these approaches can be reconciled.

Session 1 TUE MAX 415 30

Tandem repeats in coding region constitute another mechanism of adaptive radiation in cichlid fish (51770)

Langyu Gu, Walter Salzburger.

Zoological Institute, University of Basel, Basel 4051, Switzerland.

Convergent evolution provides an ideal scenario for testing the role of natural and sexual selection in adaptive radiations. However, to what extent the same genes and genetic pathways or different ones contribute to convergent phenotypes is still unclear. Cichlid fishes, which feature multiple convergent phenotypes, provide an ideal model system to answer the questions why certain key traits are important in some lineages but not in others, and how these phenotypes evolved and are maintained developmentally. Egg-dummies are an evolutionary key innovation of East African cichlids that have been suggested to contribute to their evolutionary success. Using comparative transcriptomic and genomic analyses, we identified an egg-dummy candidate gene showing cichlid-specific tandem repeats in its coding region, which represent a functional domain and are under positive selection. More interestingly, the polymorphism of these repeats is associated with species richness. We hypothesize that the repeats enlarge the available binding properties of this gene, constituting yet another mechanism of adaptive divergence in cichlids.

Session 1 TUE MAX 415 30

Correlated substitutions are rare under molecular coevolution (52722)

David Talavera, Simon Lovell, Simon Whelan.

University of Manchester; Uppsala University.

Molecular coevolution occurs when substitutions at one site influence evolutionary change at other sites. It is commonly assumed that coevolution results in correlated amino acid substitutions at groups of sites that are close together in the protein structure, and identifying such sites would be useful in (e.g.) de novo protein structure prediction. Many methods have been developed to detect molecular coevolution either directly, through phylogenetic models, or indirectly by identifying covariation, a commonly assumed outcome of coevolution. Despite decades of research these methods still have low power, even with massive alignments of 10000s of sequences.

This study examines the consequences of coevolution at the sequence level and how it affects covariation. Our theoretical results predict that all methods for detecting molecular coevolution will have extremely limited power because in order to have enough correlated substitutions to detect coevolution the strength of selection reduces evolutionary rate so much

that very few substitutions are likely to occur. These results are empirically confirmed by studying the performance of covariation methods, where true positive predictions of physical proximity are not associated with correlated mutations, but instead tend to occur from the detection of low rate sites within occur predominately in the protein core.

Session 1 TUE MAX 415 30

Disease-related mutations in proteins: a study of dynamically correlated networks and coevolved residue clusters (52814)

Yasaman Karami, Serge Amselem, Elodie Laine, Alessandra Carbone.

Université Pierre et Marie Curie, UMR 7238, Equipe de Génomique Analytique, Paris, France; CNRS, UMR 7238, Laboratoire de Biologie Computationnelle et Quantitative, Paris, France; Sorbonne Universités, UPMC Univ Paris 06, ICS, Paris, France; Service de Génétique et d'Embryologie Médicales, UMR S933 INSERM / UPMC, Hôpital Armand-Trousseau; Institut Universitaire de France, Paris, France.

Point mutations can induce effects at distant protein sites, thereby provoking diseases. Networks of dynamically correlated residues play a crucial role in propagating such perturbation signals. These residues are also expected to display high degrees of conservation and/or coevolution. We performed a consensus analysis of dynamically correlated and coevolved residue networks in three archetypal proteins. Dynamically correlated residues were detected from all-atom molecular dynamics simulations and grouped into: Communication Pathways and Independent Dynamic Segments (1), which represent two complementary media for allosteric communication. Coevolved residues were detected by sequence analysis using BIS (2) and clustered with CLAG (3). Results reveal a significant overlap between clusters of coevolution and networks of dynamical correlation. We examined the impact of two disease-related mutations on the allosteric communication of growth hormone. The comparison of wild-type and mutant showed a rewiring of Communication Pathways linking coevolved residues. Characterizing the dynamical behavior of proteins provides a means for physical understanding of coevolution signals. Understanding the role of disease-related mutations on the link between coevolution and dynamical correlation can help decipher the molecular mechanisms of mutation-induced allosteric deregulation.

1E. Laine, et al., PLoS CB (2012).

2L. Dib, A. Carbone, PLoS ONE (2012).

3L. Dib, A. Carbone, BMC Bioinformatics (2012).

Session 1 TUE MAX 415 30

Complex phylogeny of aminoacyl-tRNA synthetases (52521)

Alex Poppinga, Remco Bouckaert, Peter Wills.

Department of Computer Science, University of Auckland; Allan Wilson Centre for Molecular Ecology and Evolution; Machine Learning Group, University of Waikato; Department of Physics, University of Auckland.

All aminoacyl-tRNA synthetases (aaRSs), of all specificities from all known organisms, fall into two main classes. Each class has a core structure that has been highly conserved since the origin of life 3.8 billion years ago. The aaRSs have evolved from the simplest (core) structures, which provided the basic functional requirements for interpreting a loose binary code, into the complex present day structures that are capable of interpreting the highly specific 61-codon to 20-amino acid universal genetic code. Throughout this process, thermodynamic instabilities drove bifurcation events in the aaRS phylogeny, expanding the amino acid alphabet by one binary digit at each bifurcation. Therefore, in order to analyse the cophylogenies of Class I and Class II aaRSs before the LUCA event, it is necessary to consider epochs in which there were fewer than 20 classes of distinguishable amino acids, invalidating the use of 20 x 20 substitution matrices throughout the phylogenetic inference. To tackle this problem, we have developed an extension of BEAST, using matrices of reduced $2 \leq n \leq 20$ dimensions for each pre-organismal epoch. Results from the phylogenetic analysis are used in complement with empirical structural data to examine the transitions of specificity in these self-constructing interpreters.

Session 1 TUE POL D 33

Evolution and development of floral signals influencing pollinator behaviour (51809)

Beverley Glover.

University of Cambridge.

The morphology of flowers influences pollinator behaviour in many different ways. We are interested in how changes in flower symmetry, shape, size, colour and texture influence which pollinators visit a plant and how they interact with it. These interactions can lead to reproductive isolation and speciation. Our recent work has focused on a rare example of sexual mimicry outside the orchids, the South African daisy *Gorteria diffusa*. I will describe our analysis of the fly-mimicking petal spots of this species, focusing on their development and their variability, and discuss how this morphological variability relates to pollinator behaviour.

Session 1 TUE POL D 33

Genetic Parallelism in Flower Color Evolution (51847)

Mark Rausher.

Duke University.

A recurring question in evolutionary biology is whether parallel genetic evolution underlies parallel phenotypic evolution. Most studies addressing this question, however, are based on only two or three species, which limits conclusions that may be drawn. Using a larger sample of species allows one to perform statistical analyses to determine whether the frequency spectrum of genetic changes differs from random expectations. Using studies on the evolution of floral pigments, I apply this type of analysis to demonstrate genetic parallelism. In addition, I show how information about mutation spectra can be used to determine whether genetic parallelism is due to differences in mutation frequency or in the magnitude of deleterious pleiotropy.

Session 1 TUE POL D 33

The molecular basis of genic ecological speciation in sexually deceptive orchids (51586)

Philipp Schlüter, Khalid Sedeek, Shuqing Xu, John Shanklin, Salvatore Cozzolino, Florian Schiestl.

University of Zurich, Switzerland; Max Planck Institute for Chemical Ecology, Germany; Brookhaven National Laboratory, USA; University of Naples Federico II, Italy.

High pollinator specificity and the potential for simple genetic changes to affect pseudo-pheromone blends, and thus pollination, make sexually deceptive Ophrys orchids an interesting study system for ecological speciation. A survey of different reproductive barriers revealed that only pre-mating reproductive isolation (RI), particularly pollinator-mediated RI, has evolved between sympatric and co-flowering species. Genotyping by sequencing revealed shared polymorphism throughout the Ophrys genome. Genome scans for FST outliers identified few markers that were highly differentiated between species, identifying genes involved in floral odour production. Chemical mimicry of insect pheromones is achieved by the synthesis of alkenes with different double-bond positions, which are primarily controlled by the action of two acyl-ACP desaturase-encoding genes, SAD2 and SAD5. These loci originated by gene duplications from an ancestral, housekeeping-desaturase-like gene, and have undergone changes in both gene expression and protein function. An amino acid change during the evolution of SAD5 may have altered its enzymatic activity and released the protein from pleiotropic constraint, allowing it to carry out its specific function in alkene biosynthesis. Evolutionary modelling of this two-locus architecture of RI reveals the effect sizes of the two desaturases to be unequal and predicts potential and constraints for rapid pollinator-driven speciation in sympatry.

Session 1 TUE POL D 33

Gene flow and the genetic architecture of speciation revealed by 1043 stick-insect genomes (51629)

Patrik Nosil.

University of Sheffield.

Genome variation during the often-complex speciation process is affected by numerous factors, and can affect the likelihood of evolutionary diversification. Disentangling the processes driving patterns of genome variation is challenging, because different processes can generate similar patterns. In this talk, I will combine data from whole genome re-sequencing of natural and experimentally transplanted populations, genome wide association mapping, and theoretical modeling to test the processes driving genome divergence during ecological speciation in *Timema* stick insects. The results indicate that even the early stages of speciation can involve numerous genomic regions affected, either directly or indirectly, by divergent natural selection. However, major work remains to be done to objectively determine the traits and genomic regions directly and causally subject to selection and which are most critical for driving speciation. I will discuss how progress on this front can be made using emerging 'ecological' model systems in which genome variation can be experimentally studied in the wild.

Session 1 TUE POL D 33

Loss of function mutations in MC4R drive adaptation of *Astyanax mexicanus* through hyperphagia. (51852)

Nicolas Rohner, Ariel Aspiras, Richard Borowsky, Cliff Tabin.

Harvard; NYU.

Colonization to new environments necessitates changes to morphology, behavior, and physiology. Especially how the latter two evolve remains largely a mystery. The independently derived cavefish populations of *Astyanax mexicanus* are providing a unique opportunity to study metabolic adaptation to nutrient-poor environments. As the hallmark of cave environments is the scarcity of food, cavefish have adapted different strategies to survive, such as starvation resistance and binge eating when food becomes available. We show that while all cavefish populations tested lose weight slowly during starvation, only some consume more food than surface populations. Here we show a mutation in a conserved residue of melanocortin 4 receptor (MC4R), contributing to this insatiable appetite. Intriguingly, the same mutated residue has been shown to be linked to obesity in humans. We demonstrate that the mutation results in reduced signaling sensitivity in vitro. We further validate in vivo that the mutated allele contributes to elevated appetite and growth. The mutation is fixed in most cave populations and we provide evidence that this could be due to selection from standing genetic variation in surface populations. Our results suggest that drastic metabolic and behavioral changes can occur by coding changes in a single gene in natural populations.

Session 1 TUE POL D 33

Identifying the molecular basis of adaptation and genomic divergence in *Heliconius* butterflies (51901)

Nicola Nadeau, Carolina Pardo-Diaz, Annabel Whibley, Megan Supple, Mathieu Joron, Owen McMillan, Chris Jiggins.

The University of Sheffield; Universidad del Rosario; Muséum National d'Histoire Naturelle; The Australian National University; Smithsonian Tropical Research Institute; University of Cambridge.

The Heliconius butterflies are known for their bright wing colour patterns, which are divergently selected between populations, but convergently selected within a location, leading to mimicry between species. We have described genome-wide patterns of divergence between adjacent populations that are divergently selected for colour pattern and meet in narrow hybrid zones. This has revealed that narrow genomic regions containing the colour pattern controlling loci are differentiated between populations. We have used this information, together with genetic data from other populations and species that share colour pattern alleles, to narrow down the genomic regions and identify the particular genes underlying pattern variation. One of these genes is an unexpected candidate, belonging to a family of conserved cell cycle regulators. We find strong associations between phenotypic variation and DNA sequence variation near this gene in three different Heliconius species, as well as associations between expression of this gene and colour pattern. This gene appears to have adopted a novel function in the Lepidoptera and become a major target for natural selection acting on colour and pattern variation in this group.

Session 1 TUE GEN B 8

Caught in the crossfire: Genome defense in light of genomic autoimmunity (52618)

Justin Blumenstiel, Alex Erwin, Mauricio Galdos, Michelle Wickersheim, Chris Harrison, Kendra Marr.

University of Kansas.

For systems of immunity, a fundamental challenge is to achieve an appropriate balance between sensitivity and specificity in distinguishing self from non-self. Small RNA-based systems of genome defense identify transposable elements (TEs) via aberrant insertions or insertions into genomic regions dedicated to small RNA production. In turn, the production of anti-TE small RNAs from these insertions can mediate transcriptional and post-transcriptional TE silencing. A significant cost of genome defense is off-target gene silencing. Using a system of hybrid dysgenesis in *Drosophila virilis* as a model, we have demonstrated how effective genome defense is sensitive to the dose of multiple protective elements. These studies also show how TE destabilization can lead to increased off-target effects within and across generations. Using molecular evolutionary analysis in *Drosophila*, we find that the primary evolutionary response to increased TE burden is increased translational efficiency of the piRNA machinery. Altogether, these results support a model in which the evolution of genome defense is governed by a tension between sufficient TE repression and off-target effects. I propose that this tension - between sensitivity and specificity - is a key driver in the evolution of systems of genome defense mediated by small RNA pathways.

The punishment wars (53352)

Toby Kiers.

Department of Ecological Science, Vrije Universiteit Amsterdam.

How is conflict suppressed? In most mutualisms, an individual host associates with multiple partners that can vary dramatically in the benefit they provide. This creates a potential tragedy of the commons where less-mutualistic partners potentially share in the collective benefits, while paying less of the costs. Our focus is on understanding specific mechanisms that reduce the fitness benefits from cheating, such as sanctions and reciprocal rewards. These mechanisms can play a key role in the evolution of egalitarian cooperation. Ultimately, our aim is to identify patterns of conflict suppression and conflict resolution across diverse mutualistic systems, such as rhizosphere mutualisms.

The origins, persistence and decay of bacterial mutualisms (51759)

Lee Henry, Godfray Charles.

VU Amsterdam; University of Oxford.

Bacterial symbiosis has played a fundamental role in the evolution of eukaryotes. However, we still know little about how cooperative relationships with bacteria originate, and why they form in some host species but not others. Facultative symbionts that are beneficial, but not essential, provide unique insights into these processes. Here we use the facultative symbionts of over a hundred aphid species to test how host life history and relatedness of host species influences horizontal transmission, persistence and decay of bacterial mutualism.

‘Currency’ exchange underlying the long-term association between squid and bioluminescent bacteria (52192)

Natacha Kremer, Julia Schwartzman, Edward Ruby, Margaret McFall-Ngai.

University of Madison-Wisconsin, USA; Université Lyon 1, UMR CNRS 5558, France.

Long-term stability of horizontally transmitted symbioses must rely on negotiations between partners that result in a gain of fitness for the association. The study of invertebrate species that coevolved with simple microbial communities provides the opportunity to decipher the

chemical conversation between partners, and to highlight the ‘currency’ exchange that contributes to the stability of ‘egalitarian’ cooperative associations. In particular, the symbiosis between the Hawaiian bobtail squid and its luminescent bacterial partner, *Vibrio fischeri*, is tractable in its natural environment. The squid light organ is colonized after hatching by *V. fischeri*, which participates in the squid’s camouflaging behavior. We showed that in the mature symbiosis, host hemocytes migrate toward and release chitin into the symbiotic crypts of the light organ at dusk. This polymeric glycan is used as carbon source and catabolized by symbionts during the night, acidifying the crypt environment. Because oxygen is released from the circulating carrier protein, hemocyanin, in response to a decrease in pH, this acidification increases the amount of oxygen available to the symbionts overnight. Symbionts thus have an increased ability to produce light by their luciferase, whose activity could also be a way to limit a potential toxic effect of free oxygen.

Session 1 TUE GEN B 8

Spatial exclusion of non-cooperators from released public goods stabilizes inter-specific cooperation (52231)

Samay Pande, Filip Kaftan, Stefan Lang, Sebastian Germerodt, Ales Svatos, Christian Kost.

Experimental Ecology and Evolution group, Max Planck Institute for Chemical Ecology, Jena, Germany; Research Group Mass spectrometry, Max Planck Institute for Chemical Ecology, Jena, Germany; Department of Bioinformatics, Friedrich Schiller University Jena, Jena, Germany; Evolutionary biology group, ETH Zurich, Switzerland.

Metabolic cross-feeding interactions are ubiquitous in natural microbial communities. Explaining their maintenance, however, is challenging, because organisms should avoid investing costly resources into unrelated individuals. We hypothesized that positive assortment within structured environments such as microbial biofilms can maintain mutualistic cross-feeding. To test this, we engineered *Escherichia coli* and *Acinetobacter baylyi* to reciprocally exchange essential amino acids. Interspecific coculture experiments confirmed that non-cooperating types were selectively favoured in spatially unstructured (liquid culture), yet disfavoured in spatially structured environments (agar plates). An individual-based model and experiments with engineered genotypes indicated that a segregation of cross-feeders and non-cooperating auxotrophs stabilised cooperative cross-feeding in spatially structured environments. Finally, chemical imaging confirmed that auxotrophs were indeed spatially excluded from cooperative benefits. Together, these results demonstrate that in structured environments such as bacterial biofilms, cooperative cross-feeding between different bacterial species is favoured by excluding non-cooperators from cooperative benefits, which could help to explain the widespread distribution of these ecological interactions in nature.

Session 1 WED GEN C 2

The crucial link between ‘how’ and ‘why’ in the evolution of environmental sex determination (51813)

Lisa Schwanz.

UNSW Australia.

For many organisms, developing as a male or female depends primarily on environmental factors such as temperature or social conditions – a phenomenon known as Environmental Sex Determination (ESD). The costs of such a biological feature in a world with fluctuating or changing environments are high, and the benefits remain largely a matter of conjecture in the field of sex allocation. Instead, the benefits of Genotypic Sex Determination (GSD) seem obvious, and the challenges of transitioning away from GSD seem insurmountable. Despite this, sex-determining mechanisms are highly evolutionarily labile in some taxa, thus demanding evolutionary hypotheses. In this talk, I will discuss my theoretical and empirical research into the forces shaping the evolution of environmental sex determination (mostly temperature-dependent sex determination in reptiles). In particular, I will focus on how knowledge of the mechanisms of ESD can reveal 1) the simplicity of evolutionary transitions between sex-determining mechanisms, thus allowing ESD to evolve easily in response to selection; and 2) the plasticity in sex ratio afforded by linking developmental biology to environmental factors, thus facilitating selective advantages of ESD.

Session 1 WED GEN C 2

Sex allocation in simultaneous hermaphrodites: lessons from an emerging model organism (52767)

Lukas Schärer.

University of Basel.

Anisogamous sexual reproduction involves two fundamentally different routes to fitness, namely the male and female sexual strategies, which at their root entail making many small or fewer large gametes, respectively. These two strategies are tightly linked by the rules of sex allocation, because every zygote has one father and one mother, and so exactly one half of the fitness in a population necessarily derives from either sex function. While the two strategies can be distributed over individuals in a population in many different ways, research on sex allocation in animals has primarily focused on species with separate sexes. Over the past decade my research group has established the free-living flatworm *Macrostomum lignano* as a powerful emerging model to study sex allocation and other aspects of anisogamous sexual reproduction in simultaneous hermaphrodites, including experiments involving phenotypic plasticity, phenotypic engineering, transgenesis, transcriptomics, and experimental evolution. Among other insights this research has clearly identified local sperm competition, i.e. the competition between related sperm for fertilizations, as a key factor for hermaphrodite sex allocation. Moreover, it is becoming clear that local sperm competition also helps to clarify general aspects of the evolution of sex roles in other species with anisogamous sexual reproduction.

Session 1 WED GEN C 2

Sex allocation, juvenile mortality & the costs imposed by offspring on parents and siblings (51765)

Andrew Kahn, Michael Jennions, Hanna Kokko.

The Australian National University; The Australian National University; University of Zurich.

In general, sex-specific adult mortality is not expected to affect optimal patterns of sex allocation. Several authors have, however, made verbal arguments that this is not true for sex-specific juvenile mortality during the period of parental care. We teach this to undergraduates, but lack a model confirming the argument is sound. Here, we provide formal mathematical models exploring how such juvenile mortality affects optimal sex allocation. We confirm the prediction that biased production of the sex with higher mortality during care is favoured. Crucially, however, this is only true when this juvenile mortality frees up resources for current/future siblings (i.e. the saved investment is transferable). Furthermore, we show that while optimal sex allocation is consistent with the theory of equal investment (as asserted by previous authors, and reflecting how we teach sex allocation theory), thinking in terms of equal investment is not readily feasible in some scenarios. We also show that differences in early mortality overcome biased sex allocation such that the sex ratio at independence is generally, but not always, biased in the opposite direction from that at birth. Our models should be useful to empiricists investigating sex-specific juvenile mortality and, as importantly, to those teaching sex allocation theory to their students.

Session 1 WED GEN C 2

The evolution of unisexual flowers within inflorescences (52179)

Rubén Torices, Ana Afonso, Marcos Méndez.

Estación Experimental de Zonas Áridas (CSIC); Department of Ecology and Evolution, University of Lausanne; Centre of Functional Ecology. University of Coimbra; Biodiversity and Conservation Unit, Rey Juan Carlos University.

The evolution of unisexual flowers within inflorescences has been explained as a mechanism of avoiding self-fertilization reducing the negative effects of inbreeding. However, many species with unisexual flowers also have self-incompatibility systems making difficult generalizations of this hypothesis. An alternative hypothesis for this pattern is that flowers within inflorescences compete by resources, and that the sequential development of flowers and architectural constraints lead to a gradient on resource availability. This variation on resource availability produces distinct optima for sex allocation accordingly with the position of the flower within an inflorescence, potentially driving the evolution of sexual specialization on separated flowers. Using as a model the largest family of flowering plants (Asteraceae), we explored this hypothesis. We measured number of flowers and capitulum size to estimate flower density (as a proxy of floral competition) in 101 species with different levels of sexual specialization: hermaphroditic (only bisexual flowers), gynodioecious (bisexual and female flowers) and monoecious species (female and male flowers). We found that flower number and flower density were higher on those species with a higher degree in sexual specialization,

supporting that an increasing on floral competition might favor sex specialization of male and female functions on different flowers.

Session 1 WED GEN C 2

Genomic conflict over sex allocation in the parasitoid wasp *Nasonia vitripennis*. (51786)

Nicola Cook, Michael G Ritchie, Bart A Pannebakker, Eran Tauber, David M Shuker.

University of St Andrews; University of Wageningen; University of Leicester.

The study of sex ratios has produced an extraordinarily rich theoretical literature and provides an ideal basis to examine genetic constraints on adaptation. Here, we consider adaptive sex allocation behaviour in the parasitoid wasp *Nasonia vitripennis*, a species which allocates sex in line with Local Mate Competition (LMC) theory. Despite extensive behavioural work on sex allocation in *Nasonia*, we know rather little about the genetic basis of sex allocation in this species. However, recent theory has highlighted how genomic conflict may influence sex allocation under LMC, conflict that requires parent-of-origin information to be retained by alleles via an epigenetic signal. We manipulated whole-genome DNA methylation in *N. vitripennis* females and examined how they allocated sex. Disruption of DNA methylation did not ablate the facultative sex allocation response as sex ratios still varied in line with classical LMC theory. However, our data were consistent with predictions from genomic conflict over sex allocation theory and suggest that observed sex ratios are closer to the optimum expected for maternally- rather than paternally-inherited alleles. Our results also emphasise how elucidating the mechanism of well-understood behaviours can further enrich our understanding of them.

Session 1 WED GEN C 2

Sperm storage and the size advantage model of sex allocation in the protandrous sex-changer *Crepidula fornicata* (52232)

Thomas Broquet, Audrey Barranger, Emmanuelle Billard, Anastasia Bestin, Rémy Berger, Gaëlle Honnaert, Frédérique Viard.

CNRS - Station Biologique de Roscoff.

Sex allocation theory shows that sequential hermaphroditism is adaptive when one sex has a steeper size-fitness curve than the other. Typically, protandry (male-first sex change) is selected for when female fecundity depends on body space for the production of eggs while male reproductive value is less dependent upon size. However, size might also be decisive for males, depending upon the mating system. Which sex has the steepest increase in reproductive value with size determines the direction of sex-change. The slipper limpet *Crepidula fornicata* is a protandrous gastropod, and yet male success is thought to increase strongly with size in this species. Theory therefore predicts that large females have yet a

higher reproductive rate. We tested this prediction using size-fitness curves for each sex obtained from experimental breeding and paternity assignment. In agreement with the size-advantage theory male reproductive success increased with size due to the polygamous system but females nonetheless had a higher success than equally-sized males. Interestingly, this was partly due to sperm storage effects, which appeared a critical determinant of success of both sexes. Moreover, modeling the effect of sperm storage shows that it could hasten sex-change in protandrous species, depending on sperm replacement mechanisms.

Session 1 WED MAX 410 21

The evolution of transgenerational integration of information in heterogeneous environments (52246)

Olof Leimar, John McNamara.

Stockholm University; University of Bristol.

An organism's phenotype can be influenced by maternal cues and by directly perceived environmental cues, as well as by its genotype at polymorphic loci. In fluctuating environments, natural selection favors organisms that efficiently integrate different sources of information about the likely success of phenotypic alternatives. In such situations, it can be beneficial to pass on maternal cues for offspring to respond to. A maternal cue could be based on environmental cues directly perceived by the mother, but partly also on the cues that were passed on by the grandmother. We have used a mathematical model to investigate how the passing of maternal cues and the integration of different sources of information evolves as a response to qualitatively different kinds of temporal and spatial environmental fluctuations. The model shows that passing of maternal cues and transgenerational integration of sources of information readily evolves. Factors like the degree of temporal autocorrelation, the predictive accuracy of different environmental cues, and the level of gene flow strongly influence the expression of adaptive maternal cues and the relative weights given to different sources of information. We outline the main features of the relation between the characteristics of environmental fluctuations and adaptive systems of phenotype determination and compare these predictions with empirical studies.

Session 1 WED MAX 410 21

Maternal effect on worker size in the seed harvester ant *Pogonomyrmex rugosus* (52338)

Silvia Paolucci, Benjamin Czech, Gregory Hannon, Tanja Schwander, Laurent Keller.

Department of Ecology and Evolution, University of Lausanne, Switzerland; Cold Spring Harbor Laboratory, New York, USA.

Eusocial insects are characterized by extreme phenotypic plasticity, in which different phenotypes can be produced within the same colony depending on environmental conditions.

For example, worker sizes change dramatically across different stages of the colony life cycle. Young founding colonies produce many small workers, instead of few large ones, which are only found in established colonies. The degree to which worker size is regulated through differential feeding during development or controlled by the mother queen via maternal effects remains unknown. We tested for maternal effects influencing the size of workers in the ant *Pogonomyrmex rugosus*. A cross-fostering experiment showed that eggs laid by young founding queens developed into smaller workers compared to the ones produced from eggs laid by old queens from established colonies, when both egg types were raised by workers from established colonies. Moreover, eggs laid by old queens failed to develop when cross-fostered to founding queens. These results indicate that maternal effects influence worker size and egg survival. To further investigate how these effects can influence the developmental fate of the brood I am quantifying gene expression differences between eggs from old and young queens with a particular focus on the possible role of microRNAs.

Session 1 WED MAX 410 21

Pollution-induced non-genetic inheritance and its effect on eco-evolutionary dynamics (52395)

Stewart Plaistow, Brian Chan, Helene Collin, Steve Paterson.

University of Liverpool.

Theory suggests that genetic and non-genetic inheritance (NGI) mechanisms shape the process of phenotypic evolution, yet empirical studies demonstrating the ecological and evolutionary significance of NGI are lacking. We addressed this by testing the hypothesis that pollution induced NGI can alter the ecological and evolutionary dynamics of populations. 10 *Daphnia pulex* clones from the same source population were kept as monoclonal populations in polluted and control environments for a year. Animals from these populations were then used to set up competition trials comprising of 40 genetically identical populations (equal proportions of the 10 clones) exposed to four different combinations of ancestral and current pollution exposure (P/P, P/NP, NP/P, NP/NP). Over the following ten months persistent differences in the population dynamics of the four treatment groups were detected, including a significant effect of NGI. We used image analysis and microsatellite analysis to determine whether differences in the dynamics of the four different types of population were explained by differences in the age-structure of populations, differences in the individual 'state' dynamics of populations, or differences in the evolutionary dynamics of populations (measured as changes in the relative frequency of different clones over time).

Session 1 WED MAX 410 21

Genetic basis of variation in thermal plasticity for body pigmentation (52662)

Elvira Lafuente, Patr cia Beldade.

Instituto Gulbenkian de Ciencia.

External environmental cues can influence developmental rates and trajectories leading to the production of different phenotypes from the same genotype. This developmental plasticity sometimes results in a better match between adult phenotype and the environment the organism will experience, and thus helps organisms to cope with environmental heterogeneity. Plasticity is a complex trait that is heritable, subject to selection, and, therefore, can evolve. We know of single alleles that confer environmental sensitivity and of the polygenic nature of changes in reaction norms. However, little is known about the specific loci contributing to natural variation in plasticity. We focus on thermal plasticity in body pigmentation in *Drosophila melanogaster* to explore the genetic basis of inter-genotype variation in reaction norms. We reared flies of over 200 different genotypes at different temperatures, quantified adult color and color pattern, and unraveled genetic differences in the height, slope, and/or shape of reaction norms. These data are now being used to identify the sequence variants responsible for such differences and uncover specific loci, gene classes (e.g. enzymes vs transcription factors), and gene regions (e.g. coding vs. regulatory) that can provide raw material for evolutionary change in plasticity.

Session 1 WED MAX 410 21

Transgenerational effects of diet through the maternal and paternal lineage (52765)

Z. Valentina Zizzari, Nico M. van Straalen, Jacintha Ellers.

VU University Amsterdam.

Food shortage is an important selective factor that can influence population abundance. Yet, despite its role in shaping life-history trajectories, many aspects of the interaction between parental and offspring food environments remain unclear. In this study we used a cross-generational split-brood design where diet quantity was manipulated over two generations. Our model system is *Orchesella cincta*, a springtail found in the litter layer of forests and feeding primarily on algae. We tested for the within-generation effects of diet and the relative contribution of each parental sex on the performance of offspring reared under matched and mismatched environments. We found adverse effects of food limitation on growth rate and reproductive performance of the parental generation. Offspring life-history strategies were primed by the diet of both parents. Offspring born to food-restricted parents reached maturity faster than offspring born to well-fed parents, irrespective of their own diet. However, mismatches between adult and offspring environments also generate sex-specific adverse effects: parents on high-diet produced daughters which had a lower growth rate under a low-diet. In conclusion, we showed that in *Orchesella cincta* offspring life-history strategies may be set by the nutritional history of both parents with different outcomes in female and male offspring.

Session 1 WED MAX 410 21

Age-dependent plasticity in reproductive effort is driven by metabolic reserves and mating opportunities, not adaptive allocation strategies (52446)

Thomas Houslay, Kirsty Houslay, James Rapkin, John Hunt, Luc Bussière.

University of Stirling; University of Dundee; University of Exeter.

When males express an energetically expensive sexual signal repeatedly over their lifetime, trade-offs between current and future signal investment often cause plasticity in patterns of age-dependent signal expression. This variation in reproductive effort with age might represent alternate adaptive strategies (live fast, die young vs. slow and steady), or it could arise simply through condition-dependent constraints on allocation ('late bloomers' do not have early investment options). Testing these alternatives is difficult: resource acquisition and allocation are elusive quantities, and metabolic reserves both cause and are affected by reproductive effort.

To disentangle the causal relationships between resource acquisition and age-dependent reproductive effort, we manipulated acquisition (through diet) and sexual trait allocation (via access to potential mates) in male decorated crickets, *Gryllodes sigillatus*, while simultaneously assessing age- and signalling effort-mediated changes in metabolic storage components. Increased access to dietary resources caused increased calling effort and metabolic storage, while access to females increased both the likelihood of calling and time spent calling. Males with lower resource budgets called less than rivals, but still suffered metabolite storage loss and viability costs; our results suggest reduced signalling in lower-acquisition treatments was due to energetic constraints rather than an adaptive resource-accumulation strategy.

Session 1 WED POL A 29

Can't do it alone: Buchnera and its very different partners (52473)

Amparo Latorre.

Institut Cavanilles de Biodiversitat i Biologia Evolutiva, Universitat de València, València, Spain.

Most aphids harbour the obligate endosymbiotic bacterium *Buchnera aphidicola* that endow them with several metabolic capabilities required for their survival. Through whole genome sequencing we have determined that in the subfamily Lachninae, *Cinara tujaefilina*, *Cinara cedri* (both Eulachnini) and *Tuberolachnus salignus* (Lachnini) have established co-obligate associations with the typical *B. aphidicola* and the secondary symbiont *Serratia symbiotica*. Nevertheless, while in *C. tujaefilina* this endosymbiont is extracellular, rod shape and possesses a big genome, in *C. cedri* and *T. salignus* it is intracellular, pleomorphic and has very small genomes that have apparently emerged independently. We have previously proposed that the loss of the riboflavin biosynthesis pathway in the *Buchnera* from the Lachninae common ancestor, caused *S. symbiotica* to fix as an obligate endosymbiont. Nevertheless, some other Lachninae aphids have been found to be associated to other bacterial taxa, rather than *S. symbiotica*. We have analysed many representatives from the Lachninae and have corroborated that all possess a co-obligate endosymbiont, and while for most it is *S. symbiotica*, some members have lost this ancient endosymbiont that has been replaced by different bacterium.

How are negative fitness consequences of evolutionary trait loss compensated? (53321)

Nathan Bailey, Sonia Pascoal.

University of St Andrews.

Trait loss or reduction may evolve under favourable selective conditions, for example due to new interactions with other species or changed environmental conditions. However, the evolutionary loss of a trait is likely to cause negative pleiotropic fitness effects involving other traits. The likelihood that a mutation obliterating or reducing a trait will persist depends on how such negative effects are mitigated, either through rapid evolutionary change, phenotypic plasticity, or other mechanisms. My work tackles this problem using a field cricket that has recently lost the ability to produce calling song. The evolutionary loss of song was driven by an acoustically orienting predator, is caused by a morphological change, obeys simple patterns of Mendelian inheritance, and has demonstrable negative pleiotropic effects. I will illustrate the genomic architecture of song loss in two populations and provide evidence that despite its convergent effects, it evolved independently in each. Data from genetic mapping, gene expression profiling and proteome screens illuminate the mechanistic basis of the loss, and I test specific predictions about gene expression changes that might mitigate the mutation's detrimental effects. Understanding not only the selective forces that lead to trait loss, but also the genomic context that facilitates or constrains such evolutionary change, enhances our understanding of the evolvability of different types of adaptations in nature.

Genomic signatures of sexual trait decay in an asexual wasp (51940)

Ken Kraaijeveld, Yahya Anvar, Jeroen Frank, Johan den Dunnen, Jacintha Ellers.

VU University Amsterdam; Leiden University Medical Center.

When animal lineages switch from sexual to asexual reproduction, redundant female sexual traits consistently decay at a rapid rate. Male sexual traits, which are also redundant but not exposed to selection in asexuals, decay at a much slower rate. The genetic mechanisms underlying sexual trait decay are unknown. Genes for redundant traits may accumulate random mutations and become pseudogenes. Alternatively, the expression of sexual genes may be suppressed in asexuals. We sequenced the genomes of a sexual and an asexual lineage of the parasitoid wasp *Leptopilina clavipes* and found evidence of random mutation accumulation. After annotating the genome, we catalogued mutations that changed the amino acid sequence of the protein. Gene ontology analysis of affected genes identified several that are involved in olfactory receptors and other traits known to have decayed in the asexual lineage. While we cannot exclude that trait decay results from suppression of redundant

genes, our results suggest that at least some sexual genes have acquired loss-of-function mutations in the asexual lineage.

Session 1 WED POL A 29

Explaining siderophore loss, cross-use and exploitation in natural *Pseudomonas* communities (51954)

Elena Butaite, Rolf Kuemmerli.

University of Zurich.

Fluorescent pseudomonads typically secrete the siderophore pyoverdine (PVD) to scavenge iron from the environment. PVD production is often partially or fully lost in the laboratory because PVD is either not needed under certain culturing conditions, or favours non-producing mutants that act as cheats exploiting the PVD as a public good.

Here, we investigate the pattern of trait loss and PVD exploitation among 920 natural *Pseudomonas* strains, isolated from soil and pond habitats. We found that PVD trait loss (partial or full) was significantly more common in habitats with higher iron content and lower pH, where iron is more bioavailable. These patterns suggest that trait loss is driven by disuse. However, we also found that PVD producers and non-producers often co-existed in the same community. A mixture of cross-feeding and competition assays revealed that many non-producers could capitalize on the PVD produced by other community members. We also found evidence for local antagonistic interactions because non-producers were better at using the PVD from non-community than community members. Altogether, our data suggest that PVD loss in natural communities is driven by both social and ecological factors, and that PVD exploitation can select for novel, more exclusive variants of PVD.

Session 1 WED POL A 29

Strong selection for a loss of metabolic autonomy in bacteria (51955)

Glen D'Souza, Silvio Waschina, Christian Kost.

Experimental Ecology and Evolution Research Group, Max Planck Institute for Chemical Ecology; Theoretical Systems Biology Group, Friedrich-Schiller-Universität Jena.

Bacteria that adapt to specialised environments frequently lose biosynthetic genes, which render them dependent on an environmental uptake of the corresponding metabolites. However, it remains generally unclear whether selection or drift is driving this genome-streamlining. Here we experimentally determined the propensity of bacteria to lose biosynthetic functions when the metabolite is environmentally available. For this, we serially propagated replicate lines of the bacterium *Escherichia coli* for 2,000 generations in an amino acid-containing environment. A subsequent quantification of auxotrophic mutants revealed that genotypes that essentially required amino acids to grow evolved already after 250 generations and were highly abundant (up to 60%) in all replicate populations after 2,000

generations. Derived auxotrophic mutants were significantly more productive and fitter than the prototrophic ancestor in the presence of amino acids. However, this growth advantage was lost in amino acid-deficient environments, suggesting environmental compensation of amino acids contributed to the observed gains in fitness. Our study provides quantitative evidence that nutrient-containing environments exert a strong selection pressure for a loss of metabolic functions in bacteria and has significant implications for the evolution of microbial genomes.

Session 1 WED POL A 29

Loss and (re)gain of color vision in deep-sea fishes: uncovering the secrets of 100 teleost genomes. (52766)

Zuzana Musilova, Fabio Cortesi, Martin Malmstrøm, Ole Tørresen, Sissel Jentoft, Walter Salzburger.

University of Basel, Switzerland; University of Queensland, Australia; University of Oslo, Norway.

Color vision in vertebrates is made possible by the expression of different visual genes (cone opsins for photopic ‘color vision’ and rod rhodopsin for scotopic ‘dim-light’ vision) in retina. In teleost fishes, opsin genes have continued to duplicate creating an astonishing array of photoreceptors, considered to be crucial to adapt to the varying light conditions. Deep-sea fishes have evolved several physiological adaptations including larger eyes or rod-only retinas to counteract the low light conditions of their environment. However, the molecular mechanisms of dim-light-only vision and the loss of color vision remains poorly understood. Here we report opsin gene evolution based on 100 genomes spanning the teleost phylogeny, with emphasize on the deep-sea fish lineages. We found strong evidence for cone opsin losses and pseudogenization in many of the deep-sea fishes, confirming the absence of color vision in these lineages. Moreover fish lineages that have re-emerged from the deep-sea to colonize shallow waters, revealed a rapid expansion and functional diversification of the remaining formerly ‘green tuned’ cone opsin. Most importantly, we found that one deep-sea fish lineage had evolved multiple rhodopsins adapted to different dim-light wavelengths, assuming what may be the first evidence for rhodopsin-based color vision in vertebrates.

Session 1 WED POL B 20

Identifying locally adaptive loci by scanning for barriers to introgression (52506)

Andrea Fulgione, Joachim Hermisson, Angela Hancock.

University of Vienna.

Maintenance of locally adapted alleles in the face of gene flow is a pervasive evolutionary process, but characterizing the historical and biological details of admixture and introgression events in actual populations is a major challenge. However, continent-island systems provide

simplified cases where it is possible to reconstruct specific evolutionary events that lead to contemporary patterns of genetic variation.

The Canary Islands harbor exceptional species diversity and divergence, likely a result of ancient pre-glacial colonization events. Modern populations of *Arabidopsis thaliana* in the Canary Islands result from admixture of an anciently diverged native population and a recently introduced mainland population. To characterize demographic and adaptive histories in the Canary Islands, we collected whole-genome sequence data from natural populations of *Arabidopsis* throughout Macaronesia and leveraged data from worldwide samples. We developed a haplotype-based genome scan to perform admixture deconvolution and we identified genomic loci that represent strong barriers to gene flow as well as loci that underlie adaptive introgression from the invaders.

Session 1 WED POL B 20

A worldwide perspective on isolation-by-distance patterns in humans (52619)

Benjamin Peter, Desislava Petkova, Matthew Stephens, John Novembre.

Department of Human Genetics, University of Chicago, USA; Department of Statistics, University of Chicago, USA; Department of Statistics, University of Oxford, UK.

Human genetic diversity has been shaped by the initial expansion of humans across the globe and subsequent migration and admixture events. Throughout this history, geographical features such as mountains, oceans, and deserts have presumably shaped rates of gene flow between populations. To obtain maps that represent the spatial structure of human genetic diversity, we jointly estimate migration rates and local diversity using a recently developed, spatially explicit method (EEMS, Estimation of Effective Migration Surfaces). We apply EEMS on global, continental, and sub-continental scales, analyzing genetic data from more than five thousand individuals from multiple studies across the globe. We find many geographical features are indeed barriers with regards to effective migration. In particular, the Saharan Desert, the Mediterranean Sea, and the straits between South-East Asia and Melanesia emerge as particularly strong barriers to migration. High migration rates are found in a corridor connecting Europe with China. In contrast, we find that diversity parameters vary more smoothly, decreasing gradually with distance from Africa. Overall, our results suggest that diversity patterns are consistent with the signature of the Out-of-Africa expansion, but that migration rates are more strongly influenced by geography.

Session 1 WED POL B 20

Genetic variation linked to climate adaptation in *Arabidopsis lyrata* (52656)

Marco Fracassetti, Yvonne Willi.

University of Neuchâtel.

Global climate change has heightened the interest to understand climate adaptation and limits to such adaptive evolution. Progress in the field depends on knowing the genes under this selection and the distribution of genetic variation. We performed a genome-wide association study (GWAS), linking genetic variation with climate variables. The study organism was the North American *Arabidopsis lyrata* spp. *lyrata*, a short-lived herb occurring on sand dunes and rocky outcrops with well-separated and stable populations. We re-sequenced pools of DNA of 55 populations covering the whole geographic range of the subspecies and revealed population-level single-nucleotide-polymorphism (SNP) frequency data. Climate data based on temperature and precipitation and soil data were used for the GWAS.

We used a dual approach to detecting SNPs linked to climate variables. First, we analyzed site frequency spectra to detect signatures of selection within populations. Second, we tested SNPs for correlation with climate variables by accounting for genetic structure among populations. SNPs that were significant in both types of analyses were taken as candidates for being relevant in climate adaptation. We discuss the approach taken and the list of genes that is likely relevant for adaptation in the context of climate change.

Session 1 WED POL B 20

The role of host plant adaptation in genomic divergence and diversification of *Timema* stick insects (52805)

Moritz Muschick, Victor Soria-Carrasco, Stuart R. Dennis, Zachariah Gompert, Aaron A. Comeault, Jeffrey L. Feder, Patrik Nosil.

Department of Animal and Plant Sciences, University of Sheffield, UK; Department of Biology, Utah State University, USA; Department of Biological Sciences, University of Notre Dame, USA.

How the often-continuous processes of speciation and adaptive radiation unfold from beginning to end is poorly understood, but is of central importance for understanding biological diversification. One hypothesis is that shifts between very different peaks in the adaptive landscape, although difficult to achieve, are required to generate strong reproductive isolation. Here we test this hypothesis using a combination of ecological data, experimental estimates of reproductive isolation, and both reduced representation and whole genome sequence data from multiple species of herbivorous *Timema* stick insects. We find that extreme ecological shifts between conifer and flowering plant hosts are more rare than moderate host shifts between flowering plant families, but that such extreme host shifts generate stronger reproductive isolation. Despite clear effects of the magnitude of host shift on reproductive isolation, overall genomic divergence is more strongly promoted by geographic separation. In comparison, host adaptation causes heterogeneous, genomically localised genetic divergence. The results highlight the different but complementary roles of ecology and geography in driving transitions across the speciation continuum.

Session 1 WED POL B 20

The flexible genome: uncovering the regulatory basis of phenotypic plasticity. (52862)

Vicencio Oostra, Marjo Saastamoinen, Bas J. Zwaan, Christopher W. Wheat.

University College London (UK); University of Helsinki (Finland); Wageningen University (The Netherlands); Stockholm University (Sweden).

Phenotypic plasticity is the ability of a given genotype to express different phenotypes in response to environmental variation, often as adaptation to fluctuations in habitat quality. Studying the regulatory basis of plasticity provides insights into the mechanistic basis of this important adaptation, and into how genes and the environment interact to produce complex phenotypes. To study the genetic basis of plasticity we use the afrotropical butterfly *Bicyclus anynana*, which displays life history plasticity as adaptation to its habitat's wet-dry seasonality. We combine a full-sib quantitative genetics design with RNAseq, yielding transcriptome-wide estimates of gene expression variation as a function of genetic background, environment, and their interaction. We constructed a de novo assembly, yielding 7365 genes after filtering, and identified season-specific genes, as well as genes whose environmental response in expression was affected by genetic background, indicating genetic variation for plasticity at the transcriptome level. We then asked whether plasticity-related genes were depleted vs. enriched in nucleotide diversity compared to non-plastic genes, indicating constraints vs. potential for evolutionary responses. Our study provides new insights into the regulatory links between juvenile conditions and adult life history.

Session 1 WED POL B 20

Ecological genetics of local adaptation in *Arabidopsis thaliana* (52733)

Jon Ågren, Christopher G. Oakley, Sverre Lundemo, Douglas W. Schemske.

Dept of Plant Ecology and Evolution, EBC, Uppsala University, Norbyvägen 18 D, Uppsala, Sweden; Dept of Plant Biology, Michigan State University, East Lansing, MI 48824, USA .

Organisms inhabiting different environments are often locally adapted, yet in most cases the genetic and functional mechanisms of local adaptation are poorly understood. We mapped Quantitative Trait Loci (QTL) for total fitness and putatively adaptive traits, and determined the relationships between trait expression and fitness using a large RIL population derived from a cross between two locally adapted *Arabidopsis thaliana* populations, one in Italy and one in Sweden, and planted in field experiments at the parental sites for multiple years. We show that local adaptation is controlled by relatively few genomic regions of small to modest effect. A third of the 19 fitness QTL we detected showed evidence of trade-offs (locally favoured genotype reduces fitness elsewhere). Selection gradient analyses and mapping results indicated that QTL for flowering time and tolerance to cold contribute to fitness trade-offs. Sequence variation and functional analyses indicate that mutations in previously identified candidate genes may explain some of these trade-offs. Taken together, our results suggest that adaptation to markedly different environments can be achieved through changes in relatively few genomic regions, and that genetically based differences in both life history

and physiology contribute to adaptive differentiation and fitness tradeoffs among native *A. thaliana* populations.

Session 1 WED POL C 11

Individual variation in host health and its consequences for pathogen spread (52471)

Pedro Vale.

University of Edinburgh.

A major hurdle to reducing the burden of infectious disease is that individuals vary substantially in how sick they get and how sick they make others. Here I explore several sources of individual host variation and discuss its potential consequences for pathogen spread and evolution. Hosts may vary in how sick they get because of the variable use of damage limitation therapies. While these anti-virulence or tolerance-boosting drugs are promising “evolution-proof” alternatives to antimicrobials, I present some theoretical results highlighting that their use may, in some situations, lead to high prevalence of virulent pathogens. Hosts also vary in how sick they may make others, for example, when host heterogeneity in pathogen shedding is high, or when host behaviours increase the risk of infection spreading. I will discuss some experimental results of both viral and bacterial gut infections in *Drosophila melanogaster*. I explore how host genetics, sex and co-infection status may explain some of the heterogeneity in pathogen shedding, and test how key host behaviours are modified by infection. Behavioural responses during infection not only shed light on the risk of disease spread, they also reflect host health, revealing the more nuanced fitness costs of infection.

Session 1 WED POL C 11

Local adaptation to parasites suggests costs of migration and explains immunogenetic polymorphism in sticklebacks (52474)

Joshka Kaufmann, Tobias L. Lenz, Martin Kalbe, Manfred Milinski, Christophe Eizaguirre.

Max Planck Institute for Evolutionary Biology, Department of Evolutionary Ecology; GEOMAR Helmholtz Centre for Ocean Research; School of Biological and Chemical Sciences, Queen Mary University of London.

Local adaptation is often key to the process of speciation. Theory suggests that reduced fitness of migrants due to local maladaptation to foreign parasites could be sufficient to reduce gene flow between habitats and ultimately lead to speciation. Here, we experimentally investigated the relative fitness of migrants in foreign habitats, focusing on diverging lake and river ecotypes of three-spined sticklebacks. A reciprocal transplant experiment performed in the field revealed asymmetric costs of migration: while mortality of river migrants was increased under lake conditions, lake migrants suffered from reduced growth relative to river residents.

Focusing particularly on the parasitic environments, we found that macroparasite communities did not only differ between lake and river residents but also between the reciprocal migrants. This pattern of differential parasitisation had consequences for both the innate and the adaptive immune system, where multiple habitat-specific associations between parasite species and locally selected alleles of major histocompatibility immunogenes could be detected. Altogether, these experimental results highlight the role of selection against migrants in the early stages of ecological speciation and reveal complex resistance patterns leading to immunogenetic diversity at the meta-population level.

Session 1 WED POL C 11

Increased diversity at a locus involved in resistance to parasitism in *Daphnia magna* (52543)

Yann Bourgeois, Peter Fields, Gilberto Bento, Anne Roulin, Seanna McTaggart, Tom Little, Darren Obbard, Dieter Ebert.

Zoologisches Institut, Basel University; University of Edinburgh.

The study of processes that maintain adaptive genetic diversity have long interested evolutionary biologists. From this perspective, host-parasite coevolution provides valuable insights. In *Daphnia magna*, an emergent model species in epidemiology and evolutionary biology, it has been suggested that interaction with the obligate bacterial endoparasite *Pasteuria ramosa* fulfilled all the requirements for negative frequency-dependent selection to occur. Recently, a 150 kb candidate genomic region involved in resistance to *P. ramosa* has been identified in *D. magna*. This opens a new window to explore the effects of host-parasite interaction on natural adaptive variation in this system.

Here, we took advantage of the recent sequencing of dozens of *D. magna* genomes sampled across Eurasia. The candidate locus for resistance to *P. ramosa* displayed evidence for selection. We found increased nucleotide diversity in the 200 kb flanking this locus and an excess of alleles at higher frequencies compared to genomic background. At the resistance locus itself, we observed indel polymorphism, suggesting that resistance could be tuned by changes in copy number variation of resistance genes. We discuss the consistency of these patterns with selective processes leading to the accumulation of polymorphism, such as heterozygous advantage, negative frequency-dependent selection (Red Queen dynamics) and local adaptation.

Session 1 WED POL C 11

Variation in phenotypic selection on quantitative immune defence traits in a freshwater snail (52671)

Laura Langeloh, Jukka Jokela, Otto Seppälä.

Eawag; ETHZ.

Understanding how phenotypic selection acts on immune function is important for predicting the outcomes of host-parasite interactions. While ecological factors affecting the range of phenotypic variation in immune traits and infection risk may strongly influence the form and strength of selection on immune defence, they have mostly been neglected in previous research.

In this study, Great Pond snails (*Lymnaea stagnalis*) from 6 populations were maintained individually in two different environments for 9 weeks: water enriched with opportunistic microorganisms to impose an immune challenge, or clean water. Survival, shell length, reproductive output and the level of two immune parameters, phenoloxidase-like activity and antibacterial activity, were recorded from each snail every second week.

Immune activity and reproductive output of snails differed between water quality treatments and populations. Selection gradient analyses suggested differences in selection on the examined immune traits. While no difference between the two laboratory environments could be detected, selection gradients differed across populations. Strong family-level variation in both immune traits within populations suggests sufficient genetic variation for response to selection.

Session 1 WED POL C 11

Diversity and divergence of immune genes in four wild rodent species (52718)

Andrew Turner, Mike Begon, Amy Pedersen, Steve Paterson.

University of Liverpool; University of Edinburgh.

Individuals vary substantially in their resistance to infectious disease and experiments on laboratory rodents, such as the house mouse (*Mus musculus*), have proved invaluable in elucidating the mechanistic basis of this resistance. However, controlled laboratory studies provide few insights into the causes and consequences of genetic variation in the natural environment, where increased genetic diversity, multiple infections and fluctuating environmental conditions are the norm. The study of wild rodents represents an excellent opportunity to link the functional genetic knowledge gained from laboratory rodents with the variation in disease susceptibility observed in natural populations, including humans.

Here we examined diversity in >800 immune genes and ~500 size-matched, non-immune genes in four wild rodent species: house mice, wood mice (*Apodemus sylvaticus*), field voles (*Microtus agrestis*) and bank voles (*Myodes glareolus*). In all species, genetic diversity was significantly higher in immune genes. Through examination and comparison of diversity within and between individuals, populations and species, we investigate which genes have been subject to natural selection, and whether the same genes have been repeatedly targeted by selection across different populations and species. For example, positive selection appears to have driven divergence between species at multiple pathogen-recognition sites within Toll-like receptor (TLR) genes.

Session 1 WED POL C 11

Constitutive protection, mismatch, and secondary exposure in transgenerational immune memory in the bumblebee *Bombus terrestris* (52848)

Seth Barribeau, Paul Schmid-Hempel, Ben Sadd.

East Carolina University; ETH Zürich; Illinois State University.

A number of invertebrates show evidence of immune memory or priming. Individuals given cues of a parasite either as a clearable dose or an inactivated inoculum are better able to resist a subsequent exposure than naive individuals or those given a different priming immune exposure. This immune history can also be transferred across generations with offspring having increased resistance to parasites that their parents were exposed to. Since invertebrates lack the antibodies and T-cells of the adaptive immune system, the mechanisms behind such memory remain mysterious. Here we describe the full transcriptome expression profile of transgenerational immune memory in the European bumblebee *Bombus terrestris*. We found that daughters of mothers exposed to an inactivated inoculum of the Gram-positive bacterium *Arthrobacter globiformis* constitutively express all known antimicrobial peptides at much higher quantities than daughters that have no immune history. We also describe how a mismatch between immune history and exposure results in a fundamentally different expression pattern. Finally, we explore whether receiving a second exposure to a bacterial inoculum results in greater immune activation.

Session 1 WED POL C 11

Intracellular endosymbiont selection contributes to *Drosophila* adaptation to viral infection (52942)

Vitor G. Faria, Nelson E. Martins, Sara Magalhães, Viola Nolte, Christian Schlötterer, Luis Teixeira, **Élio Sucena**.

Instituto Gulbenkian de Ciência, Oeiras, Portugal; Centre for Ecology, Evolution and Environmental Changes, Faculdade de Ciências, Universidade Lisboa; Institut für Populationsgenetik, Vetmeduni Vienna, Austria; Departamento de Biologia Animal, Faculdade de Ciências da Universidade de Lisboa, Lisboa, Portugal.

Bacteria of the genus *Wolbachia* are intracellular symbionts of many animal species. In *Drosophila*, *Wolbachia* has been shown to confer protection to RNA virus infection in a strain-dependent manner. Through experimental evolution, we have selected an outbred *Wolbachia*-infected population of *D. melanogaster* for increased resistance to DCV, a natural viral pathogen. Whole-genome sequencing of this population, upon 20 generations of selection, revealed that a *Wolbachia* sub-strain was fixed. Moreover, we show that challenged inter-population hybrids carrying either *Wolbachia* variant differ in their fitness, confirming the adaptive value to the host of selected endosymbiont. Finally, we re-assess host genome evolution upon *Wolbachia* clearance and DCV infection over 20 more generations. These findings demonstrate that the presence of protective endosymbiont plays a role in shaping the host genome and its own evolution may have a profound effect on host adaptation.

Sexual conflict and social behaviour (52776)

Tracey Chapman.

University of East Anglia.

The intensity of sexual conflict over the level of expression of any reproductive trait value or behavior can be assessed by measuring its costs and benefits, in terms of lifetime fitness, for individuals of each sex. Though relatively underexplored, outcomes of sexual interactions between males and females can be viewed in terms of the wider context of social behaviors: i.e. Hamilton's famous quartet of social behaviors: mutual benefit (co-operation), selfishness, altruism and spite. Here I discuss how we can reclassify the outcome of interactions between males and females in this way. This reveals the potential for evolutionary disagreements between the sexes, and therefore sexual conflict, in all four types of social behavior classification – particularly so for selfish behavior. Central to this understanding is to clarify the meaning of costs and benefits in terms of positive or negative fitness consequences for males and females. Such fitness effects can be direct or indirect and although we expect sexual conflict to be low when relatedness is positive, it can still occur. I will discuss sexual conflict within this framework and provide examples.

Inclusive fitness and sexual conflict (53362)

Andy Gardner.

University of St Andrews.

I will provide an overview of the theory of inclusive fitness and explore its application to the study of sexual conflict.

The influence of relatedness on male entomopathogenic nematode aggression (51661)

Apostolos Kapranas, Maher Abigail, **Griffin Christine.**

National University of Ireland, Maynooth.

Males of entomopathogenic nematodes *Steinernema* spp. engage in aggressive contests that are fatal to losers. Previous studies suggest that males deriving from infective juveniles (IJ),

the free foraging stage that enters the insect host, are more aggressive. Theory predicts that, in closed systems with limited dispersal, intense competition should override any benefits of kin or at least higher aggression should be expected in mixed groups of relatives and non-relatives than in groups consisting solely of relatives or of unrelated animals (a dome –shaped effect). In this study, we examined how both relatedness and group size affect mortality rates among these post-IJ males in both semi-natural and natural conditions. We found that mortality rates are affected both by relatedness and group size. We discuss our findings in the context of current theory and also taking into account certain key life history characteristics of Steinernematid nematodes such as inter-specific competition and group dispersal. Entomopathogenic nematodes can provide new opportunities for testing the conflicting influence of competition and relatedness.

Session 1 WED MAX 415 7

Local mate competition mediates sexual conflict over sex ratio in a haplodiploid mite (51846)

Sara Magalhaes, Emilie Macke, Isabelle Olivieri.

CE3C: Centre for Ecology, Evolution and Environmental Changes; Aquatic Biology, IRF Life Sciences, Science & Technology, KU-Leuven; Institut des Sciences de l'Evolution de Montpellier, Université Montpellier 2.

In haplodiploids, females pass their genes on to all their offspring, whereas a male's genes are only passed on to his daughters. Hence, males always benefit from female-biased sex ratios, whereas for females the optimal offspring sex ratio depends on the level of local mate competition (LMC), ranging from highly female-biased under strict LMC to unbiased in panmixia. This generates a sexual conflict over sex ratio, the intensity of which depends on the LMC level, with most intense conflict in panmixia. Such conflicts might lead to an evolutionary arms race, with persistence traits evolving in males and resistance traits in females. Although this prediction is theoretically straightforward, it remains untested empirically. We addressed this by crossing spider mites that evolved under varying intensities of LMC (hence of sexual conflict), to mates from inbred lines. Under high levels of sexual conflict, both sexes evolved manipulative traits to shift the sex ratio to their own advantage. In females, this was partly achieved through changes in egg size. We thus show that (a) LMC levels modulate sexual conflict over sex ratio in haplodiploids, driving the evolution of manipulative traits and (b) fathers can affect sex ratio, challenging conventional assumptions.

Session 1 WED MAX 415 7

Male *Drosophila melanogaster* fight more, and sire shorter-lived daughters, when rival male are unrelated and unfamiliar (51991)

Pau Carazo, Jennifer Perry, Fern Johnson, Tommaso Pizzari, Stuart Wigby.

University of Valencia; University of Oxford.

Competition over access to reproductive opportunities can lead males to harm females. Recent inclusive fitness theory predicts that in structured populations male harm of females may be reduced when local male competitors are related. Previous empirical work has presented evidence consistent with this prediction in the fruit fly, *Drosophila melanogaster*. Here we explore the consequences of relatedness amongst rival males for the next generation. We show that groups of unrelated-unfamiliar (i.e. raised apart) males fight more intensely than groups of related-familiar (i.e. raised together) males, consistent with previous findings, and that exposure to a female is required to trigger kin-biased male-male competition. We further show that differences in male-male competition are associated with transgenerational effects: when daughters were themselves exposed to males, daughters of females exposed to unrelated males suffered higher mortality than the daughters of females exposed to related males. Collectively, these results support the hypothesis that within-male group relatedness and/or familiarity can modulate male-male competition with important transgenerational consequences.

Session 1 WED MAX 415 7

How sex-biased dispersal affects the resolution of intralocus sexual conflict (52922)

Bram Kuijper, Rufus A. Johnstone.

*Department of Genetics Evolution and Environment, University College London, UK;
CoMPLEX, Centre for Maths & Physics in the life sciences, University College London, UK;
Department of Zoology, University of Cambridge.*

Classical models on intralocus sexual conflict assume large and well-mixed populations, raising the question whether predictions extend to structured populations with interacting relatives. Here we present a model of intralocus sexual conflict in a spatially structured population with sex-biased dispersal. Strikingly, we find that sexually antagonistic traits that are beneficial to females (and detrimental to males) predominate in populations with female-biased dispersal, while male-beneficial traits prevail in populations with male-biased dispersal. For the case where females are the more dispersing sex, this can be explained by noting that philopatric males are more related than dispersing females to any juveniles in the local patch. Hence, in dying, males are more likely to be replaced by relatives than females, so that the effective cost of expressing a detrimental sexually antagonistic trait is lower for males than females. As a result of reduced selection in males, the trait evolves towards the female rather than the male optimum. In the presence of mating skew, a similar principle holds, which causes characters to evolve towards the optimum of the sex that endures the strongest competition for matings. Our findings show that the ecological context of sexual antagonism is more important than hitherto anticipated.

Session 1 WED POL D 33

Artiodactyl limb diversification: attenuated sensing of SHH by Ptch1 underlies adaptive evolution of bovine limbs (52537)

Rolf Zeller, Javier Lopez-Rios, Amandine Duchesne, Dario Speciale, Guillaume Andrey, Kevin A. Peterson, Carol Wicking, Andrew P. McMahon, Denis Duboule.

University of Basel; INRA Genetique Animale et Biologie Integrative; EPFL Lausanne and University of Geneva; University of Southern California; The University of Queensland.

A fascinating aspect is to understand how basic and robust patterning processes are altered to allow diversification. For example, the pentadactylous blueprint of the limb skeleton has been modified extensively and allowed adaptation to different habits during tetrapod evolution. Cursorial animals such as artiodactyls have modified their distal limb skeleton for fast running by reduction and loss of digits in conjunction with assuming unguligrade posture. Molecular analysis of mouse and bovine limb development reveals the progressive loss of anterior-posterior polarity in bovine limb buds. These alterations are caused by a failure to up-regulate *Ptch1* expression in the bovine limb bud mesenchyme, which renders the progenitors insensitive to graded SHH signaling. Functional genomics identified a cis-regulatory module (CRM) within the *Ptch1* locus that controls expression in the mouse limb bud mesenchyme. Strikingly, the orthologous bovine sequences are unable to activate expression in transgenic mouse embryos, establishing that the bovine CRM has degenerated. In fact, genetic inactivation of *Ptch1* in the mouse limb mesenchyme phenocopies molecular differences seen in bovine and pig limb buds. Currently, we are investigating if a microsatellite expansion in the CRM region of all artiodactyls contributes to its functional degeneration in Bovidae and other artiodactyls such as Suidae.

Session 1 WED POL D 33

Selection on flower colour in snapdragon hybrid zones (52539)

David Field, Hugo Tavares, Enrico Coen, Nick Barton.

IST Austria; John Innes Centre.

A major goal of evolutionary biology is to understand how diverging populations become distinct species. Much progress has been made in characterising genomic differentiation and the genes that contribute towards phenotypic differences and reproductive isolation. However, directly linking genes to phenotypes to fitness and reproductive isolation in nature has proved challenging. We address this gap in a uniquely tractable plant system, *Antirrhinum* (snapdragons). In this system, two subspecies with different flower colour give rise to four hybrid phenotypes across narrow hybrid zones. Flower colour is under simple genetic control, allowing us to track individuals, their phenotypes and underlying genes through space and time. Whole genomes sampled across the hybrid zone show the highest regions of genomic differentiation are located around the genes that control flower colour. The existence of steep clines for flower colour and diagnostic SNPs linked to the underlying genes indicates selection against some recombinant phenotypes. A detailed multi-generational pedigree is used to directly measure the reproductive success of the major phenotypes and determine the fitness landscape for interacting flower colour genes. By linking divergent genomic regions to phenotypic traits and how they directly influence fitness in nature, we provide an integrated understanding of the speciation process.

Adaptation to a special environment: a novel endosymbiotic bacterium living inside an ant (52725)

Antonia Klein, Lukas Schrader, Rosario Gil, Alejandro Manzano-Marín, Laura Flórez, Martin Kaltenpoth, Amparo Latorre, Andrés Moya, Jan Oettler.

Institute of Zoology/Evolutionary Biology, University Regensburg, Germany; Institut Canvanilles de Biodiversitat i Biologia Evolutiva, Universitat de Valencia, Spain; Max Planck Institute for Chemical Ecology, Jena, Germany.

Bacteria are ubiquitous in nature and have evolved uncountable adaptations to the environment. For example, so called endosymbionts live inside eukaryotic hosts. Endosymbionts often evolve mutualistic associations with their hosts, where they provide novel ecological traits to the host and in return are maintained in a sheltered environment. We discovered a novel intracellular bacterial symbiont of the invasive ant *Cardiocondyla obscurior*, ‘*Candidatus Westeberhardia cardiocondylae*’ and provide a first characterization of its association with the ant host. *Westerberhardia* shows substantial genome reduction, a typical feature of endosymbionts. Metabolic pathway analyses of the *Westerberhardia* genome, localization of *Westerberhardia* via FISH in bacteriomes and an increase of the symbiont in the pupal stage, suggest provisioning with tyrosine precursors during metamorphosis for the host’s cuticle built up as the basis of the mutualism. After hatching of the host the gut-associated bacteriomes degrade but queens maintain *Westerberhardia* in their ovaries for vertical transmission, whereas bacterial populations in adult workers and males degenerate with age. With the discovery of a naturally symbiont-free host population we have discovered a suitable system for studying ant-bacteria co-adaptation in the future.

The hemoglobin repertoire in the order of Gadiformes linked to depth adaptation (52770)

Helle Tessand Baalsrud, Ole Kristian Tørresen, Martin Malmstrøm, Walter Salzburger, Kjetill Sigurd Jakobsen, Sissel Jentoft.

University of Oslo; University of Basel.

Gene and genome duplications can promote evolutionary invention by releasing the copied genetic region from functional constraints. Natural selection acting on the new gene can result in sub-/neofunctionalization or gene loss. In teleosts, the number of hemoglobin genes varies extensively between and within lineages. This observed phenomenon is likely driven by natural selection as environmental factors such as temperature and oxygen partial pressure, which in turn depends on water depth, influence the oxygen carrying properties of hemoglobin. In the order of Gadiformes (cods and allies), species have adapted to an array of ocean depths, and it has been hypothesized that the ancestor originated from a deep-water

fish.

Here we use whole genome sequencing of 27 species to characterize the hemoglobin repertoire across this lineage. By using ancestral reconstruction and tests of natural selection we unveil that hemoglobin may have been key for the evolutionary transition from a deep-water fish to a diversity of species occupying the entire water-column, and could be involved in ecological speciation in this lineage.

Session 1 WED POL D 33

Molecular structure and functional diversity of a naturally polymorphic enzyme: PGI of *Colias* (52771)

Jason Hill, **Ward Watt**.

Stockholm University; University of South Carolina.

Reproductive success in flying insects is heavily dependent on an effective core metabolic pathway, glycolysis, in responding to rapidly fluctuating energy demands. The glycolytic enzyme phosphoglucose isomerase, PGI, is extensively polymorphic in *Colias* (Lepidoptera, Pieridae), and its polymorphs' genotypic functional differences successfully predict performance and fitness differences in the wild. The structural basis for this functional diversity has not been studied directly until now. We produced a high-resolution crystal structure for *Colias* PGI, and then used that native structure as a template to carry out 50 nanosecond molecular dynamics simulations for different allozymes of PGI. These simulations were coupled with enzyme kinetics measurements of catalytic function and thermal stability in an attempt to match structural differences between the allozymes with biochemically measured functional differences. Kinetics analysis confirmed the already known tradeoff in thermal stability vs. catalytic function in homodimers that maintains polymorphism within species and has identified the most likely mutational path between the fixed difference that separates the alpine *C. medii* and lowland *C. eurytheme*.

Session 1 WED POL D 33

The genetic basis of parallel speciation in a marine snail (52944)

Anja Marie Westram, Marina Panova, Juan Galindo, Roger Butlin.

University of Sheffield; University of Gothenburg; University of Vigo.

Parallel divergence can provide strong evidence for the role of divergent selection. However, despite parallel phenotypic evolution, loci potentially affected by selection ('outlier loci') are often not shared among geographical locations, suggesting different underlying molecular mechanisms. Alternatively, low sharing might emerge if many outliers are spurious. Low outlier sharing has e.g. been observed in the marine snail *Littorina saxatilis*, which has evolved two ecotypes - adapted to wave exposure vs. crab predation - repeatedly in Sweden,

Spain and the UK. Using capture sequencing, we re-sequenced candidate outlier and control loci in snails from two locations per country. We predicted that, if observed patterns of outlier sharing are genuine, sharing should increase on smaller geographical scales, where genetic variation is more similar and gene flow is higher. If they are caused by spurious outliers, sharing should be low even among geographically close populations, and outliers should often not be confirmable.

We found that the majority of outliers could be confirmed, and outlier sharing increased markedly among geographically close populations. Therefore, low sharing between countries is not solely due to technical reasons but can be explained by separate evolutionary histories and / or less gene flow among geographically distant instances of divergence.

Session 1 WED GEN B 35

Drosophila wing shape Integration: A multi-level approach. (52027)

Hugo Benitez, Chris Klingenberg.

University of Manchester.

Different levels of biological variation are generated from distinct sources: genetic, developmental and evolutionary variation. These levels of variation interact in morphology, being for instance observed in how correlated or independent are different traits with respect to each other. The following study applies morphometric methods in order to address questions about *Drosophila* wing shape at three levels of integration: static, developmental and evolutionary. Static integration refers to the level variation among individuals, where all specimens are at the same ontogenetic stage and belong to the same species; developmental integration is produced from the interactions between developmental processes that generate different features, and evolutionary integration is simply the covariation among evolutionary changes considering the phylogenetic structure of the data. We develop this approach in an analysis of wing evolution in 58 species across the genus *Drosophila*. The present results show that all the 58 *Drosophila* species exhibit morphological integration. Wing shape showed a noticeable developmental integration both as an overall structure and between developmental compartments. In addition, a clear evolutionary integration of wing shape was found. It is possible to conclude that wing shape shows strong internal covariation, and that the integration process has evolved in the genus.

Session 1 WED GEN B 35

The evolution of cuticular hydrocarbon profiles in ants (52700)

Thomas Schmitt, Bonnie Blaimer, Florian Menzel.

University of Würzburg; Smithsonian Institution; University of Mainz.

Insect cuticles are covered with hydrocarbons (CHC), which serve two main functions: desiccation barrier and information transfer. The CHC profiles of ants carry information on

their species identity, colony, caste, sex, etc. Intraspecific variation is usually restricted to quantitative changes in hydrocarbon composition, whereas interspecific variation is characterized by qualitative alterations i.e. variation in substance identities and substance classes. To date, little is known about the evolutionary causes of interspecific CHC variation. Moreover, we do not understand the role of phylogenetic or physiological constraints on CHC evolution. Here, we analysed the CHC profiles of 37 *Camponotus* and 39 *Crematogaster* species from around the world. CHC profiles did not appear to experience strong phylogenetic constraints. Even sister species could exhibit completely different profiles. However, we identified several physiological constraints which might be caused by the need to maintain a semiliquid texture of the epicuticular layer. Climate strongly influenced substance class composition. We explain this by variance in waterproofing requirements. Interestingly, the length of the hydrocarbon chains was not affected by climate, but was extended among ants in interspecific mutualistic associations. We conclude that CHC profiles can evolve quickly, but experience constraints posed by climatic conditions, interspecific interactions, and their physico-chemical properties.

Session 1 WED GEN B 35

Queen signalling in the honeybee (52838)

Thomas Richardson.

University of Lausanne.

In complex animal societies in which there is a reproductive division of labour, the reproductively-active individuals sometimes produce signals that advertise their fertility. In the eusocial insects, mated and reproducing queens produce queen pheromones, which can act to inhibit selfish worker reproduction, and suppress worker rearing of virgin queens.

Although the debate concerning the ultimate explanations for the evolution of queen pheromones – and in particular, whether they should be classed as honest or manipulative signals – has yet to produce a clear consensus, both hypotheses predict that mechanisms that govern the dissemination of the queen signal should preferentially target (i) older workers with functioning ovaries, as these workers have the potential to selfishly lay unfertilized eggs, and (ii) young nurse workers, as it is these workers that control the rearing of virgin queens.

Using a system for simultaneously and automatically tracking the movements of thousands of honeybees, we characterise the ages of the workers targeted by three different pathways for queen pheromone dissemination, (i) direct transmission from queen to workers via physical contacts, (ii) indirect transmission via so-called 'messenger' bees, and (iii) indirect transmission via the wax.

Session 1 WED GEN B 35

Transcriptomic underpinning of lifespan differentiation between castes in ants. (52081)

Eric Lucas, Oksana Riba-Grognuz, Miguel Corona, Yannick Wurm, Laurent Keller.

University of Lausanne; USDA; Queen Mary University of London.

Senescence presents an evolutionary puzzle: why have organisms not evolved to avoid the age-linked degeneration which occurs in most species? The disposable soma theory argues that senescence is governed by a trade-off between longevity and other life-history traits. Ants provide an excellent model for studying the evolution of senescence as they are typically characterised by extreme variation in lifespan between castes, with queens living as much as 15 times longer than workers despite being genetically identical. Furthermore, ant queens are amongst the longest-living insects, with *Lasius niger* queens living up to 29 years. Using tissue-specific high-throughput RNA sequencing of age-controlled individuals, we tested whether queens and workers of *L. niger* differ in their expression of genes involved in somatic maintenance. We found that queens over-express these genes relative to workers, but in an age-dependent manner. The difference in lifespan between castes therefore seems to stem from differential investment into maintenance at specific life stages.

Session 1 WED GEN B 35

Adaptive landscapes of transcription factor binding sites (52693)

José Aguilar-Rodríguez, Joshua L. Payne, Andreas Wagner.

University of Zurich, Inst. of Evolutionary Biology and Environmental Studies, Zurich, Switzerland; Swiss Institute of Bioinformatics, Lausanne, Switzerland; The Santa Fe Institute, Santa Fe, New Mexico, USA.

The adaptive landscape is a central concept in evolutionary theory. Recent advances in high-throughput technologies have provided us with a first glimpse at the structure and navigability of a few incomplete empirical landscapes. Here, we have studied more than one thousand complete and empirical adaptive landscapes. Each landscape describes the binding specificity of a transcription factor to all possible short DNA sequences. The architecture of such landscapes has important implications for evolution, as a transcription factor's specificity for its cognate binding site determines its influence on gene expression. We find that the adaptive landscapes of transcription factor binding specificities are far less rugged than randomized landscapes and only slightly more than additive landscapes. They contain few peaks that are accessible from throughout the landscape. These peaks do not usually comprise single sites but broad plateaus that can contain dozens to hundreds of sites, indicating the robustness of highly specific binding to mutations. The binding sites found in more accessible peaks are enriched in protein-bound regions of the mouse genome. Our findings suggest that the navigability of transcription factor binding landscapes and the robustness of their peaks may have contributed to the enormous success of transcriptional regulation as a means to achieve novel phenotypes.

Session 1 WED GEN B 35

Why shuffle genes? The dynamics of integron evolution in changing environments (52620)

Jan Engelstädter, Klaus Harms, Pål Jarle Johnsen.

University of Queensland; University of Tromsø; University of Copenhagen.

Integrons are widespread genetic elements in bacteria that function as gene capture and reshuffling devices. They consist of an array of gene cassettes (often encoding antibiotic resistance determinants), and a gene encoding an integrase that can excise and re-insert gene cassettes. In spite of their importance in clinical contexts, little is known about the evolutionary origin and maintenance of integrons.

Here, we present a mathematical model in which bacteria with and without a functional integrase compete with each other. The population is subject to a number of stressors that arise stochastically and to which the different gene cassettes provide resistance. In bacteria carrying a functional integrase, the order of the gene cassettes within the integron is reshuffled, which in turn affects their gene expression patterns.

Our model predicts that for a wide range of realistic parameters, a functional integrase can prevail in the population in spite of substantial fitness costs. Similarly to mutator genes, this advantage comes about through increasing genetic diversity within the population and is strongest when environmental conditions change at intermediate rates. We also show that under some conditions a functional integrase can prevent population extinction and explore how new integrons can emerge through horizontal gene transfer.

Session 1 THU GEN C 4

Comparing within and between-sex pleiotropy as constraints on the evolution of male and female gene expression (53323)

Stephen Chenoweth.

The University of Queensland.

Sex-specific selection is widely thought responsible for shaping multiple genomic patterns of sexually dimorphic gene expression. It is well recognised that simultaneous adaptation in males and females can be curtailed whenever alleles controlling regulatory variation have sexually-antagonistic pleiotropic effects. However, pleiotropy between the sexes is but one form pleiotropic constraint, and it may be the case that other forms, such as pleiotropy between genes co-regulated within each sex, contribute greater constraining effects on the evolution of male and female gene expression. In an attempt to address this, I will integrate results across our recent quantitative genetic studies of sex-specific fitness and gene expression, within and among natural populations of the fly, *Drosophila serrata*.

Session 1 THU GEN C 4

Sexually antagonistic epigenetic marks (53333)

William Rice.

The sexes share the same autosomal genomes yet sexual dimorphism is common due to sex-specific gene expression. When present, XX and XY karyotypes trigger alternate regulatory cascades that determine sex-specific gene expression profiles. In mammals, secretion of testosterone (T) by the testes is the master switch influencing the gene expression pathway (male vs. female) that will be followed, but many genes have sex-specific expression prior to T secretion. Environmental factors, like antiandrogens, can disrupt sexual development. However, sex-specific ontogeny can be canalized by the production of epigenetic marks (epi-marks) produced during early ontogeny that increase sensitivity of XY embryos to T and decrease sensitivity of XX embryos. Here I will integrate and synthesize the evidence indicating that canalizing epi-marks are produced during early ontogeny. I will also describe the evidence that such epi-marks sometimes carry over across generations and produce mosaicism in which some traits are discordant with the gonad. Such carry-over epi-marks are sexually antagonistic because they benefit the individual in which they were formed (via canalization) but harm opposite-sex offspring when they fail to erase across generations and produce gonad-trait discordances.

Session 1 THU GEN C 4

Resource competition and the evolution of sexual dimorphism (51570)

Stephen De Lisle, Locke Rowe.

University of Toronto; University of Toronto.

Theory suggests the evolution of sexual dimorphism in ecologically relevant traits can evolve purely through competition between the sexes for a shared resource. Although more parsimonious hypotheses exist for the evolution of ecological sexual dimorphisms, there are some underappreciated reasons to expect that resource competition may often play some role in the evolution of sexual dimorphism. Here, we outline a set of minimal criteria for empirically demonstrating a role for resource competition in the evolution of dimorphism. Using a series of experiments, we compare the geometry of fitness surfaces across density and sex frequency manipulations in a pond-breeding salamander (*Notophthalmus viridescens*). We find consistent disruptive selection on multivariate sexual dimorphism in feeding morphology, that increases in strength with density. Fitness and the strength of divergent selection are negative-frequency dependent in the manner expected under competition-driven divergence between the sexes. Taken together, our results constitute evidence of resource competition between the sexes as a contributor to sexually antagonist selection and the evolution of sexual dimorphism. We suggest that resource competition may often contribute to sexual divergence jointly with selection stemming from anisogamy, especially when ecological opportunity is sex-specific

Session 1 THU GEN C 4

Sexual selection drives short- and long-term evolution of the avian Z chromosome (51711)

Alison Wright, Peter Harrison, Fabian Zimmer, Stephen Montgomery, Marie Pointer, Judith Mank.

University College London; University of Oxford.

Comparisons between sex chromosomes and autosomes are important for understanding the magnitude of sexual conflict acting throughout the genome. We investigated the role of sexual selection in shaping gene expression and coding evolution of the Z chromosome in the Galloanserae, a clade of birds with the full range of sexual selection. Our results reveal that over long-term evolutionary history, the Z chromosome has been convergently and successively masculinized (Wright et al. 2012 Genetics), consistent with theoretical predictions that Z-linked genes should be more often selected for male-benefit alleles due to their unequal inheritance pattern. We next examined the role of mating system in driving masculinization of the Z chromosome over shorter evolutionary timespans, using phylogenetically controlled comparisons among species with high and low levels of sexual selection. Our results, combining coding sequence, polymorphism and gene expression with phenotypic measures of sexual selection, indicate that variance in male reproductive success in promiscuous species reduces the effective population size of the Z chromosome (Wright et al. in review), leading to relaxed purifying selection acting on the coding content. This in turn limits the adaptive role of the Z chromosome in general, and in particular its potential role in encoding sexually selected traits.

Session 1 THU GEN C 4

Insights on Sexually Antagonistic Selection in the Human Genome (51817)

Elise Lucotte, Romain Laurent, Evelyne Heyer, Laure Ségurel, **Bruno Toupance**.

Muséum national d'Histoire Naturelle; Max Planck Institute for Evolutionary Anthropology.

Sexually antagonistic selection can occur when, within a species, the two sexes have different fitness optima for a trait. If a trait under sexually antagonistic selection is encoded by the same set of genes in the two sexes, an Intralocus Sexual Conflict (IASC) can arise, leading to the evolution of sexual dimorphism. A classical theoretical model predicts that the X chromosome should be a hotspot for the accumulation of loci under IASC, as compared to the autosomes. Although numerous studies have been conducted to test this hypothesis, they provided conflicting results and, so far, no study attempted to map loci under IASC at the genome-wide level in natural populations. Here, we designed a methodological framework to detect loci under IASC using genomic data. Applying this method on a human genome-wide SNP dataset (HapMap, 11 worldwide populations), we show that SNPs exhibiting signatures of ongoing IASC are preferentially located on the X chromosome as compared to autosomes. Moreover, they are enriched in genes involved in the determination of traits known to be sexually dimorphic in humans, including external appearance, metabolism and immune system, supporting an implication of sexually antagonistic selection in the evolution of sexual dimorphism.

Genetic architecture of aggression and cooperation in the California harvester ant *Pogonomyrmex californicus* (52324)

Juergen Gadau, Jennifer Fewell, Alexander Mikheyev.

Arizona State University; Okinawa Institute of Science and Technology.

Aggression is an adaptive behavior that is shown in many different contexts in solitary and social organisms. The regulation of aggression, when, where and how much aggressive behavior is shown, is however an important component that determines whether aggression is adaptive or non-adaptive. Abnormal/non-adaptive aggression in humans is often associated with psychological disorders that are based on an underlying genetic predisposition that can be elicited by a diverse array of environmental factors. Newly mated queens of *P. californicus* found nests either alone (haplometrosis) or in groups of unrelated yet cooperative individuals. This population differences have a strong genetic basis that manifests itself in significant differences in aggression and conflict escalation during colony founding when queens of the haplometrotic population are paired artificially with queens of their own or the pleometrotic population. We studied the genetic and regulatory mechanisms of aggression and, by corollary, cooperation by comparing the differences in brain gene expression profiles of aggressive and non-aggressive *P. californicus* foundresses. This allowed shed further light on the evolution of both social phenotypes in *P. californicus*, and the genetic and regulatory basis of aggression and cooperation.

Convergent molecular signatures of plastic phenotypes in eusocial evolution (53354)

Seirian Sumner.

School of Biological Sciences, Bristol Life Sciences Building, University of Bristol.

Convergent phenotypes are apparent across the tree of life, despite contrasting evolutionary histories, ecologies and selection pressures. To what extent does convergence at the phenotypic level reflect convergence at the molecular level? To address this we sequenced and compared the genomes and 23 brain transcriptomes of two eusocial insect species with simple societies, the paper wasp *Polistes canadensis* and the dinosaur ant *Dinoponera quadriceps*. Both exhibit simple, behavioural castes with comparable highly plastic phenotypes, but the wasp evolved from a solitary ancestor, representing basal eusociality, whereas the ant evolved via a secondary reversion from a complex eusocial ancestor. We found evidence of shared molecular traits associated with phenotypes that are likely to be hallmarks of simple eusocial castes, irrespective of evolutionary history, and putative molecular signatures of plastic phenotypes. These included little molecular differentiation between castes at the gene, network, regulatory or functional level; molecular specialization

in queens but not workers; a role for both conserved and taxon-restricted genes in phenotypic differentiation. We also found molecular traits specific to the wasp that are putative signatures of basal eusocial evolution and included absence of worker-biased transcription, reflecting the generalist behavioural strategies of subordinate social animals. Ant-specific traits we found that are likely to be remnants of inherited complex eusociality included equal transcriptional investment in castes, increased molecular differentiation and role for taxon-specific genes. Identifying the contrasting, as well as conserved molecular processes that underlie convergent phenotypes has the potential to unlock the pathways by which evolution repeatedly solves recurring problems.

Session 1 THU MAX 410 24

Bold individuals live in risky environments: nature, nurture or both? (51807)

Benedikt Holtmann, Shinichi Nakagawa.

University of Otago.

A new hypothesis states that animals choose their habitats according to their personality (phenotypic habitat-selection hypothesis). If sensitivity to predation risk (e.g. shy or bold) exists and if the environment is heterogeneous, this hypothesis predicts that variation in personality would be maintained. Yet, a traditional view is that animals become adjusted to their chosen habitat after settling (habituation hypothesis). This hypothesis predicts that individuals change their levels of responsiveness to predators over time. Here, we test these contrasting hypotheses using a population of dunnocks (*Prunella modularis*) in a public park where human disturbance risk is heterogeneous over space but constant over time. We found that boldness (i.e., flight-initiation distance) was highly repeatable. Bold birds were found in most disturbed areas while shy birds were found in least disturbed areas. In contrast vigilance was more plastic and birds became less vigilant over time. Although these findings support both hypotheses, clearly, personality plays an important role in habitat selection. We also detected a strong behavioural syndrome between boldness and vigilance, highlighting the importance of examining traits with different degrees of flexibility together. In addition, we investigated associations between boldness and the two candidate genes: DRD4 and SERT (dopamine and serotonin receptor genes).

Session 1 THU MAX 410 24

Direct and indirect genetic effects shape the social phenotype of great tits (52114)

Reinder Radersma, Joshua A. Firth, Colin J. Garroway, Bernhard Voelkl, Ben C. Sheldon.

Edward Grey Institute of Field Ornithology, Department of Zoology, University of Oxford, UK; Département de Sciences Biologiques, Université de Montréal, Canada.

Many animals regularly engage in interactions with conspecifics. Because those interactions can have fitness consequences, there is scope for selection on social traits. For selection to operate traits need to have a heritable component; however, we know little about the genetic basis of social traits. Here we estimate heritability of social traits derived from six large social networks of foraging great tits (*Parus major*) from one pedigreed population in six winters. Networks consisted of 753-1,166 individuals engaging in 12,740-132,143 flocking events each winter. We derived three social traits from association indices: gregariousness, unevenness of relationships and clustering. Because individuals affect each other's social phenotypes, the heritability of social behaviour is potentially overestimated. To account for this we introduced indirect genetic and environmental effects in the models. We found within-individual repeatabilities of 34-46% when we did not account for indirect effects and 27-35% when accounting for indirect effects. Heritabilities were 13-17% without indirect effects and 12-14% with indirect effects. We show that indirect genetic and environmental effects can shape the social phenotype. As social selection may act faster and more efficiently than other forms of selection, this study opens up a new perspective on the evolution of social behaviour.

Session 1 THU MAX 410 24

Baffling: an alternative signalling strategy using self-made tools (52122)

Rittik Deb, Rohini Balakrishnan.

Centre for Ecological Sciences, Indian Institute of Science.

In order to reduce the costs of finding mates animals often use different modes of communication. From the sexual selection perspective, the general trend has been that males advertise (signal) and females respond. These signals are also used by males for intra-sexual competition and by females to choose between males. One of the consequences of inter-male competition and female choosiness has been the evolution of alternative strategies. Often these are simple behavioral modifications but occasionally involve extraordinary tools and complex behavioral patterns. In our study species, a tiny tree cricket, *Oecanthus henryi*, it was found that though the dominant strategy was to call from leaf edge to attract females, some males have evolved an alternative signalling strategy. This strategy encompassed making and use of a complex tool (a precise acoustic baffle) that enhanced their communication efficiency. Field observations and controlled experiments revealed that though all males could make baffles, very few males implemented this strategy in the wild. Following this we examined who were the males that were adopting this strategy and what were their advantages (proximate and ultimate). Further ecologically relevant experiments and simulations were conducted to understand the ecological context and evolution of such an alternative behavioral strategy.

Session 1 THU MAX 410 24

The influence of age and gene expression on division of labor in a social insect (52144)

Philip Kohlmeier, Foitzik Susanne, Feldmeyer Barbara.

Johannes Gutenberg University Mainz.

In complex societies of eusocial insects, workers specialize in certain tasks. Whether an individual acts as a forager or a nurse depends on the colony's needs and is modulated by individual variation in task thresholds. These are influenced by the expression of behavioral genes, which in turn are affected by age, physiology, and environmental factors, among others. For example, old honeybee workers are more likely to forage than younger individuals showing lower titers of vitellogenin but higher expression of octopamine. However, how these factors interact, influence behavioral gene expression, and finally determine behavior, is poorly understood. To disentangle them, we manipulated colony composition in the ant *Temnothorax longispinosus* to control for worker age and task requirements. Behavioral observations revealed that young workers focus on inside tasks, whereas older individuals take over foraging. However, in manipulated colonies, old workers responded to the young worker removal by increasing their brood care activity, whereas in the reverse case young workers failed to switch to foraging. Whole transcriptomes of designated brood carers and foragers of both ages were then analyzed using RNA-Seq. We here report on the results of behavioral observations and on the genes and functional categories associated with behavioral caste and age.

Session 1 THU POL A 32

How likely is rapid adaptation? Lessons from eco-evolutionary population modelling (53338)

Katja Schiffrers.

Biodiversity and Climate Research Centre (BiK-F).

Recent evidence for rapid adaptive changes in populations exposed to environmental change suggests that projections of species range dynamics based on the premise of ecological niche conservatism may be overly pessimistic. However, eco-evolutionary theory has shown that there exist a number of genetic and demographic constraints that may hamper rapid adaptation and evolutionary rescue. To evaluate the importance of adaptive processes for species' range dynamics, we need to better understand the coupling between ecological and evolutionary processes.

In this talk, I will present two studies based on stochastic simulations of joint allelic and demographic dynamics of spatially-structured populations that examine the prerequisites for evolutionary adaptation. The first study evaluates the equivocal effects of dispersal in heterogeneous habitats on a population's evolutionary potential under changing climate. The second one explores how landscape structure and genetic architecture jointly drive rates of niche evolution. Results of both studies demonstrate the high sensitivity of adaptive processes to genetic, demographic and environmental factors and show that a multitude of prerequisites have to concur to allow populations to rapidly adapt to new environmental conditions.

Mapping life-cycle phenology of plant genotypes in space and time (53572)

Liana Burghardt, C. Jessica E. Metcalf, Amity M. Wilczek, Daniel E. Runcie, Johanna Schmitt, Kathleen Donohue.

Duke University.

Predicting how the environment affects the expression of genetic variation remains a perennial challenge to evolutionary ecologists. We have developed a model that predicts environment-dependent timing of plant life-stage transitions and life-cycle expression. Life-cycle expression strongly influences fitness because it determines the environmental conditions to which each differentially tolerant life stage will be exposed. This model, parameterized for *A. thaliana*, generates predictions of whole life-cycle phenology of different genotypes in complex environments. First, we simulate life cycles in four locations and compared multiple “genotypes” by varying two parameters associated with natural genetic variation in phenology: seed dormancy and floral repression. The model predicts variation in life cycles across locations that qualitatively matched observed natural phenology and suggests that dormancy variation across the range is necessary to maintain an annual life cycle. We also use this framework to predict the reproductive environment *A. thaliana* is exposed to across the range. Reproductive environments are important because they influence dormancy levels and reproductive rates. We show that a genetic cline in dormancy reduces the breadth of reproductive environments experienced and may contribute to local adaptation in this species. Lastly, we use this framework to explore how changes in temperature and moisture across the European range due to temporal climate change will influence life-cycle expression of these same genotypes.

The accumulation of mutation load and range dynamics. (51883)

Roslyn Henry, Aurélie Coulon, Kamil Bartoń, Justin Travis.

The University of Aberdeen; Centre d'Ecologie et des Sciences de la Conservation, Paris; Centre d'Ecologie Fonctionnelle et Evolutive, Montpellier.

Periods of climate change can alter the nature of biological processes within species' ranges, thus the eco-evolutionary dynamics of range formation and expansion are important for understanding and predicting species distributions. Here, we focus on a process that has thus far been overlooked in both contexts; the accumulation of mutation load. For range formation we show that the accumulation of deleterious mutations severely reduces the extent of a range across an environmental gradient, especially when dispersal is limited, growth rate is low and mutations are of intermediate deleterious effect. For range expansion, we demonstrate that the accumulation of mutation load can substantially slow the rate of range expansion however the evolution of dispersal mediates this effect to some extent. Our results illustrate the important role deleterious mutations can play in range dynamics and as such we highlight the incorporation of mutation load as a necessary focus for further work, noting particularly the

potentially opposing effects that mutation load and migration load may have for species' range dynamics.

Session 1 THU POL A 32

Local adaptation versus inbreeding depression in marginal populations of a Mediterranean alpine plant: are they worthy of conservation in a context of climate change? (52284)

Javier Morente-López, Alfredo García-Fernández, Carlos Lara-Romero, Maria Luisa Rubio-Teso, Raquel Ruiz, Ainhoa Sánchez, José María Iriondo.

Universidad Rey Juan Carlos.

Silene ciliolata is a chamaephytic cushion plant that grows in alpine cryophytic pastures of the Mediterranean mountains. In the Sistema Central of the Iberian Peninsula, populations occur along an altitudinal gradient from 1900 to 2500 m. Populations that grow at the lower elevations are marginal from the standpoint of the ecological range of the species. However, the higher temperature and lower precipitation regimes that take place in these sites are likely to expand to the rest of the distribution area of the species as a consequence of global warming. In this context, we were interested in contributing to the debate on whether marginal populations are able to locally adapt to the existing limiting environmental conditions or, on the contrary, are genetically impoverished and maladapted. We have implemented an experimental design that involved artificial cross-pollination of mother plants from various marginal populations using pollen from the same population, other marginal populations and central populations. The performance of the resulting seeds was assessed in situ at experimental sowing plots located nearby the marginal populations. This experiment has been complemented with common garden studies implemented in an ex-situ experimental facility to ascertain genetic differences in vegetative, phenological and reproductive traits of the species.

Session 1 THU POL A 32

Forecasting the demographic and evolutionary response of perennial Alpine plants (52404)

Olivier Cotto, Wilfried Thuiller, Frédéric Guillaune.

UNC Chapel Hill; Université de Grenoble I, CNRS; University of Zurich.

Predicting how climate change will affect species distributions is a major challenge for biologists. Most previous attempts to answer this challenge used projections of the current ecological niche to assess future species distributions. Species niche can change over time due to evolutionary processes and species demography can be deeply affected by selective pressures resulting from climate changes. We used genetically explicit individual based simulations with overlapping generations to investigate the roles of evolution and species

demography for predicting future species distributions. We modeled the life histories and current distributions of four endemic Alpine perennial plant species. We used the latest regional climatic simulations to model the environment up to 2090. We assumed that selection and intraspecific competition occur at the seedling stage. We found that the extinction rate of these species would not change over time. However, the size of local populations would drop accompanied by modifications in age-structure. Old maladapted adults persist and block the recruitment of adapted juveniles. We further found that stopping climate change allow an immediate increase in local population sizes with no extinction debt. Overall we show that, for long-lived species, climate warming would deteriorate the state of local populations without change in extinction rate, possibly until a massive and sudden extinction event.

Session 1 THU POL A 32

Are plastic changes in tree phenology adaptive in the context of climate change? Insights from a mechanistic model. (52492)

Ophélie Ronce, Anne Duputié, Alexis Rutschmann, Isabelle Chuine.

ISEM CNRS.

Concerns are rising about the capacity of species to adapt quickly enough to climate change. In long-lived organisms such as trees, genetic adaptation is slow, and how much phenotypic plasticity can help them cope with climate change remains largely unknown. Here, we assess whether, where and when phenological plasticity is and will be adaptive in three major European tree species. We use a process-based species distribution model, parameterized with extensive ecological data, and manipulate plasticity to suppress phenological variations due to interannual, geographical and trend climate variability, under current and projected climatic conditions. We show that phenological plasticity is not always adaptive and mostly affects fitness at the margins of the species' distribution and climatic niche. Under current climatic conditions, phenological plasticity constrains the northern range limit of oak and beech and the southern range limit of pine. Under future climatic conditions, phenological plasticity becomes strongly adaptive towards the trailing edges of beech and oak, but severely constrains the range and niche of pine. Our results call for caution when interpreting geographical variation in trait means as adaptive, and strongly point towards species distribution models explicitly taking phenotypic plasticity into account when forecasting species distribution under climate change scenarios.

Session 1 THU POL B 18

Functional genomics of marine and freshwater sticklebacks (52566)

Felicity Jones.

Friedrich Miescher Laboratory of the Max Planck Society.

Colonisation of new freshwater habitats has resulted in the repeated adaptive divergence of freshwater sticklebacks from their ancestral marine ecotype. We use these powerful biological replicates of the evolutionary process to identify and functionally dissect the molecular mechanisms underlying adaptive divergence and reproductive isolation. I'll describe how we are using whole genome sequencing and population genomics of stickleback species pairs to identify high-resolution sets of loci underlying parallel adaptive divergence. Many loci fall in non-coding parts of the genome, suggesting non-coding regulatory elements may be particularly important in adaptation. We use a range of methods to functionally dissect the phenotypic effect of these loci. These include transgenic methods to test for divergence in the regulatory potential of marine and freshwater adaptive haplotypes, and powerful new genome editing techniques to knock-out and knock-in adaptive loci. Our ultimate aim is to understand the fitness effects of these loci in natural populations. To do this we study the fitness and survival of naturally occurring recombinant individuals in contact zones between marine and freshwater forms. The ability to identify and functionally dissect adaptive loci in sticklebacks provides powerful insights into the molecular mechanisms underlying adaptation in natural populations.

Session 1 THU POL B 18

The genetic basis for the rapid diversification of male genital morphology among *Drosophila* species (51763)

Kentaro M. Tanaka, Corinna Hopfen, Matthew R. Herbert, Christian Schlötterer, David L. Stern, John P. Masly, Maria D. S. Nunes, **Alistair P. McGregor**.

Oxford Brookes University; Veterinärmedizinische Universität Wien (Austria); MPI for Biology of Ageing (Cologne, Germany); Janelia Research Campus (VA, USA); University of Oklahoma (OK, USA).

Identifying the genetic and developmental bases of phenotypic evolution is crucial to understanding organismal diversity and the evolutionary forces involved. The morphology of the external genitalia of males of *Drosophila simulans* clade species has evolved rapidly since their last common ancestor. For example, male *D. simulans* and *D. mauritiana* exhibit striking differences in the size, shape and bristle composition of their claspers, posterior lobes and anal plates. To identify the underlying loci we used high-resolution introgression mapping. We detected several small regions on chromosome 3 that contribute to interspecific differences in either the claspers or the posterior lobe and anal plates. While generally these loci affect each trait in the same direction and act additively, we also found evidence for epistasis. We then performed an RNAi screen to investigate if positional candidate genes that are differentially expressed between sexes or species also regulate genital development. We found six genes that are required for development of genital traits consistent with the effects of the introgressed regions in which they are located. We are currently using CRISPR/Cas9 in *D. mauritiana* and *D. simulans* to identify which of these candidate genes have contributed to the evolution of genital differences between these two species.

Session 1 THU POL B 18

Functional characterization of an adaptive cis-regulatory polymorphism in *Drosophila melanogaster* (51637)

John Parsch, Amanda Glaser-Schmitt.

University of Munich (LMU).

Drosophila melanogaster, which presently has a worldwide distribution, expanded from its ancestral home range in sub-Saharan Africa within the past 15,000 years. This expansion into new habitats is thought to have been accompanied by extensive adaptation. However, the genes involved in this adaptation are almost completely unknown. Transcriptomic studies found that the gene CG9509, which encodes a choline dehydrogenase, consistently shows higher expression in cosmopolitan populations than in sub-Saharan populations. The expression difference is caused by sequence variation in an upstream enhancer that shows population genetic evidence for a selective sweep in cosmopolitan populations. Detailed molecular genetic analyses have revealed three SNPs that contribute to the expression difference. Interestingly, two SNPs with moderate effects on expression are fixed in cosmopolitan populations, while a third SNP, which has a large effect on expression, is at intermediate frequency. Using RNAi knockdown and a null mutant, we show that high expression of CG9509 is associated with diminished larval growth rate, smaller adult body size, and reduced wing load - phenotypic traits that may be advantageous in temperate environments. Our results demonstrate how large-scale transcriptomics can be combined with population genetic, molecular genetic, and phenotypic studies to characterize the functional effects of regulatory changes on gene expression and organismal traits.

Session 1 THU POL B 18

From genome to function: Timing adaptations in the intertidal insect *Clunio marinus* (52203)

Tobias S. Kaiser.

Max F Perutz Laboratories.

The marine midge *Clunio marinus* (Diptera: Chironomidae) lives in the intertidal zone of the European Atlantic coast. Its life cycle is timed to the rhythm of the tides by circadian and circalunar clocks. As the pattern of the tides differs along the coastline, *C. marinus* populations show a variety of local genetic adaptations in circadian and circalunar timing. Population genetic analysis suggests that timing adaptations evolved within the last 20,000 years. QTL mapping indicates that the timing adaptations are controlled by few major effect loci.

In order to pinpoint the adaptive timing loci, we sequenced, assembled, annotated and genetically mapped a *C. marinus* reference genome, leading to a full reconstruction of the three chromosomes. Then we re-sequenced pools of 300 individuals from five populations of *C. marinus*, which differ in circadian and circalunar timing. Genome-wide we detected timing-associated genes based on the correlation of genetic divergence with timing differences. The distribution of genetic variation in the QTLs suggests that timing adaptation

happened from standing genetic variation and involves regulatory changes. Subsequent molecular analysis substantiated that adaptation in circadian timing relies on modulating alternative splicing of a metabolic enzyme.

Session 1 THU POL B 18

Characterization of the wing colour patterning supergene in a mimetic butterfly (52256)

Suzanne Saenko, Florence Prunier, Violaine Llaurens.

Museum National d'Histoire Naturelle.

Identification and experimental validation of genes underlying adaptive phenotypic variation is crucial for our understanding of evolution. Heliconius butterflies are famous for their extreme diversity in wing colour patterns, associated to aposematism and Müllerian mimicry. While the majority of Heliconius species are locally monomorphic and vary geographically, *H. numata* maintains a high local polymorphism throughout its geographical range, with 7-10 forms coexisting in the Amazon populations, each mimicking different species of Melinaea butterflies. This dramatic polymorphism is controlled by alleles of a single supergene P, containing at least 18 genes. Polymorphic inversions at the P locus suppress recombination, maintaining the favourable genetic combinations that produce mimetic colour patterns. However, the exact nature of the wing patterning genes within the supergene has not yet been investigated. Here, we use RNA-sequencing in combination with 'classical' approaches such as qPCR and in situ hybridizations to test the involvement of candidate genes from the P supergene in wing pattern formation in *H. numata*. Remarkably, this locus harbors the genes involved in colour patterning in other species of Lepidoptera and therefore represents a genomic hotspot of evolutionary change in multiple clades.

Session 1 THU POL C 10

Ecological and evolutionary determinants of disease dynamics (51727)

Anna-Liisa Laine.

University of Helsinki.

Several key theories have been proposed to explain the diversity of pathogen populations and to predict evolutionary trajectories of disease. Among the key theories are the Red Queen hypothesis, life-history trade-offs, and competition for resources under multiple infection, and while each has been relatively intensively studied also empirically, to date we understand remarkably little about the relevance of these processes for realized epidemiological dynamics under conditions that support spatial and environmental complexity. In this talk I will synthesize what we currently about ecological and coevolutionary processes jointly shaping disease dynamics in the metapopulation of fungal pathogen *Podosphaera plantaginis* infecting its host across a heterogeneous landscape.

Side effects of parasitism in microbes (53332)

Alex Hall.

ETH Zürich.

Parasitism creates selection for resistant hosts, but can also alter the frequencies of other alleles not directly related to the host-parasite interaction. I will describe some experiments with bacteria and their viral parasites showing that parasitism can alter the spread of alleles that determine bacterial drug resistance, mutation rate and growth rate in the abiotic environment. These effects can come about through mechanisms such as genetic hitchhiking or epistasis, and our results show that they depend strongly on ecological factors, which modify the strength of selection for resistance to parasites and their effects on other phenotypic traits.

Parasite evolution in heterogeneous and spatially structured host populations (51787)

Sébastien Lion.

CEFE, Montpellier, France.

Evolutionary epidemiology aims at understanding how host-parasite interactions evolve in response to various ecological factors. However, theoretical studies often assume that the host population is well-mixed, thereby neglecting potential selective pressures caused by genetic and epidemiological spatial structuring. I will present some theoretical and experimental results in order to elucidate the evolutionary impacts of parasite and host dispersal patterns. I will first focus on a population where all hosts have the same quality, and show that the predictions of non-spatial theory are altered by kin competition for susceptible hosts. I will then examine what happens in a heterogeneous population in which a fraction of the hosts are vaccinated. I show that different types of vaccines lead to different evolutionary outcomes, which depend on the interplay between vaccine efficacy, vaccination coverage, and spatial structure. Kin selection is shown to be a key conceptual tool to understand epidemiological feedbacks on parasite traits and to generate predictions for the management of infectious diseases.

Relative fitness of a generalist parasite on alternative hosts: a cross-infestation experiment of the hen flea among sympatric passerine hosts. (51793)

Anaïs APPELGREN, Karen McCOY, Heinz RICHNER, Blandine DOLIGEZ.

UMR CNRS 5558 - LBBE (LYON, FR); EEL-IEE (BERN, CH); MIVEGEC (MONTPELLIER, FR).

Host range is a key element required to understand a parasite's ecology and evolution and can vary greatly depending on the spatial scale considered. Several studies suggest that generalist parasites frequently show local population structure in relation to alternative sympatric hosts (i.e., host races), and are thus less "generalist" than described. Here, we tested this hypothesis for a common nest-based parasite, the hen flea *Ceratophyllus gallinae* exploiting two abundant host species that share the same breeding habitat, the great tit *Parus major* and the collared flycatcher *Ficedula albicollis*. We performed a cross-infestation experiment of fleas between the two host species during a single breeding season and recorded the reproductive success of both hosts and parasites. Hosts were recaptured the following year to assess the long-term impact of cross infestation. Results suggest the presence of local host-specialized parasite populations, with variation in the relative virulence on the two hosts modulated by the host population locality and history.

Session 1 THU POL C 10

Parasite evolution in a host sexually dimorphic world (51858)

David Duneau, Nicolas Buchon, Brian Lazarro.

Cornell university.

The evolution of the interactions between hosts and their parasites is multifactorial as it depends on the combination of many factors in both the host and the parasite. In a growing number of infectious disease, host sex is one of the key factors that generates strong differences in the outcome of the disease. The mechanisms underlying the effect of the host heterogeneity due to sexual dimorphism remain poorly characterized. We used *Drosophila melanogaster*, a powerful genetic model organism, to investigate the sexual dimorphism of the response to infection, its underlying mechanisms and its consequences on parasite evolution. We characterized the sexual dimorphism in response to a broad spectrum of parasites covering different types of pathogens. We found that male hosts imposed a stronger selective pressure on bacteria probably because of an adaptive reduction of immune sensitivity of female recognition of infection. We described in depth the immune components involved in the dimorphic response to *Providencia rettgeri*, a natural pathogenic Gram negative bacteria of *D. melanogaster* populations. Then, we investigated the consequence of sexual dimorphism on the evolution of bacteria via an experimental evolution approach.

Session 1 THU POL D 9

A behavioural ecologists' view of bacterial life in the lung (53335)

Ashleigh Griffin.

University of Oxford.

Behavioural ecologists use evolutionary theory to provide adaptive explanations for observations of animals living in their natural environment. Success relies on accurately identifying selection pressures acting upon traits of interest. For this reason, we have made limited progress in understanding the adaptive significance of behavioural traits in microbes. To observe a bacterial cell, we typically isolate it from its natural environment first before bringing it into the lab for examination. This process releases cells from the very selection pressures we wish to understand. Furthermore, the bacteria we are most interested in – human pathogens – live in one of the most inaccessible and irreproducible environments – living human beings. In this talk, I will present evidence that selection to optimise fitness from social interactions can drive long-term phenotypic dynamics in *Pseudomonas aeruginosa* infecting patients with cystic fibrosis. After ten years of studying *P. aeruginosa* in precisely controlled experimental evolution studies, we were interested to know if the competitive dynamics of co-operators and cheats in our experiments had any relevance to the real world. But first we had to overcome the challenge of identifying selection pressures inside a human lung.

Session 1 THU POL D 9

Cooperation, cheating, and collapse in microbial populations (53366)

Jeff Gore.

Natural populations can suffer catastrophic collapse in response to small changes in environmental conditions, and recovery can be difficult even after the environment is restored to its original condition. We have used laboratory microbial ecosystems to directly measure theoretically proposed early warning signals of impending population collapse. Our experimental yeast populations are subject to catastrophic collapse because they cooperatively break down the sugar sucrose, meaning that below a critical size the population cannot sustain itself. The cooperative nature of yeast growth on sucrose also makes the population susceptible to "cheater" cells, which do not contribute to the public good and reduce the resilience of the population.

Session 1 THU POL D 9

Rock-paper-scissors dynamics maintain cooperation and diversity in well-mixed bacterial communities (51679)

Rolf Kümmerli, Fredrik Inglis, Jay Biernaskie, Andy Gardner.

University of Zürich; Swiss Federal Institute of Aquatic Science and Technology (EAWAG); University of Oxford; University of St. Andrews.

Cooperation and diversity abound in nature despite the fact that cooperators risk exploitation from cheats and weak competitors risk displacement by superior ones. This is especially true in unstructured, well-mixed environments where cooperators and weak competitors are fully

exposed to exploitative and superior forms. Here, we use theory and experiments with bacteria to demonstrate a simple mechanism that promotes cooperation and diversity in well-mixed conditions: coexistence between cooperators and cheats is stabilized by the presence of loners who sidestep social interactions. This three-way Rock-Paper-Scissor system occurs in communities of the bacterium *Pseudomonas aeruginosa*: cooperators secrete shareable siderophore molecules to scavenge growth-limiting iron, thereby outcompeting loners who have an independent yet less efficient iron-uptake system; loners outcompete cheats who can only exploit the cooperator's but not the loner's iron uptake system; and cheats outcompete cooperators. This circular interaction network maintains cooperation and strain diversity over time. Thus, our analyses establish a general mechanism for explaining trait, strain and species diversity, even in natural settings like aquatic habitats, where individual dispersal is high.

Session 1 THU POL D 9

Sibling cooperation mitigates effects of low parental care in earwigs: a new perspective on the early evolution of family life (51744)

Jos Kramer, Julia Thesing, Joël Meunier.

Dept. of Evolutionary Biology, Institute of Zoology, University of Mainz.

The evolution of family life requires net fitness benefits for offspring, which are commonly assumed to mainly derive from parental care. However, an additional source of benefits for offspring is often overlooked: cooperative interactions among juvenile siblings. In this study, we examined how sibling cooperation and parental care could jointly contribute to the early evolution of family life. Specifically, we tested in the European earwig *Forficula auricularia* whether the level of food transferred among siblings (sibling cooperation) (1) depends on the level of maternal food provisioning (parental care), and (2) shapes fitness traits measured in family members. We show that the expression of these two behaviors is negatively correlated, reflecting a compensatory relationship between sibling cooperation and maternal care. Furthermore, the level of sibling food transfer did not influence offspring survival, but was associated with negative effects on the production of the second and terminal clutch by the tending mothers. These findings indicate that sibling cooperation mitigates the detrimental effects on offspring survival that result from being tended by low quality mothers. More generally, they are in line with the hypothesis that sibling cooperation is an ancestral behavior that can be retained to compensate for insufficient levels of parental investment.

Session 1 THU POL D 9

Kin Selection and Maternal Effects: the confusion, consequences and case study. (51893)

Caroline Thomson, Jarrod Hadfield.

University of Oxford; University of Edinburgh.

There is abundant evidence in many taxa for positive directional selection on body-size, and yet little evidence for microevolutionary change. In species where variation in body-size is caused by variation in parental care, a proposed explanation is a negative genetic correlation between direct and parental effects; selecting genes that increase body-size causes a correlated reduction in parental care, which reduces body-size in the following generation. However, empirical evidence seems to suggest that this genetic correlation is not sufficiently negative (less than -0.9) to explain evolutionary stasis. Here we show that these arguments implicitly assume that parental care is cost free, and including a cost could allow evolutionary stasis without requiring such extreme genetic architectures. Using a large cross-fostered population of blue tits, we estimate selection on parental care (i.e. the cost) and show that evolutionary stasis would be possible under more reasonable genetic correlations. Thus, we highlight the importance of accounting correctly for the complete selection acting on traits across generations.

Session 1 THU POL D 9

The role of antimicrobials in the evolution of cooperation (51986)

Marie Vasse, Clara Torres-Barceló, Michael E. Hochberg.

Institut des Sciences de l'Evolution-CNRS Université de Montpellier, France; Santa Fe Institute, USA.

Cooperation is a pervasive phenomenon in biological systems and despite considerable study, its establishment and maintenance are incompletely understood. Theoretical and empirical work on social behaviors in single species indicates that cooperation is fostered by positive assortment. However, numerous studies on more complex systems have shown that environmental and social factors may influence the ecological and evolutionary dynamics of cooperation. Using both experimental evolution and theoretical approaches, we studied the impact of antimicrobial compounds on the dynamics of public good cooperation within a bacterial population. *Pseudomonas aeruginosa* is an opportunistic human pathogen that facultatively produces iron-scavenging molecules called siderophores in response to iron limitation. Siderophore production is costly for the producer and benefits other local individuals carrying the siderophore receptors, and therefore may be subject to evolution as a cooperative trait. Comparing a wild-type and a mutant strain lacking the most important siderophore producing gene, separately or in competition, we showed that the deleterious effects of antimicrobials can shape bacterial populations and affect public good dynamics. Our results highlight the importance of considering environmental factors when studying the evolution of cooperation.

Session 1 THU MAX 415 26

The role of epistasis in the evolution and epidemiology of multidrug-resistant tuberculosis (53373)

Sebastien Gagneux.

Multidrug-resistant tuberculosis (MDR-TB) is a global public health emergency. Although much is known about the mechanisms of resistance to the different anti-TB drugs, little is known on the evolutionary trajectory of *Mycobacterium tuberculosis* exposed to prolonged drug pressure and its impact on the spread of MDR-TB. Recent studies by our group and others suggest that this evolutionary trajectory is more complex than previously thought. In particular, epistatic interactions between drug resistance-conferring mutations, compensatory mutations and different strain genetic backgrounds play an important role. For example, we recently identified mutations in *rpoA* and *rpoC* of RNA polymerase of *M. tuberculosis* resistant to rifampicin. These mutations compensate for the fitness cost associated with the resistance-causing mutations in *rpoB*. Moreover, these compensatory mutations are associated with ongoing transmission of MDR-TB, indicating that compensatory evolution contributes to the success of highly drug-resistant strains of *M. tuberculosis* in countries with a high burden of MDR-TB. Using an *M. smegmatis* model, we observed sign epistasis between *rpoB* mutations causing resistance to rifampicin and mutations in *gyrA* conferring resistance to fluoroquinolones, indicating that mutations causing resistance to different drugs can compensate for each other's fitness costs. Intriguingly, the particular combinations of *rpoB* and *gyrA* mutations exhibiting the highest in vitro fitness were also the more common in clinical strains. Taken together, our findings suggest that epistasis is an important driver of MDR-TB epidemics, and that it should be considered in the development and deployment of new anti-TB drug regimens.

Session 1 THU MAX 415 26

Convergent evolution and adaptation of *Pseudomonas aeruginosa* within patients with cystic fibrosis (51623)

Rasmus Lykke Marvig, Lea M. Sommer, Søren Molin, Helle K. Johansen.

Department of Clinical Microbiology, Rigshospitalet, Copenhagen, Denmark; Department of Systems Biology, Technical University of Denmark, Lyngby, Denmark.

Only little is known about how within-host evolution compares between genotypically different strains of the same pathogenic species. We sequenced the whole genomes of 474 longitudinally collected clinical isolates of *Pseudomonas aeruginosa* sampled from 34 children and young cystic fibrosis patients. Our analysis of 36 *P. aeruginosa* lineages identified convergent molecular evolution in 52 genes. This list of genes suggests a role in host-adaptation for remodeling of regulatory networks and central metabolism, acquisition of antibiotic resistance, and loss of extracellular virulence factors. Furthermore, we find an ordered succession of mutations in key regulatory networks. Accordingly, mutations in downstream transcriptional regulators were contingent upon mutations in upstream regulators, suggesting that remodeling of regulatory networks may be important in adaptation. Characterization of genes involved in host-adaptation may help prediction of bacterial evolution in cystic fibrosis patients and design of future intervention strategies.

Omics of endosymbiosis adaptation during experimental evolution of legume symbionts (52222)

Camille Clerissi, Delphine Capela, Marta Marchetti, François Li, Rachel Torchet, Stéphane Cruveiller, Carine Gris, Eduardo PC Rocha, Catherine Masson-Boivin.

INRA, LIPM, UMR 2594/441, 24 chemin de Borde Rouge-Auzeville, 31326, Castanet-Tolosan, France; CEA/FAR, Institut de Génomique, 2 rue Gaston Crémieux, 91057, Evry, France; Microbial Evolutionary Genomics, Institut Pasteur, 28 rue Dr. Roux, 75015, Paris, France; CNRS, UMR3525, 28 rue Dr. Roux, 75015, Paris, France.

Cooperation between legumes and bacteria collectively called rhizobia fixed a fourth of the atmospheric nitrogen each year. Rhizobia are phylogenetically disparate bacteria that have diversified through horizontal transfer of key symbiotic genes converting soil bacteria into legume symbionts. Making the transition to an intracellular lifestyle is a dramatic ecological change. Each plant indeed represents a complex ecosystem to which the bacterium may adapt. How and which re-adjustments allow the shift to endosymbiosis is still poorly unknown. To tackle this issue, we took advantage of the experimental evolution of a pathogenic *Ralstonia solanacearum* chimera carrying the symbiotic plasmid of the rhizobium *Cupriavidus taiwanensis* into legume symbionts. Eighteen lineages of chimeric *Ralstonia* were adapted to nodule tissues for 16 infection cycles. Evolution was very fast, since most lineages acquired and improved the two first major symbiotic steps, nodulation and intracellular infection. To get an integrated view of adaptive changes driving symbiotic adaptation, we performed a combined genomic, transcriptomic and metabolomic analysis of the 18 final clones. The clones exhibit convergent changes that may reflect their capacity to face new endosymbiotic conditions. Our work highlights the potential of coupling experimental evolution with omic approaches to get insight into the emergence of plant endosymbionts.

Rapid evolution of bacterial pathogens co-infecting an animal host (52348)

Kayla King, Michael Brockhurst, Steve Paterson, Greg Hurst.

University of Oxford; University of York; University of Liverpool.

Co-infections, when multiple pathogen species coexist within an individual, are very common in nature. Studies in natural populations have provided compelling evidence that competitive interactions between pathogen species in a given host species strongly alter pathogen fitness and transmission. Thus, we hypothesised that co-infection would alter patterns of pathogen evolution. We tested this by experimentally evolving two opportunistic, bacterial pathogens – *Enterococcus faecalis* and *Staphylococcus aureus* – separately and together within *Caenorhabditis elegans* nematodes in the lab. Using a combination of phenotypic and genomic analyses, we show that the speed and direction of in vivo evolution of pathogen virulence and other infection-related traits were affected by a co-infecting competitor. The evolution of a pathogen, therefore, cannot be understood without knowledge of others infecting the host.

Phylogenetic analysis of a mycobacterium tuberculosis outbreak (52913)

Denise Kühnert, David Stucki, Mireia Coscolla, Lukas Fenner, Tanja Stadler, Sebastian Gagneux.

Institute of Integrative Biology, ETH Zürich, Zürich, Switzerland; Swiss Tropical & Public Health Institute, Basel, Switzerland; Department of Biosystems Science & Engineering, ETH Zürich, Zürich, Switzerland.

The fast evolution of pathogenic viruses gave rise to a number of phylogenetic approaches to extract information about the epidemiological characteristics of viral genomes. Here we apply these approaches to the more slowly evolving bacterial genomes of mycobacterium tuberculosis.

Around 1991 the city of Bern, Switzerland, was struck by a small but severe outbreak of tuberculosis. Two initial cases were observed in 1987 and 1988, the majority of patients were sampled between 1991-1998, and up to 2011 patients infected with related strains were observed. Overall 75 infected patients were sampled, and 68 of the resulting bacterial isolates were genetically related and therefore sequenced.

In this study we aim at understanding the epidemiological dynamics of the Bernese tuberculosis outbreak. We analyze the genomes with BEAST2, using a birth-death tree prior that allows to incorporate an exposed phase in which patients are infected but not yet infectious. Piecewise constant changes in the reproduction number allow us to estimate changes in epidemiological dynamics through time.

Our results suggest that the majority of transmissions took place before 1993, supporting previous suggestions that more recently sampled cases may have been latent for years, before being reactivated. We estimate an average latent period of 2-5 years.

Parallel evolution of a global regulator ameliorates the cost of plasmid carriage (52435)

Ellie Harrison, Steve Paterson, Andrew Spiers, Micheal Brockhurst.

University of York; University of Liverpool; Abertay University.

Conjugative plasmids present a paradox. Although many carry useful bacterial genes, all plasmids exert a burden on their host. Therefore selection should favour plasmid loss and retention of any useful genes on the bacterial chromosome. Previous studies have shown that evolution can resolve this paradox by ameliorating the cost of plasmid carriage, yet the mechanisms for this are poorly understood. We combine experimental evolution, microarray

analysis and whole genome sequencing to investigate how evolution resolves this plasmid paradox.

We experimentally evolved replicate populations of *Pseudomonas fluorescens* carrying the mercury resistance plasmid pQBR103. Prior to evolution plasmid carriage was associated with widespread up-regulation of translation-associated genes, suggesting that pQBR103 exerts a translational burden on its host. Following evolution however this was reversed. Sequencing of evolved clones revealed parallel evolution targeting two bacterial genes: *gacA* and *gacS*, a two-component regulator that positively regulates translation of extracellular proteins. Knockouts confirmed that loss of *gacA/S* function ameliorates the cost of plasmid carriage. As disruption of *gacA/S* increases post-transcriptional repression of bacterial genes, these data suggest that the bacteria ameliorate the cost of plasmid carriage by reducing their own translational workload to accommodate that of the plasmid.

Session 1 THU GEN B 35

A theoretical study of sympatric divergence of whitefish in Scandinavia (52756)

Xavier Thibert-Plante, Per-Arne Amundsen, Kimmo Kahilainen, Kim Praebel, Kjartan Østbye, Sergey Gavrilets.

Umeå University; The Arctic University of Norway; University of Helsinki; University of Oslo; University of Tennessee, Knoxville.

We have a better understanding of the role of divergent selection and assortative mating in parapatric speciation event. Unfortunately, the application of those theoretical concepts is not straightforward in complex empirical systems of contemporary speciation. One of such complex system is the divergence of whitefish in Scandinavia. There is a large number of lakes in northern Scandinavia where divergence occurred. In some of those lakes, as much as three morphotypes have diverged in situ. We use a large scale individual-based numerical simulation to model the divergence of whitefish in Scandinavia. Our aim is to distinguish the role of different driving factors (such as habitat preference, divergence in resource distribution, divergence in mating time and divergence in spawning site) in this divergence. Speciation and adaptive radiation are the result of a complex intertwined factors. The leading factor is the divergence in resource types, but reproductive isolation is the result of a much more complex interaction between habitat preference and assortative mating. It is fairly instructive to apply theoretical models to empirical systems, as we learn how the different driving factors interact during speciation.

Session 1 THU GEN B 35

Genomic imprinting and its systematic perturbation in abortive interspecific tomato seeds (51694)

Ana Marcela Florez Rueda, Margot Paris, Anja Schmidt, Alex Widmer, Ueli Grossniklaus, Thomas Städler.

Institute of Integrative Biology, ETH Zurich, Universitätstrasse 16, CH-8092 Zurich, Switzerland; Institute of Plant Biology, University of Zurich, Zollikerstrasse 107, CH-8008 Zurich, Switzerland .

Hybrid seed failure represents an important postzygotic barrier to interbreeding among species of wild tomatoes (*Solanum* section *Lycopersicon*) and other angiosperm groups. We studied this phenomenon in the closely related *S. peruvianum* and *S. chilense*; hybrid crosses between these species yield very high proportions of inviable seeds due to endosperm failure and arrested embryo development. Based on seed size differences in reciprocal hybrid crosses and developmental evidence implicating endosperm failure, we hypothesized that (perturbed) genomic imprinting might be involved in this strong postzygotic barrier. Consequently, we surveyed endosperm transcriptomes obtained via laser-microdissecting developing seeds representing both intra- and interspecific pollinations. We implemented a novel approach to estimate parent-of-origin-specific expression using both homozygous and heterozygous nucleotide differences between the two parents and identified hundreds of candidate imprinted genes. Importantly, we uncovered systematic shifts of the ‘normal’ (intraspecific) maternal:paternal transcript proportions in hybrid endosperms; the average maternal proportion of gene expression increases in both directions of the hybrid cross but is strongly negatively correlated with ‘normal’ maternal proportions. This genome-wide shift almost entirely eliminates paternally imprinted gene expression in hybrid endosperms but also affects maternally imprinted genes (which on average shift to lower maternal proportions) and all other genes.

Session 1 THU GEN B 35

Why are ring species so rare? (52898)

Ayana B. Martins, Marcus A. M. de Aguiar.

Instituto de Física Gleb Wataghin, Universidade Estadual de Campinas; Instituto de Biociências, Universidade de São Paulo.

Ring species are groups of organisms that dispersed along a ring shaped region in such a way that the two expansion fronts, that meet after many generations, are reproductively isolated despite ongoing gene flow. Here we study the formation of ring species by simulating population expansion around a central geographic barrier. We combine different strategies of parameter space exploration and compare two models with independent sets of assumptions to propose the conditions for ring species formation by speciation by distance. If population expansion takes less than 10000 generations, ring species formation occurs when the time to contact secondary and the time to reproductive isolation are of the same order. We show that both these times depend on landscape, population and individual features. However, in ring shaped scenarios, population structuring leading to the acquisition of reproductive isolation is better explained by landscape configuration than by local mating. The conditions that allow ring species formation appear to be limited, which could by itself explain their rarity. Furthermore, these complexes are most likely to

form for extremely narrow species distributions which are unlikely to persist in nature, and, therefore, are expected to be rare in nature.

Session 1 THU GEN B 35

Male barn swallows mimic nestlings to attract females (51938)

Masaru Hasegawa, Emi Arai, Mamoru Watanabe, Masahiko Nakamura.

Sokendai; Tohoku University; University of Tsukuba; Joetsu University of Education.

Courtship behaviors of male birds often resemble the food-begging behavior of their young, at least from a human perspective. However, it is still unclear whether such behavior in males is objectively similar to nestling behavior and, if so, how such similarity is evolved and maintained. The sensory trap hypothesis proposes that this similarity is a consequence of signal evolution, whereby male signals mimic stimuli to which females respond in other contexts (i.e., parental care, in this case). We demonstrated that the enticement calls of male barn swallows structurally resemble the food-begging calls of nestlings, compared with the other three male vocalizations (i.e. songs, alarm calls and contact calls). In addition, we found that females were attracted to the playback of nestlings' food-begging calls during the courtship period, despite nestlings being absent at this time. The response of females to food-begging calls was similar and positively correlated with their response to male enticement calls. To our knowledge, this is the first study to demonstrate the objective similarity as well as a similarity in receiver response towards the two behaviors during courtship, supporting the sensory trap hypothesis. We discuss the evolutionary importance of nestling mimicry in this model species of sexual selection.

Session 1 THU GEN B 35

How sick are sexy males? Testing Hamilton & Zuk hypothesis with a meta-analytical approach. (52575)

Zofia Prokop, Mateusz Buczek, Agata Plesnar-Bielak, Shinichi Nakagawa, Lukasz Michalczyk.

Jagiellonian University, Krakow, Poland; University of Otago, Dunedin, New Zealand.

Female preferences for specific male phenotypes have been documented in many animal species, including those where males contribute only gametes to offspring production. However, selective pressures responsible for the origin and maintenance of such preferences remain elusive. The Hamilton and Zuk hypothesis proposes that female preferences target those male traits that reliably signal heritable disease resistance, and hence preferences evolve by indirect selection – because offspring of choosy females inherit disease resistance alleles from their fathers. One of the predictions of this hypothesis is a negative correlation between secondary sexual traits and disease in males. We use meta-analysis to evaluate empirical evidence for this prediction. Our preliminary results (analysis of ~75% of the final data base)

do not support Hamilton and Zuk hypothesis: the meta-analytic mean for the correlation between sexual traits and disease measures, calculated across studies and taxa, is not significantly different from zero ($r=-0.14$, CI: -0.32 to 0.05). Interestingly, however, we find a substantial effect of phylogeny on the magnitude of this correlation. In further analyses, we also test for the effects of several moderators related to biology of host and pathogen taxa, and to methodology of the study, on the magnitude of the effect.

Session 1 THU GEN B 35

Worldwide patterns of bird colouration on islands and associated mechanisms (52146)

Claire Doutrelant, Matthieu Paquet, Julien Renoult, Pierre-André Crochet, Arnaud Grégoire, Rita Covas.

CEFE-CNRS Montpellier, France; ACTE- CNRS Paris, France; CIBIO Porto, Portugal.

Islands are natural simplified replicates around the world that harbour original selective environments and offer unique opportunities to investigate patterns of convergent adaptation, referred as syndromes. Communicative traits are decisive to animal fitness, mediating interactions with the environment. However, whether and how these traits are part of an insularity syndrome is still unclear. We quantitatively analyzed with spectrophotometry and a model of avian vision, the plumage colouration of 232 bird species comprising island endemics from around the world and their close mainland relatives. We found that both plumage brightness and colour conspicuousness (volume in a bird colour space) were reduced on islands in both sexes, and further evidenced a decrease in colourfulness (number of distinct colour patches) in males. We then investigated the ‘species recognition’ and ‘life-history trade-offs’ hypotheses as two of the possible explanations for these changes and found some support for both. Hence, our results reveal convergent colour changes on islands worldwide and confirm that interspecific interactions and trade-offs are two of the important underlying mechanisms affecting the evolution of bird plumage colouration.

Session 1 FRI GEN C 19

The promise of reverse ecology (53311)

Matthew Rockman.

New York University.

Unbiased genome-wide population-genetic analyses hold remarkable promise for revealing the molecular variants whose frequencies have changed in response to selection within and among populations and species. These methods have been applied to two classes of question. One question centers on the roles of selection, linkage, and demography in shaping the dynamics of genetic variation. A second question centers on discovering specific loci that have been targets of selection and inferring the causes of selection. Approaches to the second

question are sometimes called reverse ecology, by analogy to reverse genetics, which starts with mutations and then seeks impacted phenotypes. Reverse ecology promises to provide an unbiased view of the selective forces operating on populations, but we lack a principled method for connecting genetic variants discovered in such screens to the ecological factors that act on them. This gap is especially acute for genetic variants whose known phenotypes are cell-biological rather than organismal. I will illustrate the challenges with evidence for ongoing selection on meiotic genes in *Caenorhabditis* nematodes and the alternative models of natural selection that can account for the patterns.

Session 1 FRI GEN C 19

Human adaptation to life in the high arctic (53312)

Rasmus Nielsen.

UC Berkeley.

The native people of Greenland, the Inuit, are of special interest to anthropologists and evolutionary biologists because of their extreme adaptations to life in the high arctic. In particular, Inuit traditionally have a diet based primarily on hunting marine mammals, which have a high content of polyunsaturated fatty acids. Inuit provide an opportunity to investigate genetic adaptations to such a diet. We analyze SNP chip data and exome sequencing data from 191 and 18 Inuit, respectively, in order to identify regions targeted by positive selection specifically in Inuit related to metabolic processes. We find extreme selection signals in several loci and using association mapping, we show that alleles associated with positive selection in these loci are strongly associated with multiple phenotypes, including weight. Our study illustrates the use of small understudied populations for understanding the genetic basis of human biological variation.

Session 1 FRI GEN C 19

Genomic basis of the evolution and variation in *Drosophila* immunity against parasitoids (52187)

Bregje Wertheim, Laura Salazar-Jaramillo, Sylvia Gerritsma, Kirsten M. Jalvingh.

Groningen Institute for Evolutionary Life Sciences; University of Edinburgh ; Universite de Lausanne.

To understand the intricate genetic networks that underlie variation in immunity, and to map how the genome changes during the evolution of immunity, we use the *Drosophila*-parasitoid interactions as model system. The ability to survive parasitoid attack varies hugely both among and within species of the *Drosophila* genus, from absent to high resistance. Combining phenotypic assays, comparative genomics, population genomics and experimental evolution approaches, we identified genome changes associated with gains, losses and increases of parasitoid resistance. Comparing 11 sequenced *Drosophila* species, we showed that evolution

of parasitoid resistance coincided with the acquiring of a novel type of differentiated hemocyte (i.e. insect blood cell) and with the duplication of 11 genes that are up-regulated during the immune response after parasitization. To characterize the impact of a selective sweep for parasitoid resistance on the genome, we used experimental evolution followed by genome sequencing. Several narrowly defined genomic regions showed strong signatures of selection and candidate genes were identified that potentially confer increased parasitoid resistance. Comparing 8 natural *D. melanogaster* populations, we find that physiological and genetic mechanisms underlying phenotypic variation differ substantially among populations. Combined, this emphasizes that short- and long-term evolutionary responses can result in markedly different genome changes.

Session 1 FRI GEN C 19

A complementary method to genome scans for selection against maladaptive gene flow (52429)

Simon Aeschbacher, Graham Coop.

University of California, Davis.

We quantify the genome-wide signal of selection against maladaptive gene flow, such as in the context of local adaptation or hybridisation. Combining the concept of effective migration rate with the structured coalescent, we predict the aggregate effect of selection against locally deleterious alleles as a function of recombination. Given a linkage map and estimates of between-population diversity, we infer the selection intensity per basepair, the time of onset of selection, and the baseline migration rate. Our method complements genome scans for candidate loci. In particular, it avoids issues of F_{st} outlier approaches such as their inability to distinguish between global background selection and selection against gene flow. It also borrows strength across multiple sites of weak effect, many of which would be missed by genome scans. Analytical approximations suggest that it is difficult to separate the average selection coefficient from the genomic density of selected sites, but their compound effect can be identified. We test our approach against simulations and apply it to two datasets from the yellow monkeyflower (*Mimulus guttatus*), one in which we detect the signal of local adaptation to serpentine soils, and another where we show evidence for selection against introgression from the sister species *M. nasutus*.

Session 1 FRI GEN C 19

The genomic consequences of local adaptation in deer mice (52614)

Susanne P. Pfeifer, Stefan Laurent, Matthieu Foll, Brant Peterson, Jeffrey D. Jensen, Hopi E. Hoekstra, Rowan D.H. Barrett.

School of Life Sciences, Ecole Polytechnique Fédérale de Lausanne (EPFL), Switzerland;
School of Life Sciences, Ecole Polytechnique Fédérale de Lausanne (EPFL), Switzerland;

Department of Organismic and Evolution Biology, Harvard University, USA; Department of Biology, McGill University, Canada.

Although natural selection is the major force driving phenotypic evolution and adaptation to new environments, uncertainty persists concerning the magnitude and causes of genomic changes that occur when populations evolve under novel ecological conditions. Moreover, ecological sources of selection and the genomic basis of adaptive traits are often complex, limiting the predictability of local adaptation. To determine whether natural selection may indeed have predictable effects on specific phenotypes and their underlying mutations, we identified the genetic polymorphisms responsible for adaptive pigmentation traits in wild deer mouse populations (*Peromyscus maniculatus*) inhabiting the Nebraska Sand Hills, formed 8,000 to 10,000 years ago, and directly estimated the consequences of natural selection on these phenotypes. We conducted a large-scale field-based selection experiment that involved the introduction of 480 wild deer mice (with known genotypes and phenotypes) into replicated field enclosures, representing the two extremes in substrate color found in their natural habitat. These observations were used to estimate the targets and strength of selection acting on pigmentation traits at the phenotypic level. Additionally, we characterized genome-wide changes in allele frequencies in order to estimate how local adaptation can shape broader patterns of evolution at the genotypic level.

Session 1 FRI GEN C 19

The genetic architecture of recombination rate variation in a wild population. (52859)

Susan Johnston, Jon Slate, Josephine Pemberton.

University of Edinburgh; University of Sheffield.

Genome scans provide a useful tool for detection of genomic regions underlying both local adaptation between populations (e.g. FST outlier analyses) and fitness-related variation within populations (genome-wide association studies). To date, most studies have focused on detecting the effects of single markers, yet recent work shows that such approaches may fail to capture loci of moderate or small effects on phenotype. Therefore, multi-locus frameworks are more likely to accurately characterise genetic variation segregating within and between populations, especially when the trait has a polygenic architecture. In this study, we used information from a high density SNP chip to calculate individual recombination rate variation in wild Soay sheep. We then investigated the genetic architecture of this moderately heritable trait ($h^2 \approx 0.13$) using chromosome partitioning and regional heritability mapping. This integration of traditional quantitative genetic approaches and multi-locus information allowed us to identify regions of the genome associated with recombination rate variation, but also allowed us to estimate the proportion of heritable variation caused by additional polygenic effects at unknown loci. We describe additional steps taken to prevent identification of false-positive signals, and show how these statistical approaches allow more accurate investigation of trait evolution both within and between populations.

Genetic and neural basis for the evolution of schooling behavior in sticklebacks (53318)

Catherine L. Peichel, Anna K. Greenwood, Abigail R. Wark, Margaret G. Mills.

Fred Hutchinson Cancer Research Center; Graduate Program in Neurobiology and Behavior, University of Washington; Graduate Program in Molecular and Cellular Biology, University of Washington.

The formation of social groups is prevalent across the animal kingdom, but can vary dramatically among different species, within species, and even across the lifetime of an individual. Schooling behavior in fish provides a particularly dramatic example of social group formation. To study the proximate genetic and neural mechanisms that contribute to the evolution of schooling behavior, we developed the “model school assay” and used it to demonstrate that there are heritable differences in schooling behavior between threespine stickleback (*Gasterosteus aculeatus*) populations adapted to divergent marine and freshwater benthic habitats. Marine sticklebacks have both a stronger tendency to school and a better ability to maintain a parallel body position when schooling than benthics. Our genetic mapping studies revealed that differences in these two components of schooling behavior are controlled by distinct genetic modules. These studies also revealed that the Ectodysplasin (Eda) gene is tightly linked to body position while schooling. Interestingly, the Eda gene is also tightly linked to variation in the patterning of the sensory hair cells (neuromasts) of the lateral line sensory system, which had been implicated in schooling behavior. To test whether the Eda gene is responsible for variation in both lateral line patterning and schooling behavior, we used transgenic methods to broadly express the marine version of the Eda cDNA in benthic sticklebacks. These transgenic sticklebacks have a marine-like pattern of neuromasts, and the presence of the transgene causes benthic sticklebacks to school in a more parallel orientation. This change in schooling behavior seems to be mediated by the effects of Eda on the lateral line system. Our results thus provide mechanistic insight into how and why fish form schools and yield one of the first genes known to shape vertebrate behavior in an evolutionary context.

Using live bearing fish as short generation time models in the study of vertebrate brain evolution (52743)

Niclas Kolm.

Stockholm University Zoology/Ethology.

Brain morphology variation is ubiquitous in the animal kingdom. Yet the evolutionary processes and mechanisms that have generated this variation remain poorly understood. Till now, the study of the causes and consequences of this variation has mainly used comparative analyses to investigate correlations between brain morphology and behavior, ecology, sexual selection and life histories. Using artificial selection experiments of brain size in the guppy, a

live bearing fish with short generation time, we study multiple hypotheses concerning the costs and benefits of evolving a larger brain. I will present some of our findings on these selection lines regarding the genetic architecture of brain size and how several traits, including behavior, investment into other organs, sexual traits, immune competence and fitness, are affected by rapid evolution of brain size. Finally, I will present how we use new artificial selection experiments on the guppy to unravel the evolutionary possibilities and consequences of rapid evolution of separate brain region sizes and how brain morphology is affected by artificial selection of social abilities. My aim is thus to show that short generation time vertebrates such as live bearing fish may form new models for the study of evolutionary and ecological neurobiology.

Session 1 FRI MAX 410 23

Innate differences in auditory perception and reproductive isolation in an avian species pair (51804)

David Wheatcroft.

Uppsala University.

Vocal learning is a defining characteristic of human intelligence. Researchers have used the song learning process in birds, where over 4000 species learn their vocalizations, to understand the cognitive basis and evolution of vocal learning. The vocal learning process in birds is based on innate auditory preferences that bias young birds to learn the songs of their own species. Divergence across species in the genes underlying song perception may play a key role in the build up of reproductive isolation between species, but their evolutionary origin remains mysterious. Here, I compare innate auditory preferences in two closely related species of songbirds, the collared and pied flycatchers (*Ficedula* spp.). I demonstrate that juveniles from both species innately recognize their own species' songs. I use immunohistochemistry to investigate the neural and genetic basis of these behaviours, and present behavioral data suggesting that early perceptual differences influence adult song production and preferences. My results imply that genes involved in auditory perception play a driving role in the vocal learning process, which in turn affects sexual isolation between these species.

Session 1 FRI MAX 410 23

From the jungle to the barn: Independent genetic control for increased brain and body size and Mosaic brain evolution in chickens during domestication (52310)

Rie Henriksen, Leif Andersson, Per Jensen, **Dominic Wright.**

Linköping University; Uppsala University; Linköping University; Linköping University.

The evolution of brain size and its relationship with body size and brain substructure composition has proven to be both enduring and perplexing to disentangle. By crossing a domestic breed of chicken with its wild counterpart for multiple generations, we can address this problem by looking at the genes that control intra-specific species variation (and specifically inter-population variation) for overall brain size, body size and brain substructure size independently. We show (i) these traits have entirely separate genetic architectures, with different genes governing these traits. (ii) In contrast to popular belief, domestic chickens have larger, not smaller, brains than their wild counterparts, but as these genes are confounded by LD with the genes for extreme growth in pure domestic populations, this effect is masked by standard allometric measurements. (iii) Different regions control the development of different substructures, and that the cerebellum and cerebral hemisphere is enlarged in domestic birds. (iv) Brooding behaviour (a key behaviour missing from domestic hens) correlates negatively with cerebellum size in this intercross. These results have far-reaching consequences for the use of allometry in brain size study, and highlight how within-species variation can be used to answer general questions regarding the evolution of brain size.

Session 1 FRI MAX 410 23

Evolution of acid-sensing olfactory circuits in *Drosophila* (52332)

Lucia Prieto Godino, Rapahel Rytz, Steeve Cruchet, Liliane Abuin, Benoite Bargeton, Ana Silbering, Vanessa Ruta, Matteo Dal Peraro, Richard Benton.

Centre for Integrative Genomics, University of Lausanne, Lausanne, Switzerland; Rockefeller University, New York, USA; Ecole Polytechnique Federale de Lausanne, Lausanne, Switzerland.

Nervous systems evolve to adapt animals' behavior to their ecological niches, but the genetic and cellular changes underlying this process are poorly understood. We have compared the olfactory circuits of the specialist fly species *Drosophila sechellia*, which feeds and breeds exclusively on the acid-rich fruit of *Morinda citrifolia*, with its generalist cousins *D. melanogaster* and *D. simulans*, which are associated with a wide range of fermenting fruits. We have identified both loss and gain of sensory responses to acids in *D. sechellia* and link these to single nucleotide differences within a tandem array of olfactory receptor genes, IR75a-IR75b-IR75c. These receptor functional differences are accompanied by multigenic-dependent changes that shape the species-specific neuroanatomical organization of acid-sensing pathways in the periphery, while leaving the organization of second order central neurons largely conserved. Importantly, we show that these peripheral traits can account in part for the distinct behavioral preferences of these species toward environmentally relevant odors, thereby linking chemosensory ecology to adaptive genetic changes influencing nervous system structure and function.

Session 1 FRI MAX 410 23

Communication scenes of weakly-electric fish recorded in natural habitats challenge sensory processing (52598)

Jan Benda, Jörg Henninger, Rüdiger Krahe.

University of Tübingen, Germany; McGill University, Montreal, Canada.

The importance of using naturalistic stimuli for studying the neurophysiology of sensory information processing has been generally recognized. However, knowledge of species-specific natural stimuli in natural habitats - relevant for the evolution of the neural systems - is largely missing to date. We demonstrate that automated, large scale observations of electro-communication scenes of the neotropical gymnotiform weakly electric fish *Apteronotus rostratus* in natural habitats provide unexpected and novel insights to both neurophysiological and evolutionary aspects of animal communication. We continuously monitored electric fish behavior and communication interactions during courtship, spawning, and aggression using an array of 60 electrodes over many days. From the data we reconstructed frequencies and amplitudes of electrosensory stimuli received by the fish and compared them to the filter properties of electrosensory receptor neurons. While during male-male interactions the signal frequencies matched the tuning of the electrosensory periphery the signal amplitudes could be dramatically low. Conversely, during male-female interactions the signal amplitudes were much larger, but the frequencies clearly exceeded the receptors' best frequency. Electro-communication is thus used at the limits of electrosensory processing. Our field data provide novel naturalistic stimuli for studying sensory processing and raise interesting questions about the coevolution of sensory and motor systems.

Session 1 FRI POL A 31

Nucleotide polymorphism and physiological diversity underlying pigmentation variation in *Drosophila melanogaster* (52481)

Aya Takahashi.

Department of Biological Sciences, Tokyo Metropolitan University.

Natural variation in pigmentation intensity in *D. melanogaster*, which is likely to be under some form of natural selection, is mainly caused by changes in cis-regulated gene expression level of a melanin biosynthesis gene, *ebony*. We found that knocking down this gene by RNAi changes desiccation resistance, which may be one of the pigmentation-associated physiological traits under selection. We also conducted a fine-scale quantification of the cis-regulated expression levels and sequence analyses of this gene using the sampled alleles from *Drosophila* Genomic Resource Panel (DGRP). Detailed comparisons between nucleotide and expression polymorphisms showed that there are multiple functional cis-regulatory alleles segregating in the population. Also, a long range LD was detected in the upstream region of this gene, which suggested an existence of complex interactions between nucleotide variants within the region. The detailed analyses on within population variants of this gene revealed a more complex picture compared to the simple model of expression divergence among species by changes in modular enhancers. In addition to the results on *ebony*, associations detected between various pigmentation traits and other genes in the melanin biosynthesis pathway will also be discussed.

Do good genes induce a higher metabolic rate? A study in the colour polymorphic barn owl (52555)

Alexandre Roulin, Robin Séchaud, Paul Béziers.

University of Lausanne; University of Lausanne; University of Lausanne.

Variation in the degree of melanin-based coloration can have a strong underlying genetic basis. Colour morphs often differ in a number of other phenotypic attributes and it is not rare to observe that one morph better performs than other morphs in a large number of situations. This begs the question about how colour variation is evolutionary stable. In the barn owl (*Tyto alba*), females displaying larger black feather spots better cope with a number of stressful factors raising the question of how variation in spot size persists. We show here that larger-spotted female nestlings consume more oxygen independently of ambient temperature. This suggests that to sustain costly physiological processes that help cope with stressful environmental conditions, larger-spotted females invest more energy and hence have a higher metabolic rate. Large-spotted barn owls may therefore adopt a high cost/high benefit strategy and small-spotted barn owls a low cost/low benefit strategy. Our study may explain why polymorphism in the degree of melanin-based coloration is evolutionary stable. From a proximate point of view, our findings may due to the melanocortin system.

Tests of the thermal melanism and melanisation desiccation-resistance hypotheses in New Zealand *Hemideina maori* (Orthoptera: Stenopelmatidae). (51925)

Keith King, Brent Sinclair, Jon Waters, Graham Wallis.

Department of Zoology, University of Otago, Dunedin, New Zealand; Department of Biology, University of Western Ontario, London, ON, Canada; Department of Zoology, University of Otago, Dunedin, New Zealand; Department of Zoology, University of Otago, Dunedin, New Zealand.

The New Zealand alpine tree weta (*Hemideina maori*) has melanic and yellow colour morphs. Melanism appears to have evolved repeatedly in this species, occurring sporadically in seven of eight clades mitochondrial DNA clades. The adaptive significance of melanism in *H. maori* has not been established. There is no evidence that melanism is associated with either increased immune response or incidence of parasitism. We investigated two additional hypotheses; thermal melanism and melanisation-desiccation resistance. Heat gain was measured in weta directly exposed to a heat source (basking simulation) as well as indirectly exposed (microhabitat simulation). In both simulations, thermal melanism was not supported as heat gain was not significantly increased in melanic morphs, compared to yellow. Weight was the significant covariate, with heat gain slower in heavier weta. We used open flow-through respirometry to compare water-loss rates between morphs. Melanic morphs had significantly lower rates of cuticular water loss than yellow morphs, thus supporting the

melanisation-desiccation resistance hypothesis. However, melanic *H. maori* are typically found at lower (and presumably less-desiccating) elevations than yellow morphs, suggesting that desiccation resistance is not the primary adaptive mechanism for melanism in *H. maori*.

Session 1 FRI POL A 31

Effects of MC1R gene on sexual dimorphism in barn owls and the potential conflict between natural and sexual selection on melanin-based colorations (51974)

Luis San José Garcia, Anne-Lyse Ducrest, Valerie Ducret, Paul Béziers, Céline Simon, Kazumasa Wakamatsu, Alexandre Roulin.

University of Lausanne; Fujita Health University.

The melanocortin-1 receptor (MC1R) gene has been repeatedly observed to underlie adaptive colour variation in vertebrates. MC1R induces large changes in melanin-based colourations favoured by natural selection as an adaptation to diverse processes such as predator-prey interactions and thermoregulation. However, melanin-based colourations are often sexually dimorphic, suggesting that sexual selection could interact or even conflict with natural selection if MC1R also induces changes in the degree of sexual dimorphism. This hypothesis has not been tested despite evidences support that more sexually dimorphic galliform species accumulate more synonymous mutations at the MC1R. We present results confirming that MC1R colour effects induce correlated changes in sexual dimorphism in the barn owl, *Tyto alba*. Plumage colour traits in this species vary from white to red and from unspotted to heavily marked with black spots and depend on natural and sexual selection. Although males and females exhibit any phenotype, males are on average whiter and less spotted. MC1R largely explains variation in coloration but, more importantly, certain MC1R alleles allow for larger sexual dimorphism. These findings indicate that MC1R could epistatically act with factors determining sexual dimorphism, supporting that evolution of adaptive colouration through MC1R may interact with sexual selection.

Session 1 FRI POL A 31

Could melanin-based plumage colouration be adaptive in environments polluted with trace metals? (52028)

Marion CHATELAIN, Julien GASPARINI, Adrien FRANTZ.

Institute of Ecology and Environmental Sciences of Paris.

Anthropogenic activities release significant amounts of trace metals in the biosphere, several of which are known to have deleterious effects on animals. Because of their toxicity, these trace metals may induce selective pressures and select for detoxification mechanisms. Interestingly, metals can bind to both keratin and melanin, resulting in high concentrations of metals in feathers. Metal chelation may consequently constitute one of the main current

biological functions of melanin. We aimed at investigating the adaptive role of melanin by testing 1) the selective pressures that zinc and lead exert on wild birds, 2) the relation between plumage melanin colouration and metal concentrations in both feathers and blood, and 3) the beneficial effect of highly melanic plumages in habitats with high amounts of trace metals. Indeed, we found noxious effects of a low but chronic experimental exposure to lead on feral pigeons' reproductive success and immunity. Positive correlations between both zinc and lead concentrations and plumage melanin colouration suggest that this pigment may allow eliminating circulating metals and may consequently be selected in environments polluted with toxic trace metals. The heterogeneity of metal concentrations in the environment may participate to the evolutionary maintenance of melanin-based plumage colouration polymorphism.

Session 1 FRI POL A 31

Larval UV exposure impairs adult immune function through a trade-off with larval investment in cuticular melanin (52344)

Sara Debecker, Ruben Sommaruga, Tim Maes, Robby Stoks.

*Laboratory of Aquatic Ecology, Evolution and Conservation, University of Leuven;
Laboratory of Aquatic Photobiology and Plankton Ecology, Institute of Ecology, University of Innsbr.*

Despite the strong impact of ultraviolet (UV) radiation on invertebrates, it is unknown whether immune function is affected across metamorphosis. More general, the mechanisms on how larval stressors bridge metamorphosis and shape adult fitness remain poorly understood. We studied whether cuticular melanin content is upregulated under UV exposure in the larval stage of the damselfly *Coenagrion puella* and whether this is traded off across metamorphosis against a key component of the invertebrate immune response, the melanotic encapsulation response, in the adult stage. Larvae exposed to UV increased the melanin content in the exoskeleton and metamorphosed later and at a smaller mass than animals reared without UV. Across metamorphosis, this was associated with a reduced melanotic encapsulation response, thereby constituting the first proof for a UV driven impaired immune response in an invertebrate. Path analysis indicated that the immunosuppressive property of larval UV exposure was not mediated by age and mass at metamorphosis, but instead that the adult immune response was traded off against larval cuticular melanin investment. This melanin-based trade-off across metamorphosis provides a new pathway by which effects of larval stressors are carried over to the adult stage and thereby advances our understanding of the mechanisms of carryover effects of larval stressors across metamorphosis.

Session 1 FRI POL B 17

Whole genome duplications and recruitment of ecologically relevant genes in alpine Mustards (52011)

Céline Geiser, Amélie Bardil, Terezie Mandáková, Béatrice North, Kevin Leempoel, Martin Lysak, Stéphane Joost, **Christian Parisod**.

Institute of Biology, University of Neuchâtel, Switzerland; Central European Institute of Technology, Masaryk University, Czech Republic; Laboratory of Geographic Information Systems, École Polytechnique Fédérale de Lausanne, Switzerland.

Polyploid taxa represent excellent models to address the underpinnings of genome evolution and the building up of new species in heterogeneous environments. Here, I present an overview of recent works in the alpine *Biscutella laevigata* autopolyploid complex (Brassicaceae). Transcriptomics inferred recurrent whole genome duplication (WGD) events specific to clade of species and that were used to infer processes fostering genome evolution across different timescales:

(i) After a 7-8 million years old WGD event, intense chromosomal repatterning selected for clusters of retained duplicates enriched in functions associated with responses to abiotic stresses. Low coverage genome sequencing unraveled the dynamics of several retrotransposons, supporting interplay between genome reorganization and environmental opportunities in shaping the evolution of paleopolyploids.

(ii) Retrotransposons in autotetraploids having recolonized the Alps after the ice ages showed considerable dynamics going along with ecological radiation following this recent WGD. Ecological genomics involving transplant experiment indeed supported distinct autopolyploid gene pools firmly associated with contrasted habitats despite gene flow. These ecotypes demonstrated adaptive differentiation at loci whose functions match habitat requirements. WGDs thus recurrently fostered genome reorganization and adaptive recruitment of genes responding to environmental factors, indicating that similar proximate and ultimate factors of genome dynamics may consistently act through time.

Session 1 FRI POL B 17

Application of Associative Transcriptomics to polyploid crops (53307)

Andrea Harper.

University of York.

Associative Transcriptomics is designed to be rapidly applied to diverse crop species, and has proven particularly useful in polyploid species as, by focussing on transcribed sequences, it reduces the level of complexity that often complicates genetic analyses. Even without access to high quality genomic references, the method enables identification and ordering of both gene sequence and gene expression markers, which can then be associated to traits of interest. By using both types of marker, the method often simplifies the identification of candidate genes, and can uncover valuable information about the causative nature of the underlying variation. In this presentation, the approaches used to adapt the method to the allopolyploids oilseed rape and bread wheat will be discussed.

Session 1 FRI POL B 17

Zinc accumulation, transcriptomics and asymmetric adaptation in the allopolyploid *Arabidopsis kamchatica* (51574)

Timothy Paape, Masaomi Hatakeyama, Jun Sese, Rie Shimizu-Inatsugi, Kentaro Shimizu.

University of Zurich; Tokyo Institute of Technology.

A feature that makes gene duplication through allopolyploid hybridization interesting compared to that of autopolyploidization (autosomal duplication within a single diploid ancestor) is that homeologous copies are not ancestrally identical but have unique evolutionary histories as a result of each diploid progenitor's evolution and their respective adaptations. Uniquely derived ancestral gene copies therefore have the potential to result in the retention of phenotypes that were present in either of the ancestors. Using de novo reference assemblies of both diploid ancestors and a newly developed bioinformatics pipeline to separate homeologous RNAseq reads, we have demonstrated that zinc accumulation in *A. kamchatica* is largely the result of transcriptional patterns and polymorphism derived from the diploid hyperaccumulating ancestor *A. halleri* ssp. *gemmifera* despite hybridization with a non-accumulating *A. lyrata* ancestor. Moreover, allopolyploid hybridization of the diploid parents which each possess highly divergent metal tolerance and hyperaccumulation phenotypes is equivalent to having diverse F1 crosses but without allelic recombination disrupting linkage as the ancestral gene copies evolve as homozygous homeologs. Our findings therefore allow us to explore the dynamic genome evolution of an allopolyploid species when asymmetric adaptations can be measured when stress conditions are applied.

Session 1 FRI POL B 17

Evolutionary analysis and demographic inference for polyploid genomes using ABC (52703)

Camille Roux, John Pannell.

UNIL; UNIL.

Polyploidization is a major contributor to diversification of both plants and animals. However, despite its high incidence, the population genetic and evolutionary study of polyploid species has been seriously limited by challenges associated with multiple-copy genomes. Until now, for example, it has been difficult to infer important details histories of polyploid lineages, including the mode of polyploidisation and patterns of gene exchange between genomes and diverging lineages. These challenges stem both from complications arising during data acquisition (e.g., the need to attribute sequences to genome copies) and data analysis. Here, we present the use of approximate Bayesian computation (ABC) for the analysis of sequence data from non-model polyploid species using short-read NGS technologies to expose the recent evolutionary and demographic history of polyploid populations. Our study uses both simulated datasets and real nucleotide sequences from species in the Brassicaceae. We find that ABC is a powerful tool for discriminating between an autopolyploid vs. allopolyploid origin of a tetraploid species, is robust for detecting signatures of introgression between tetraploid populations and their close diploid relatives, and allows parameter estimation for a range of competing evolutionary and demographic models.

Molecular basis of ecological diffusion after recurrent allopolyploidization in *Dactylorhiza* (52831)

Ovidiu Paun, Francisco Balao, Maria Lorenzo, Daniel Diehl, Bao-Hai Hao, Emiliano Trucchi, Mikael Hedrén.

University of Vienna; University of Sevilla; University of Lund.

Early-generation allopolyploids need to accommodate divergent genomes into one nucleus by adjusting organization and function, thereby influencing the ecological properties and adaptive success of resulting lineages. To identify the drivers of adaptation to distinct environments after iterative genome doubling, we investigate ecologically-divergent, sibling allopolyploids *Dactylorhiza majalis* and *D. traunsteineri* (Orchidaceae). By using RADseq we document a genome-wide absence of genetic differentiation between these allopolyploids, despite their phenotypic divergence. In addition, we bring evidence of frequent gene flow between the polyploids in sympatry, which points toward a strong divergent selection required in order to maintain the observed phenotypic divergence. By using the sibling allopolyploids of different ages in their native environmental context we investigate with RNAseq the progression through time of gene expression alterations after allopolyploidization, and their importance to the ecological properties of the polyploids. We observe a general trend of increased overexpression in the younger polyploid, whereas the transcriptome of the older resembles more closely those of the diploid parents. The differential expression between the polyploids is mainly driven by parental dominance in opposite directions and affects genes related to metabolic processes and response to stimulus. We discuss the importance of qualitative versus quantitative expression alterations in allopolyploid genomes, and their role for diversification in general.

Whole genome duplication events and evolution of the self-incompatibility system are strongly associated within the Brassicaceae (52955)

Xavier Vekemans, Laura Henocq, Vincent Castric, Céline Poux.

CNRS-Universite Lille1.

Recent studies using phylogenetic approaches, mapping of trait evolution, and quantification of species diversification have shown that transitions from outcrossing to selfing and from diploidy to polyploidy are associated with large reductions in species diversification rates. However, the joint evolution of polyploidy and mating system genes has rarely been addressed. We studied the impact of whole genome duplication events on the evolutionary dynamics of the self-incompatibility system in Brassicaceae. A clear signature of strong genetic bottleneck, followed by allelic re-diversification at the S-locus has been detected in three unrelated groups. In all three cases, this bottleneck appears to be associated with an

historical event of polyploidy. Detailed analyses of the S-locus genomic region in two cases have revealed common patterns (deletion of the S-locus in its ancestral position, evolution of a new S-locus at a different position), as well as striking differences (the genes involved in pollen-pistil recognition at the new S-locus are either orthologous or non-orthologous to the SCR and SRK genes of the ancestral Brassicaceae). These results suggest a scenario with temporary loss of self-incompatibility after polyploidization, followed by re-establishment of SI at a different genomic location with rapid allelic re-diversification caused by strong balancing selection.

Session 1 FRI POL C 12

The effects of deleterious mutations on patterns of influenza A/H3N2's evolutionary dynamics (53349)

Katia Koelle.

Duke University.

Recent phylogenetic analyses indicate that RNA virus populations carry a substantial deleterious mutation load. This mutation load has the potential to shape patterns of adaptive evolution via genetic linkage to beneficial mutations. Here, we examine the effect of deleterious mutations on patterns of influenza A subtype H3N2's antigenic evolution in humans. By first analyzing simple mathematical models of influenza that incorporate a mutation load, we show that deleterious mutations act to slow influenza's rate of antigenic evolution, while making it more punctuated in nature. These models further predict three distinct molecular pathways by which antigenic cluster transitions occur, and we find phylogenetic patterns consistent with each of these pathways in influenza viral sequences. Simulations of a more complex phylodynamic model incorporating both antigenic and deleterious mutations further indicate that deleterious mutations act in concert with antigenic mutations to reproduce influenza's spindly hemagglutinin phylogeny, antigenic co-circulation, and high annual attack rates.

Session 1 FRI POL C 12

Estimating heritability: old-school parent-offspring versus next-gen phylogenetics (52186)

Gabriel Leventhal, Sebastian Bonhoeffer.

Institute of Integrative Biology, ETH Zurich.

The heritability of a trait is one of the most used tools to quantify how fast a trait will evolve in a population. As a result, many different methods have been proposed to measure heritability in real populations. With the rise of the availability of genetic data, traditional methods such as parent-offspring regression or sibling analysis have been superseded by phylogeny-based methods to estimate heritability. However, as with all phylodynamic

models, tree-based methods for heritability estimation require an underlying model that describes how the trait evolved along the tree. Using set-point viral load in HIV as an example, I will show that tree-based estimates of heritability are very sensitive to model misspecification such as the absence of selection. In contrast, estimates from parent-offspring (donor-recipient) regression are more robust to such misspecification. The difficulty of obtaining good parent-offspring pairs must thus be weighed against potentially strongly biased estimates of heritability.

Session 1 FRI POL C 12

New routes to phylogeography (51904)

Nicola De Maio, Daniel Wilson.

nuffield Department of Medicine.

The inference of migration from pathogen genomic data is important to investigate routes of transmission, within-host infection dynamics, and sources of outbreaks. Statistical investigation is usually performed with discrete trait analysis models (i.e. MUGRATION) and similar, or with structured coalescent-based methods (e.g. MultiTypeTree). We propose a new method called BaStA (BAYesian STructured coalescent Approximation) based on an efficient approximation to the structured coalescent. We implemented BaStA in BEAST2. Furthermore, we performed a thorough comparison of the three approaches using both simulations and real data. Simulations show that our approach has comparable accuracy to MultiTypeTree, but much broader applicability. In contrast, MUGRATION showed generally unreliable estimates of both migration rates and ancestral locations. These differences were recapitulated in an analysis of zoonotic transmission events in real-world outbreaks, where MUGRATION inferred diametrically opposite results from the alternative approaches. Finally, we applied BaStA to an HIV compartmentalization dataset beyond the computational feasibility of MultiTypeTree and other structured coalescent-based methods due to the elevated number of demes.

Session 1 FRI POL C 12

Heterogeneity in antibody range and the antigenic drift of influenza A viruses (52307)

Gabriela Gomes.

Instituto Gulbenkian de Ciencia.

In this paper we explore the consequences of a heterogeneous immune response in individuals on the evolution of a rapidly mutating virus. We show that several features of the incidence and phylogenetic patterns typical of influenza A may be understood in this framework. In our model, limited diversity and rapid drift of the circulating viral strains result from the interplay

of two interacting subpopulations with different types of immune response, narrow or broad, upon infection. The subpopulation with the narrow immune response acts as a reservoir where consecutive mutations escape immunity and can persist. Strains with a number of accumulated mutations escape immunity in the other subpopulation as well, causing larger epidemic peaks in the whole population, and reducing strain diversity. Overall, our model produces a modulation of epidemic peak heights and patterns of antigenic drift consistent with reported observations, suggesting an underlying mechanism for the evolutionary epidemiology of influenza, in particular, and other infectious diseases, more generally.

Session 1 FRI POL C 12

Phylogenetic analysis of poliovirus outbreak (52809)

Lucy Li, Nicholas C Grassly, Christophe Fraser.

Imperial College London.

Background: Traditional surveillance of polio via Acute Flaccid Paralysis (AFP) reporting under-estimates the number of poliovirus infections as <1% of infections are symptomatic. Poliovirus genetic sequences collected from positive patient samples can provide an additional information to help quantify the size of the infected population. By concurrently analysing incidence data from AFP surveillance and viral sequence data from molecular surveillance, a more accurate estimate the prevalence of infection could be obtained.

Method: We jointly analysed the epidemiological and genealogical data from a poliovirus outbreak in Tajikistan to infer epidemiological parameters and reconstruct the epidemic trajectory. The likelihood of the epidemic trajectory depended on the incidence of reported cases and on the coalescent times of the viral genealogy.

Results: We found that the estimate of the infected population size depended on both the case-to-infection ratio and the heterogeneity in transmission. The variance in the number of secondary infections cause by each case was found to be high, suggesting the presence of super spreaders in the population. We also quantified the contribution of the viral genealogy to our estimated parameter values and epidemic trajectory.

Session 1 FRI POL C 12

Phylogenetic inference for bacterial and viral populations using BEAST 2 (52622)

Timothy Vaughan, Gabriel Leventhal, Alexei Drummond, David Welch, Tanja Stadler, Nigel French.

Department of Computer Science, The University of Auckland, New Zealand; Department of Biosystems Science and Engineering, Swiss Federal Institute of Technology (ETH Zürich); Institute of Veterinary, Animal and Biomedical Sciences, Massey University, New Zealand.

Since its introduction by Grenfell et al. (Science, 2004), the term "phylodynamics" has been used to describe a wide variety of relationships between the population and evolutionary dynamics of rapidly evolving organisms. In this talk I will present our work on two distinct phylodynamic inference methods which exploit these relationships in order to learn about population dynamics from sampled genetic sequence data.

Firstly, I will present our progress toward developing and implementing an algorithm for inferring the population dynamics of rapidly evolving bacterial populations in the presence of gene conversion. Our algorithm is based on the work of Didelot et al. (Genetics, 2007; Genetics, 2009). I will briefly introduce the algorithm and demonstrate its application to both simulated and real bacterial genetic data.

Secondly, I will discuss some results from our recent investigations into the use of the Particle Marginal Metropolis-Hastings algorithm (Andrieu et al., JRSSB, 2010) to perform exact phylodynamic inference under stochastic variants of compartmental epidemiological models such as SIR and SEIR. The method also allows for inference under arbitrary birth-death models; including models with spatial structure. I will present some encouraging first steps and discuss our future ambitions for this project.

Session 1 FRI POL D 22

Epigenetic origin of adaptive phenotypic variants in the blood-fluke *Schistosoma mansoni* (52321)

Sara Fneich, André Theron, Céline Cosseau, Jérôme Buard, David Duval, Nathalie Arancibia, Jérôme Boissier, Guillaume Mitta, **Christoph Grunau**.

Laboratoire Interactions Hôtes-Pathogènes-Environnements (IHPE) UMR5244 CNRS/University of Perpignan; CNRS, UPR1142, Institute de Génétique Humain (IGH), Montpellier; INRA, UMR 1198 Biologie du Développement et Reproduction, Jouy en Josas, France.

Adaptive evolution is impossible without the generation of phenotypic variants. The origin of variation has been a central topic in evolutionary biology. It is now commonly accepted that genetic variation is the only cause of phenotypic variants. The term "mutant" is even often used interchangeable to designate a genetic or a phenotypic variation. However, epigenetic information is emerging as a complementary source of heritable phenotypic variation. It is currently not clear what the relative importance of genetics and epigenetics in generating this variation is. We used a host-parasite system to address this question. The human blood fluke *Schistosoma mansoni* can adapt rapidly to new intermediate snail hosts. The interaction between parasite and mollusk is characterized by a compatibility polymorphism. The principal molecular marker for compatibility (infection success) is the expression pattern of polymorphic mucins (SmPoMuc). We show here that chromatin structure changes at the SmPoMuc promoters are the principal cause for SmPoMuc transcription polymorphism

leading to phenotypic novelty and increase in infection success i.e. fitness. We establish that epigenetic changes can be the major if not only cause of adaptive phenotypic variants in *Schistosoma mansoni*, suggesting that epimutations can provide material for adaptive evolution in the absence of genetic variation.

Session 1 FRI POL D 22

Facing environmental predictability with different sources of epigenetic variation (52392)

Christelle Leung, Sophie Breton, Bernard Angers.

Université de Montréal.

Epigenetic processes have been proposed as a key mechanism enabling living organisms to cope with environmental challenges and explaining the ecological success of genetically identical organisms. Two contrasting but not mutually exclusive strategies are expected in response to environmental predictability: phenotypic plasticity resulting of epigenetic-environment interactions and diversifying bet-hedging resulting of random epigenetic changes would be respectively selected in stable and unstable environments. Using the asexual fish *Chrosomus eos-neogaeus* as a biological model, this study aimed to test whether the clonal lineages from distinct environments (lakes vs temporary streams) display different epigenetic variability. Results reveal striking differences in the partition of epigenetic diversity among lineages, suggesting that the clones were selected according to the type of environment. This study provides the first empirical support linking environmental predictability to different sources of epigenetic variation in natural populations.

Session 1 FRI POL D 22

Epigenetic contribution to natural heritable variation within apomictic dandelion lineages (52587)

Koen Verhoeven.

Netherlands Institute of Ecology.

Asexual taxa are convenient models to explore the role of epigenetics in adaptation, because heritable epigenetic effects are more easily exposed and arguably also more relevant for adaptation when genetic variation is limited. To gain insight into the epigenetic contribution to heritable variation in asexual plants, we study epigenetic differences that build up between clone members of apomictic dandelion lineages. At the scale of several generations, we exposed clone members to different experimental environments and followed DNA methylation patterns for several subsequent generations, for which we explore a bisulfite sequencing GBS marker approach. At the scale of (micro-)evolutionary divergence, we compared different accessions from a single, geographically widespread apomictic lineage collected from different European countries. Accessions showed heritable differences in

flowering time, which was correlated with genomewide DNA methylation patterns. Flowering time differences between accessions disappeared after experimental in vivo demethylation, demonstrating that accession-specific DNA methylation causally contributes to heritable flowering time differences. Together, these studies shed light on the extent and evolutionary potential of epigenetic variation that builds up in asexuals. But important questions remain to be addressed and I will discuss some of the prospects and challenges for uncovering the adaptive role of epigenetic variation in natural systems.

Session 1 FRI POL D 22

Importance of pollution induced epigenetic inheritance for phenotypic diversification in *Daphnia pulex* (51724)

Helene Collin, Steve Paterson, Stewart Plaistow.

University of Liverpool.

The transmission of phenotypic novelty from parents to offspring is more than Mendelian inheritance. Although epigenetic inheritance can result in the transmission and persistence across generations of non-genetic effects, empirical evidence that epigenetic inheritance does create such effects is still sparse. Moreover, the underlying molecular mechanisms involved in epigenetic inheritance remain poorly understood. We addressed this shortfall by performing multi-generation experiments in which we exposed three clones from a natural population of water fleas (*Daphnia pulex*) to sub-lethal doses of a novel freshwater pollutant (herbicide, heavy metal and endocrine disruptor). We then quantified phenotypic changes and epigenetic inheritance patterns (gene expression, micro-RNA expression and DNA methylation) over the next generations among the different clones. Transcriptional profiles generated with microarrays enabled the identification of genes and pathways differentially expressed in three generations of descendants whose ancestors were exposed to pollutants. We then used whole genome bisulphite sequencing and micro-RNAseq to pin down epigenetic modifications across the genome and test the hypothesis that epigenetic inheritance interacts with genetic inheritance to promote phenotypic variation. Overall, we provide an ecologically relevant test of the hypothesis that environmentally induced non-genetic inheritance mediated by epigenetic modifications has important consequences for phenotypic and evolutionary diversification.

Session 1 FRI POL D 22

Associations of climate with DNA methylation polymorphisms provide evidence of local response to environment in a California oak, *Quercus lobata* (51731)

Victoria Sork, Paul Gugger.

University of California Los Angeles.

Epigenetic variation in natural populations may provide a mechanism to improve population response to environmental conditions. DNA methylation may promote or restrict gene expression that enhances plant performance and local adaptation. Our previous studies of epigenetic differentiation among three populations of *Quercus lobata* suggests that CpG methylation is either directly a target of natural selection or tightly linked to adaptive genetic variation. If DNA methylation plays a role in local adaptation, some methylation polymorphisms should be strongly associated with climate gradients. Here, we test this hypothesis in populations of *Quercus lobata* using bud and leaf tissue from 60 adults sampled throughout the species range. We generated reduced-representation bisulfite sequencing libraries (BS-Seq) to identify nucleotide and cytosine methylation polymorphisms (SNPs and SMPs). To identify outliers that are significantly correlated with climate variables, we conducted an environmental association analysis that controls for background demographic history. We found numerous SMPs that were strongly associated with climate. Many of them varied independent of the SNPs and some SNPs also showed significant association with climate. Our findings have important implications for the mechanisms underlying local adaptation to climate, especially in species with long-generation time, and the potential role of epigenetic mutations in adaptive evolution.

Session 1 FRI POL D 22

A role for methylation in responding to environmental stress in a wild rodent (52729)

Angela Sims, Joannes van Cann, Esa Koskela, Tapio Mappes, Phill Watts, **Joannes van Cann**.

University of Jyväskylä; University of Oulu.

Individuals often require rapid responses to environmental change that can provide effects that are longer-term than those produced by individual plasticity yet shorter than evolutionary change. Bank voles (*Myodes glareolus*) experience population cyclicity which induces environmental stress, such as increased population density or reduced food availability. By giving females ecologically-relevant stressors it is possible to reveal the effects of early life stress upon fitness as well as the underlying epigenetic mechanisms. Pregnant females were given social stress or food stress (in a 2x2 factorial design) during pregnancy and were profiled for DNA methylation. Animals were released in field enclosures to ascertain subsequent differences in offspring fitness when they are introduced to high and low density environments. Not only do mothers respond to stress during pregnancy by altering the number and size of offspring, but the stressors also impact the size and number of offspring in the subsequent generation with support for an epigenetic (DNA methylation) mechanism associated with these fitness effects. The implication is that the epigenetic response of a parent to its immediate environment can have lasting fitness effects on offspring and thus may play a vital evolutionary role in adaptation to a cyclic environment.

Session 1 FRI POL D 22

Epigenetic divergence and parallel evolution in *Heliosperma pusillum* (Caryophyllaceae) (52742)

Emiliano Trucchi, Ruth Flascher, Maria Lorenzo Romero, Bozo Frajman, Peter Schönschwetter, Ovidiu Paun.

University of Vienna; University of Innsbruck.

Epigenetic modifications are expected to occur at a faster rate than genetic mutations, and to be a flexible way to respond to stress conditions and to rapidly generate variation that can be visible to natural selection, even in the absence of genetic mutations. We then expect epigenetics to be particularly important in the early phases of adaptation and divergence. The alpine plant *Heliosperma pusillum* and its recently and recurrently diverged, low-montane sibling *H. veselskyi* constitute a perfect model system to test this hypothesis. They occur in distinct ecological conditions with divergent morphologies (dense trichomes versus glabrous plants), stable and heritable in common garden settings. However, genome-wide data (AFLP, RADseq) fail to group them according to observed phenotypes. Employing a novel approach (bisulfite-converted RAD sequencing – bsRADseq), we screened the DNA methylation patterns across more than 200,000 nucleotide positions in six population pairs of the two ecotypes. Comparing by sequencing the DNA methylation state and context (CpG, CHG, CHH) in 120 individuals, we demonstrate that epigenetic patterns are much more conserved across representatives of the two ecotypes than predictions given the distinct native environments and that several candidate loci for convergent epigenetic modification during parallel adaptation to a similar environment are present.

Session 1 FRI GEN B 35

The genetic sex determination system predicts adult sex ratio in tetrapods (51723)

Mark Kirkpatrick, Ivett Pipoly, Veronika Bókony, Tamás Székely, András Liker.

University of Texas; University of Pannonia; University of Bath.

Adult sex ratio (ASR) has critical effects on behaviour, ecology and population dynamics, but the causes of variation in ASR are unclear. Here we study how the type of genetic sex determination influences ASR variation across 354 species from 118 tetrapod families. Taxa with male heterogamy (XY systems) have a more female-biased ASR than taxa with female heterogamy (ZW systems). The effect is strong: the mean proportion of males is 0.48 for XY systems vs. 0.58 for ZW systems, and the type sex determination system explains 22% to 35% of variation between species in ASR. We develop models to understand the genetic factors that may contribute to this pattern, including meiotic drive and sex-linked deleterious mutations. Regardless of their causes, the effects of the genetic sex determination on the adult sex ratio are likely to have profound impacts on social behaviour of diverse tetrapod lineages.

Session 1 FRI GEN B 35

A quantitative genetic signature of senescence in a short-lived perennial plant (51800)

Benoit Pujol, Pascal Marrot, John Pannell.

CNRS - Laboratoire Evolution & Diversité Biologique; CNRS - Centre d'Ecologie Fonctionnelle & Evolutive; University of Lausanne.

Senescence (the physiological decline of organisms with age) poses an apparent paradox because it represents a failure of natural selection to increase the survival and reproductive performance of organisms. The paradox can be resolved if natural selection becomes less effective with age, because the death of post-reproductive individuals should have diminished effects on Darwinian fitness. A substantial body of empirical work is consistent with this prediction for animals. In plants however, conclusions from demographic studies support the hypothesis that plants have avoided the evolution of senescence. Unlike animals, the survival and reproductive success of plants can increase with age. Such phenomenon is often attributed to the fact that reproduction is diffuse and modular across the soma in the plant kingdom. Here, we show that the necessary conditions for senescence to evolve can be found in many plants. We also provide experimental evidence for a quantitative genetic basis of senescence in the short-lived perennial plant *Silene latifolia*. We found a marked increase with age in the additive genetic variance of traits closely associated with fitness, as expected under the evolutionary theory of senescence. This result thus extends to plants the quantitative genetic support for the evolutionary theory of senescence.

Session 1 FRI GEN B 35

Bauplan constraints on the evolution of lifespan in Vertebrates (52342)

Alexander Scheuerlein.

Max Planck Institute for Demographic Research.

Lifespan in vertebrates ranges from months to approximately 300 years. Here I will show using mortality data from 4000+ vertebrate species that average lifespan correlates with the shape of mortality trajectories in mammals, but not in other vertebrates. Specifically, it is the variation in lifespan within a species that is reduced at large body size in mammals. This is not the case in birds, amphibians, reptiles, or fish, where inter-individual variation in lifespan remains high. I will discuss this finding in the light of bauplan constraints that may hinder the evolution of long lifespans in mammals, despite large body size.

Session 1 FRI GEN B 35

Early-life reproduction is associated with increased mortality risk but enhanced lifetime fitness in humans (51922)

Virpi Lummaa, Adam Hayward, Ilona Nenko.

University of Sheffield.

The physiology of reproductive senescence is well-understood, but the drivers of variation in senescence rates are less so. Evolutionary theory predicts that early-life investment in reproduction should be favoured by selection at the cost of reduced survival and faster reproductive senescence. We tested this hypothesis in humans using data collected from preindustrial Finnish church records. Reproductive success of women increased up to age 25 and was relatively stable until a decline from age 41. Women with higher early-life fecundity (producing more children before age 25) subsequently had higher mortality risk, but high early-life fecundity was not associated with accelerated senescence in annual breeding rate. However, women with higher early-life fecundity experienced faster senescence in offspring "quality" (survival to adulthood). Despite these apparent costs, early-life fecundity was under positive selection: individuals with higher early-life fecundity had higher lifetime reproductive success. These results are consistent with evolutionary theory predicting trade-offs between early reproduction and later-life survival, and of interest in the light of recent increases in maternal ages in many societies and the potential consequences for offspring health and fitness.

Session 1 FRI GEN B 35

Repair or reproduce? Trying to solve an open question - an experimental study on zebra finches (51929)

Joanna Sudyka, Giulia Casasole, Joanna Rutkowska, Mariusz Cichoń.

Institute of Environmental Sciences, Jagiellonian University.

Somatic deterioration in ageing animals reflected in telomere decay may arise from differential allocation of resources. Telomeres are especially susceptible to the action of reactive oxygen species (ROS) damaging cellular structures. The link between reproduction, telomeres and oxidative stress has been repeatedly explored, but this enquiry remains inconclusive. We employ experimental approach (brood size manipulation) and a challenge with energetically costly burden (low ambient temperature) in zebra finches (*Taeniopygia guttata*) to evaluate if an array of ageing-related molecular markers: telomere length (qPCR), ROS and antioxidant levels (d-Rom and OXY tests) and DNA damage are influenced by enhanced reproductive effort. Individuals reproducing beyond their chosen rate should lose more telomeric sequences, and negative effect of reproductive effort has indeed been confirmed. Here we aim at revealing underlying mechanisms of this telomere decay. We hypothesize that telomere loss may stem from negative action of free radicals. We confirm that telomere decay in reproducing animals is faster and make this picture complete by showing that oxidative stress and defence are higher among parents experiencing enhanced reproductive effort.

Session 1 FRI GEN B 35

Reproductive costs in males: does it really matter? (52067)

Marlène Gamelon, Josefa Bleu, Bernt-Erik Sæther.

Centre for Biodiversity Dynamics - NTNU; Institute of Ecology and Environmental sciences - Paris (IEES - Paris), Université Pierre et Marie C.

Reproductive cost is a central concept in life-history theory. Reproduction requires resources that cannot be allocated to other functions resulting in a trade-off between current reproduction and future survival and/or future fecundity. Understanding such trade-offs, shaping life history traits, is crucial for evolutionary studies but also for demographic analyses. While examples of reproductive costs are widespread in the wild in females, there is no study investigating the overall support of direct reproductive costs in males. We screened the literature to gather studies testing the existence of direct costs of reproduction in male mammals and birds. We described the patterns of co-variations between current and future reproduction, and compared the differences between mammals and birds. Then, we examined the influence of paternal care and of the mating system on reproductive costs within birds. Finally, we discussed the possible bias that can mask reproductive costs in males. Because reproductive costs at the individual scale may have demographic consequences at the population scale, and while recent works have pointed out the need to integrate males into population models, we propose to explicitly take into account costs of reproduction in males into population models.

Session 1 FRI GEN B 35

Slow development as an evolutionary cost of long life (52549)

Martin Lind, Hwei-yen Chen, Sara Meurling, Ana Cristina Guevara Gil, Hanne Carlsson, Martyna Zwoińska, Alexei Maklakov.

Uppsala University.

Long life is not for free, but is subjected to trade-offs with other life-history traits, which themselves are often under selection in natural populations. There is a growing appreciation that by focusing on the trade-off between reproduction and lifespan, we overlook the trade-off between development and lifespan. We investigated this trade-off in two independent selection experiments. First, by manipulating extrinsic mortality rate (high/low) and mortality source (random/heat-shock) we showed that high mortality rate under heat-shock leads to the evolution of increased lifespan and fecundity in outcrossing *Caenorhabditis remanei* nematodes, but at the cost of longer development time. The evolutionary link between development and lifespan was then independently assessed in a separate selection experiment by selecting *C. remanei* populations for short or long development time. This confirmed our findings above, since selection on slow development resulted in evolution of long lifespan. Because our experimental lines did not differ in body size, our results highlight the key role of development (differentiation of the soma) in the evolution of lifespan. Since development rate is often under strong selection in time-constrained natural populations of many species, reduced somatic maintenance and thus short intrinsic lifespan may be a widespread cost of adaptation to seasonal environments.

Whole genome meiotic drive in Arthropods (53337)

Laura Ross.

The University of Edinburgh.

Sexual reproduction tends to be a remarkably “fair” and symmetrical process: a mother and father provide equal shares of their genes to their offspring, and each these has an equal chance of being passed on to future generations. Yet this symmetry has frequently broken down. Among thousands of species of insects and mites mothers monopolize the production of male offspring, by producing sons that eliminate their father's genome from their germline (Paternal genome elimination, PGE). Here I present theoretical and comparative analyses aimed at understanding the phylogenetic distribution and evolutionary dynamics of this unusual reproductive system. In addition I present empirical work on the epigenetic mechanisms by which the paternal genome is eliminated and on its implications for sex determination.

Origin, evolution and consequences of sex chromosome drive in stalk-eyed flies (53336)

Gerry Wilkinson, Josephine A. Reinhardt, Kimberly A. Paczolt.

Department of Biology, University of Maryland.

Meiotic drive is a selfish genetic element in which a chromosome is passed preferentially to gametes. When it involves a sex chromosome, biased offspring sex ratios occur and, if unchecked, can quickly cause extinction. Sex chromosome drive can persist either by balancing selection or because it is masked by some form of suppression. Multiple examples of sex chromosome drive have been uncovered in interspecific crosses of *Drosophila* where a cryptic drive system is exposed due to the absence of appropriate suppressors. Diopsid stalk-eyed flies provide a fascinating group in which to study sex chromosome drive because 1) they possess a neo-X chromosome, 2) populations of multiple species contain drive X chromosomes at frequencies up to 30%, 3) several phenotypic traits, including eyespan, differ among drive and nondrive males, and 4) crosses between populations reveal both cryptic X and Y drive. In this talk I will summarize these findings and then present recent data derived from de novo assembly of testes transcriptomes from 17 different diopsid species, which include both drive and nondrive males from four different species, to reconstruct the evolutionary history of drive and nondrive X chromosomes in the genus *Teleopsis* and identify genes associated with drive in two independent lineages. I will also describe the extent of divergence between drive and nondrive X chromosomes using pooled genome resequencing data aligned to a reference genome. Finally, I will describe results from an experimental evolution study in which mating has been manipulated each generation either to exclude sexual selection, permit sperm competition without mate choice, or allow mate choice in either the presence or absence of a drive X chromosome. Collectively, these results provide

new insights into a novel sex chromosome drive system in which the genomic landscape of the sex chromosomes is highly dynamic.

Session 1 FRI MAX 415 16

Mating system shifts and transposable element evolution (51670)

J Arvid Ågren, Stephen I Wright.

Univeristy of Toronto.

With respect to abundance, transposable elements (TEs) are an unrivalled success story among selfish genetic elements. TEs make up about half of the human genome and more than 80% of some plant genomes. Replicating faster than the rest of the genome allows TEs to spread despite their deleterious effects. However, this cannot explain why TEs are so common in some species, but not in others. Mating system is predicted to play an important role the evolutionary dynamics of TEs. Shifts to selfing from outcrossing, or from sexual to asexual reproduction, will affect both the ability of TEs to spread to new lineages and the efficacy of the selection acting on them. However, whether mating system shifts should lead to a net accumulation or loss of TEs remains unclear. We discuss results from several whole genome studies of TE abundances, genome distributions, and population frequencies, of multiple plant genera to suggest that shifts to selfing or asexuality may initially lead to an increase in TE copy number but that over longer evolutionary timescales asexual and selfing genomes will lose TEs. We discuss what this balance between transmission and selection can tell us about the evolution of selfish genetic elements more broadly.

Session 1 FRI MAX 415 16

Spore killer genomics: elucidating causes and consequences meiotic drive in *Neurospora* (52515)

Jesper Svedberg, Ruxandra I. Molnar, Thomas M. Hammond, **Hanna Johannesson**.

Uppsala University; Illinois State University.

Conflict caused by selfish genetic elements is a driving force for evolutionary innovation, and hence, of fundamental importance for all aspects of evolution. Nevertheless, empirical data on the topic is largely lacking. Here, we introduce *Neurospora* as a novel study system of the evolutionary significance of meiotic drive. In this sexual eukaryote model system, the meiotic drive element Spore killer is found. The Spore killer and its resistance factor have been mapped to an approximately 2 Mbp large region of suppressed recombination on LG3. We have introgressed the Spore killer element, the resistance and sensitive alleles into uniform genetic background, and are screening the phenotypic effects of carrying the element. Furthermore, we have sequenced 90 genomes, representing all known Spore killers as well as sensitive and resistant strains of *N. sitophila* and *N. intermedia* using Illumina HiSeq (to 30x coverage). From seven of these we have also gathered MiSeq (100x) and Pac Bio (50x) data

to create high quality, full chromosome assemblies. This data has revealed a complex pattern of inversions, insertions and deletions that may play an essential role in maintaining the region of suppressed recombination and in explaining the birth and death of Spore killers over evolutionary time.

Session 1 FRI MAX 415 16

The Molecular Basis of Paris Sex Ratio Meiotic Drive in *Drosophila simulans* (52788)

Quentin Helleu, Pierre R. Gérard, Raphaëlle Dubruille, David Ogereau, Bastien Saint Léandre, Benjamin Prud'homme, Benjamin Loppin, Catherine Montchamp-Moreau.

EGCE, CNRS UMR9034, Université Paris-Saclay - Gif sur Yvette; CG ϕ MC, CNRS UMR5534, Université Claude Bernard - Lyon; IBDM, CNRS UMR7288, Aix-Marseille Université.

Sex Ratio segregation distorters are selfish genetic elements that promote their own transmission by subverting the meiotic process to their advantage. The spread of an X-linked distorter in populations results in an excess of females, which triggers a genetic conflict between the X chromosome and the rest of the genome. Such conflicts are important drivers of genome evolution, but little is known about the molecular nature and function of the Sex Ratio selfish elements. I will present our recent work on the Paris Sex Ratio system of *Drosophila simulans*, in which two distorter elements on the X chromosome co-operate to prevent Y chromosome sister chromatids segregation during meiosis II. We mapped a gene in one of the distorter loci and achieved the functional validation of its involvement in sex-ratio distortion. It is a young and rapidly evolving gene that belongs to a well-known gene family involved in chromatin state regulation. It emerged through duplication about 15-22 Myrs ago and has experienced multiple independent cis-duplications, loss or pseudogenization throughout its evolutionary history. This suggests that this gene could have been involved in multiple genetic conflicts. These findings should help understanding the molecular basis of genetic conflicts and the evolutionary impact of heterochromatin regulation during meiosis.

Session 1 FRI MAX 415 16

Genome size variation and song attractiveness in grasshoppers: sexual selection against large genomes? (52928)

Holger Schielzeth, Corinna Streitner, Ulrike Lampe, Alexandra Franzke, Klaus Reinhold.

Bielefeld University.

Genome size evolution is affected by a conflict between selfish-genetic elements and the host genome, such that selfish genetic elements tend to increase genome size to a degree that impairs the fitness of the host. We have studied the impact of genome size on male attractiveness in the bow-winged grasshopper *Chorthippus biguttulus*. Grasshoppers exhibit

particularly large variation in genome size due to the high prevalence of supernumerary chromosomes that are considered (mildly) selfish, as evidenced by non-Mendelian inheritance and fitness costs if present in high numbers. We ranked male grasshoppers by song characteristics that are known to affect female preferences in this species and scored genome sizes of attractive and unattractive individuals. We then tested if attractive and unattractive singers differ in their genomes sizes, which would demonstrate that genome size is reflected in male courtship songs and that females select songs of males with small genomes. Such mate preferences would effectively select against further increase in genome size and could suggest an underappreciated route of how choosy females could gain indirect benefits. The data can also provide a novel example of how sexual selection can reinforce natural selection and act as an agent in an intragenomic arms race.

Session 2 MON GEN C 1

Diversity and the maintenance of sex by parasites (51799)

Ben Ashby, Kayla King.

University of Exeter; University of Oxford.

The Red Queen hypothesis predicts that parasite-mediated selection will maintain sexual individuals in the face of competition from asexual lineages. The prediction is that sexual individuals will be difficult targets for coevolving parasites if they give rise to more genetically diverse offspring than asexuals. However, increasing host genetic diversity is known to suppress parasite incidence, which could provide a short-term advantage to clonal populations and lead to the extinction of sex. We test these ideas using a stochastic individual-based model that fully incorporates ecological dynamics. We find that if parasites are readily transmissible, then sex is most likely to be maintained when host diversity is high, in agreement with the Red Queen hypothesis. If transmission rates are lower, however, we find that sexual populations are most likely to persist for intermediate levels of diversity. Our findings thus highlight the importance of genetic diversity and its impact on epidemiological dynamics for the maintenance of sex by parasites.

Session 2 MON GEN C 1

Geographical parthenogenesis in *Hieracium alpinum* (Asteraceae): molecular evidence for multiple origin of asexuality and replacement of sexual diploids by asexual triploids (52584)

Patrik Mráz, Matthias Hartmann, Pavel Zdvorák, Delphine Rioux, Philippe Choler, Jindřich Chrtěk, Pierre Taberlet.

Department of Botany, Charles University in Prague, Czech Republic; Laboratoire d'Ecologie Alpine, J. Fourier University, Grenoble, France; Institute of Botany, Academy of Sciences of the Czech Republic, Pruhonice, Czech Republic.

Many asexual species occupy larger ranges than their sexual relatives, a pattern referred to the term 'geographical parthenogenesis'. Various hypotheses have been proposed to explain such patterns, nevertheless evidence for any of them is lacking because of limited number of empirical studies. *Hieracium alpinum* is an arcto-alpine species spreading from the far North (Greenland, Iceland, Fennoscandinavia) to the southerly situated mountains (Alps, Carpathians, Sudetes). While sexual diploids occur solely in the Southern-eastern Carpathians, apomictic autotriploids cover the rest of the range. Using straightforward combination of various approaches, we aim to test the hypotheses putatively underlying the origin, distributional success and adaptive potential of asexual triploids. Molecular data based on AFLPs and three plastid loci show highly congruent patterns and indicate (i) relatively high level of molecular variation within asexuals with, however, a predominance of one widespread genotype; (ii) multiple origin of asexual lineages which did not arise from extant diploids but they are rather remnants of extinct diploid lineages which have been completely replaced by asexuals. This potentially superior fitness / colonization ability of asexuals, when compared, to sexuals is discussed in the light of field data focusing on reproduction / dispersal potential, frequency of apomixis and biotic interactions.

Session 2 MON GEN C 1

Interactions between genetic and ecological effects on the evolution of life cycles (52675)

Marie Rescan, Thoma Lenormand, Denis Roze.

Station Biologique de Roscoff, UMI 3614 CNRS/UPMC; CEFÉ, UMR 5175 CNRS/UM2 .

Sexual reproduction leads to an alternation between a haploid and a diploid phase, whose relative development varies widely across taxa, with vegetative growth occurring in one phase only (haploidy or diploidy) or in both (biphasic cycles). Previous genetic models showed that either diploidy or haploidy can be favored, depending on the dominance of beneficial/deleterious alleles and on effective recombination rates. By contrast, ecological models showed that niche differentiation between phases stabilizes biphasic life cycles.

Here, we explore the interplay between genetic and ecological factors, considering that mutations affect the ecological properties of haploids and diploids, and may have differential effects between phases. We show that selection on a modifier gene affecting the relative length of both phases can be decomposed into a direct selection term favoring the phase with the highest mean fitness (due to ecological differences or to differential effects of mutations), and an indirect selection term favoring the phase in which selection is more efficient. When deleterious alleles occur at many loci and in the presence of ecological differentiation between phases, evolutionary branching often occurs and leads to the stable coexistence of alleles coding for haploidy and diploidy, while temporal variations in niche sizes stabilize biphasic cycles.

Session 2 MON GEN C 1

Evidence for inter-individual genetic transfers among the genus *Adineta vaga* (52791)

Nicolas Debortoli, Xiang Li, Cuong Q Tang, Boris Hespeels, Diego Fontaneto, Jean-François Flot, Karine Van Doninck.

UNamur; Imperial College London; National Research Council; University College London.

Bdelloid rotifers have survived and diversified into more than 400 morphospecies over the past 40 My asexually. Genomic data suggest that chromosome pairing, and thus conventional meiosis, is impossible within the bdelloid rotifer *Adineta vaga*. Hence, their persistence and diversification as ancient asexuals is puzzling and suggest that they have developed alternative mechanisms to evolve and diversify. Using a population genetic approach combining nuclear and mitochondrial markers, distinct species delineation methods (GMYC, ABGD and Haplowebs) and genomics, we demonstrate for the first time inter-individual genetic transfers within a bdelloid rotifer lineage.

Our results indicate the existence of 6-7 distinct species in which most individuals reproduce clonally. However, two distinct patterns suggesting inter-individual genetic transfers were observed: (1) seven individuals were assigned to different species depending on the marker considered and (2) three cycles of allele-sharing in a [A||B, B||C, C||A] fashion were reconstructed. This could indicate a form of non-meiotic recombination among bdelloids such as parasexuality during which two whole chromosome sets are merged followed by random chromosome losses to re-establish the original ploidy. Alternatively, desiccation could promote horizontal gene transfers through frequent DNA double-strand breaks and genome repair upon rehydration.

Session 2 MON GEN C 1

The Red Queen and the bdelloid rotifers: host-parasite interactions in the long-term absence of sex (51907)

Christopher Wilson, Antonios Kriezis, Timothy Penny, Joshua Potter, Timothy Barraclough.

Imperial College London.

Bdelloid rotifers are a class of microscopic invertebrates that abandoned males and meiosis millions of years ago. We present a new multi-locus, fossil-calibrated phylogenetic analysis indicating that a specialised clade of fungal parasites, Rotiferophthora, has been evolving and diversifying with bdelloids for at least twenty million years. This longstanding association seemingly challenges the prominent hypothesis that asexuals cannot keep up with coevolving parasites. Ecology offers a possible explanation: when their habitats dry up, bdelloids can persist for months as dormant, desiccated propagules that disperse widely by wind. Rotiferophthora cannot tolerate extreme drought stress, and is destroyed or left behind, potentially interrupting the coevolutionary process and rescuing asexual hosts. To investigate this hypothesis, we challenged bdelloid clones from three global locations with twenty phylogenetically resolved fungal isolates, sympatric and allopatric. As predicted, Rotiferophthora isolates showed no local adaptation to bdelloid populations, partly because they had rather broad host ranges, as expected if they cannot follow specific hosts through

space and time. We also found some bdelloid clones that detected and destroyed ingested Rotiferophthora spores, demonstrating that although these ancient asexuals frequently 'run' from longstanding enemies, they can also mount an immunological fight, whose basis is an intriguing target for future investigation.

Session 2 MON GEN C 1

No evidence for parasites maintaining sex in natural stick insect populations (52405)

Chloé Larose, Tanja Schwander.

UNIL, Department of Ecology & Evolution.

Sex is a conundrum of evolution! Since only females can directly produce offspring, asexual reproduction avoids the cost of producing males inherent to sexual reproduction. Nevertheless, asexuality is rare while obligate sex is widespread. One of the main hypotheses to explain the maintenance of sex is the Red Queen theory. This theory suggests that sex allows organisms to respond more effectively to continual changes in their environment, which is particularly relevant in the case of coevolution with parasites. However, we found no evidence for parasites maintaining sex in natural Timema stick-insect populations. We first identified a fungal parasite that infects a large proportion of individuals in their natural habitat, but found no evidence that sexuals are less infected by the parasite compared to related asexual species. By experimentally infecting individuals, we confirmed that infection induces an immune response, and has negative fitness effects for the host. Infection rates following reciprocal transplantation in the field further indicate local co-evolution between hosts and parasites, but no differences between sexual and asexual hosts. These results suggest that coevolution with this parasite is not selecting for sexual reproduction in Timema.

Session 2 MON GEN B 5

Sexually antagonistic effects on development and transcriptomic maturity in Drosophila (52779)

Brian Hollis, Laurent Keller, Tadeusz J Kawecki.

University of Lausanne.

Sexually antagonistic selection exists whenever the evolutionary interests of males and females diverge and is an ultimate explanation for sexual dimorphism. The sexes must share most of the genome, however, so the evolution of sexual dimorphism is likely to be constrained in many ways. Here we will report the results of an experimental evolution study in Drosophila where selection on one sex has been greatly relaxed for over 150 generations by the elimination of all mating competition. This has resulted in parallel evolutionary change in the sexually dimorphic transcriptome of replicate populations. Beyond this, measures of sex-

specific maturation rate, at both the level of gene expression and egg-to-adult developmental timing, show elevated female performance and reduced male performance. Together, these experimental results represent the signature of an evolutionary process by which the genome is being optimized for female function at the expense of males.

Session 2 MON GEN B 5

Sex-specific effects of serotonin on behavior and gene expression in a stalk-eyed fly (52813)

Jaime Grace, Andrew Bubak, Michael Watt, Kenneth Renner, John Swallow.

University of Colorado Denver; University of South Dakota.

Stalk-eyed flies, *Teleopsis dalmanni*, experience intense sexual selection, both intersexual and intrasexual, as males compete over access to territories and females. Males with longer eyestalks are both more attractive to females and more likely to win aggressive contests with other males. Serotonin (5-HT) plays a critical role in aggressive behavior: males with artificially elevated 5-HT levels are more likely to win competitions with size-matched opponents over a food source. However, the increase in aggression in response to elevated 5-HT may be sexually dimorphic. We first examined whether females treated with 5-HTP (5-hydroxytryptophan, the serotonin precursor that is converted to serotonin in the brain) are more likely to exhibit aggressive behaviors towards other females in size-matched contests. We then performed RNA sequencing on the brains of males and females treated with 5-HTP to determine which genes are differentially expressed relative to controls. Intriguingly, we found that females treated with 5-HTP exhibited fewer aggressive behaviors and were less likely to win aggressive competitions. We also describe candidate genes that may contribute to this dimorphic behavioral response. These studies illuminate the sexually dimorphic role of serotonin in modulating aggression and highlight other genes that may contribute to these sexually dimorphic aggressive behaviors.

Session 2 MON GEN B 5

Convergent evolution of female-limited color dimorphism in *Drosophila* (52828)

Amir Yassin, Héloïse Bastide, Justin Lack, Jean David, John Pool.

University of Wisconsin Madison, USA; Laboratoire EGS, CNRS, France.

Drosophila melanogaster abdominal pigmentation is a paradigm trait for the study of the genetics of sexual dimorphism. This pattern is highly variable between species, but the genetic basis and evolutionary causes of its liability remain unclear. In *D. erecta* (melanogaster group) and circa 20 species of the montium group, the dimorphism is restricted only to females, with one female morph resembling monomorphic males. By combining intra- and inter-specific introgression mapping and comparative genomics we showed that female-

limited color dimorphism (FLCD) is associated with the X-linked tan locus in *D. erecta*, and with the autosomal transcription factor pdm3 in three species of the montium group. Population genetics revealed the presence of a partial selective sweep on the dark allele in *D. erecta* (where males are dark), and an interspecific introgression of the light allele between two montium species (where males are light). We hypothesize that male mimicry evolution is due to female alternative strategies for optimal mating rate, and test this hypothesis using population cages under different sex-ratio regimes. Given the unique genetic tools available for these species, we believe that *Drosophila* FLCD may present a prime model for the study of the recurrent evolution of sexual dimorphism in action.

Session 2 MON GEN B 5

Trans-regulation of sexually discordant expression from the *Drosophila melanogaster* X chromosome (52930)

Michael Stocks, Rebecca Dean, Björn Rogell, Urban Friberg.

University of Sheffield; University College London; Stockholm University; Linköping University.

The X chromosome constitutes a unique genomic environment because it is present in one copy in males, but two copies in females. This simple fact has motivated several theoretical predictions with respect to how standing genetic variation on the X chromosome should differ from the autosomes. In this study we tested for the amount and the type of genetic variation on the X chromosome within a population of *Drosophila melanogaster*, by comparing the proportion of X linked and autosomal trans-regulatory SNPs with sexually concordant and discordant effect on gene expression. We find that the X chromosome is depleted for SNPs with a sexually concordant effect, but hosts comparatively more SNPs with a sexually discordant effect. Interestingly, this enrichment only concerns SNPs with a larger influence on expression in females than expression in males. The distribution of these SNPs is shifted towards regions where dosage compensation is predicted to be less complete. These results suggest that intrinsic properties of dosage compensation influence either the accumulation of different types of trans-factors and/or their propensity to accumulate mutations. These results have general implications for X chromosome evolution, as well as the genetic basis of sex-specific evolutionary change.

Session 2 MON GEN B 5

Sexual selection drives evolution and rapid turnover of male-biased genes (51628)

Peter W. Harrison, Alison E. Wright, Fabian Zimmer, Rebecca Dean, Stephen H. Montgomery, Judith E. Mank.

University College London.

The rapid rates of evolution for sex-biased genes has led to the widespread assumption that they are the genomic manifestation of sexual selection. However, we still lack a clear understanding of the connection between sexual selection and transcriptional dimorphism. To assess the role of sexual selection in shaping evolutionary patterns of sex-biased genes, we assembled transcriptomes from an avian clade representing the full range of sexual selection. Using phylogenetically-controlled comparative methods, we show for the first time that sexual selection drives both rate of turnover in sex-biased expression as well as the degree of transcriptome sexualization. Our data also indicate that the rapid turnover in sex-biased gene expression occurs primarily through male expression evolution, and this is true for both male- and female-biased genes. Finally, our results suggest that the elevated rates of sequence evolution often observed for male-biased genes may not actually be due to adaptive evolution, and therefore sexual selection. Rather, our results implicate relaxed purifying selection as the principal cause of elevated rates of evolution. Taken together, our results provide the first direct links between sexual selection and evolutionary properties of sex-biased genes, highlighting the power of sexual selection in shaping gene expression and genome evolution.

Session 2 MON POL A 28

Evolution by r- and K-selection in fluctuating environments (51771)

Bernt-Erik Saether, Steinar Engen, Visser Marcel E, Grøtan Vidar.

Centre for Biodiversity Dynamics, NTNU; Centre for Biodiversity Dynamics, NTNU; Netherlands Institute of Ecology; Centre for Biodiversity Dynamics, NTNU.

More than half a century ago r – and K –selection was proposed as a general process for producing evolutionary change, provided that phenotypic fitness depends on population size. Such density dependent selection will favour phenotypes with large growth rates r at small population sizes and phenotypes with high competitive skills when populations are close to the carrying capacity K . Here we present a new stochastic modelling framework that enables us to partition phenotypic selection in fluctuating environments into components due to population growth rate at low densities and strength of density dependence. Using the number of eggs laid in a season in a small song-bird, the great tit, as a phenotype, there is strong evidence for phenotypic variation in the strength of selection, resulting in balancing selection favouring large clutch sizes (r-selection) at small population densities and smaller clutches (K-selection) in years with large populations. Fluctuations in population size thus affect the fitness of individuals that lay different clutch size differently. This provides clear empirical evidence for r- and K-selection as an important selective agent in natural populations, which in turn may contribute to evolutionary rescue of populations affected by environmental perturbations such as climate change.

Session 2 MON POL A 28

Maintenance of polymorphism through small-scale spatial variation in selection (51814)

Rolanda Lange, Keyne Monro, Dustin Marshall.

Monash University.

How does trait diversity persist even though it is effectively depleted by selection? In theory, polymorphisms can be maintained by spatial and temporal variation in selection. To quantify such variation, we measured selection in a marine bryozoan along a depth gradient of only three meters - a small spatial scale relative to dispersal potential. Using life-time reproductive output in the field as a fitness measure we estimated multivariate selection on five phenotypic traits relating to individual size, colony growth and phenology. We found strong spatial variation in both linear and quadratic selection in several traits. Our results suggest that selection can vary over remarkably small environmental gradients, limiting the ability of dispersive marine species to adapt to any one environment and maintaining trait diversity.

Session 2 MON POL A 28

Variation in selection in a wild insect population (51888)

Tom Tregenza, Rolando Rodríguez-Muñoz, David Fisher, Jon Slate, Ian Skicko, Sophie Kendall, Xingping Liu, Paul Hopwood, Carlos Rodríguez del Valle.

University of Exeter; University of Sheffield; Jiangxi Agricultural University.

Quantifying variation in selection in natural populations is essential for understanding its evolutionary importance. There are now a number of long term field studies that have successfully documented patterns of selection in plants and wild vertebrates. Short-lived exothermic animals are likely to experience greater variation in selection across generations than longer lived species. However, despite their abundance, measures of selection across years in wild invertebrates remain scarce. We have remotely monitored an individually tagged population of wild crickets using a network of up to 130 day-night video cameras distributed across individually marked burrows. This allows us to capture detailed information about naturally and sexually selected traits and life-history parameters, and to combine these data with local climatic variables. We have analysed >400,000 hours of video, recording >100,000 behavioural events. Over 9 years of monitoring, annual population size has fluctuated between 51 and 541 adults. There has also been substantial variation among years in sex ratio and traits including adult emergence dates, body size, male wing morphology and lifespan. Our data reveal individual mating patterns, dominance hierarchies, mortality sources and other key events. We combine these data with individual genotyping of the population, to provide insights into variation in selection in a wild insect population.

Session 2 MON POL A 28

A general condition for adaptive genetic polymorphism in temporally and spatially heterogeneous environments (51891)

Hannes Svoldal, **Claus Rüdfler**, Joachim Hermisson.

Gregor Mendel Institute, Austrian Academy of Sciences, Vienna; Animal Ecology, Department of Ecology and Genetics, Uppsala University; Mathematics and Biosciences Group, Department of Mathematics, University of Vienna.

Both evolution and ecology have long been concerned with the impact of environmental variability on levels of diversity. We model the evolution of a quantitative trait under selection that fluctuates in both space and time, and derive an analytical condition for when these fluctuations promote genetic diversification through adaptation to different environmental conditions. As ecological scenario we use a generalized island model with soft selection within patches in which we incorporate generation overlap. We allow for arbitrary fluctuations in the environment including spatio-temporal correlations. Using the concepts of invasion fitness and evolutionary branching, we derive a simple and transparent condition for the adaptive evolution and maintenance of genetic diversity. This condition relates the strength of selection within patches to expectations and variances in the environmental conditions across space and time. Our results unify, clarify, and extend a number of previous results on the evolution and maintenance of genetic variation under fluctuating selection. Individual-based simulations show that our results are independent of the details of the genetic architecture and whether reproduction is clonal or sexual. The onset of increased genetic variance is predicted accurately also in small populations in which alleles can go extinct due to environmental stochasticity.

Session 2 MON POL A 28

Spatio-temporal heterogeneity of natural selection in the wild: an experimental approach towards understanding life history adaptation of *Arabidopsis thaliana*. (52035)

Moises Exposito-Alonso, Adrian Brennan, Carlos Alonso-Blanco, F. Xavier Picó.

Max Plank Institute for Developmental Biology, 72076 Tuebingen, Germany; School of Biological and Biomedical Sciences, University of Durham, DH1 3LN Durham, UK; Spanish National Center for Biotechnology, Spanish National Research Council, 28049 Madrid, Spain; Doñana Biological Station, Spanish National Research Council, 41092 Sevilla, Spain.

The model annual plant *Arabidopsis thaliana* has become a useful model for evolution and ecology but just a few studies have addressed selection gradients on life history traits. Because *A. thaliana* shows a duality of life cycle - i.e. winter or spring cycles - we hypothesize enormous adaptive potential via life cycle adjustment in changing environments. We performed common garden experiments with 50 Iberian accessions (with the same genetic background to avoid bias) in two natural settings at different altitudes (350 and 1650 m) and starting at autumn and spring within every year for four years (2010-2014). We recorded germination rate, survivorship, flowering time, number of reproductive individuals, and number of seeds per plant. We detected huge plasticity of life cycle among genotypes, something that allowed good performance under very different conditions. Using integrated fitness, we found significant directional selection for flowering time and germination rate by experiment. Magnitude and sign of selection changed across locations and years. In the light of these results, we confirmed the importance of life cycle adjustment for climatic adaptation.

We also predict that environmental heterogeneity, and hence selection, can maintain phenotypic and genetic diversity in different environments, although at different frequencies.

Session 2 MON POL A 28

Tempo does not infer mode in evolution (52645)

Kjetil Voje.

Centre for Ecological and Evolutionary Synthesis (CEES), University of Oslo.

We lack a consensus on evolutionary rates in biology. The claimed dominance of almost no lineage evolution (stasis) in the fossil record does not rest well with the observation of high evolvability of virtually any quantitative trait studied in contemporary populations. This ‘paradox of stasis’ makes the long-term history of life seem almost decoupled from the evolutionary process we study on shorter time-scales. I analyze the rate of evolution in a large number of fossil time series that fit different modes (e.g. stasis, directional change) using novel statistical tools. I find no relationship between the mode of evolution and rate of change in the fossil record. The fluctuations observed in traits during stasis represent the same distance traveled in phenotype space compared to traits that fit different modes of evolution, including directional change. The result holds for fossil time series on various time scales. The observation of a similar rate of evolution during stasis and directional change in the fossil record has implications on several contemporary debates in evolutionary biology, and may increase our ability to explain macroevolutionary patterns with microevolutionary processes.

Session 2 MON POL A 28

Consequences of multiple-scale variation in selection on microgeographic adaptation (52197)

Philippe Cubry, Sylvie Oddou-Muratorio, Ivan Scotti, François Lefèvre.

INRA URFM "Ecologie des Forêts Méditerranéennes", UR629.

Local adaptation is generally considered at a large geographic scale, due to the common idea that high gene flow at microgeographic scale (i.e. within dispersal neighborhood) should prevent sub-populations to evolve traits conferring them a better fitness in their micro-habitat. However, environmental heterogeneity within populations can be huge, and was shown to result in microgeographic adaptation in some recent empirical studies.

Here we used NEMO simulation framework to simulate patterns of environmental heterogeneity both within (microgeographic scale) and among populations. Considering different strengths of selection, demographic parameters and genetic architectures, we evaluate local adaptation at microgeographic and population scales by using hierarchical F_{st} and Q_{st} on quantitative loci.

Our results demonstrate that local adaptation at microgeographic scale occurs even under relatively low selection intensities. The decoupling between Q_{st} and F_{st} appears higher at the microgeographic scale than at higher population scale, likely because the relative contribution of allelic combinations (compared to changes in allele frequencies) to local adaptation is higher at this microgeographic scale due to higher gene flow. This study sheds light on the potential of microgeographic adaptation to maintain local genetic diversity and to contribute to the evolvability of the population.

Session 2 MON POL B 15

Adaptive genome remodeling by massive changes in gene content and gene transfers across gene fungi (52106)

Antoine Branca, Jeanne Ropars, Ricardo Rodríguez de la Vega, Manuela López-Villavicencio, Jérôme Gouzy, Erika Sallet, Emilie Dumas, Joëlle Dupont, Tatiana Giraud.

University Paris-Sud CNRS - ESE; University of Ottawa - CIAR; Museum National d'Histoire Naturelle CNRS - SEB; INRA/CNRS - LIPM.

Cheesemaking has been an essential innovation for the transformation of milk, a highly perishable food, into a long-term preservable product. Two key *Penicillium* species have been used for the maturing of cheese: *Penicillium roqueforti* for blue cheeses and *P. camemberti* for Brie-type cheeses. These two distantly related molds have been independently selected for growth in a human-made nutrient-rich environment. Here we compared the genomes of ten *Penicillium* species isolated from various environments, including five newly-sequenced genomes. We show that *Penicillium* fungi have adapted to the cheese medium through the convergent expansions of multigene families and multiple recent horizontal transfers of crucial metabolic genes. We found in cheese-making *Penicillium* high numbers of lineage-specific genes family expansions involved in the utilization of the nutrients present in the cheese, such as lactate and phospholipids. Most of these species-specific gene expansions co-occurred in recently horizontally transferred regions, with almost 100% identity between distant species, and flanked by specific transposable elements. Laboratory assays linked the presence of a cheese fungus-specific horizontally-transferred region to both faster growth and greater competitiveness on cheese. Our results have both industrial and food safety implications, and improve our understanding of the genomic processes of adaptation to rapid environmental changes.

Session 2 MON POL B 15

Transcriptome comparisons within a species complex: Half a million years is enough to remove half of the genetic diversity in coding sequences, but not enough for morphological differentiation. Influence of life history (52218)

Anne CHENUIL, Nicolas GALTIER, Laurent ABI-RACHED, Alexandra WEBER.

IMBE - Centre National de la Recherche Scientifique - Aix-Marseille Université - IRD; ISEM - Centre National de la Recherche Scientifique- Université Montpellier 2 ; URMITE - Centre National de la Recherche Scientifique - INSERM - IRD - Aix-Marseille Université.

Complexes of closely related species are interesting models especially when species are sympatric and display contrasted traits. *Ophioderma longicauda* (Echinodermata) was recently characterized as such. Although typically reproducing via lecithotrophic larvae, some lineages brood their offspring. Transcriptomes from few individuals of those species were sequenced. While whole transcriptome comparisons show that genetic diversity in the brooding species is about half that of the species with larvae, this difference increases to 3-to-4 fold when assessed on numerous individuals (with fewer genetic markers). Species delimitation within the complex was established by discriminant analysis of principal components (DAPC) based on multilocus genotypes (32 multiallelic loci). Divergence times between species were obtained using Approximate Bayesian Computation (ABC) and a calibration with a pair of *Ophioderma* species separated by the Isthmus of Panama, which closed about 3.5 mya. ABC also estimated that effective sizes were much lower in the brooder than in ancestral and broadcasting species. Thus, in only 550000 years (ca 100,000 generations), genetic diversity drastically decreased in the brooders, probably owing to increased genetic drift. We discuss whether this evolution would have been as rapid if a species with a large effective size had emerged from a smaller effective size ancestor.

Session 2 MON POL B 15

Evolutionary dynamics of bacterial pan-genomes (52245)

Jane Charlesworth, Daniel Wilson, Derrick Crook.

MMM, University of Oxford.

Bacterial genomes are dynamic landscapes. Gene gain/loss events are common in many bacteria, such that strains within a species may vary quite a lot in gene content. As a result of this extreme genome plasticity, bacteria are commonly described as having ‘core’ and ‘accessory’ genomes, where core genes are present in all, or virtually all examined isolates of a species and accessory genes are variably present and absent. The complete gene repertoire available to a bacterial species, or ‘pan-genome’, is an important resource for investigating the genetic basis of phenotypes such as pathogen virulence (for example by looking at the association of gene gain/loss events with phenotypes of interest) but constructing this set is computationally very challenging. Using whole genome sequencing data, our work aims to investigate which functional groups accessory genes represent and the phylogenetic distribution of gene gain/loss events in population-level datasets from a diverse range of bacterial species, including *Staphylococcus aureus* and *Escherichia coli*. We have developed a bioinformatics pipeline to rapidly obtain the set of all genes present in thousands of sequenced bacterial samples and are investigating the consequences of increasingly diverse and comprehensive sampling on estimates of bacterial pan-genome content and size.

Session 2 MON POL B 15

Avian phylogenomic analyses revealed the macroevolution patterns of bird genomes (52249)

Guojie Zhang.

Centre for Social Evolution, Department of Biology, University of Copenhagen, Copenhagen, Denmark; National Genebank, BGI, Shenzhen, China.

Characterization of genomic biodiversity through comprehensive species sampling has the potential to change our understanding of evolution. To study evolution across a major vertebrate class, dissect the genomics of complex traits, and resolve a centuries-old debate on the avian species tree, we formed a consortium focused on sequencing and analyses 48 bird genomes covered all 30 neognath orders, representing a wide range of avian evolutionary diversity. The phylogenomic analyses with full genome data produced a highly supported avian order phylogeny that resolves many debates on the timing and topology of their radiation. Whole genome comparison for all bird species with other vertebrate species revealed several distinct macroevolution patterns of avian genome. The small genome size of bird was a consequence of massive loss of repeat elements and thousands of functional genes at ancestral stage. Avian genomes furthermore show a remarkably high degree of evolutionary stasis at the levels of nucleotide sequence, gene synteny, and chromosomal structure. Despite this pattern of conservation, we detected many non-neutral evolutionary changes in protein-coding genes and noncoding regions. These analyses reveal that pan-avian genomic diversity covaries with adaptations to different lifestyles and convergent evolution of traits.

Session 2 MON POL B 15

Fixation of gene duplications due to beneficial increases in gene expression (52436)

Margarida Cardoso-Moreira, J. Roman Arguello, David Riccardi, Srikanth Gottipati, Lawrence G. Harshman, Jennifer K. Grenier, Andrew G. Clark.

Department of Molecular Biology and Genetics, Cornell University, USA; Center for Integrative Genomics, University of Lausanne, Switzerland; Translational Medicine and Think Team, Otsuka Pharmaceutical Development and Commercialization, Inc; School of Biological Sciences, University of Nebraska-Lincoln , USA.

Gene duplications are a crucial source of genetic innovation and serve as major contributors to phenotypic evolution. Despite their evolutionary importance there are critical gaps in our understanding of how gene duplications fix in natural populations. Two outstanding questions remain: 1) Are gene duplications more often fixed by genetic drift or by positive selection?, and 2) If gene duplications are fixed by positive selection, what are the targets of selection? Here we address these two questions using the *Drosophila* Global Diversity lines, a novel resource of 84 *D. melanogaster* genomes derived from 5 geographically diverse populations that is well-suited for studies of local adaptation. We detected ~2,200 polymorphic duplications, including ~500 whole-gene duplications. We investigated the potential impact of these duplications by generating gene expression profiles for each line. We found that ~50% of gene duplications lead to significant increases in gene expression, and that these changes in

dosage are usually deleterious. However, the high-frequency gene duplications, for which we found evidence of positive selection, also had significant increases in gene expression. Our work suggests that gene duplications can be driven to fixation by positive selection in *Drosophila*, probably due to beneficial increases in gene dosage.

Session 2 MON POL B 15

Adaptive Evolution of a Clinal Inversion Polymorphism in *Drosophila melanogaster* (52643)

Martin Kapun, Chloé Schmidt, Jérôme Goudet, Paul Schmidt, Thomas Flatt.

Department of Ecology and Evolution, University of Lausanne, Lausanne, Switzerland;
Department of Biology, University of Pennsylvania, Philadelphia, USA.

In(3R)Payne, a common cosmopolitan inversion in *D. melanogaster*, exhibits steep latitudinal clines across multiple continents, but whether this pattern is due to spatially varying selection or demography remains unclear. To address this fundamental question we first estimated inversion frequencies by applying diagnostic marker SNPs to pool-seq data from 10 populations along the North American east coast. By comparing our estimates to published records we find that the inversion cline has remained stable for over thirty years. Consistent with this cline being maintained by selection, QST-FST analysis suggests that In(3R)P evolves non-neutrally. In further support of an adaptive scenario, SNP-wise regression reveals numerous inversion-associated alleles differentiated in parallel between the North American and Australian clines. Second, we sequenced pools of isochromosomal lines of In(3R)P karyotypes from the endpoints of the North American cline and identify major inversion-specific genetic differentiation among karyotypes. Finally, again paralleling observations from Australia, we find that In(3R)P makes a major contribution to the well-known body size cline in North America. Together, these results provide compelling evidence that In(3R)P is maintained by spatially varying selection across multiple continental clines.

Session 2 MON POL B 15

Whole genome sequencing reveals an antibiotic resistance determinant driving rapid evolutionary change via several mechanisms in a multi-species outbreak (52688)

Anna Sheppard, Nicole Stoesser, Adam Giess, Robert Sebra, Andrew Kasarskis, Tim Peto, Derrick Crook, Costi Sifri, Amy Mathers.

MMM Consortium, Nuffield Department of Clinical Medicine, University of Oxford, Oxford, UK; Icahn School of Medicine, Mount Sinai, New York, New York; Public Health England, Microbiology Services, London, UK; Department of Medicine, University of Virginia Health System, Charlottesville, Virginia; Office of Hospital Epidemiology, University of Virginia Health System, Charlottesville, Virginia; Department of Pathology, University of Virginia Health System, Charlottesville, Virginia.

The presence of the *Klebsiella pneumoniae* carbapenemase (KPC) gene blaKPC confers resistance to last line antimicrobial therapies, resulting in higher mortality in human infections. Although first described in *K. pneumoniae*, blaKPC has been acquired by multiple species of gram-negative bacteria and is usually found in association with the mobile transposon Tn4401. Here we describe an outbreak of blaKPC-positive Enterobacteriaceae from patients at a single US hospital prospectively collected over five years. We performed Illumina sequencing of 291 isolates from 189 patients, as well as long-read (Pacific Biosciences) sequencing of a subset to generate closed genomes. Twelve species were identified, with high intra-specific diversity, indicating frequent horizontal transfer of blaKPC within and between species. Two fully sequenced blaKPC plasmids carried by isolates from the index patient were each found in multiple species, demonstrating plasmid transfer as a mechanism for blaKPC spread. A number of unrelated plasmids carrying blaKPC were also identified, indicative of Tn4401 transposition between different plasmids. This work demonstrates that short-term evolution of bacterial pathogens can be driven by inheritance at multiple levels; in addition to vertical inheritance, we found a high frequency of horizontal transmission, facilitated either through promiscuous, highly mobile blaKPC plasmids or Tn4401 transposition.

Session 2 MON POL C 14

The effects of increasing parasite diversity on the evolution of resistance/infectivity and host/parasite growth (51903)

Alex Betts, Craig Maclean, Kayla King.

Oxford University.

Bacteriophages, the viral parasites of bacteria, have been suggested as an alternative to antibiotics in the face of increasing resistance in harmful bacteria. However, unlike antibiotics, bacteriophages can coevolve to counter new resistant phenotypes. While, most work on bacteria-bacteriophage coevolution has focussed on pairwise combinations of one phage against one bacterial species, phages naturally exist in parasitic communities. Phages vary in their ability to suppress bacterial populations and in the resistant phenotypes they select for in hosts. Phage community diversity may thus have complex ecological and evolutionary consequences in harmful bacterial populations of therapeutic relevance. We investigated the effects of phage community complexity on bacterial population growth and the evolution of resistance and infectivity using *Pseudomonas aeruginosa* PAO1 and a panel of lytic, dsDNA bacteriophages. Parasite diversity was manipulated by creating different combinations of phage up to a 5 phage cocktail. The bacteria and bacteriophage communities were allowed to coevolve and resistant phenotypes emerged very rapidly. Clones showing resistance to a 5 phage cocktail emerged within 24 hours. Additionally we observed reduced phage titres in more diverse communities, possibly an effect of inter-phage competition. These findings could have potentially important implications for application of bacteriophages as biological control agents.

Session 2 MON POL C 14

Evolution of competitive ability in multispecies bacterial communities is sensitive to community composition (51942)

Tarmo Ketola, Lauri Mikonranta, Jouni Laakso, Johanna Mappes.

University of Jyväskylä; University of Helsinki.

Very few studies have experimentally assessed the evolutionary effects of species interactions within the same trophic level. In such communities, the need for fast exploitation of resources could drive the evolution of increased resource competition and growth rate. Accordingly, when *Serratia marcescens* bacteria evolved in 20 different four species communities, their growth rate exceeded the growth rate of the clones that had evolved alone. In addition to the community effects the existence of key species that control much of the community's functionality is often emphasized in the ecological literature. Here we show experimentally that some species can also strongly affect the evolutionary effects in communities where all the members occupy the same trophic level. This result shows that evolution can lead to vastly different outcomes depending on the community structure, which could complicate prediction of consequences environmental changes on species living in multispecies communities.

Session 2 MON POL C 14

The role of dispersal and interspecific competition on local adaptation (52045)

Dries Bonte, Karen Bisschop, Rampal S. Etienne, Dries Bonte.

Ghent University; University of Groningen.

Besides selection, biological interactions and non-selective forces can influence the rate at which a species can adapt to a new habitat. However, experimental evidence is usually scarce. Here, using experimental evolution we investigate the role of dispersal and interspecific competition on the rate to which the spider mite (*Tetranychus urticae*) can adapt to a new host plant. Additionally, we test whether an increase in adaptation leads to an increase in competitive ability. Our results show a humpback shaped relation between dispersal and adaptation and a negative impact of competition on adaptation. We also show that populations that adapt to a new host without the presence of a competitor increase their competitive abilities when later exposed to competition.

Session 2 MON POL C 14

Rescued by evolution - problems ahead: Adapting to fluctuating environment increases invasiveness (52169)

Kati Saarinen.

University of Jyväskylä.

Evolving in a disturbed environment might select for traits that promote invasiveness; rapid population growth, plasticity and persistence. Disturbed and heterogeneous environments might also be more prone to invasions than non-disturbed. These are interesting theories especially now, when the climate change causes increasing amounts of disturbances. These timely ideas were put into practice in an experiment utilizing *Serratia marcescens* bacterial strains evolved for 2.5 months at rapidly fluctuating or constant temperature, and by following *S. marcescens* invasion success to bacterial communities under thermal fluctuations or under constant temperature. We found very clear evidence that the fluctuation adapted strains had evolved a better ability to invade bacterial communities than the ones from the constant environment. This phenomenon got even more pronounced as invasion proceeded further. Moreover, thermal fluctuations during invasions clearly promoted the invasion. It is ironic that the very same strains that had avoided extinction by evolution, evolved to become more invasive. Thus, climate change induced environmental fluctuations do not only impose threat on biota by driving species extinct. If species can evolve ways to cope fluctuations, evolutionary rescue can also lead to the emergence of invasive genotypes - pests and pathogens.

Session 2 MON POL C 14

Life after death: The fate of the microbiota of a dying host (52493)

David Preiswerk, Jean-Claude Walser, Dieter Ebert.

Zoological Institute, University of Basel; Genetic Diversity Centre (GDC), ETH Zürich.

From a microbial perspective living organisms represent dynamic, transient ecosystems. The transition of a living host to dead organic matter implies profound changes in habitat properties which will find expression in microbiota composition. The microbiota dynamics before and beyond host death can in turn shed light on lifestyle and ecology of the respective microbes.

We examined the temporal dynamics of the microbiota of the planktonic crustacean *Daphnia magna* through 16S amplicon Illumina MiSeq sequencing. Conventional clonal animals were starved to death under axenic conditions and left for four days of decomposition. Over the entire timeframe samples were collected in 12 hourly intervals.

We found strong temporal dynamics in microbiota composition. Most prominently the genera *Limnohabitans* and *Rubrivivax* (both Betaproteobacteria) increased during starvation but decreased strongly towards and after host death. *Pseudomonas* (Gammaproteobacteria) and *Rhodobacter* (Alphaproteobacteria) however only appeared before host death and increased strongly during decomposition. These results suggest an important, unexplored role of the dead host in microbiota ecology. For opportunistic bacteria the strategy to persist in the living host and subsequently exploit its remains for efficient proliferation could be very successful. The decaying host would thus act as an environmental reservoir for colonization of novel hosts.

Session 2 MON POL C 14

The effect of interspecific competition on the evolutionary response of photosynthetic algae to elevated CO₂ (52706)

Diane Lawrence, Sinéad Collins.

University of Edinburgh.

Species' evolutionary responses to novel environments are often shaped by biotic interactions such as predation and competition. Experimental work has demonstrated that in some cases competitive pressures may push adaptation to proceed more quickly but also that competition may hinder adaptation, for example, due to trade-offs. Here we ask what the evolutionary consequences of interspecific competition are when the initial growth response to the novel environment is positive, as will often be the case with photosynthetic species in acidifying oceans. We tested the prediction that interactions between species would inhibit adaptation to elevated CO₂ using experimental evolution with the marine algae *Ostreococcus*. We selected 6 *Ostreococcus* lineages for approximately 200 generations in monoculture and in cocultures at average pCO₂ of 430µatm and 1000µatm in fluctuating and stable CO₂ regimes. Here we discuss the evolutionary response to elevated CO₂, the impact of species interactions on adaptation to elevated CO₂ and the effect that interspecific competition during evolution had on the capacity of the organisms to respond to further abiotic and biotic changes. The results of this experiment will contribute to our understanding of the impacts that biotic interactions have on species adaptation to favourable novel environments.

Session 2 MON POL C 14

The interaction of *Saccharomyces paradoxus* with its natural competitors on oak bark (52807)

Vienna Kowallik, Duncan Greig.

Max Planck Institute for Evolutionary Biology, Plön, Germany; Department of Genetics, Evolution, and Environment, University College London, London, UK.

We studied the ecology and interactions of *Saccharomyces paradoxus*, the closest related species of the model organism *S. cerevisiae*, in natural oak bark medium. In nature, *S. paradoxus* is often found on oak trees but it is unclear whether the yeast's association with oaks is an artifact of biased sampling methods or whether it is adapted to this habitat. We show that *S. paradoxus* grows surprisingly well on sterilized oak bark medium, but its growth is largely suppressed by the oak bark community in nonsterilized oak bark. We cultured and identified a set of twelve common fungal and bacterial species from oak. High-throughput DNA sequencing of oak bark samples verified that these microbes were representative of the oak microbial community. We then tested how each of the twelve microorganisms affected the growth of *S. paradoxus* in direct competition in oak bark medium at temperatures representing summer and winter conditions. We identified positive and negative interactions: one *Pseudomonas* species produced a diffusible toxin that killed *S. paradoxus*, whereas a *Mucilaginibacter* species had the opposite effect and facilitated *S. paradoxus*' growth. Further experiments indicated a mutualistic interaction between these two species that was only apparent in the complex, natural medium.

Bias in the Heritability of Preference and its Potential Impact on the Evolution of Mate Choice (51734)

Derek Roff, Daphne Fairbairn.

University of California; University of California.

The evolution of mate choice is a function of the heritability of preference. Estimation in the laboratory is typically made by presenting a female with a limited number of males. We show that such an approach produces a downwardly biased estimate, which we term the heritability of choice. Because females in the wild typically survey on average less than 5 males we argue that the heritability of choice may be more meaningful than the heritability of preference. The restricted number of males surveyed can lead to a reduction in the phenotypic variance of the preferred trait in the group of males selected by the females if the phenotypic variance in preference is equal to or less than the phenotypic variance in the referred trait. If the phenotypic variance in preference exceeds that of the preferred trait the opposite occurs. A second effect of the restricted number of males sampled is that females are likely to mate initially with males that are not the most preferred. The failure to find the most preferred male may account for the common observation of multiple matings and extra-pair copulations. We suggest that current explanations for polyandry need to take this failure into account.

Heritability of heterozygosity leads to transgenerational effects of heterozygosity and inbreeding (51802)

Pirmin Nietlisbach, Lukas Keller, Erik Postma.

University of Zurich.

Although many studies have shown that heterozygosity is subject to natural and sexual selection, its response to selection is rarely considered. Indeed, despite the fact that heterozygosity has previously been shown to be heritable whenever allele frequencies are unequal, this mathematical inevitability remains largely unknown. Furthermore, quantitative predictions of heritability of heterozygosity have so far only been possible for bi-allelic loci. Here we use newly developed theory for multi-allelic loci, as well as a long-term individual-based dataset and 160 microsatellite markers for an island population of song sparrows (*Melospiza melodia*) to show that the empirically estimated heritability of heterozygosity of 0.31 closely matches our theoretical predictions. Combined with a correlation between heterozygosity and fitness, this allows for a response to selection of heterozygosity. Additionally, because heterozygosity is heritable, the heterozygosity of descendants of inbred individuals will be reduced, irrespective of their own inbreeding level. In line with this, we show that ancestral inbreeding is a predictor of heterozygosity in song sparrows. Interestingly, this effect is expected to have fitness consequences that may confound those of purging. In

conclusion, heterozygosity being a heritable trait allows for a response to selection, and for transgenerational fitness consequences of inbreeding and heterozygosity.

Session 2 MON MAX 410 6

Genetic compatibility underlies benefits of mate choice in an external fertilizer (52053)

J. David Aguirre, Mark W. Blows, Dustin J. Marshall.

Massey University; University of Queensland; Monash University.

Mate choice is a universal feature of sexually-reproducing species. In species with external fertilization however, direct interactions between reproductive partners are dramatically reduced and instead, mate recognition and choice typically occur at the level of gametes. Here, we examine the mechanisms underlying the benefits of gamete-level mate-choice (GMC) for paternal quality or compatibility in an externally fertilizing ascidian in the field. A manipulative mate-choice assay confirmed that offspring viability was greater in clutches where we allowed GMC relative to clutches where we precluded GMC. Additionally, we demonstrated that these benefits of GMC were driven by sexual selection rather than ecological genetic diversity effects, and that sexual selection was strongest during the early life-cycle stages. Subsequent quantitative genetic experiments revealed that paternal quality effects on offspring viability were generally weaker than parental compatibility effects, and that there was significantly more variation in parental compatibility for the trait combination underlying the benefits GMC. Overall, we provide evidence suggesting that the most compatible combinations of gametes produced the greatest number of viable offspring, and therefore that mate choice for genetic compatibility enhanced reproductive success in the field for a species where mate choice occurs predominantly among gametes.

Session 2 MON MAX 410 6

The structure of the mating network as a framework to understand mating systems: theory and tests (52251)

Grant McDonald, Lewis Spurgin, Eleanor Fairfield, David Richardson, Tommaso Pizzari.

University of Oxford; University of Gronigen; University of East Anglia; University of East Anglia; University of Oxford.

Multiple mating by females (polyandry) is a key component of mating systems, influencing the opportunity for both pre- and post-copulatory sexual selection on males. Yet empirical studies have provided conflicting results for the way polyandry impacts the operation of sexual selection. Recent work suggests that this may be further complicated by the relationship between male promiscuity and that of his partners (“mating structure”) which determines the reproductive value of male mating success. Reconciling conflicting empirical results across systems, requires: i) predictions for the effects of polyandry and mating

structure on sexual selection under biologically meaningful scenarios, and ii) empirical investigations to test predictions under realistic conditions. Here, we first use a simulation approach to predict the effects of polyandry and mating structure on the operation of pre- and post-copulatory sexual selection. We then employ an experimental approach using Red junglefowl (*Gallus gallus*) to test such predictions, and demonstrate how polyandry and mating structure combine to shape the operation of pre- and post-copulatory sexual selection. This study provides a framework to understand the response of sexual selection to variation in polyandry across mating systems and reveal the subtle yet powerful role of mating structure in modulating the influence of polyandry.

Session 2 MON MAX 410 6

The breakdown of self-incompatibility during a range expansion (52406)

Francisco Encinas-Viso, John Pannell, Andrew Young.

CSIRO; University of Lausanne.

It is commonly observed that for species that vary in their mating system among populations, range margins are enriched for increased selfing rates. This has often been attributed to a response to selection under mate and/or pollinator limitation. However, previous theoretical studies have shown that a reduction of inbreeding depression could facilitate the breakdown of self-incompatibility (SI) and therefore the invasion of self-compatibility (SC); we might thus expect that, during a range expansion SC could be favoured by selection in populations in which inbreeding depression has been purged. Here, we present results from a spatially explicit individual-based simulation model of a 2-dimensional range expansion, in which both inbreeding depression and the number of S-alleles at an SI locus can evolve, and in which there are recurrent mutations to SC. We find that under certain conditions (low recombination and migration rates), SC evolves and completely displace SI. Under other conditions, SC and SI are able to coexist in the expanded metapopulation, with spatial segregation of SC and SI populations. Importantly, our results indicate that evolution of inbreeding depression during a range expansion can be entirely sufficient for the evolution of SC at range margins, and that mate or pollinator limitation is not necessary.

Session 2 MON MAX 410 6

The intersection of the mating system and strong selection: herbicide resistance is related to increased inbreeding in *Ipomoea purpurea*, the common morning glory (52523)

Regina Baucom, Adam Kuester, Shu-Mei Chang.

University of Michigan; University of Georgia.

Human-mediated influences on plant mating systems can lead to significant ecological and evolutionary outcomes for plant populations. While it has been shown that increased

inbreeding is associated with habitat fragmentation, the influence of strong selective agents, such as herbicide, on plant mating is rarely considered. Here we examine the potential that the evolution of resistance to glyphosate, which is the main ingredient in the widely used herbicide RoundUp, has influenced the mating system of *Ipomoea purpurea*, the common morning glory, a species of agricultural weed that employs a mixed mating system. Using a progeny array of replicate maternal lines sampled from 23 populations collected in the US, and a greenhouse resistance assay, we uncovered a significant positive correlation ($r = 0.53$; $P < 0.008$) between estimates of the selfing rate (F) and the level of herbicide resistance. We hypothesize there are two potential explanations for this result: first, demographic changes following herbicide exposure may lead to greater self-fertilization and/or sib-mating in resistant populations; second, evolutionary changes in the mating system may occur concomitant to the evolution of increased resistance. Our results are broadly relevant to organisms with labile mating systems subjected to strong selective forces.

Session 2 MON MAX 410 6

Inherited Inbreeding: evidence of sex-specific, additive genetic variances in the degree of inbreeding (52592)

Matthew Wolak, Pirmin Nietlisbach, Lukas Keller, Peter Arcese, Jane Reid.

University of Aberdeen; University of Zurich; University of British Columbia.

Inbreeding has the potential to profoundly shape mating system evolution. A pervasive assumption in evolutionary theory is that the degree to which individuals inbreed will evolve in response to selection stemming from inbreeding depression. Such evolutionary response requires non-zero additive genetic variance in the degree of inbreeding, but this has never been tested. We developed a novel analysis that facilitates estimation of additive genetic variance in the degree of inbreeding and applied this to long-term data from a free-living song sparrow population. Specifically, we estimated female- and male-specific genetic variances contributing to variance in the kinship between socially-paired mates, while simultaneously estimating effects of immigration and of each individual's own coefficient of inbreeding on the mean kinship between mates. Female and male additive genetic variances in the kinship between mates both exceeded zero and the cross-sex genetic correlation was close to one, meaning that there was substantial total additive genetic variance in the degree of inbreeding. Effects of immigration and of each individual's coefficient of inbreeding on the kinship between mates were negative and positive respectively. We provide the first evidence that the degree of inbreeding shows additive genetic variance in nature and might consequently evolve in response to selection.

Session 2 MON POL D 34

Recombination rate variation and differential gene flow shape the genomic landscape of speciation in sea bass (52219)

Pierre-Alexandre Gagnaire, Nicolas Bierne, François Bonhomme.

Institut des Sciences de l'Evolution, ISEM CNRS-UM2-IRD, Montpellier, France.

The genomic landscape of species divergence provides a static picture of the dynamic process of speciation. Therefore, reconstructing the history of speciation is fundamental to understand how this picture captures the complex interplay between migration, recombination and selection as speciation unfolds. Here, we combine RAD-sequencing in natural populations and whole-genome sequencing in mother-father-child trios to investigate patterns of genome-wide divergence between naturally hybridizing lineages of Atlantic and Mediterranean sea bass (*Dicentrarchus labrax*). We find that variation in local recombination rates influences both nucleotide diversity within lineages and differentiation between lineages. Genomic islands of differentiation map disproportionately to low-recombining regions of reduced diversity, but some are also found in regions of high diversity and high recombination rates. Fitting alternative demographic models that explicitly account for genomic variation in demographic parameters revealed that the genomic landscape of divergence between sea bass lineages was generated both by selection at linked sites during divergence and varying rates of introgression across the genome after secondary contact. Therefore, genomic islands in sea bass are not simply an incidental consequence of reduced diversity in low-recombining regions, but also the product of reduced gene flow in these regions.

Session 2 MON POL D 34

The repeatability of genomic architecture in a homoploid hybrid species (52266)

Anna Runemark, Cassandra N. Trier, Fabrice Eroukhmanoff, Jo S. Hermansen, Tore O. Elgvin, Glenn-Peter Saetre.

University of Oslo.

The genomic revolution suggests a more important role for hybridization and introgression in speciation than has previously been recognized. The potential of hybridization to form novel variation depends on whether different genomic mosaics can arise, or if only certain combinations are viable. To investigate the creative potential of hybridization we re-sequence the whole genomes of three island populations of the homoploid hybrid Italian sparrow *Passer italiae*, which appear to result from three independent hybridization events. First, we investigate whether the hybridization events are independent by examining if genetic material inherited from the respective parent species on Crete, Corsica and Sicily originate from different parent populations, and whether the proportion of the genome inherited from the parent species and the size and distribution of genomic areas from the parent species differ between these islands. Then, we investigate whether the same genomic regions are more frequently inherited from the same parent species than expected by chance, genome wide, for coding genes only, and for specific gene classes. Finally, we investigate whether recombination frequency distribution and estimated time of hybridization differ between islands. Our study system provides a rare opportunity to investigate the creative potential of – and the genomic landscapes resulting from – hybridization.

The genomic landscape of the speciation continuum in the killer whale (52440)

Andrew D. Foote, Nagarjun Vijay, María C. Ávila-Arcos, Matteo Fumagalli, Thorfinn Sand Korneliussen, Michael D. Martin, Philip A. Morin, M. Thomas P. Gilbert, Jochen B. W. Wolf.

Department of Evolutionary Biology, Evolutionary Biology Centre, Uppsala University, Uppsala, Sweden; Centre for GeoGenetics, Natural History Museum, University of Copenhagen, Copenhagen, Denmark; Department of Integrative Biology, University of California, Berkeley, USA; Southwest Fisheries Science Center, La Jolla, USA.

To better understand the progression and chronology of adaptation and reproductive isolation during the early stages of speciation we sequenced 49 genomes and analysed whole-genome divergence between pairs of killer whale *Orcinus orca* ecotypes, which we demonstrate fall along the speciation continuum. The study system provides a useful comparison to genomic evolution in hominins, given the similar life histories, and the role of gene-culture coevolution in a recent, rapid radiation to a global distribution. We find that genetic diversity is lost through population splits and founder effects and the subsequent formation of reproductive isolation. This combined with subsequent population expansion has facilitated rapid shifts in allele frequencies and therefore the build up of genomic differentiation through stochastic processes (drift) and selection. We find outlier regions containing significantly differentiated SNPs in exons and potential regulatory regions in all pairwise comparisons. GO analyses suggest links to local adaptation, for example due to differences between fish- and mammal-eating ecotypes, or climate differences. We compare genome-wide estimates of F_{st} with D_{xy} and find a negative correlation, which we argue suggests that reproductive isolation has developed first, followed by the build up of heterogeneous differentiation, in-part due to heterogeneous levels of selection across the genome.

What causes "genomic islands" of excess F_{st} ? (52460)

Nick Barton, Hugo Tavares, David Field.

IST Austria; John Innes Institute; IST Austria.

Genes responsible for adaptation and for reproductive isolation may be identified by local increases in F_{st} along the genome. However, such "genomic islands" may be produced in two ways: through gene flow, which prevents or erases divergence everywhere except close to loci that are kept different by divergent selection, or by processes such as background selection or selective sweeps, which reduce diversity within populations, and hence increase F_{st} . I compare these different scenarios, and show that while selective sweeps can produce sharp "islands", gene flow tends to produce broad "islands", especially around clusters of selected loci. These theoretical arguments are illustrated by the *Antirrhinum* flower colour hybrid zone, where two closely linked loci determine sharp clines in flower colour

Recombination rate and the chromosomal distribution of gene flow between species of *Heliconius* butterflies (52752)

Simon Martin, John Davey, Chris Jiggins.

University of Cambridge.

Speciation is often complex, leaving behind a messy history of genealogies across the genome. The discordant histories of different genomic regions reflect both incomplete lineage sorting and gene flow, which, in turn depend on geography, natural selection, effective population size, and genomic features such as inversions and recombination rate variation. Using whole-genome sequencing of sympatric and allopatric populations of three species of *Heliconius* butterflies, we show that the genealogical history of a locus depends strongly on where in the genome the locus lies and on the time scale of speciation. Specifically, between one pair of species, gene flow is greater near chromosomes ends and on small chromosome, where recombination rates are higher. Between another pair, the distribution of gene flow across the genome is more even. We propose that this difference reflects differences in the timing of hybridisation between these pairs of taxa. This work helps to disentangle the effects of various factors on the emergence of reproductive isolation between incipient species.

FUNCTIONAL SPECIATION GENOMICS OF THE ANOPHELES GAMBIAE COMPLEX (51792)

Frederic Tripet, Fred Aboagye_Antwi, Nahla Alhafez, Abdoulaye Niang, Gareth Weedall, Doug Paton, Jessica Brothwood, Sharanjit Kandola, Abdoulaye Diabate.

School of Life Sciences, Keele University, United Kingdom; Department of Animal Biology and Conservation Science, Faculty of Sciences University of Ghana Legon; Institut de Recherche en Sciences de la Santé/Centre Muratz, Bobo-Dioulasso, Burkina Faso; Centre for Genomic Research, University of Liverpool, Liverpool, UK.

Anopheles gambiae exhibits complex populations and a number of cryptic taxa have been described. Genome-wide studies have shown that speciation in this species occurs through the divergence of a few loci characterized by reduced recombination and divergent selection. Such 'islands of speciation', located in pericentromeric regions of chromosomes X, 2L and 3L are thought to contain genes responsible for assortative mating in complex *An. gambiae* populations. We took two functional genomic approaches in order to identify which of these island(s) is crucial for assortative mating. In the first, laboratory recombinant strains differing only at their X-island were created by selective introgression. Recombinant strains that mated consistently assortatively were identified and their genome re-sequenced in order to broadly map assortative mating genes to the X-chromosome island of speciation. In the second approach we performed SNP genotyping of wild individuals captured from swarms from an

area with introgression between cryptic taxa. Genetic analyses of these natural recombinants enabled us to confirm the strong association between the X-island and swarm spatial segregation in field populations. Both approaches emphasize the importance of X-island loci for the speciation process and constitute fundamental steps towards the identification of genes of pre-mating reproductive isolation in this important species complex.

Session 2 MON POL D 34

Ant hybrids reveal genomic features underlying speciation (51826)

Jonna Kulmuni, Kishor Dhaygude, Pekka Pamilo, Roger Butlin.

University of Sheffield; University of Helsinki.

Ants have rarely been used in speciation studies, yet they offer unique advantages. Their haplodiploidy, where males are haploid and females diploid, can aid in discovering genetic elements underlying speciation. We have discovered a hybrid ant population, which displays a rugged genomic landscape of differentiation with gene flow. Specifically, we find two groups of haploid males, representing parental gene pools, and females that are hybrids between these gene pools. This means introgression is permitted in diploid females but selected against in haploid males. Accordingly, we observe strong selection in haploid males: hybrid individuals are present at egg stage, but die during development. This provides a unique opportunity to study genome areas underlying reproductive isolation because, rather than relying on genome scans of differentiation, we can observe selection directly. To identify genomic regions that are responsible for hybrid male death and reduced gene flow between the parental gene pools, we are comparing the genomes of males and females. When analyzing the most variable regions of the genome, preliminary results identify SNPs in several contigs involved in hybrid male death and so reproductive isolation. Future analysis will reveal the identity, size and distribution of these genomic regions harboring barriers for gene flow.

Session 2 MON MAX 415 13

The role of hybridization in the evolution of alpine *Coenonympha* butterflies (52339)

Thibaut Capblancq, Laurence Després, Jesus Mavarez.

Laboratoire d'Ecologie Alpine (LECA), Grenoble, France.

Hybridization events have become central elements in animal evolution studies during the last decade and new methods in population genomics and model testing now allow for disentangling complex evolutionary histories. Interspecific crosses are recognized to be involved in key evolutionary processes such as local adaptation, colonization of new environments, speciation and extinction. We evaluated the role of hybridization in diversification and adaptation in complex of three *Coenonympha* butterfly taxa present in the Alps. Morphological, genetic and ecological analyses allowed us to prove the hybrid origin of

one of them: the Darwin's Heath (*C.darwiniana*). This lineage emerged after hybridization events between the Pearly (*C.arcania*) and the Alpine Heath (*C.gardetta*) approximately 10,000 years ago and with different parental contributions. It is now completely stable in two distinct restricted areas where its intermediate phenotype seems locally advantageous considering the fact that it completely excludes its parent species. Moreover, current contact zones show contrasting ongoing hybridization patterns, and although species seem to keep their integrity the reproductive isolation between them is far from complete. The analysis of introgression patterns, discussed in regards to climatic variables discriminating populations and species, promise new insights for understanding the role of hybridization in adaptation for this butterfly complex.

Session 2 MON MAX 415 13

Nestedness and turnover in the genetic diversity of marine species across the Indo-Pacific Ocean (52352)

Libby Liggins, Eric D. Crandall, J. David Aguirre, Michelle R. Gaither, Chris E. Bird, Rob J. Toonen, DIPnet members, Cynthia Riginos.

Massey University, Auckland; University of Hawaii; Durham University; Texas A&M University - Corpus Christi; Diversity of the Indo-Pacific Network; The University of Queensland.

The Indian and Pacific Oceans contain much of the world's marine biodiversity, but species and genetic lineages are not evenly distributed throughout this region. Understanding the generality of genetic breaks and genetic diversity gradients is important for describing the evolution of biodiversity and assembly of marine communities in this region; however the large population sizes and high dispersal of many marine species result in consistently high genetic diversity across species ranges (based on haplotype/nucleotide diversity) and obscure genetic breaks (based on distance measures and fixation indices). Here we complement traditional population genetic measures with measures originally conceived for comparing species compositions among communities. We applied nestedness and partitioned beta-diversity measures to mitochondrial genetic datasets for >100 marine species contributed by DIPnet (formed by the National Evolutionary Synthesis Center working group 'Advancing genetic diversity research in the Indian and Pacific Oceans'). We describe genetic diversity gradients considering nestedness and turnover to identify evolutionary 'sinks' (where immigration predominates) and 'sources' (where mutagenesis is evident), and reveal the significance of nestedness and turnover in forming genetic breaks. These measures, commonly used in community ecology, provide a nuanced understanding of genetic patterns in the Indo-Pacific that cannot be detected using traditional population genetic measures.

Session 2 MON MAX 415 13

Specificity of the microbiome: insights from *Daphnia* hosts. (52516)

Samuel PICHON, Mahendra MARIADASSOU, Dieter EBERT.

University of Basel, Switzerland; INRA Jouy-en-Josas, France.

Environmental and host genetic factors shape the composition of host-associated microbiota. To estimate the relative importance of each of both factors, we characterized the structure of the bacterial communities by amplicon pyrosequencing in three sympatric *Daphnia* species and of their environments (pond water and sediments). The three *Daphnia* species harbor a unique and diverse microbiota dominated by Proteobacteria, including members of the Comamonadaceae family. Previous results and the global similarity of these three symbiotic communities suggest that some of these associations may be evolutionary stable. However, differences among *Daphnia* species resemble the host phylogenetic relationships, suggesting that the hosts evolved with specific microbiota and that genetic factors are predominant in structuring their microbiota. We developed a local specificity index and introduce a permutation based test to assess the significance of the specificity. Analysis of multiple datasets (*Daphnia*, humans, etc.) suggests that microbial species that are specific to one habitat are most abundant in that habitat. The positive association between abundance and specificity was found in every dataset. We suggest that this relationship is a main structuring force of microbiota.

Session 2 MON MAX 415 13

From neutral theory to competition-dispersal trade-off: dispersal polymorphism effects on species diversity patterns (52634)

Fabien Laroche, **Philippe Jarne**, Thomas Perrot, François Massol.

AgroParistech - CEFÉ; CNRS - CEFÉ; CNRS - GEPV.

Neutral models provide important insights on patterns of species diversity in metacommunities. Introducing some variance in the carrying capacity of local communities may select for dispersal polymorphism under otherwise neutral conditions in metapopulation models. We extend this approach to a neutral metacommunity using a multi-species, multi-community model and show that dispersal polymorphism may readily emerge both within- and among-species depending on community carrying capacity distribution. Importantly small communities are occupied by dispersing species (“drifters”) while large communities harbours species with limited dispersal (“dwellers”). When dispersal converges toward a unique evolutionarily stable equilibrium, diversity within communities and dissimilarity among communities do not differ qualitatively from neutral expectations. This is no more true when a dispersal polymorphism can emerge, suggesting that deviation from neutral predictions can be detected when comparing diversity indices among communities differing in carrying capacity. We discuss how our model contributes to unify two classical approaches in metacommunity ecology, namely neutral and competition-colonization models.

Session 2 MON MAX 415 13

Evolution of ecological communities through the lens of an island chronosequence (52653)

Rosemary Gillespie, Andrew Rominger, Jun Ying Lim, Fernanda Valdavinos, John Harte, Kari Goodman, Daniel Gruner, Kerry Shaw, Donald Price.

University of California; Pacific Ecoinformatics; University of Maryland; Cornell; University of Hawaii Hilo.

Islands are bedrock model systems in the development of ecological and evolutionary theory. The Hawaiian Islands in particular have expanded our understanding of island biogeography, with phylogeographic studies of rapid diversification and the dynamics of adaptive radiation overlaid upon a detailed understanding of ecosystem development and senescence. These studies demonstrate the overriding importance of in situ speciation in biodiversity patterns of highly isolated archipelagoes, beyond the reach of equilibrium colonization dynamics. We synthesize ecological and evolutionary perspectives to analyze processes driving emergent patterns of island biodiversity. We apply this approach to a simple and relatively isolated system that occurs across a 5 million-year space-for-time chronosequence provided by the island hotspot. We use this natural experiment to develop a novel analytical pipeline that combines both macroecological (interaction networks and maximum entropy inference) and evolutionary (population genetics and phylogenetics) approaches and hence build a predictive understanding of the interplay between ecology and evolution in dynamically shaping the macroecology of complex ecosystems.

Session 2 TUE GEN C 3

Coevolution of the sex chromosomes in *Drosophila melanogaster* (52014)

Katrine Lund-Hansen, Edward H. Morrow, Jessica K. Abbott.

University of Sussex; Lund University.

Theory predicts that the Y chromosome may accumulate genes beneficial for males, even if these are harmful to females. As the Y chromosome is not present in females, selection does not act directly against these sexually antagonistic genes. Genes on the X chromosome would then be predicted to evolve to counteract the harmful Y genes or become resistant to them. To test this, we carried out a sex chromosome replacement experiment in males from five outbred, wild type, lab-adapted *Drosophila melanogaster* populations with different geographic origins. We replaced either the X or the Y chromosome and found that half of the novel genotypes had a significantly higher reproductive fitness than their source population. This change in fitness was not caused by interactions with the autosomes, but by the mismatching of the sex chromosomes, indicating that coevolution of the sex chromosomes must have occurred. We will present data on the effect of the introduction of a novel sex chromosome on various components of male fitness. We will also present a novel theory about the nature of sexually antagonistic coevolution on the X and Y.

Session 2 TUE GEN C 3

Evolution of an unusual sex determination system in a Mammal, the African pygmy mouse *Mus minutoides* (52017)

Paul Saunders, Ophélie Ronce, Pierre-André Crochet, Frédéric Veyrunes.

*Institut des Sciences de l'Evolution de Montpellier, CNRS, Université de Montpellier, France;
Centre d'Ecologie Fonctionnelle et Evolutive, CNRS, Montpellier, France.*

All therian mammals have a similar XX/XY sex determination system (SDS) except for a dozen species. In the African pygmy mouse *Mus minutoides*, males are XY, and there are three types of females: XX, XX* and X*Y (the asterisk designates a sex-reversal mutation on the X chromosome). The evolution of such a system is a paradox as sex-reversal mutations lead to sterility or subfertility in mammals, precluding departure from the standard system. Nevertheless, the X* is old (>0.9My) and highly prevalent in this species. To investigate the evolutionary forces involved in the emergence and maintenance of this system, an empirical approach and mathematical modelling are combined.

Data gathered from our laboratory colony reveal (i) that X*Y females have a greater reproductive success and (ii) the existence of sex chromosome transmission distorters. These findings can be related to two hypotheses proposed to explain transitions in SDS: Fitness differences between genotypes and sex-ratio selection. Our mathematical models suggest that either feature could be responsible for the appearance of the X* and that they both participate in its maintenance. These results provides valuable insight into understanding the constraints acting on SDS with highly heteromorphic sex chromosomes and conditions that can loosen these constraints.

Session 2 TUE GEN C 3

The PhyloSex project: towards a better understanding of sex determination diversity and sex chromosome evolution in fish. (52201)

Jennifer Anderson, Christophe Klopp, Hugues Parrinello, Laurent Journot, John H. Postlethwait, Yann Guiguen, **Manfred Schartl**.

*INRA, Laboratoire de Physiologie et Génomique des Poissons, 35042 Rennes Cedex, France;
INRA, SIGENAE, UR875, INRA Auzeville, BP 52627, 31326 Castanet-Tolosan Cedex,
France; MGX (Montpellier Genomix), 34094 Montpellier Cedex 05, France; University of
Oregon, Institute of Neuroscience, Eugene OR 97403, USA; University of Wuerzburg,
Physiological Chemistry, Biocenter, 97074 Wuerzburg, Germany.*

Fish show a great variety of sex determination mechanisms, which in the case of genetic sex determination is linked to a similarly high variability of sex chromosome differentiation. Curiously, neither phenomenon follows any obvious phylogenetic pattern. To obtain a better understanding of the biological meaning of the diversity of sex determination and the mechanisms driving sex chromosome evolution we are attempting to decipher the molecular basis of the primary sex determination mechanisms and the structure and genetic organization of sex chromosomes across a broad diversity of rayfin fish. On the one hand we are analyzing a collection of species that represent major branches of the fish tree of life and on the other

hand we focus on closely related species within branches of the phylogenetic tree (Esociformes, Danios, Poeciliids). We use high throughput marker mapping in 40 species as well as transcriptomics and long insert clone sequencing to delineate sex-specific chromosomal regions and to identify candidate sex determining genes. Our first results indicate that many species harbor very poorly differentiated sex-chromosomes. Our RAD-tag based approach led to the identification of sex-specific markers, allowing to delineate the extent of recombination suppression. We also identified candidate sex determining genes in some species.

Session 2 TUE GEN C 3

Evolution of sex-determining modes in amniotes: transitions, stability and ancestral state (52534)

Lukas Kratochvil, Michail Rovatsos, Marie Altmanova, Jasna Vukic, Martina Pokorna.

Charles University, Prague; Czech Academy of Sciences, Libechov.

It is believed that in contrast to mammals and birds frequent turnovers of sex chromosomes and transitions between genotypic sex determination (GSD) and environmental sex determination (ESD) in both directions are typical for poikilothermic amniotes. Nonetheless, using comparison of genes linked to X and Z sex chromosomes across wide species sampling, we demonstrate that sex chromosomes are highly conserved for dozens million of years in iguanas and snakes. Current knowledge on the homology of sex chromosomes among particular GSD clades as well as on the phylogenetic distribution of GSD and ESD is in agreement with ancestral ESD for amniotes. Transitions from ESD to GSD were frequent, but transitions in the opposite direction were rare (if any). Previously, we argued that this stability of GSD with respect to ESD could be attributed to the stability of well-differentiated sex chromosomes. However, within reptiles, we have recently found two independent disappearances of highly differentiated sex chromosomes. Still, even here the derived states represent again GSD, not ESD. We call for a general explanation of the resistance of GSD to the invasion by ESD and suggest that it may be based on the wider potential to resolve sexual conflict under GSD.

Session 2 TUE GEN C 3

The evolution of sexual specialization in an artificial dioecious fungus (52652)

Bart Nieuwenhuis, Hanna Johannesson, Simone Immler.

Department of Evolutionary Biology, Uppsala University; Department of Systematic Biology, Uppsala University.

One possible scenario for the evolution of males and females is the occurrence of mutations in a simultaneous hermaphroditic ancestor acting as sex determining loci, which render individuals male or female. This division into male and female individuals not only should

lead to phenotypic divergence but also to rearrangements in the underlying genomic architecture. To study this important first steps in the evolution of two separate sexes from a hermaphroditic ancestor, we created mating-type specific male-sterile and female-sterile strains of the haploid fungus *Neurospora crassa*. Effectively this creates dioecious individuals, in which the mating type locus has become a sex-determining locus. Using experimental evolution with these dioecious strains, we studied how the strains adapt to their novel role as male or female, both at the phenotypic and the genetic level. Sexually antagonistic traits are expected to become associated with the sex determining locus, either due to mating type regulated expression or through linkage. We will present measurements on male and female fitness contributions from competition essays between dioecious and hermaphroditic individuals. Then we will describe phenotypic and genetic changes in the male and female strains after 15 generations of experimental evolution.

Session 2 TUE MAX 410 21

Non-genetic transmission and sex-linked inheritance of prenatal maternal effects in a precocial bird (51834)

Barbara Tschirren, Ann-Kathrin Ziegler, Monika Okuliarova, Michal Zeman, Joel Pick, Mathieu Giraudeau.

University of Zurich; Comenius University Bratislava.

Resources and developmental cues provided by the mother during the first stages of life can have pronounced and long-lasting consequences for offspring morphology, physiology and behavior. Whereas the role of such prenatal maternal effects in mediating offspring phenotypic plasticity is well documented, their potential consequences for subsequent generations are still debated. Important mediators of prenatal maternal effects in birds are hormones that are transmitted from the mother to the eggs. Using a breeding experiment over three generations in Japanese quail (*Coturnix japonica*), we show that maternal yolk hormone deposition is inherited exclusively along the maternal line, suggesting W-chromosome linkage. Furthermore, we demonstrate that an experimental manipulation of yolk hormones in the eggs, mimicking environmentally-induced maternal effects, affects the daughters' egg composition later in life, thereby influencing the grand-offspring's developmental trajectories. We assess the adaptive value of such a non-genetic transmission of information across generations and the role of sex-specific selection in shaping the evolution of sex-linked inheritance of maternal effects.

Session 2 TUE MAX 410 21

Does molecular pleiotropy constrain evolution, plasticity or both? A proteomic perspective in a salmonid fish metapopulation (51853)

Spiros Papakostas, Asbjørn Vøllestad, Matthieu Bruneaux, Tutku Aykanat, Joost Vanoverbeke, Mei Ning, **Craig Primmer**, Erica Leder.

University of Turku; University of Oslo; KU Leuven.

The significance of gene expression pattern modification as a mechanism promoting rapid evolution has received considerable attention recently but the relative roles of plastic vs evolutionary expression change remain unclear. We conducted a common garden experiment and studied the proteomic expression profiles of European grayling (*Thymallus thymallus*) sub-populations that have adapted to different thermal environments in just 25 generations. The proteome expression changes included both evolutionary and plastic components, with each component having an independent, but complementary, effect on the expression profile. A QST–FST analysis indicated that the observed differences in proteomic expression profile between cold and warm origin sub-populations likely included an adaptive component. We also found that temperature-driven gene expression changes were constrained by the level of gene pleiotropy estimated by either the number of protein interactions or gene biological processes. Genes with low pleiotropy levels were the main drivers of the observed changes in both plastic and evolutionary global expression profiles, while highly pleiotropic genes had a limited expression response to temperature treatment. These findings provide important insights into the molecular mechanisms facilitating rapid adaptation in changing environments and suggest that gene pleiotropy should be considered more carefully when interpreting gene expression profiling data

Session 2 TUE MAX 410 21

Evolutionary and ecological plasticity in short order: genome-wide evidence for in-situ evolution and adaptation in invasive Florida Burmese pythons (52049)

Todd Castoe, Daren Card, Drew Schield, Margaret Hunter, Kristen Hart.

University of Texas Arlington; United States Geological Survey.

Substantial evolutionary changes are thought to happen over long time periods in most species, making analyses of natural selection and its effects on the genome difficult. Invasive species, however, represent a promising model for analyzing the processes of evolution and adaptation on timescales that are tractable for study, and have been shown to demonstrate rapid evolutionary responses and high plasticity over short or ‘ecological’ timescales. The invasive Burmese python (*Python molurus bivittatus*) is ideal for studying rapid evolution due to its recent establishment and proliferation in sub-tropical Florida, a location with climatic conditions that are notably different from those in the species' native range of tropical Southeast Asia. Among other major selective events that have impacted this introduced population, a significant die-off (>50%) of individuals in the Florida python population (FPP) occurred during a 2010 freeze event. We used genome-wide SNP sampling of the FPP (via RADseq) before (2007) and after (2013) the freeze event to test for evidence of evolution and locus-specific selection. We found multiple regions of the genome that appear to show major shifts in heterozygosity over a surprisingly short time period (time of a single generation), indicating in situ evolution and adaptation in the FPP.

Bridging Ecology and Evolution by Symbiotic and Epigenetic Mechanisms (52052)

Yoav Soen.

Weizmann Institute of Science.

While adaptations to novel environments extend over evolutionary timescales, a new environment can emerge already within a single generation and can immediately impact the physiological and epigenetic state of the organism. Whether and how the initial response might be connected to longer-term establishment of new adaptations are not clear.

We take an experimental approach to address these questions by studying responses of flies to novel scenarios of stress. We identified epigenetic- and symbiotic-mediated mechanisms which promote increased developmental plasticity under stress, influence the germline, and contribute to non-Mendelian transfer of variation across generations.

I will discuss these epigenetic- and symbiotic-mediated processes and their potential contribution to the establishment of initial adaptations that can bridge part of the gap between ecological and evolutionary processes.

Plastic vs genetic responses to temperature acclimation: quantitative traits to transcripts. (52063)

Allannah Clemson, **Marina Telonis-Scott,** Carla Sgro.

Monash University.

Relating environmental variables to a range of phenotypes expressed by a genotype is a ‘tried and true’ method for studying responses to varying environments. Given the critical role of temperature in shaping the geographic distributions in terrestrial organisms, attention is now shifting to consider thermal performance when assessing the potential impacts of climate change. Examining populations that inhabit diverse thermal environments provides insights into traits and genes that are important in environmental adaptation, and can enhance predictions of species’ ability to mitigate any deleterious effects of a changing environment. Here we use the fruit fly *Drosophila melanogaster* as a model to understand how environmental adaptation affects thermally responsive traits and genes. We collected two outbred populations along the Australian eastern coast (north and south) and developed them at six temperatures. We then compared the expression of temperature responsive candidate genes as well as life-history traits to understand the link between genotype and phenotype driving thermal adaptation. Our goal is to develop an approach to link climatic preference with stress performance, life-history, morphology and molecular processes. Ultimately, can genes that respond differentially to developmental temperature explain fitness differences

across environmental gradients, and thus provide insight into future responses to climate change.

Session 2 TUE MAX 410 21

Adult transcriptome variation is determined by egg to adult development time in a desert drosophilid (52041)

William J. Etges, Cassia de Oliveira, Subhash Rajpurohit, Allen Gibbs.

University of Arkansas; Lyon College; University of Pennsylvania; University of Nevada, Las Vegas.

Complex life cycles offer an opportunity to investigate the genetic influences of early life stage variation on later components of the life history. We investigated whole genome transcriptional variation in populations of *Drosophila mojavensis* by day of preadult development time (DEVT) in aged adults reared on different host plants. Because DEVT variation is genetically correlated with sexual isolation between populations as well as cuticular hydrocarbon differences, transcriptional variation in adults differing in DEVT is of direct consequence to understanding host plant related adaptation, life history evolution, and reproductive isolation. We found hundreds of genes enriched for different functions in adults that varied due to DEVT including those influencing gene regulation, mitochondrial energetics, and cuticular hydrocarbon production.

Session 2 TUE MAX 410 21

Within and across generation life-history responses to nutritional stress during development (51875)

Marjo Saastamoinen.

University of Helsinki.

Organisms in the wild are constantly faced with a wide range of environmental variability, such as fluctuation in food availability. Understanding the processes and underlying mechanisms that allow organisms to cope with such environmental variation is a key challenge in evolutionary ecology. I will synthesise across studies in which we have assessed the influence of short-term nutritional stress during development on adult life-history variation in the Glanville fritillary butterfly (*Melitaea cinxia*). Poor developmental conditions often have a negative impact on fitness-related traits, such as reproduction and lifespan. However, conditions experienced during development can sometimes be used as cues for the likely environmental condition the individual will encounter later on in life (i.e. predictive adaptive responses). Accordingly, individuals can shape their adult physiology or life history in a way that allows them either to deal with the predicted conditions later on in life or to move away from these deteriorating environments. Predictive adaptive responses seem to occur also across generations, as mothers that experienced nutritional stress during their own

development produce offspring that have improved compensatory strategies to cope with nutritional stress. We are currently assessing whether differences in methylation underlie these observed phenotypic differences in response to developmental nutritional stress.

Session 2 TUE POL A 28

Antagonistic coevolution with competing consumers alters the dynamics of selection over time (52528)

Frickel Jens, Becks Lutz.

Community Dynamics Group, Dept. Evolutionary Ecology, Max Planck Institute for Evolutionary Biology.

Coevolutionary changes in antagonistic interacting populations can constantly change the mode, strength and direction of selection through a link between ecological and evolutionary dynamics on the same time scale. To explore the role of eco-evolutionary dynamics and their effects on variation in selection over time, we conducted a series of experimental evolution studies using host-virus systems. We will present results from experiments where we compared the evolutionary and ecological dynamics of experiments when host and virus coevolved with and without an additional consumer for the host (predator). We found that predator and virus could only coexist after the host evolved a general resistance against the virus and that coexistence of the two consumers shifted the ecological dynamics towards cyclic populations compared to the experiments with only host and virus. Most importantly, the presence of the predator changed the evolutionary dynamics from fluctuating selection when host and virus evolve alone, to constant selection when virus, host and predator coexisted. Overall, our study shows the important consequences of rapid evolutionary change and highlights that the details of coevolutionary dynamics matter for community stability (cycles vs. stability) and structure (coexistence), which in return determines type of selection (fluctuating vs. constant).

Session 2 TUE POL A 28

Stress response of mutation accumulation lines of the green algae *Chlamydomonas reinhardtii* across two environmental gradients (52130)

Susanne Kraemer, Andrew Morgen, Peter Keightley, Nick Colegrave.

University of Edinburgh.

Understanding the distribution of fitness effects (DFE) of novel mutations is central to many areas of evolutionary biology. Importantly though, mutational effects are not fixed but will depend on the environment that the organism experiences. However, the effect of the environment on DFE, expressed as changes to the mean and variance of fitness, has been rarely investigated experimentally. Intuitively it might be expected that selection coefficients against deleterious mutations will increase in stressful environments but experimental tests so

far have produced conflicting results. Clones of the green algae *Chlamydomonas reinhardtii* were previously subjected to a mutation accumulation experiment. Here, we measured fitness of two independent MA lines and their ancestors across two different environmental gradients, increasing salt and decreasing phosphorous. We investigated changes in expressed genotypic variation and the consistency of the genetic response to environments between the two MA lines, between the two different stressors, between MA lines and their ancestors and in relation to the severity of stress. This allowed us to determine how DFE changes in response to stressful conditions, which, in turn, will determine the future capacity for adaptation in this model plant.

Session 2 TUE POL A 28

Geographical variation in predation pressure toward warning signals of an Arctiid moth *Parasemia plantaginis* (52702)

Katja Rönkä, Bibiana Rojas, Emily Burdfield-Steel, Swanne Gordon, Ossi Nokelainen, Tönis Tasane, Janne Valkonen, Johanna Mappes.

University of Jyväskylä; University of Tartu.

The wood tiger moth (*P. plantaginis*) is an aposematic species of which hind wing coloration can be white, yellow, orange or red combined with variable amount of black pigmentation. Throughout its Holarctic distribution both monomorphic and polymorphic populations exist. We asked whether differences in frequency dependent selection by predators could explain geographic differences in warning signals. We recorded local passerine and Lepidoptera communities during large-scale field experiments in four geographic locations (in Estonia, Scotland, Georgia and Southern Finland) where artificial moths of white, yellow and red hind wing coloration were exposed to natural predators. In Estonia white morphs, in Scotland yellow morphs and in Caucasus red morphs dominate whereas in Finland white and yellow morphs coexist. Predation pressure differed between the populations and natural selection seemed to favor locally common morphs in Scotland (yellow) and in Georgia (red) as expected according to the theory of aposematism. However, in Finland and Estonia we did not find evidence of positive frequency dependent selection. In addition to the local wood tiger moth population, we found some evidence that the structure of predator populations as well as local alternative prey communities influence the strength and direction of selection contributing to warning signals.

Session 2 TUE POL A 28

Environmental suitability influences the evolvability of morphological traits: linking biogeography and evolutionary dynamics (52708)

Jesus Martinez-Padilla, Alba Estrada, Regan Early, Francisco Garcia-Gonzalez.

Estación Biológica de Doñana; CIBIO/InBIO, Universidade de Evora; College of Life and Environmental Sciences, University of Exeter; Centre for Evolutionary Biology, The University of Western Australia.

Natural selection is the main mechanism driving evolution. Yet, our knowledge on how evolution works under different environmental circumstances is extremely limited in wild populations. Here we explore how environmental variation influences the evolvability of phenotypic traits of European wild bird populations. We reviewed studies that provided, or allowed calculation of, the coefficient of additive genetic variation (CVA) as a proxy of the ability of populations to respond to natural selection. We obtained 132 estimates of CVA of morphological traits from 13 species of 19 populations. We built Species Distribution Models of those species in Europe at a resolution of 50x50Km² considering spatial, topographical and climatic variables with the favourability function. We then matched the environmental suitability of the location with the CVA of each population and species we had data from. We explored the association between favourability and CVA. We found that CVA of morphological traits was higher at intermediate environmental suitability and lowest in very favourable or unfavourable environments. Our results highlight the need to consider the populations' environmental context to accurately contextualize evolutionary potential.

Session 2 TUE POL A 28

Climate-change driven evolution of an ornament in a wild bird (52921)

Simon Evans, Lars Gustafsson.

Department of Animal Ecology, Uppsala University.

Despite extensive empirical research, and theoretical expectations of rapid adaptation in response to selection, empirical evidence for contemporary evolution of secondary sexual traits is scarce. We explored this issue in a population of collared flycatchers (*Ficedula albicollis*), in which the heritable (~35%) ornamental forehead patch of males has shown a marked phenotypic decline in size over 34 years. Based on estimates of annual fitness selection, we report a reversal in selection on forehead patch size over the study period, driven by climate-dependent viability selection (interannual survival) on males: early in the study, males with larger ornaments had higher survival. Conversely, in latter years, when temperatures at the breeding ground have been higher, less ornamented males had higher survival. Using a Bayesian animal model to quantify genetic and environmental variation in forehead patch size, we find a highly significant temporal decline in the breeding value of males, and show via simulations that genetic drift is unlikely to account for this. Our study thus demonstrates evolutionary reduction of ornamentation in the wild within the timeframe of a contemporary study and in response to climate change.

Session 2 TUE POL B 20

Genomics of local adaptation in the Mediterranean blue tit *Cyanistes caeruleus* (52007)

Marta Szulkin, Pierre-Alexandre Gagnaire, Nicolas Bierne, Anne Charmantier.

CEFE CNRS; ISEM CNRS; ISEM CNRS; CEFE CNRS.

Demonstrating local adaptation in nature requires establishing connections not only between genotype, phenotype and fitness, but also between genomic differentiation and its covariation with habitat heterogeneity. Here, we investigated the origins of a strong habitat-linked phenotypic differentiation across Mediterranean populations of wild blue tits (*Cyanistes caeruleus*) breeding in a highly heterogeneous environment. First, we tested for population genomic structuring related to habitat type. By applying a RAD-Seq approach to generate c. 12 000 SNPs, we detected large-scale and fine-scale genetic differentiation between populations. This included differentiation in adjacent habitats within Corsica less than 6 km apart, which was unexpected in highly mobile organisms such as birds. Complementary population genomic analyses revealed a pattern of isolation-by-environment (IBE) where genetic differentiation correlated with habitat type independently of geographic difference. Second, we established a quantitative genomic framework to study local adaptation in the Mediterranean blue tit. We compare pedigree and marker-based heritability for key reproductive traits, which are also known to differ between habitats. Third, we discuss the importance of using sample replicates and complementary statistical inference for genomic data validation to generate reliable insight into the genomics of local adaptation.

Session 2 TUE POL B 20

Utilizing large sampling frames to investigate the genomic determinants of short-term adaptation in *Mycobacterium tuberculosis* (52282)

Jessica Hedge, Timothy Walker, Sarah Walker, Derrick Crook, Tim Peto, Daniel Wilson.

University of Oxford; Wellcome Trust Centre for Human Genetics.

Short-term adaptation plays a major role in the success of *Mycobacterium tuberculosis*, the aetiological agent of TB disease in humans. The most obvious example is the emergence of drug resistance under the strong selective pressure from antimicrobial drugs. We have also identified signatures of short-term selection outside of genes associated with any known resistance, suggesting that *M. tuberculosis* must also adapt to different local environments within hosts. Although the exceptionally low clock rate of this species makes studies of within host adaptation challenging, intensive population-level sampling frames can increase the sensitivity to detect variants occurring over the short term. By performing phylogenetic analyses of 3651 *M. tuberculosis* whole genome sequences representing the global diversity of this pathogen, we have investigated the genetic pathways involved in local adaptation to the host environment over the short-term. The genetic variants identified in this way may help to explain why *M. tuberculosis* occasionally leaves the lungs, from where it can successfully transmit to other hosts and easily enter the bloodstream, to infect other tissues, which represent an evolutionary dead-end. By testing for associations between sites under selection and disease manifestation, we can begin to characterise the genomic signatures of adaptation in this pathogen.

Signatures of selection in an admixed feral chicken population (52293)

Martin Johnsson, Eben Gering, Pamela Willis, Thomas Getty, Dominic Wright.

IFM Biology, Linköping University, Linköping, Sweden.; Zoology Department, Michigan State University, East Lansing, Michigan, U.S.A.; Biology Department, University of Victoria, Victoria, Canada.

Feralisation is the evolutionary process that occurs when a population of domestic animals is returned to wild conditions. Domestication as well as feralisation can serve as models of adaptation to new environments. Our observations of phenotypes and genetic data suggest that feral chickens of Kauai are an admixed population of wild and domestic chickens. We performed whole-genome SOLiD sequencing on 23 Kauai chickens (~ 5X individual coverage), called single nucleotide variants and performed selective sweep mapping by sliding window pooled heterozygosity. As a comparison, we reanalyzed a dataset of selective sweeps in domestic chickens. Consistent with their probable admixed origin, the Kauai population had on average higher heterozygosities than domestic chickens. We found 37 putative selective sweeps on Kauai, largely separate from those in domestic chickens, and potentially driven by feralisation and adaptation. One among the potential sweeps on chromosome 13 is close to a candidate gene for relative comb mass identified in a laboratory cross between wild and domestic chickens. We speculate that this is due to restoration of natural and sexual selection on comb size on previously domesticated genotypes. High heterozygosities suggest ongoing feralisation on Kauai that may offer an opportunity to map this process in real time.

Experimental genomic tests for pollution driven rapid evolution in the Mediterranean mussel (52305)

Anamaria Štambuk, Stuart Dennis, Dorotea Polović, Maja Šrut, Víctor Soria-Carrasco, Zachariah Gompert, Vid Baković, Goran Klobučar, Patrik Nosil.

Department of Biology, Faculty of Science, University of Zagreb, Rooseveltov trg 6, 10000 Zagreb, Cr; Department of Animal and Plant Sciences, University of Sheffield, Sheffield S10 2TN, UK; Department of Biology, Utah State University, Logan, UT 84322, USA.

Anthropogenic disturbance can rapidly and substantially alter the environment such that exposed organisms are challenged to quickly adapt to these changes. We studied evolutionary responses to pollution in marine environments using the Mediterranean mussel *Mytilus galloprovincialis*. We sampled 15 natural populations along a pollution gradient and used a subset of these to perform transplant experiments between clean and polluted environments in both the wild and in lab mesocosms. The results of the experiments showed consistent differential survival between treatments and source populations driven by an acclimatization effect in the wild transplant and by population by environment interactions in the mesocosm experiment. For over 1800 mussels used in these studies we collected genome wide SNP data

using a genotype-by-sequencing approach. These SNPs were analysed to test for genetic structure in natural populations and the genomic architecture of survival (i.e., fitness) in the experiments. By combining data obtained from the native populations and two types of transplant experiments we identified interactions between environment, genotype, and fitness, thus providing new insight into pollution driven evolution and the effect of adaptive processes on the mussel genome.

Session 2 TUE POL B 20

Parallel and non-parallel genomic signatures of selection in three-spine sticklebacks from different regions (52380)

Shenglin Liu, Anne-Laure Ferchaud, Michael M. Hansen.

Aarhus University; Université Laval.

Multiple independent colonizations of freshwater areas by marine three-spine stickleback represent some of the most well-known examples of parallel evolution, both at the phenotypic (especially lateral plate polymorphism) and genomic levels. However, whereas high degrees of parallelism are observed in some geographical regions (e.g. American northern Pacific), parallelism appears less pronounced in other regions (e.g. the North Sea and Baltic Sea in Europe). We test the hypothesis that the degree of similarity of environments and ecosystems between freshwater bodies also explains the degree of parallelism. Using RAD sequencing we analyze marine and freshwater sticklebacks from 1) Greenland, where ecosystems are very simple and similar across lakes, with only few fish predators present and 2) Denmark, where ecosystems are complex and differ strongly between habitats. In accordance with our hypothesis, we do find pronounced phenotypic and genomic parallel evolution in Greenland, but only limited parallel evolution in Denmark. We furthermore estimate divergence time between marine and freshwater sticklebacks and demographic history of populations in the two regions in order to rule out that different time since founding or strong bottlenecks could explain the differences of results.

Session 2 TUE POL B 20

Extreme local adaptation in *Drosophila* chemosensory perception (52494)

J. Roman Arguello, Margarida Cardoso-Moreira, Jaaved Mohammed, Jennifer K. Grenier, Srikanth Gottipati, Andrew G. Clark, Richard Benton.

University of Lausanne, Center for Integrative Genomics; Cornell University, Department of Molecular Biology and Genetics; Cornell University, Department of Biological Statistics and Computational Biology; Translational Medicine and Think Team, Otsuka Pharmaceutical Development and Commercialization, Inc.

How organisms adapt to new environments is of fundamental biological interest but is poorly understood at the level of genes and neurons. A particularly interesting question regarding

local adaptation is how sensory systems and perception are altered during this process. To investigate the extent to which selection has shaped the chemosensory perception within *D. melanogaster* - a preeminent model for studying sensory neurobiology – we have analyzed genome-wide polymorphism and divergence data from the Global Diversity Lines (84 *D. melanogaster* genomes derived from 5 geographically diverse populations). By coupling population genomic analyses of chemosensory protein families within parallel analyses of all other large protein families we demonstrate that, surprisingly, chemosensory proteins do not stand out as outliers with respect to signals of adaptive differences between species. However, chemosensory proteins do experience local adaptation at extremely high rates, often displaying the strongest signals of selection among large protein families. We show that adaptation has operated almost exclusively on standing variation, and that positively selected genes often harbor unanticipated levels of diversity. Our curated set of selected chemosensory proteins is currently guiding functional studies aimed at understanding the phenotypic impacts of the variants under selection.

Session 2 TUE POL C 11

Toll-like receptors in birds: diversifying selection, pseudogenization and gene duplication (51989)

Hana Bainova, Maria Weronika Gutowska, David W. Burt, Michal Vinkler.

*Department of Zoology, Faculty of Science, Charles University in Prague, Czech Republic;
Department of Genomics and Genetics, The Roslin Institute and R(D)SVS, University of
Edinburgh, UK.*

Toll-like receptors (TLRs) form an essential class of pattern recognition receptors that plays a key role in the first line of vertebrate innate immune defence against various pathogens. Avian TLR family comprises in its original state ten receptors, where each receptor homodimer or heterodimer is capable of recognizing a distinct set of microbe-associated molecular patterns. Herein we present the result of our investigation of avian TLR evolution. We analysed all TLR sequences available from 65 bird species covering major avian clades. The sequence data were extracted from whole genome sequences obtained within the Avian Genomes project as well as from public sequence repositories. Our selection analyses revealed that positive diversifying selection acts more on extracellular than on endosomal TLRs. Furthermore, we described the unique phenomenon of TLR5 pseudogenization recently published in passerines also in other bird taxa (e.g. in Psittaciformes, Cariamiformes, Trogoniformes, Phaethontiformes, Eurypygiformes and Apodiformes). TLR7 duplication predicted until today only in passerines seems to be common also in other avian taxa as e.g. in Charadriiformes, Cuculiformes and Mesitornithiformes. The assessment of evolutionary patterns explaining the genetic variability in genes of the TLR family may shed light on selective pressures shaping host-parasites interactions on large evolutionary scales.

Session 2 TUE POL C 11

Diversity through alternative splicing: Do Dscam1 splice variants respond to bacteria exposure? (52023)

Sophie Armitage, Wei Sun, Xintian You, Joachim Kurtz, Dietmar Schmucker, Wei Chen.

University of Münster; Max-Delbrück Center for Molecular Medicine Berlin; VIB University Leuven.

One way that a host can evolve diversity in immune recognition and effector molecules is through alternative splicing. It has been proposed that the extensively alternatively spliced gene Dscam1 (Down syndrome cell adhesion molecule), might be involved in pancrustacean immune responses against diverse parasites. It has been proposed that the phenotypically variable isoforms (combinations of exons) that it can produce may be involved in the recognition of diverse parasite epitopes, although evidence to support this is sparse. One prediction is that the Dscam1 gene expression of alternatively spliced exons is influenced by exposure to an immune elicitor. To test this hypothesis, for the first time in an immune context, we used Pacific Biosciences long read RNA sequencing methods to investigate splicing patterns after exposing *Drosophila melanogaster* and a cell line to live *Escherichia coli*. Using long reads allowed us to examine the expression of different isoforms. Contrary to our prediction, we found no significant changes in exon or isoform expression in response to bacterial exposure. However, these data represent only one of a vast number of possible host-microbe interactions. In order to test the general significance, future studies are needed to test other host-parasite combinations and more ecologically relevant conditions.

Session 2 TUE POL C 11

Major-effect mutations provide resistance to viruses in natural *Drosophila* populations (52031)

Chuan Cao, Rodrigo Cogni, Michael Magwire, Frank Jiggins.

University of Cambridge; University of São Paulo; Syngenta.

Coevolutionary arms races between hosts and parasites mean that there is continual selection for novel ways to resist infection. We have used the powerful tools of *Drosophila* genetics and genomics to understand the evolution of resistance. By combining high-resolution QTL mapping and association studies we have found that there are a small number of major-effect polymorphisms that control virus resistance in natural *Drosophila* populations. For three of the genes involved, we have modified them to experimentally confirm the exact mutations involved, showing that diverse molecular changes can lead to resistance. A single amino acid change in the restriction factor pastrel dramatically increases the resistance against *Drosophila* C Virus. A transposable element insertion in gene *CHKov1* results in a new transcript, which protects flies against sigma virus infection. Meanwhile, a large deletion in the protein *Gel* makes flies resistant to sigma virus infection, likely by altering its role in RNA degradation. In all cases the resistant allele is the derived state and the genes often show signs of strong selection. Together our results indicate that major-effect mutations that provide resistance to viruses continually arise and are driven through populations by natural selection.

Bumblebee immune response upon faecal transplant and microbiota community structure in host-parasite interactions (52154)

Kathrin Nöpflin, Paul Schmid-Hempel.

ETH Zürich.

Microbial symbionts are suspected to closely interact with the host immune system. Recently, their role in mediating levels of resistance in host-parasite interactions has thus come into focus. So far, however, experimental investigations of the impact of the microbiota on the host immune system and vice versa are virtually absent. Experiments done in the bumblebee, *Bombus terrestris*, demonstrated that the microbiota both provides a protective function against the trypanosome gut parasite, *Crithidia bombi*, and mediates the specificity of the host-parasite interaction. Here, we investigated how the crosswise transplantation of "resistant" and "susceptible" faecal microbiota into "resistant" and "susceptible" backgrounds of microbe-free worker bees affects the activity of the host immune system. In a first step, we measured the primary immune gene expression response to the transplant. In a second step, we investigated if these gene expression patterns are associated with differences in the microbiota community structure as described by 16s rRNA sequence data. Our results underline the importance of the host genotype (i.e. resistance background) in host-parasite interactions. Most likely, the host genotype is able to exert selection via differences in gene expression upon the establishing gut community.

Evolution of anti-parasitic behaviors in monarch butterflies (52207)

Jaap de Roode.

Emory University.

Hosts have evolved a wide variety of defenses against parasites, including anti-parasitic behaviors. Monarch butterflies (*Danaus plexippus*) are commonly infected with the protozoan parasite *Ophryocystis elektroscirrha*, which strongly reduces monarch survival, mating ability and fecundity. Monarchs are specialized on milkweeds as their larval food plants, and milkweed species with high concentrations of cardenolides (secondary toxic chemicals) reduce parasite infection and virulence. We investigated whether monarchs can use medicinal milkweeds to prevent or cure disease, and whether monarch medication behaviors depend on parasite risk in natural populations. Our experiments suggest that infected female butterflies preferentially lay their eggs on medicinal milkweeds that make their offspring less sick. Moreover, the type of medication behavior depends on parasite risk in natural populations. In eastern and western North America, where parasite risk is low, only infected monarchs had a preference for medicinal plants, indicating therapeutic medication. In contrast, in South Florida, where parasite risk is high, both infected and uninfected monarchs preferred to lay

eggs on medicinal milkweed, indicating prophylactic medication. Overall, our results suggest that monarchs can use medicinal milkweeds to mitigate the negative effects of their prevalent protozoan parasites, and that variation in parasitism risk contributes to variation in medication behavior.

Session 2 TUE POL C 11

The effectiveness and costs of pathogen resistance strategies in a long-lived host (52294)

Hanna Susi, Anna-Liisa Laine.

University of Helsinki.

Hosts have evolved different strategies to resist pathogens but little is known about how variable, effective, and costly these mechanisms are in long-lived hosts. In the interaction between *Plantago lanceolata* and its powdery mildew causing fungus *Podosphaera plantaginis* the same host may block infection by some strains of the pathogen while being susceptible to others and once infected, hosts may quantitatively mitigate disease development. We conducted a laboratory experiment to assess variation in resistance strategies across 41 plant genotypes originating from 8 *P. lanceolata* populations. To test stability and costs of different resistance strategies, we established multi-year experimental populations of plants possessing qualitative resistance, quantitative resistance, or susceptibility to disease. We found variation among the resistance phenotypes in laboratory with no evidence for trade-offs between qualitative and quantitative resistance strategies. Throughout the three year study qualitative resistance efficiently blocked infections but quantitative resistance was not effective against infection in the experimental populations. We detected fitness costs of resistance in the absence of the pathogen for qualitative and quantitative resistance compared to susceptible plants. Our results demonstrate that different resistance strategies can be maintained in a natural population by costs of resistance and by shifts in resource allocation under infection.

Session 2 TUE POL C 11

Trade-off between dual roles of the gut in nutrient acquisition and immune defense: experimental evolution and physiological basis (52313)

Tadeusz Kawecki, Roshan Vijendravarma.

University of Lausanne.

In addition to its role in digestion and absorption of nutrients, the digestive tract is the first line of defense against enteric pathogens, and thus the site of potential evolutionary trade-offs between nutrient acquisition and immunity. We will present evidence for such a trade-off from experimental evolution, with *Drosophila* as the study system. We found that populations adapted during 160 generations of experimental evolution to chronic larval malnutrition became more efficient at extracting the diluted nutrients, but also more susceptible to

intestinal infection with the bacterial pathogen *Pseudomonas entomophila*. Detailed experiments reveal an unexpected mechanism of this trade-off: elevated predisposition to loss of intestinal integrity upon infection, leading to sepsis. These results provide a potential evolutionary explanation for the maintenance of genetic susceptibility to opportunistic intestinal pathogens.

Session 2 TUE MAX 415 27

The adaptive value of within-individual covariation between floral signals and rewards. (51709)

Santiago Benitez-Vieyra.

Instituto Multidisciplinario de Biología Vegetal (Universidad Nacional de Córdoba - CONICET).

When pollinators visit a sequence of flowers they experience a continuum of variation in advertisement traits and in the amount and quality of reward, ranging from full rewarding to deceptive flowers. They can combine this information, evaluate the reliability of plant signals and use previous knowledge to decide when to leave that plant. Hence, in most plant species the within-individual covariation among signals and rewards could be the target of pollinator-mediated selection if pollinators verify the reliability of floral signals and penalize cheating individuals. We examined whether within-individual signal-reward correlations evolve under selection at micro- and macroevolutionary levels, detecting the occurrence of current phenotypic selection on natural populations and testing the adaptive divergence of floral signals in plants visited by different pollinators. In the latter case, we used a sample of Neotropical *Salvia* species and took advantage of the differential use of floral signals by bees and hummingbirds to predict which specific traits are predominantly associated with nectar reward at the within-individual level. Our findings support the idea that signal honesty is selected by pollinators and highlight the adaptive value of within-individual variation.

Session 2 TUE MAX 415 27

Learning about natural variation of floral odors sets boundaries for generalization among flowers with the same reward value (51798)

Brian H. Smith, Fernando F Locatelli, Patricia C Fernandez.

Arizona State University; Universidad de Buenos Aires; INTA EEA Delta del Paraná y FAUBA.

Floral odors are typically mixtures. Mixtures that have the same meaning – e.g. food - can vary in composition from flower to the next. Therefore a central problem in recognition of floral odors is generalization among flowers that differ but have the same meaning. We propose that mechanisms of plasticity in early sensory processing in the brain are central to solving this problem. Accordingly, plasticity should work to improve grouping of odors that

have the same meaning. Using synthetic mixtures that mimic natural odor variation, we studied how honey bees learn about and generalize among floral odors. We conditioned honey bees on a discrimination problem using synthetic mixtures that mimic natural variation among snapdragon flowers. We then employed bioimaging of calcium responses in projection neurons of the antennal lobe, which is the first synaptic relay of olfactory sensory information in the brain, to study how ensembles change as a result of conditioning. We show how neural networks in the antennal lobes become 'tuned' through plasticity to improve grouping of odors that have the same meaning. We argue that this tuning allows more efficient use of the immense coding space of the antennal lobe to solve the generalization problem with floral odors.

Session 2 TUE MAX 415 27

Paternity analysis reveals mating patterns in an *Antirrhinum* hybrid zone incorporating sibships and phenotypes (51642)

Thomas Ellis, David Field, Nick Barton.

IST Austria.

Pedigree estimation of natural populations allows a direct and powerful insight into mating patterns of wild organisms and the traits which contribute to variation in reproductive success. I will present data on paternity for open-pollination seedlings from an *Antirrhinum* hybrid zone. Here yellow and magenta subspecies hybridise and form transgressive white, orange and pink pigmentation phenotypes. Comprehensive phenotypic sampling permits joint estimation of paternity and the strength of selection on floral characters. This is performed in a new Bayesian framework which combines information on phenotypes and shared alleles among siblings to assign relationships, which is efficient for modern SNP genotype datasets.

Session 2 TUE MAX 415 27

The double role of *Salvia viridis*' extrafloral display (51644)

Yoram Gerchman, Tamar Keasar.

University of Haifa at Oranm.

Salvia viridis is a Mediterranean annual plant, growing in small groups ("patches"), and characterized by an extra-floral structure, a group of conspicuous purple tufts of leaves ("flags"), which terminate each vertical inflorescence. We have studied the role of these flags in the interaction of the *S. viridis* plant with different animals, both pollinators and herbivores, and found that removal of the flags increased herbivory. Furthermore, removal of the flags from whole patches, but not from individuals within patches, reduced pollinator visits. Chemical analysis suggested that the flag leaves' purple color is due to a high content of anthocyanin. Comparison of reflectance data for flags and leaves suggest that they can be visually discriminated by both pollinators and herbivores. Finally we have also looked into

the biomass 'cost' of the flag and concluded that it is probably negligible. Our results shed light on visual based selection for extra-floral traits by pollinators and herbivores.

Session 2 TUE MAX 415 27

Heritability of floral volatiles and pleiotropic responses to artificial selection in *Brassica rapa* (52051)

Pengjuan Zu, Florian Schiestl, Wolf Blankenhorn.

Institute of Systematic Botany, University of Zurich; Institute of Systematic Botany, University of Zurich; Institute of Evolutionary Biology and Environmental Studies, University of Zurich.

Plants produce a large diversity of volatile organic compounds that serve fundamental functions such as pollinator attraction and herbivore deterrence. Plant volatile emission is often highly variable and sensitive to environmental factors. To date, nothing is known about heritability of plant volatiles, and whether individual compounds can evolve independently or merely in concert with the whole volatile bouquet. To fill this gap in our understanding of plant volatile evolution, we conducted bi-directional artificial selection on four target floral volatiles representing four main chemical groups to estimate heritability and correlated pleiotropic responses in fast cycling *Brassica rapa*. The realized heritability of the four target volatiles ranged from 20% to 45%, as estimated from the “high amount” selection lines. The average narrow-sense heritability of all 13 analyzed floral volatiles was 18% based on parent-offspring regressions. There were pleiotropic effects of the selected volatile compounds on other volatiles, on flowering time, and on some morphological traits. We found that the whole floral scent bouquet changed even when there was selection on only single compounds. Our study demonstrates that floral scent can evolve fast under phenotypic selection, but this can come with additional correlated responses in traits that are not direct targets of selection.

Session 2 TUE MAX 415 27

Are florivores agents of selection on floral colour? Review and Synthesis (51743)

Mahua Ghara, Yuval Sapir.

Tel Aviv University.

Colour in flower is an advertising signal, important to visually attract pollinator which in turn acts as an agent of selection on colour. Floral tissues such as petals, style, pollen, or ovules are consumed by insects (florivores) that may use colour to visually orient themselves to host. Florivores cause loss of fitness directly through consumption of gametes (pollen and ovules), and indirectly through alteration of signals important for pollinator attraction. Florivores are likely to impose selection on floral colour. We systematically reviewed available literature for evidences on pollinator- and florivore-mediated selection on floral colour, and for evidences on selection mediated by interaction between pollinators and florivores. Although

publications on pollinator-mediated selection were abundant, the role of florivores as agent of selection on floral colour remained relatively uninvestigated. A few studies provided evidence for florivores as agents of selection and some studies that failed to provide evidence for pollinator-mediated selection alluded to the possibility of selection mediated by florivores. The review summarizes the studies on florivore-mediated selection on floral colour, and suggests a frame-work to estimate the role of florivores in floral colour evolution. A possible cause for such shortage in studies on florivore-mediated selection, as compared to pollinators is discussed.

Session 2 TUE POL D 33

Multiple morphological and behavioural modifications converge into a function that promotes invasion and diversification within a new adaptive zone (52191)

Antonin Crumière, Abderrahman Khila.

IGFL.

Evolutionary key innovations may open new ecological opportunities and facilitate adaptive radiations. However, the adaptive value of key innovations during initial stages of the colonization of new niches and genetic mechanisms underlying their emergence are rarely established. The Gerromorpha, a monophyletic group of semi-aquatic Heteroptera, transited from terrestrial life to life on the water surface, and radiated into remarkable forms that colonized a vast array of sub niches. Using phylogenetic mapping, we discovered that the transition to water surface life is associated with an increase in the frequency of leg strokes and an increase in leg length which is exploited by Gerromorpha to cover larger stroke amplitudes during water surface locomotion. The combined modification in these biomechanical parameters contributes to increase locomotion efficiency compared to exclusively terrestrial relatives. The emergence of these traits at the base of the Gerromorphan phylogeny coincides with the novel deployment of the Hox gene *Ultrabithorax* in the second thoracic segment. Using RNAi knockdown we highlight the importance of *Ubx* in the emergence of these traits and the role of fluid substrate as a selective force in the evolution of Gerromorpha. Therefore, evolutionary changes in highly pleiotropic genes can generate multiple discreet phenotypic changes, which can have a spectacular impact on organismal ecology and diversification.

Session 2 TUE POL D 33

Natural Arabidopsis BRX Loss-of-Function Alleles Confer Root Adaptation to Acidic Soil (52240)

Christian Hardtke.

University of Lausanne.

To understand gene action at the cellular, tissue and organismal levels is the ultimate goal of developmental biology and can connect to ecological-evolutionary aspects through analysis of corresponding natural genetic variation. In our lab, we have isolated a regulator of root growth vigor in *Arabidopsis thaliana* named BREVIS RADIX (BRX) through the natural variation approach. Although generally highly conserved, hyperactive as well as loss-of-function BRX alleles exist in nature. A physiological feature of brx null mutants, proton pump hyperactivity, could explain their occurrence, because on overly acidic media or soil this feature confers more robust growth and increased fitness as compared to wild type. In these conditions, the fitness advantage might over-compensate for the loss of root meristem growth, for which BRX is essential. In summary, the existence of independently maintained brx loss-of-function alleles in nature and their association with low pH soils supports the notion that they are advantageous in acidic soil pH conditions. Physiological assays based on brx characteristics now enable us to map other genes that confer adaptation to acidic soil and to rapidly identify their causal allelic variants through next generation sequencing approaches.

Session 2 TUE POL D 33

The genomic architecture of adaptation and speciation in ecologically divergent forest trees (*Populus* spp.) (52358)

Margot Paris, Stölting Kai N. , Meier Cécile, Heinze Berthold, Castiglione Stefano, Bartha Denes, Macaya Sanz David , Gonzalez-Martinez Santiago, Lexer Christian .

University of Fribourg; Federal Forest Research Centre Vienna; University of Salerno; West Hungarian University; INIA-CIFOR.

Recent advances in sequencing technologies offer great opportunities to address the molecular basis of adaptation and ecological speciation. In Eurasia, several phenotypically differentiated forms within the ‘model tree’ genus *Populus* have diverged in the face of gene flow. *Populus* provides a promising model to explore the determinants of adaptation and divergence along a continuum, ranging from differentiated populations and phylogeographic lineages to divergent species with fairly strong postzygotic barriers. We report a whole genome sequencing effort involving multiple populations of Eurasian *Populus alba* and *P. tremula* including multiple post-glacial recolonization lineages within the former. We find a complex genomic architecture of adaptive differentiation from both, standing genetic variation and new mutations. In Central European *P. alba* alone, screening of 14 million sequence polymorphisms reveals 430 highly differentiated genes mainly linked to soil adaptation (e.g. ion transport, root development, and water stress response). High divergence between hybridizing species appears to be maintained by widespread coupling effects, whereas 4% of the studied genome windows do not exhibit any fixed between-species polymorphism. Some of these regions also exhibit intraspecific footprints of selection, thus suggesting that introgression contributes to the functionally important variation available for adaptation.

Session 2 TUE POL D 33

The origin and spread of premating isolation driving incipient speciation in *Mimulus* (52401)

Matt Streisfeld, Sean Stankowski, James Sobel.

University of Oregon; Binghamton University.

Speciation is a continuous process that occurs across a broad range of spatial settings and scenarios. Yet, the historical events contributing to the origin and spread of traits that generate reproductive isolation are poorly understood. We elucidate the ecological genetic changes driving the early stages of divergence in a classic example of incipient speciation in *Mimulus aurantiacus*. Red- and yellow-flowered ecotypes are parapatrically distributed and partially isolated due to differences in habitat and pollinator behavior. However, postmating barriers are weak, resulting in gene flow across much of the genome and a narrow hybrid zone where ranges overlap. Nevertheless, a small set of loci remain differentiated, demonstrating the preliminary stages of genomic divergence. Indeed, six floral traits associated with pollinator isolation vary clinally in nature, providing strong evidence for divergent selection despite gene flow. Our molecular studies have revealed a cis-regulatory mutation in the *MaMyb2* gene that is primarily responsible for red floral pigmentation. We show that this adaptive allele entered the red-flowered ecotype via introgressive hybridization with a more distantly related subspecies, a result that not only sheds light on the complex history of divergence but also the power of ecological adaptation to drive the early stages of speciation.

Session 2 TUE POL D 33

Sexual isolation and the genetics of chemical cues involved in speciation in *Heliconius* butterflies (52450)

Claire Mérot, John Davey, Richard Merrill, Sarah Barker, Ene Leppik, Brigitte Frérot, Chris Jiggins, Mathieu Joron.

ISYEB UMR 7205, Muséum National d'Histoire Naturelle, Paris; Department of Zoology, University of Cambridge; UMR 1392 iEES, INRA Versailles ; UMR 5175, CNRS-Centre d'Ecologie Fonctionnelle et Evolutive, Montpellier.

Speciation with gene flow implies the evolution of reproductive isolation under selection favouring lineage differentiation. Understanding how divergent selection leads to speciation requires characterizing the ecological, phenotypic and genomic modalities of reproductive isolation. *Heliconius* butterflies are now an established example of ecological speciation driven by a “magic trait”, wing colour pattern, because a shift in this trait triggers disruptive selection for mimicry, as well as sexual isolation involving the same trait as a mating cue.

However, sibling species with similar wing patterns exist in sympatry, meaning that other traits maintain or accompany reproductive isolation. To understand the multidimensionality of speciation, we investigated *Heliconius* sister-species with similar patterns. Behavioural experiments show that pattern similarity interferes with mate location, yet species isolation remains strong due to mate choice based on short-distances cues. Chemical analyses on genitalia and wing scents demonstrated species-specific chemical signatures, suggesting

chemical communication participates to reproductive isolation. Using genome-wide RAD-mapping of interspecific crosses, we revealed the genetic architecture of pheromone profiles, analyzed it in the light of the genomic landscapes of divergence, and tested the linkage with other loci involved in speciation. This opens the possibility to explore the coupling and order of appearance of the different speciation modalities.

Session 2 TUE POL D 33

Key Physiological Innovations during Colonizations of Fresh Water and Land (52488)

Carol Eunmi Lee, Seong-il Eyun, Marijan Posavi, Gregory Gelembiuk, Jane Remfert, Guy Charmantier, Mireille Charmantier-Daures.

University of Wisconsin; University of Nebraska; Université de Montpellier.

Arthropods are the most successful animal phylum on the planet, both in terms of number of species and total biomass. While arthropods evolved originally in the sea, they have become extraordinarily successful across an extremely wide range of habitats and ecological niches. Arthropods now dominate many marine, freshwater, hypersaline, and dry environments across the globe. While most marine invertebrates have no need to osmoregulate, invading freshwater habitats requires the active uptake of scarce ions, whereas invading land adds the additional challenge of also regulating water (at times to reduce water loss). In addition, challenges are imposed by the differences in physical properties between water versus air. Yet, arthropods have invaded freshwater and terrestrial environments multiple times independently. This talk discusses some key adaptations that occurred during the transitions from marine to freshwater to terrestrial habitats, based on results from laboratory selection experiments, comparative physiological studies, and genome sequence analyses. Evolution of ion transporter function appears to be critical for the transition from marine to freshwater habitats, and these functions appear to be concentrated in the legs in many arthropods. Additionally, across the phylum Arthropoda we observe curious gains and losses of chemoreceptor gene families in arthropod lineages.

Session 2 TUE POL D 33

Distinct genetic mechanisms of parallel speciation in phytophagous ladybird beetles (52536)

Kei Matsubayashi, Victor Soria-Carrasco, Zachariah Gompert, Romain Villoutreix, Moritz Muschick, Akemi Togashi, Haruo Katakura, Hideki Ueno, Patrik Nosil.

The University of Sheffield; The University of Sheffield; Utah State University; The University of Sheffield; The University of Sheffield; Hokkaido University; Hokkaido University; Niigata University; The University of Sheffield.

Adaptation to similar environments can create new species and this process can occur repeatedly to result in replicate species pairs (i.e., parallel speciation). The genetic basis of this process is poorly understood but is assumed to usually occur by new pairs of species forming via divergence from a single shared ancestor. By combining genomic analyses with experimental estimates of several isolating barriers we found that parallel speciation in phytophagous ladybird beetle species involves distinct historical and genetic processes in different species pairs in Japan. In one geographic region a species pair was formed by divergence from a single common ancestor and specialization on different host plants. In contrast, in another locality a new species was formed by hybridization between two different closely related parental species. Although the latter case also involved host adaptation, it was facilitated by hybridization between the two parental species. The results indicate that individual species can contain much genetic variation due to variation derived from distinct ancestors, and that hybridization between populations can generate new highly distinct species even in the early stages of ecological speciation. The collective results illustrate complex origins of different species with a potential role for hybridization in facilitating this process.

Session 2 TUE GEN B 8

How do beneficial microbiomes form and adapt within mutualisms? (52278)

Tabitha Innocent, Mahmoud Al-Bassam, Morten Schiøtt, Douglas W. Yu, Matthew I. Hutchings, Jacobus J. Boomsma.

Centre for Social Evolution, Department of Biology, University of Copenhagen; University of East Anglia, School of Biological Science, Norwich NR4 7TJ, Norfolk, England; Chinese Academy of Science, Ecology, Conservation and Environment Center (ECEC), Kunming Institute o.

The fungus-farming attine ants live symbiotically with multiple species of antibiotic-producing actinobacteria. We know the diversity of bacterial species provides a diversity of antibiotics, thus maintaining long-term protection against pathogens that attack the ant's fungal mutualist. However, only one of these actinomycete species is vertically transmitted by the ants, so it has remained unclear how and at what life stages more diverse beneficial microbiomes are established by selective recruitment of additional actinomycete strains from the environment.

This is an important general problem: how do the dynamics of bacterial competition lead to the formation of a microbiome that benefits a host and mutualistic partner? While mutualisms between bacteria and other species are both abundant and influential (e.g. multiple insects, crop plants, coral systems), these systems tend to be difficult to experimentally manipulate in the lab. With the attine ant model we can empirically test the latest evolutionary theories on mutualism stability with ramifications well beyond this system.

In this light, I will present genomic and experimental data covering several genera of attine ants suggesting the ants promote interference competition among bacteria, and this competition favours beneficial actinobacterial communities.

Mutualism in a community context: lessons from ants, aphids and their gut microbiomes (52797)

Aniek B.F. Ivens, E. Toby Kiers, Daniel J.C. Kronauer.

The Rockefeller University, New York, USA; VU University Amsterdam, NL.

Ant-aphid interactions are classic examples of interspecific cooperation. The ants depend on honeydew excreted by the aphids for sugar; the aphids depend on the ants for protection and hygiene. Such mutualistic interactions are inherently prone to destabilizing conflicts of interest. Several mechanisms can align the partners' interests, such as partner fidelity through reduced rates of aphid dispersal and partner choice based on honeydew quality.

Although historically regarded as two-species interactions, mutualisms are now increasingly recognized as complex multispecies networks. Using genetic barcoding, we show that an interaction of subterranean *Lasius* ants tending *Prociphilus* aphids in fact comprises a mutualistic community of multiple species of ants and aphids. Moreover, aphids harbor specialized endosymbiotic bacteria, which facilitate feeding on specific plants; likewise the ants' gut microbiome likely facilitates honeydew digestion.

In our experiments, we aim to identify the roles these microbes play in the mutualism's evolutionary stability. Their impact is potentially huge: by influencing honeydew quality, aphid endosymbionts can affect partner choice. Likewise, ant gut microbes can affect partner fidelity by determining on which aphids' honeydew the ants can feed and thus with whom they can associate. Including additional organisms can thus drastically change our understanding of the evolutionary ecology of mutualism.

Colony fusion as a route to cooperation without kinship in ant supercolonies (52676)

Ea B. M. Hørsving, Louise S. Pedersen, Dóra B. Huszár, Luigi Pontieri, Jacobus J. Boomsma, Jes Søren Pedersen.

Centre for Social Evolution, Department of Biology, University of Copenhagen, Universitetsparken 15,.

One of the most spectacular cases of cooperation among unrelated individuals is ant supercolonies, where large networks of interconnected nests may extend over hundreds, or even thousands, of kilometres without territorial aggression. Several species exclusively form supercolonies and always as genetically closed lineages that have emerged by budding from existing ones (fission). Alternatively, here we asked whether fusion of colonies has the potential to lead to the emergence of new supercolonies in the common red ant *Myrmica rubra*. We found that two colonies do not fuse only if they are both tight families headed by a single queen. All other *M. rubra* colony combinations always fused, even when the

geographic origin was as distant as Denmark and Finland (different haplotype groups). This indicates that supercolony formation in *M. rubra* is more dependent on family structure than genetic distance, and that multiple-queen colonies can expand in the habitat and merge. Genetic evidence for mixed origins of supercolonies indicates that fusion indeed happens in the field. These complexities suggest that there may be more than a single evolutionary route to the paradoxical state of supercoloniality, and that colony fusion could lead to cooperation without kinship in evolutionarily derived ant lineages.

Session 2 TUE GEN B 35

Specialist and generalist oviposition strategies in butterflies: maternal care or precocious young? (52208)

Alexander Schäpers, Sören Nylin, Mikael Carlsson, Niklas Janz.

Department of Zoology, Stockholm University.

Herbivorous insects specialized on a narrow set of plants are believed to be better adapted to their specific hosts. Species with a broader diet breadth seem to pay a cost through decreased oviposition accuracy. Despite many studies investigating oviposition behavior we lack knowledge on how larvae cope behaviorally with their mothers' egg-laying strategies. We examined how five nymphalid butterfly species with different host plant ranges differed in female oviposition preference and in neonate larval behavior in several disadvantageous situations. We found a general synchrony between female and larval abilities, where species with more "caring", discriminating females had larvae that were less able to deal with a suboptimal initial feeding site. Conversely, relatively indiscriminate females had more precocious larvae with higher abilities to cope with suboptimal sites. Remarkably, despite similarities between the tested species with similar host ranges, there were also striking differences. Generalist and specialist species can be found side by side in many clades, with each clade having a specific evolutionary history. Such clade-specific, phylogenetically determined preconditions apparently have affected precisely how a broad or narrow diet breadth can be realized.

Session 2 TUE GEN B 35

Factors affecting the evolution of host-switching in infectious diseases (52407)

Alethea Wang, Magda Meier, Francois Balloux.

UCL; UCL; UCL.

Although new infectious diseases have become increasingly prevalent in the past several decades, the underlying factors leading to their emergence remain unclear. Epidemics have frequently been linked to pathogen host switching, but few studies have broadly examined the overall prevalence of host switching across pathogen groups. Here, we examine how two evolutionary factors - host taxonomic relatedness and pathogen host range - influence a

pathogen's ability to infect new host species. Although pathogens often infect closely related species, there are also many cases in which the original and new hosts are taxonomically diverse. Second, pathogens vary considerably in their host ranges, with some being specialists that only infect a single species and others capable of infecting hosts from a number of different taxonomic groups. We conducted a comprehensive literature review of ~550 bacterial pathogens of humans and animals to quantify whether host taxonomic relatedness and breadth of host range are important factors underlying the potential for pathogen host switching. This understanding will improve our ability to predict, prevent and control future disease outbreaks.

Session 2 TUE GEN B 35

The long reach of a tapeworm parasite in its social host (52951)

Sara Beros, Evelien Jongepier, Felizitas Hagemeyer, Susanne Foitzik.

Institute of Zoology, Department of Evolutionary Biology, Johannes Gutenberg University.

Parasite-induced alterations are well-known on the individual level, but the consequences of parasite infections for social groups are less clear. Manipulative parasites with complex life cycles could extend their influence to non-infected group members by chemical or behavioural manipulation to ensure their own survival and transmission. An infection with the tapeworm *Anomotaenia brevis* induces multidimensional changes in its intermediate host, the ant *Temnothorax nylanderi*. Despite having a deviant chemical profile that would usually lead to social rejection, infected ants are tolerated and well-cared for in their colonies, as evident in their increased survival rate. Here, we tracked infection-mediated effects by manipulating the composition of ant colonies through addition and removal of infected workers, and determined colony aggression. Our results reveal that the presence of infected ants clearly influences the colonies' response to intruders. Parasitized colonies behaved less aggressive towards conspecifics, and this change was based on a lower aggression in non-infected ant workers. We argue that this lower aggression might be the outcome of behavioural manipulation and could ensure the care for infected workers, consequently increasing parasite fitness. In summary, individual parasite infections can have far-reaching consequences in social groups, hereby influencing the behavioral performance on the colony level.

Session 2 TUE GEN B 35

Wing pigmentation and immune response in the Glanville fritillary butterfly (51704)

Elena Rosa, Marjo Saastamoinen.

University of Helsinki.

Melanin production in insects is typically involved in pigmentation and immune response, and both of these traits depend on the phenoloxidase enzyme pathway. During attacks by

exogenous pathogens, encapsulation response is activated, resulting in clotting and melanisation of the foreign bodies. In butterflies, melanin production is important in the cuticle and adult wing pigmentation, and it has a key role in thermoregulation. However, as melanin production is costly, trade-offs among competing life history traits are expected, especially under restricted resource conditions.

In Finland, the Glanville fritillary butterfly occurs in its northern range limit and is restricted to the Åland archipelago, where a conspicuous variation in wing darkness among individuals has been observed. Our aim is to investigate within and among population level variation in the relationship between immunity and pigmentation. Darker patterns are predicted to be influenced also by developmental conditions: individuals under cool environmental conditions are expected to be darker as a predictive adaptive response to allow faster heat absorption and increased activity under those conditions. However, immune challenge during early life may activate melanin production and influence its allocation to wing patterns, or to adult immune response.

Session 2 THU GEN C 4

Field estimates of parentage reveal sexually antagonistic selection on body size in a population of *Anolis* lizards (51824)

Katie Duryea, Patrick Bergeron, Zachary Clare-Salzler, Ryan Calsbeek.

Lund University; University of Sherbrooke; University of Montana; Dartmouth College.

Sexual dimorphism evolves when selection favors different phenotypic optima between the sexes. Such sexually antagonistic selection creates intralocus sexual conflict when traits are genetically correlated between the sexes. We investigated sexually antagonistic selection on body size in the brown anole lizard, *Anolis sagrei*. Brown anoles are highly sexually dimorphic: males are on average 30% longer than females and 150% more massive in our study population. Viability selection on body size is sexually antagonistic and directional selection favors larger males whereas stabilizing selection constrains females to remain small. Here, we measure reproductive components of fitness over three generations in a population of brown anoles. We estimated the number of offspring produced by an individual that survived to the following year, a measure of individual fitness that includes aspects of both individual reproductive success and offspring survival. Using this measure of fitness, we found directional selection on male body size, consistent with previous studies of viability selection. However, selection acting on female body size varied among years, including periods of positive directional selection, stabilizing selection, and no selection. Thus, selection acts differently in the sexes through both survival and reproduction and sexual conflict appears to be a persistent force in this species.

Session 2 THU GEN C 4

Identification and characterisation of sexually antagonistic loci in *Drosophila melanogaster* (51842)

Mark Hill, Ted Morrow, Kevin Fowler, Max Reuter.

University College London; University of Sussex.

Divergent evolutionary interests between the sexes generate sexually antagonistic selection, where opposing trait values are selected in males and females. However, a response to these selective pressures is constrained by the sexes' shared genome, leading to 'intralocus sexual conflict' (IASC). Despite our increasing understanding of the taxonomic prevalence of IASC and the traits affected, the identity of antagonistic loci remains almost entirely unknown. Here, we present the results of a study addressing this question. We identified antagonistic loci in *D. melanogaster* by combining genomic data from a set of sexually antagonistic haplotypes with an evolve-and-resequence experiment. Both studies identify well-supported candidate loci and significantly overlapping sets of genes. Enrichment analyses show that antagonistic genes are predominantly involved in developmental and regulatory processes and, interestingly, include a significant number of genes involved in the sex-determination cascade. Collectively these studies represent the first detailed information regarding the genetic basis of IASC and provide a good foundation for studying the functional genetics of sexual antagonism and elucidating its evolutionary dynamics.

Session 2 THU GEN C 4

Male-male competition in the pistil causes rapid sexually antagonistic evolution in a plant and a correlated response on a mating-system related floral trait (51995)

Åsa Lankinen, Sofia Hydbom, Maria Strandh.

Swedish University of Agricultural Sciences, Sweden; Lund University, Sweden.

Adaptive evolutionary change in response to sexual selection and sexual conflict can be surprisingly fast in animals. In plants, however, such knowledge is limited, as experimental evolution studies manipulating the strength of sexual selection have not been conducted. In *Collinsia heterophylla*, a 'mixed-mating' annual that combine outcrossing and self-pollination, early fertilizations are associated with female fitness costs, which is in accordance with a sexual conflict over timing of pistil receptivity to pollen. To test how sexual conflict influences trait evolution we conducted artificial selection on pollen by creating monogamous and polyandrous lines (crossed with one or two pollen donors, respectively, at early floral stages). After four generations of artificial selection we found increased pollen competitive ability and enhanced female fitness costs in the polyandrous selection line compared to the monogamous selection line and a control line, showing rapid sexually antagonistic evolution of pollen. Additionally, we found evidence for a correlated positive effect on timing of anther-stigma contact, a trait that determines timing of self-pollination. In conclusion, our study suggests that artificial sexual selection on pollen can lead to rapid evolutionary change in plants, female fitness costs and correlated effects on mating system-related traits.

Session 2 THU GEN C 4

Sex biased expression as a sexually antagonistic trait (52078)

Paris Veltsos, Yongxiang Fang, Andrew R Cossins, Rhonda R Snook, Michael G Ritchie.

Centre for Biological Diversity, University of St Andrews; Centre for Genomic Research, University of Liverpool; Centre for Genomic Research, University of Liverpool; Animal and Plant Sciences, University of Sheffield; Centre for Biological Diversity, University of St Andrews.

Sexually antagonistic traits such as growth rates, colouration or immunity are often under sexual selection. The availability of transcriptomic data has led to comparisons of gene expression levels under different sexual selection treatments, linking gene expression and sexually antagonistic trait studies. We have experimentally manipulated the strength of sexual selection, by either enforcing monogamy or exposing females to higher than natural number of male partners, for over 150 generations in lab populations of *Drosophila pseudoobscura*. Such manipulation may influence one sex more than the other and can result in the inversion of sex bias for some genes. By employing replicated sampling over two tissues and mating statuses we demonstrate that, in most cases, the expression of sex biased genes responded to experimental sexual selection more than unbiased genes. However the direction of the shift in gene expression was difficult to predict and sensitive to both tissue and mating status. We conclude that sex biased gene expression can be considered a sexually antagonistic phenotype, but the direction of change in response to sexual selection can vary within the same organism.

Session 2 THU GEN C 4

Sexual conflict and sex-biased gene expression throughout development (52134)

Fiona Ingleby.

University of Sussex.

Sexual dimorphism offers a potential resolution to intralocus sexual conflict, by allowing males and females to express their optimum trait phenotype when fitness optima differ between the sexes for a shared trait. As most of the genome is shared between the sexes, sex-biased gene expression is likely to account for most sexual dimorphism. Our research examines how sex-biased gene expression relates to sex-specific fitness throughout development as well as across different genotypes, therefore examining developmental and genetic sources of variation in sexual conflict. Using data from sex-specific fitness assays in *Drosophila melanogaster*, I show changes in sexual conflict between larval and adult stages, and show genetic variation for sexual conflict. I also use preliminary gene expression data from an RNA-sequencing experiment to begin to relate sex-specific fitness to patterns of sex-biased gene expression at each developmental stage.

Session 2 THU GEN C 4

Evolution of haploid selection in predominantly diploid organisms (52393)

Sarah P Otto, Michael F Scott, Simone Immler.

University of British Columbia; Uppsala University.

Diploid organisms shape the extent to which their haploid gametes and gametophytes experience selection. While animals are thought to experience only mild selection in the haploid stage, plants often experience strong haploid selection. When should parents limit exposure of gametes to haploid selection and when should they strengthen this selection? We develop mathematical models that consider the "selective arena" within which male gametes or gametophytes (sperm or pollen) compete for fertilization, examining how this selective arena evolves when controlled by the mother or by the father. In the presence of deleterious mutations, increased haploid selection purges the gamete pool and leads to higher quality offspring. Thus, mothers should maximize selection in the haploid phase as long as all their eggs/ovules can still be fertilized. Fathers, however, are primarily selected to maximize the proportion of offspring that they sire. Therefore, fathers often evolve to mask haploid expression, creating the potential for parental conflict. Furthermore, we include sex chromosome linkage and the effect of alleles that are not strictly deleterious. That is, alleles can have different fitnesses in males and females (sexually antagonistic selection) or in haploids and diploids (ploidy antagonistic selection), which modifies the optimal intensity of the selective arena.

Session 2 THU GEN C 4

Sexually antagonistic selection in canaries not generated by testosterone-related intralocussexual conflict (52841)

Arne Iserbyt, Marcel Eens, Wendt Müller.

University of Antwerp.

A current debate exists on the extent to which males and females constrain each other's evolution. On the one hand intersexual genetic correlations may cause a fundamental evolutionary problem when selection favors sex-specific phenotypic optima. On the other hand genetic mechanisms may evolve that resolve this intralocus sexual conflict by decoupling developmental pathways in males and females. Circulating testosterone (T) levels received increased research interest in this context, given its important role in mediating suites of physiological, morphological and behavioural traits and given its marked differential fitness effects in male and females. Here, we applied a full-sib (brother/sister) comparison in a pedigreed canary population to continue this debate. We show that parental fitness is negatively correlated between siblings, indicating sexually antagonistic selection. Furthermore, plasma T levels of brothers and sisters were positively correlated, indicating a significant intra-sexual genetic correlation with a heritable component (h^2) estimated at 0.41 ± 0.31 . However, T levels could not explain the fitness variation between siblings, contrasting the hypothesis of intralocus sexual conflict. The mechanism(s) underlying sexually antagonistic selection yet remain to be identified.

DNA methylation in the clonal raider ant *Cerapachys biroi* (52304)

Romain Libbrecht, Peter Oxley, Laurent Keller, Daniel Kronauer.

Rockefeller University; University of Lausanne.

Division of labor is at the root of the ecological success of insect societies, yet the mechanisms regulating reproduction and behavior are not fully understood. The clonal raider ant *Cerapachys biroi* has no distinct queen and worker castes, and is characterized by an alternation between reproductive phases (ants lay eggs inside the nest) and brood care phases (ants do not lay eggs but nurse the brood and forage for food). The opportunity to compare queen-like (reproductive phase) and worker-like (brood care phase) individuals, combined with the possibility to control for age, experience and genetic background (all known to influence reproduction and behavior), makes *C. biroi* a great model system to study division of labor. In the past few years, there has been a growing interest in the role of epigenetic mechanisms (e.g. DNA methylation) in division of labor. Our aim is to properly investigate the role of DNA methylation in regulating reproduction and behavior in *C. biroi*, by comparing whole-genome DNA methylation patterns (using bisulfite sequencing) between brains of individuals collected in reproductive and brood care phases. This project also provides important insights into the function and mode of action of DNA methylation in insects.

Correlated experimental evolution of behaviour and life history in *Drosophila* (52373)

Katja Hoedjes, Martin Kapun, Bas Zwaan, Thomas Flatt, Laurent Keller.

University of Lausanne; Wageningen University.

Selection on one trait often results in changes in other, seemingly unrelated traits, due to pleiotropy or linkage. For example, correlated responses between behaviour (learning ability) and life history (longevity) have been reported in the fruit fly, *Drosophila melanogaster*. However, the molecular basis of correlations between behaviour and life history remains poorly understood. To begin to uncover these mechanisms we have employed experimental evolution (EE) in the fruit fly. We used two independent selection regimes: populations adapted to poor larval nutrition and populations that were selected for reproduction at old age. In both selection regimes significant evolutionary responses in life history traits were observed, including in development time and longevity, with little evidence for interactions between the regimes. To examine correlated behavioural responses, we measured learning and locomotory behaviour in adults of the EE populations. We also sequenced pooled genomic DNA samples of 250 individuals per EE population and analyzed these genomes for variation in single nucleotide polymorphism frequencies. This approach allows us to identify candidate

genes or pathways that might underpin correlations between learning and locomotion and the observed differences in life history.

Session 2 THU MAX 410 24

The social niche experienced early in life influences the behavioural phenotype (52467)

Valentina Balzarini, Michael Taborsky, Joachim G. Frommen.

Behavioral Ecology, Institute of Ecology and Evolution, University of Bern, Switzerland.

According to the social niche theory of animal personality, multidimensional social options select for fine-tuned specialisations due to multi-niche frequency dependence. In addition to negative frequency dependence stabilizing the coexistence of alternative behavioural tactics, the development of different personalities is triggered by positive feedback favouring behavioural consistency due to benefits of specialisation and the avoidance of the costs of switching between strategies. This hypothesis has been rarely tested; a critical test requires a system that is characterized by a combination of high social complexity with experimental accessibility. The cooperatively breeding cichlid *Neolamprologus pulcher* combines these requirements. We studied the influence of individual social experience during ontogeny on the development of personality traits in these highly social fish. We experimentally assigned 14 days old fry to one of two alternative roles, either to be subordinate or dominant to a group of 4 unrelated fry. We kept focal fish in their respective roles for 3 months and monitored their social behaviour weekly. Subsequently, we tested their personality traits, including social interaction, exploration and helping propensities. Our data reveal that early life experience in an experimentally assigned social role affects the entire behavioural phenotype of an individual throughout extended periods of their life.

Session 2 THU MAX 410 24

Genomic changes associated with behavioural plasticity: selection for improved learning behaviour (52472)

Maartje Liefting, Ken Kraaijeveld, Cecile Le Lann, Bregje Wertheim, Jacintha Ellers.

VU University Amsterdam; Université Rennes 1; University of Groningen.

Learning is considered a form of behavioural plasticity through which an organism can adjust its performance to changes in the environment. Evolution of learning behaviour and memory dynamics of species is highly context dependent, giving rise to inter- and intraspecific variation in learning rates. Despite significant progress in unravelling the neurobiology and memory pathways underlying such variation, our understanding of the genetic support of variation in cognitive abilities and the relevance in an evolutionary ecological context remains incomplete. In addition, little is known on how selection on one aspect of learning may result in correlated evolution of other cognitive skills. We performed an artificial selection

experiment with the parasitoid wasp *Nasonia vitripennis* to improve learning of host-associated visual cues in females. Selection lines readily evolved improved learning skills, which also extended to other (olfactory) cues, suggesting general learning ability was targeted by selection. These improved cognitive skills of the selection lines even extended to male learning. Subsequently, we used high throughput sequencing to characterize changes in the genome associated with improved learning. SNP analysis identified multiple genomic changes associated with cognitive skills, and we discuss genes within these regions that form putative targets of selection.

Session 2 THU MAX 410 24

Maladaptive reproductive investment and behavioral variation in urban habitat (52607)

Virginie Demeyrier, Arnaud Grégoire, Marcel Lambrechts, Anne Charmantier.

Cefe UMR 5175 - Cnrs.

Increasing urbanisation imposes novel constraints for many organisms. While urbanisation is considered as an extreme situation where humans significantly influence wildlife, it can also provide opportunities to study mechanisms of adaptation. Within the artificial cocktail present in towns, artificial cavities are clearly potential evolutionary-traps for cavity-nesting birds. In this study, we performed an experiment where urban insectivorous cavity-nesting great tits (*Parus major*) were offered three nest-box sizes, covering the natural cavity range, in the city of Montpellier, France. Following a four-year monitoring of breeding phenology and using measures of anthropogenic perturbations and resource abundance, we show that great tits are more attracted to, lay larger clutches in, and finally produce fewer fledglings in, large rather than smaller artificial cavities. Increasing family size according to cavity size has previously been described. However, our results reveal that this strategy is maladaptive when large artificial cavities are placed in urbanized invertebrate-poor environments. Additionally to this experiment, open-field trials over two years allowed to compare great tit personalities in a deciduous forest near the city of Montpellier and along an urban gradient within the city. The results show contrasted personalities in rural versus urban environments and shed light on behavioural adaptation and maladaptation in an urban context.

Session 2 THU MAX 410 24

The role of state-behavior feedbacks in explaining adaptive personality differences (52710)

Maria Moiron, Kimberly J. Mathot, Niels J. Dingemanse.

Max Planck Institute For Ornithology; Royal Netherlands Institute for Sea Research; Ludwig-Maximilians University of Munich.

In recent years it has become widely accepted that individuals within single populations often exhibit consistent differences in behavior across contexts and over time (called ‘animal personality’). However, it is much less evident how behavioral consistency can be explained from an adaptive viewpoint. State-behavior feedback loops have been proposed as an evolutionary explanation for personality-related differences. The feedback mechanism between state and behavior exists because an individual’s state affects its optimal behavior, which in turn affects its state. This feedback dynamics has been theoretically well-developed but never empirically tested. Here we first provide a statistical framework based on repeated measures and multi-level random regression modelling that enables one to capture variation in state-behavior feedbacks. Next, we experimentally explore feedback loops between sampling (information acquisition) and body condition that may explain why individuals differ in sampling behavior using wild passerine birds (great tits) as a model species. We present data on the occurrence of between- and within- individual variation in sampling; and we provide an empirical test of how positive feedback loops lead to within individual state-behavior covariance and between individual positive intercept-slope correlations of temporal reaction norms, while negative feedback loops lead to the opposite outcome.

Session 2 THU MAX 410 24

Behavioural interactions of a planktonic crustacean with pond sediments (52929)

Roberto Arbore, Alexandra Mushegian, Jason Andras, Dieter Ebert.

University of Basel; Mount Holyoke College.

Planktonic species differ in the degree to which they interact with the bottom sediment surfaces. Some species, although primarily pelagic, might display important connections with the benthic habitat. The freshwater crustacean *Daphnia magna* can adopt a sediment browsing behaviour, alternative to suspension filter feeding. Such behaviour, while conferring the ability to exploit benthic food sources, also increases the exposure to multiple risks as, for instance, infection from sediment spore banks and benthic predation. We found genetic variation for this behaviour within an experimental population (F2 recombinant panel) and between clones from natural populations of different ecological contexts (e.g. presence/absence of fish predation). A QTL analysis provided evidence for a complex genetic architecture underlying this behavioural trait. In order to get further insights on the nature of the selective pressures possibly acting on the evolution of this behaviour, we performed a series of experiments using clones with high and low browsing activities. Here we examine a scenario involving both costs (e.g. risk of parasite infection) and benefits (e.g. foraging opportunities, microbiota acquisition) associated with sediment browsing and its environmental effects (e.g. conspecific infection risk due to sediment bioturbation).

Session 2 THU POL A 32

Coevolution of genetic variance and species’ range in a changing environment (52491)

Jitka Polechova, Nick Barton.

IST AUSTRIA.

As the environment changes in time, species change their range: they adapt, diversify or perhaps go extinct. The standing genetic variation of a species is crucial for its adaptation to changing conditions, and gene flow across a phenotypic gradient can maintain a large genetic variance. Yet, most studies of adaptation to a changing environment either neglect the effect of gene flow, or assume that genetic variance is constant. We model the joint population dynamics and evolution of the trait mean and its variance, via change in allele frequencies. When mutation contributes little to the standing genetic variation, a straightforward extension of the theory for panmictic populations predicts the critical rates of spatial and temporal change that a population can track. Large populations adapted to a steep environmental gradient can also adapt to a faster temporal change, because gene flow across a steep phenotypic gradient generates high local genetic variance. Further, we show that when the number of mutations per generation in the selected loci is high, ‘cline reversals’ (paired such that gradient in trait mean does not change) can increase the genetic variance fast enough to prevent demographic collapse due to maladaptation, and hence allow adaptation to a faster temporal change.

Session 2 THU POL A 32

The role of sex and recombination in evolutionary rescue (52499)

Hildegard Uecker, Joachim Hermisson.

IST Austria; University of Vienna.

Environmental change, if severe, can drive a population extinct unless the population succeeds in adapting to the new conditions. How do sexual reproduction and recombination affect the survival chances of an endangered population? We consider the probability of evolutionary rescue after a sudden deterioration of the environment when survival of the population is contingent on mutations at multiple (two) loci or the formation of mutant homozygotes. Such situations arise, for example, in combination drug therapy or the application of herbicide mixtures. We compare the rates of rescue in random mating, selfing, and clonal populations under these conditions. Recombination and likewise segregation during sexual reproduction generically have two opposing effects: they generate and they break up favorable gene combinations. We investigate how the population dynamics affect the interplay of these two effects and consequently the rate of adaptation from standing genetic variation and de-novo mutations. We find that, even in the absence of density-dependent fitness, a fast eradication of the wildtype population can enhance rescue in a sexually reproducing population. On the other hand, recombination and segregation can prevent rescue when the wildtype disappears slowly.

Session 2 THU POL A 32

Environmental marginality and the evolutionary potential of peripheral populations in *Arabidopsis lyrata* (52568)

Julie Lee-Yaw, Yvonne Willi.

University of Neuchatel.

Theoretical models of species' geographic range limits are often premised on environmental gradients, with species experiencing increasingly marginal conditions towards the edge of their range. Range limits arise where adaptation to these conditions ultimately fails. However, whether the range limits of most species conform to this scenario remains unclear. Using spatial data and ecological niche models we explore these assumptions in North American *Arabidopsis lyrata*. Specifically, we ask whether peripheral populations occupy sites of low suitability relative to more central populations and whether range limits coincide with predicted niche limits. We further ask whether genetic diversity and the transition from outcrossing to selfing (restricted to peripheral populations in this system) is associated with particularly poor-quality habitat, thus testing the link between range position, habitat quality and demography. Our results suggest that latitudinal range limits in this system are well explained by the abiotic environment. Peripheral populations occupy regions of low suitability relative to more central populations, with genetically impoverished and selfing populations at the range edge occupying some of the lowest-quality sites. We will discuss the implications of these results for our understanding of the evolutionary potential of peripheral populations.

Session 2 THU POL A 32

Evolution of seasonal timing in a changing world: how empirical evidence and phenological models can help us to forecast the rate of adaptation (52721)

Lucia Salis, Marcel Visser.

Netherlands Institute of Ecology (NIOO-KNAW).

In a changing world, species need to adapt to their new environment. In the winter moth, the synchronization between timing of egg hatching and the bud burst of its food plant, the oak, has been disrupted by climate change. Using both long-term (18 years) observational data and experiments we show that timing of egg hatching has changed genetically, resulting in closer synchrony of egg hatching with oak bud burst. We explore using an eco-evo-devo framework what the limitations are of this genetic adaptation. We first developed a novel phenological model that accurately describes how an insect's developmental rate is affected by the interaction between developmental state and temperature. Accounting for this interaction improved the predictive power of the model and therefore contributed to a better understanding of the mechanisms underlying insect development. Next, we use this model to study the genetic variation in the model's parameters and to test whether there is additive genetic variation in these parameters, and thus whether these parameters can be altered by selection. As temperature are forecasted to continue increasing, eco-evo-devo studies that couple empirical findings with phenological models offer a unique opportunity to unravel the potential of future insect's adaptive responses to climate change.

From genes to ecosystems: the molecular mechanisms of eco-evolutionary feedbacks from rapid adaptation of herbivore consumers to nutrient limitation (52843)

Spiros Papakostas, Steven Declerck.

University of Turku; Netherlands Institute of Ecology.

Humans alter biogeochemical cycles of essential elements such as phosphorus (P). Prediction of ecosystem consequences of altered elemental cycles requires integration of ecology, evolutionary biology and the framework of ecological stoichiometry. We studied micro-evolutionary responses of populations of a herbivorous rotifer species to P-limited food and the potential consequences for its population demography and for ecosystem properties. We subjected field-derived, replicate rotifer populations to P-deficient and P-replete algal food, and studied adaptation in common garden transplant experiments after 103 and 209 days of selection. We quantified about 30000 transcripts using next-generation sequencing and 1000 proteins using high-resolution mass spectrometry. When fed P-limited food, populations with a P limitation selection history suffered 37% lower mortality, reached twice the steady state biomass, and reduced algae by 40% compared to populations with a P-replete selection history. Adaptation involved no change in rotifer elemental composition but reduced investment in sex. Selection history had a profound impact on the expression profile of the rotifers and several transcripts and proteins showed an expression profile specific to each condition pointing towards the molecular basis behind those adaptations. We demonstrate potentially strong eco-evolutionary feedbacks from shifting elemental balances to ecosystem properties and study the underlying functional molecular mechanisms.

Estimating evolutionary potential in the wild : role and stability of the G matrix (51978)

Céline Teplitsky, Stéphane Chantepie, Anders P. Moller, Shinichi Nakagawa, Florentino de Lope, Lars Gustafsson, James A. Mills, Nathaniel Wheelwright, Anne Charmantier.

Département Ecologie et Gestion de la Biodiversité UMR 7204 CNRS / MNHN / UPMC, Muséum National d'Hi; Laboratoire d'Ecologie Alpine, UMR CNRS 5553, Université Joseph Fourier, Grenoble I, BP 53, 38041 Gr; Laboratoire d'Ecologie, Systématique et Evolution, CNRS UMR 8079, Université Paris-Sud, F-91405 Orsa; Department of Zoology, University of Otago, PO Box 56, Dunedin, New Zealand ; Department of Zoology, Biology Building, University of Seville, E-41012 Seville, Spain; Department of Animal Ecology, Evolutionary Biology Center, Uppsala University, SE75236, Sweden; 10527 A Skyline Drive, Corning, New York 14830, USA; Department of Biology, Bowdoin College, Brunswick, Maine 04011, USA; Centre d'Ecologie Fonctionnelle et Evolutive UMR 5175 CNRS, F-34293 Montpellier, France.

Global environmental change represents a major threat to biodiversity today. The habitats of species are being modified at a fast rate, raising an important question: will populations manage to adapt to the new conditions? One strong constraint on microevolutionary responses is the fact that traits within an organism are not free to evolve independently, but form integrated units. There is growing evidence that the genetic correlations between traits can slow down the rate of adaptation in wild populations. However, the importance of such constraints will depend on their stability, i.e., if genetic correlations are changing rapidly, the G matrix should not represent a strong constraint on evolutionary responses and evolutionary responses would be difficult to predict.

We investigated the stability of the G matrix across five bird species, comparing conditional evolvability and autonomy over 5 year time periods. These variables can be estimated using animal models (MCMCglmm software) on long term data sets of wild bird populations for which detailed pedigrees are available. The G matrix for morphological traits is stable in all the populations considered. We compare this to expectations based on estimates of selection within the populations, and assess whether G is aligned with selection.

Session 2 THU POL A 32

Adaptation lags in bet-hedging traits during periods of climate change (52047)

Tom JM Van Dooren.

Institute for Ecology and Environmental Sciences iEES Paris.

Bet-hedging occurs as an adaptation to unpredictable environments. It is nature's insurance policy against uncertain events. Our theories assume that such adaptation is to an unpredictably fluctuating but stationary environment. There are little or no predictions on how such traits would evolve during periods where environmental variables are not stationary, but change with trends in means and variances. With such trends, adaptive states are what one would find eventually if evolving populations would adapt to repeated sampling from the instantaneous state of the probability distributions of environmental parameters. Adaptive lags are then the differences between such adaptive states and the actual state of a population. By means of the main textbook example of bet-hedging evolution, namely that of an evolving probability of germination in annual plants with a seed bank, I show that gradual unidirectional change in environmental parameters can lead to an intermittent window where bet-hedging is not adaptive. The adaptive lag in the actual response in germination probability can then reverse in sign: first plants germinate too little. When bet-hedging has become adaptive again, they germinate too much. I extend my example with an evolving plastic germination probability, and scenarios of environmental change with a tipping point.

Session 2 THU POL B 18

An island model for unraveling adaptive history: Cape Verde Arabidopsis (52468)

Andrea Fulgione, Stéphanie Arnoux, Joachim Hermisson, **Angela Hancock**.

University of Vienna; Gregor Mendel Institute; University of Vienna; University of Vienna.

Islands have been central to evolutionary biology since Darwin and Wallace. They represent natural laboratories, where fundamental principles of the evolutionary process can be revealed. We combine a tractable island system and a well-studied model organism to unravel the historical route to local adaptation in an extreme environment.

A single *Arabidopsis* sample was collected 30 years ago in the Cape Verde Islands, a climatic extreme in the *Arabidopsis* species distribution. Due to its surprising location and phenotypic divergence, the resulting line (Cvi-0) is an enigma to the *Arabidopsis* community. Over the years, Cvi-0 has been the subject of extensive QTL mapping efforts and functional follow-up analyses, so that we have a wealth of information about the genetic basis of its intriguing phenotypic divergence. This backdrop provides an ideal opportunity to access the specific events that led to local adaptation in this population. To this end, we collected and sequenced population samples from Cape Verde to reveal a striking signature of strong positive selection on pleiotropic functional variants as well as parallel adaptation across islands. Our study design provides a framework for combining knowledge from trait mapping, population genetics, functional variant identification, and field studies of natural populations to characterize the details of adaptive dynamics in nature.

Session 2 THU POL B 18

The Genetic Architecture of Recombination Rate Variation in *Drosophila melanogaster* (52479)

Nadia Singh, Chad Hunter.

North Carolina State University.

Meiotic recombination is an essential biological process, necessary for proper chromosome segregation in many organisms. Despite this critical function, rates of recombination are highly variable within and between populations and species. The genetic architecture of this variation remains poorly understood, especially in the model organism *Drosophila melanogaster*. We sought to identify the genetic basis of recombination rate variation using whole genome association mapping. We leveraged the *Drosophila* Genetic Reference Panel for this purpose and measured rates of meiotic recombination on two chromosomes in 205 fully sequenced inbred lines using a classical genetic approach. We scored over a 500,000 progeny and revealed 2-3 fold variation in crossover frequency among lines. Much of this variation is genetic, and we used genome-wide association mapping to identify genetic factors contributing recombination rate. We used RNAi, mutant analysis, and expression assays to functionally confirm a subset of candidates revealed by this approach. Our results thus provide comprehensive insight into the scale and scope of population-level variation in recombination rate in *Drosophila* and the first insight into the genetic architecture of population-level variation in recombination rate in this model system.

Tracking genomic changes during rapid life history evolution (52853)

Nina O. Therkildsen, Stephan B. Munch, David O. Conover, Stephen R. Palumbi.

Hopkins Marine Station, Stanford University; NOAA Southwest Fisheries Science Center; Stony Brook University; Hopkins Marine Station, Stanford University.

Multi-generational selection experiments offer a powerful approach for directly observing how the genome responds to known selection pressures over time. We have returned to a seminal experiment that demonstrated substantial evolution in growth rate (resulting in a nearly two-fold difference in adult size) in response to size-selective fishing over just five generations in the Atlantic silverside. Based on 'in silico' capture of genomic sequence, we compared allele frequencies at >800K SNPs distributed across ~80% of the exome in large vs. small selected lines. We identified strong differentiation at 1118 SNPs, including nearly fixed differences in 17 genes. High divergence occurs in bone morphogenic proteins and macrophage stimulating factors, previously linked to growth. However, selected genes maintain high overall levels of diversity, indicating that selection has primarily acted as 'soft' sweeps on old alleles. Because natural variation in size selection across latitudes has driven strong clinal adaptation in growth rate in the Atlantic silverside, we compare the sweep signatures from the experiment with genome scans of wild populations. This integrated analysis of responses to natural and artificial selection on the same complex trait offers parallel insights into the genomic basis for life history adaptation evolved over various time scales.

The genetic basis of parallel evolution in an introduced species (52994)

Billie Gould, **John Stinchcombe**.

University of Toronto.

The goal of identifying the genes or even nucleotides underlying quantitative and adaptive traits has been characterized as the 'QTN programme' and has recently come under severe criticism. Part of the reason for this criticism is that much of the QTN programme has asserted that finding the genes and nucleotides for adaptive and quantitative traits is a fundamental goal, without explaining why it is such a hallowed goal. Here we outline motivations for the QTN programme that offer general insight, regardless of whether QTNs are of large or small effect, and that aid our understanding of the mechanistic dynamics of adaptive evolution, illustrating with examples from research we have done on introduced populations of the model plant, *Arabidopsis thaliana*. We combine outlier scans (XTX), molecular population genetic tests of selection, and the rich list of flowering time candidate genes to test for regions of the genome involved in parallel adaptation. Our results indicate that parallel adaptation in

the introduced range has been achieved through independent genetic mechanisms, suggested little pleiotropic constraint on adaptive evolution.

Session 2 THU POL B 18

A Clinal Polymorphism in Insulin Signaling Has Major Effects on *Drosophila* Life History (52690)

Esra Durmaz, Subhash Rajpurohit, Nicolas Betancourt, Paul S. Schmidt, Thomas Flatt.

Department of Ecology and Evolution, University of Lausanne, Lausanne, Switzerland; Department of Biology, University of Pennsylvania, Philadelphia, USA; Department of Biology, University of Pennsylvania, Philadelphia, USA; Department of Biology, University of Pennsylvania, Philadelphia, USA; Department of Ecology and Evolution, University of Lausanne, Lausanne, Switzerland.

Several life history traits in *Drosophila melanogaster* exhibit strong clinal differentiation across latitude, for example along the North American east coast, from Florida to Maine. Similarly, at the genetic level, we have recently identified major genome-wide patterns of clinal differentiation, likely shaped by spatially varying (clinal) selection. Interestingly, we find particularly strong clinal variation in numerous genes involved in insulin/insulin-like growth factor signaling (IIS), a pathway known from laboratory mutant and transgenic studies to physiologically regulate fitness traits. However, whether natural allelic variants in genes of this pathway affect life history remains poorly understood. Here, we have examined life history effects of a naturally occurring, clinally varying candidate haplotype in dFOXO, a downstream effector of IIS. We used recombinant inbred (DGRP) lines to establish two sets of synthetic recombinant populations either fixed for the northern or southern allelic state. Our results show, for the first time, that a clinally varying, naturally occurring polymorphism in dFOXO has major pleiotropic effects upon starvation resistance and body size, two important fitness traits known to be strongly clinal.

Session 2 THU POL C 10

Parasitoid adaptation to hosts with symbiont-conferred resistance (51859)

Alice Dennis, Christoph Vorburger.

ETH Zurich & EAWAG; ETH Zurich & EAWAG.

In host-parasitoid systems, variation in host defenses create a set of environments to which parasitoids must adapt in order to reproduce. For the parasitoid wasp *Lysiphlebus fabarum* this also includes evolving responses to the diverse, heterogeneous, microbiome of their aphid host. To investigate the genomic basis of varied wasp infectivity, we have experimentally evolved wild-caught wasps on three different aphid hosts: two lines possessing different defensive strains of the symbiont *Hamiltonella defensa*, and one un-infected line. In just 10 generations, this has produced wasp lines with different, and non –reciprocal, infective

abilities, presumably by selection of pre-existing genetic variation from the wild populations. Using RNAseq, we have identified differentially expressed genes associated with each selected wasp infectivity-phenotype. We are now using these to examine the functional genomic basis of the infective abilities of the evolved lines and to screen natural populations of *L. fabarum* for the relevant molecular variation over time and space.

Session 2 THU POL C 10

Endosymbiotic bacteria protect aphids against natural enemies in a natural wet meadow habitat (51915)

Jan Hrcek, H. Charles J. Godfray.

Department of Zoology, University of Oxford.

Endosymbiont mediated protection is a widespread phenomenon with potential to allow rapid adaptation by horizontal transfer. Pea aphids harbour endosymbiotic bacteria which protect them against parasitoids and fungal pathogens. We ask whether the spatial and temporal heterogeneity in natural enemy pressure and the specificity of the endosymbiont mediated protection allow the protection previously demonstrated in laboratory experiments to affect aphid mortality rates under natural conditions.

We deployed sentinel populations of aphids with and without protective endosymbionts for ten days at five naturally managed meadows in a 15km circle around Oxford, UK, three times during 2014 season. Sentinel aphids were attacked by a rich community of parasitoids and fungal pathogens of up to six species per site. Endosymbionts protected aphids in the field in accordance with predictions from laboratory experiments. However, the complexity of multiple concurrent antagonistic interactions and high specificity of the bacterial protection led to increased aphid survival only in some of the spatio-temporal replicates.

This work shows that the phenotypic effects of endosymbionts identified through a decade of laboratory research on aphids are ecologically relevant in a natural habitat and demonstrates the importance of field experiments in revealing the outcome of attack by a community of natural enemies.

Session 2 THU POL C 10

All aboard! Tracking host-parasite historical associations in the Canary Islands. (51930)

Fátima Jorge, Ana Perera, Robert Poulin, Vicente Roca, Miguel A. Carretero.

CIBIO Research Centre in Biodiversity and Genetic Resources, InBIO, Universidade do Porto, Vairão, P; Departamento de Biologia, Faculdade de Ciências da Universidade do Porto, Porto, Portugal; Department of Zoology, University of Otago, Dunedin, New Zealand;

Departament de Zoologia, Facultat de Ciències Biològiques, Universitat de València, València, Spain.

Host parasite associations are the outcome of historical events and current ecological conditions. Several cophylogenetic events can shape such intimate interactions, i.e. cospeciation, host switching and missing the boat. Given their long term isolation and structure, the Canary Islands provide an ideal environment for studying the origin and evolution of host-parasite associations. Did parasites follow the colonisation of islands by their host or did they undergo other events such as host switches? In our study, we reconstructed the origins of the current associations between parasitic nematodes and all their reptile hosts from the Canary Islands. Parasite phylogeny was inferred from molecular data with maximum Likelihood and Bayesian methods. The most likely evolutionary history of these associations was reconstructed on the basis of our estimated parasite phylogeny and on published host phylogenies. Results suggest at least three different colonisations events in the Canary archipelago and some level of evolutionary congruence with their hosts. One lineage probably originated from a host switch between skinks and lacertids but evolving separately since. Overall, while island colonisations by parasites are initially determined by stochastic events (whether or not they get in the boat), how they evolve subsequently may be mainly dependent on parasite adaptation (specificity).

Session 2 THU POL C 10

Population size shape reciprocal adaptations in the experimental host-parasite coevolution (51967)

Andrei Papkou, Rebecca Schalkowski, Mike-Christoph Barg, Ines Braker, Hinrich Schulenburg.

Evolutionary Ecology Genetics, University ofKiel.

Genomic regions involved in host-parasite interaction are subjected to intense selection. This may lead to either rapid allele fixations or continuous frequency oscillations. However, the resulting allele dynamics is not solely determined by selection, but additionally depends on genetic variation and random drift. Population size (N) is, therefore, an important characteristic in this respect as it influences genetic diversity and selection-drift interplay. Surprisingly, little is known about the role of N in coevolution, despite the fact that N varies considerably across host and parasite species and changes frequently due to their interaction and external factors.

To examine empirically how N influences antagonistic adaptation, we initiated experimental coevolution between the nematode *Caenorhabditis elegans* and its pathogen *Bacillus thuringiensis* in large, small and periodically changing populations. The effect of N was already evident after 23 host generations. In particular, we found that changes in host fecundity and parasite virulence varied depending on population size. Moreover, a time-shift experiment revealed the patterns of negative frequency-dependent selection in the large populations, but not in the small populations. Next, we used population genomics and infection transcriptomics approaches to identify candidate regions, and to assess the contribution of different evolutionary forces to the underlying genetic changes.

Testing for genetic differentiation along altitudinal gradients in ticks (*Ixodes ricinus*) (52121)

Mélissa Lemoine, Barbara Tschirren.

Institute for Evolutionary Biology and Environmental Studies.

Due to its broad host range and its wide distribution, the European sheep tick (*Ixodes ricinus*) has for a long time been considered as a generalist vector. Recent genetic studies suggest however that locally adapted populations exist, specialising on different host species. Since eggs and larvae of *Ixodes* ticks are highly vulnerable to temperature and humidity, both abiotic and biotic factors may potentially play a role in shaping spatial genetic differentiation of tick populations. Therefore *I. ricinus* is an excellent study system for examining the contributions of isolation-by-ecology vs isolation-by-distance to spatial genetic divergence. Using larvae collected from voles in 12 sites among altitudinal gradients in Swiss Alps, we estimated the contributions of temperature and humidity as well as geographical and host genetic distances to genetic divergence of tick populations using neutral markers. This study helps to understand whether the current rapid colonisation of new environments by *I. ricinus* is linked with the colonisation of these environments by its hosts or with its intrinsic evolutionary potential.

Eco-evolutionary dynamics in coevolving host-virus systems (52276)

Jens Frickel, Lutz Becks.

Community Dynamics Group, Dept. Evolutionary Ecology, Max Planck Institute for Evolutionary Biology.

Eco-evolutionary dynamics - the interplay of ecology and evolution on the same time scale - have been shown to influence population and community as well as evolutionary dynamics in many complex ways. However, coevolution in the framework of eco-evolutionary theory has not been addressed directly. Using experiments with an algal host and its virus, we show here for the first time eco-evolutionary feedback dynamics in antagonistic coevolving populations. Specifically, we found that the continuous reciprocal adaption of resistance and infectivity in host and virus drove the ecological dynamics of the system leading ultimately to a shift from consumer-resource cycles to stable population sizes. The coevolutionary dynamics were initially driven by arms race dynamics with consecutive selective sweeps, but shifted towards fluctuating selection as a result of an evolutionary constraint in the virus and the evolution of a trade-off between host resistance range and growth rate. Importantly, our results show that the role of selection and demography changes continuously over time as a result of the eco-evolutionary feedback. Consequently, the entanglement of ecology and evolution has

important consequences and might substantially lower the predictability of the mode and tempo of adaptive change.

Session 2 THU POL C 10

Host age structure as a source of heterogeneity in host-parasite interactions (52545)

Frida Ben-Ami.

Tel Aviv University.

Understanding the interplay between the epidemiology and ecology of host and parasite populations is of utmost importance in light of recent epidemics and growing resistance towards drug treatments. Particularly in microparasites, where ecological dynamics such as within-host competition can strongly influence evolutionary change, they must be studied conjointly to understand disease evolution. While genetic heterogeneity has received considerable attention in both theoretical and experimental studies of host-parasite interactions, there is very little data on how host age, an intrinsic and highly dynamic property of the host population as well as a key epidemiological factor, impacts ecological and evolutionary dynamics of host and parasite populations. Using the *Daphnia magna*-*Pasteuria ramosa* system, I will present results from several recent experiments that demonstrate the complex interplay between host demography and the ecology of host and parasite populations. In particular, I will show that host age at exposure can affect parasite infectivity, virulence and reproduction as well as within-host competition and parasite diversity. I will also make a case for incorporating age-dependent epidemiological parameters into stage-structured theory and virulence modeling. Ultimately, elucidating the underlying dynamics will improve our understanding of disease ecology and virulence evolution.

Session 2 THU POL D 9

Testing inclusive fitness theory in a lower termite (51905)

Judith Korb, Katharina Hoffmann.

University of Freiburg; University of Osnabrueck.

Inclusive fitness theory predicts that interactions between relatedness and ecological costs and benefits determine altruism, however empirical studies in social insects commonly concentrate on relatedness. Less studied termites offer a promising test case to study the interaction between relatedness and altruism because different termite castes vary in degree of altruism: Soldiers are always sterile and can only gain indirect fitness. In contrast, workers of wood-dwelling lower termites are immature instars that are less altruistic and have the full capability to become reproductives. By manipulating local resource availability and the opportunity to reproduce in colonies of varying degree of relatedness, we show that the importance of relatedness differed for different castes and that nepotism always was context

dependent. Sterile soldiers adjusted their behaviour more strongly to relatedness than the less altruistic workers which can themselves reproduce. For all castes the adjustment was a phenotypic plastic response and it only occurred when helping increased the chance of relatives to become reproductives. Furthermore, strong local resource competition negated the effect of relatedness. Our study is one of very few social insect studies that demonstrates how ecological factors interact with relatedness in flexibly shaping social interactions and cooperation.

Session 2 THU POL D 9

An evolutionarily significant unicellular strategy in response to starvation in *Dictyostelium social amoebae* (51912)

Clement Nizak, Minus van Baalen, Darja Dubravcic.

CNRS - ESPCI ParisTech; CNRS - Ecole Normale Supérieure.

The social amoeba *Dictyostelium discoideum* is widely studied for its multicellular development as a response to starvation. Aggregates of up to 10^6 cells form fruiting bodies containing (i) dormant spores (~80%) that can persist for months in the absence of nutrients, and (ii) dead stalk cells (~20%) that promote the dispersion of the spores towards nutrient-rich areas.

Using a new quantitative approach based on time-lapse fluorescence microscopy and a low ratio of reporting cells, we have quantified the fraction of non-aggregating cells. In realistic starvation conditions, up to 15% of cells do not aggregate. Non-aggregating cells have an advantage over cells in aggregates since they resume growth earlier upon arrival of new nutrients, but have a shorter lifespan under prolonged starvation. We find that phenotypic heterogeneities linked to cell nutritional state and genetic factors bias the representation of cells in the aggregating vs. non-aggregating fractions. In addition, interactions between clones in mixtures of non-isogenic cells affect the partitioning of each clone into both fractions. We further build a numerical model to test the evolutionary significance of the non-aggregating cell fraction. The partitioning of cells into aggregating and non-aggregating fractions is optimal in fluctuating environments with an unpredictable duration of starvation periods.

Session 2 THU POL D 9

Cheating on the edge: spatial self-organization promotes cooperation in expanding bacterial colonies (52077)

Alexandre Jousset, Anna Hille, Stefan Scheu, Katrin Meyer.

Utrecht University; Georg-August University Göttingen.

Understanding the mechanisms underlying the evolution and stability of cooperative behaviors in microorganisms is one of the most exciting topics of microbial evolutionary biology. Many unicellular microorganisms engage in complex social behaviors in fighting

against enemies, scavenging for nutrients or forming complex structures in a joint effort. However, social behaviors are predicted to be unstable as defectors can readily live on the costs of their faithful neighbors, potentially disrupting cooperation. Here we show that expanding colonies show self-organization patterns that maintain cooperation. We follow the growth of *Pseudomonas fluorescens* colonies on a solid medium containing albumin as sole carbon source. Prior to uptake, albumin must be broken down by extracellular proteases, which function as public good. Using a combination of individual-based models and microscopy, we show that in expanding communities defectors first accumulate on the border of the colony, but their growth is restricted by low diffusion of public goods. As cooperators expand they engulf defectors thereby confining them to the center of the colony. Therefore, resource exploitation at the edge of expanding microbial colonies stabilizes cooperation in a spatially explicit context.

Session 2 THU POL D 9

Long Life, Promiscuity and the Origin of Cooperation in Birds (52360)

Philip Downing.

Department of Zoology, University of Oxford.

Long life is a common feature of cooperative societies in taxa as diverse as mammals and ants. However, it is not clear whether it is a cause or a consequence of cooperation. Theory predicts that the likelihood of cooperation evolving is higher in long-lived species because it ensures a long reproductive lifespan and therefore high direct fitness benefits. However, the effect of long life on cooperation also depends on whether individuals gain indirect fitness while helping, which is determined by female promiscuity: high promiscuity lowers indirect fitness benefits making the direct fitness gained from long life vital for cooperation to evolve. We tested these predictions comparatively by reconstructing ancestral states of breeding system and survival across birds and investigating the interaction between promiscuity and life span. As predicted by theory, we found that long life facilitates the evolution cooperation and that species with low indirect fitness are exceptionally long-lived, driving the difference in lifespan between cooperative and non-cooperative breeders. These results clarify the importance of life-history traits in the evolution of cooperative breeding. Furthermore, they suggest that promiscuous species can make the evolutionary transition to cooperation because long life compensates for the reduction in indirect fitness.

Session 2 THU POL D 9

Diversity in parent-offspring communication in birds: shifting between signals and cues (52636)

Shana Caro, Ashleigh Griffin, Camilla Hinde, Stuart West.

University of Oxford, United Kingdom; Wageningen University, The Netherlands.

Evolutionary theory has helped us understand communication in the natural world as a cooperative behaviour relying on the alignment of interests of both signaller and receiver. There is, however, a lack of empirical consensus for basic theoretical predictions even in one of the best studied systems: offspring begging their parents for food. Existing theory predicts both that offspring should display honest signals of need and that offspring should display honest signals of quality; these contrasting predictions have both received empirical support. We present the results of a meta-analysis, which resolve the current lack of synthesis by showing that parents integrate signals of need or quality differently depending on brood reduction strategy and environmental conditions. As food availability increases, parents in brood-reducing species allocate food more by begging intensity, but less by signals of quality like gape coloration and size cues. Offspring signalling strategies also shift with parental response strategies: the smallest offspring beg the most intensely only when partial brood starvation is unlikely. A separate, within-species, in-depth analysis on great tits found the same flexible response within a population. These empirical results demonstrate the need to account for ecology and dynamic strategy sets in signalling models.

Session 2 THU POL D 9

Developing social evolution theory into a set of tools for analyzing microbial data (52960)

jeff smith.

Washington University in St Louis.

Social evolution theory is a valuable guide for empirical research, but in many studies of microbial cooperation it is often only used as a verbal heuristic. Here I test the usefulness of different theoretical approaches in social evolution as tools for analyzing experimental data. I re-analyze published microbial data sets that share a common experimental design and identify the pros and cons of different approaches in terms of data visualization, ease of application, statistical power, theoretical interpretation, and generalization across systems. The regression-based approach of the Price equation that underlies many kin selection and multilevel selection models is often a poor choice for the large, nonlinear fitness effect common in microbial systems. Some measures of fitness are better than others. The functional form of frequency dependence is potentially very informative, but at present there is almost no theory with which to interpret it. These findings show that there is still a substantial need to formulate social evolution mathematics in a way that makes theory a useful guide for data collection and analysis.

Session 2 THU POL D 9

Fitness costs in spatially structured environments (51856)

Florence Débarre.

wissenschaftskolleg zu berlin.

The clustering of individuals that results from limited dispersal is a double-edged sword: while it allows for local interactions to be mostly among related individuals, it also results in increased local competition. In this talk, I will show that, because they mitigate local competition, fitness costs such as reduced fecundity or reduced survival are less costly in spatially structured environments than in non spatial settings. I will first present a simple demographic example to illustrate how spatial structure weakens selection against fitness costs. Then, I will illustrate the importance of disentangling the evolution of a trait from the evolution of potential associated costs. I will use an example taken from a recent study investigating the effect of spatial structure on the evolution of host defense -- a social trait, since fighting against parasites indirectly protects your neighbors. In this example indeed, the differences between spatial and non-spatial selection gradients are entirely due to differences in the fitness costs, thereby undermining interpretations of the results made in terms of the trait only. This illustrates the need to consider fitness costs as proper traits in both theoretical and empirical studies, and of not neglecting the effect of ecological feedbacks on evolution.

Session 2 THU MAX 415 25

Functional trade-offs and phenotypic diversity in cellular migration (53350)

Thierry Emonet.

Yale University.

Bacteria perform chemotaxis in a wide variety of environmental tasks, from scavenging nutrients to infecting host tissues. As such, it would seem unlikely that one type of chemotactic behavior would be equally suited to all tasks. Indeed, some species have many chemotaxis systems and switch between them. Others have one, but behavioral diversity is still observed in clonal wildtype cells. What are the trade-offs that bacteria face in performing chemotaxis in different environments? Can population diversity be tailored to resolve these trade-offs? I will discuss our recent theoretical and experimental efforts to uncover the functional role of phenotypic heterogeneity in cellular migration and understand how biological systems may resolve functional trade-offs.

Session 2 THU MAX 415 25

Bacterial Genomic Diversity in Light of Environmental Selection (53365)

Martin Polz.

Massachusetts Institute of Technology.

Many bacterial and archaeal lineages have a history of extensive gene acquisition and loss, evident as large genome content differences even among otherwise closely related isolates. Explaining the co-existence of the resultant vast genotypic diversity in light of selection remains one of the biggest challenges in microbial biology. Using marine vibrios as a model, we show that in spite of such high gene turnover, genotypic clusters representing ecologically

cohesive populations can be identified. These populations display many hallmarks of animal and plant populations, including speciation, social interactions and ecological tradeoffs. Population genomics shows that interactions among genotypes, e.g., via public good production and cheating, and with predators, e.g., via variation of surface antigens, lead to gene content variation among closely related genotypes. This provides a functional explanation how biological interactions may select for coexisting high genomic diversity.

Session 2 THU MAX 415 25

Is HIV short-sighted? Insights from a multistrain nested model (51615)

Katrina Lythgoe, Lorenzo Pellis, Christophe Fraser.

Imperial College London; University of Warwick.

An important component of pathogen evolution at the population level is evolution within hosts. Unless evolution within hosts is very slow compared to the duration of infection, the composition of pathogen genotypes within a host is likely to change during the course of an infection, thus altering the composition of genotypes available for transmission as infection progresses. We develop a nested modelling approach that allows us to follow the evolution of pathogens at the epidemiological level by explicitly considering within-host evolutionary dynamics of multiple competing strains and the timing of transmission. We use the framework to investigate the impact of short-sighted within-host evolution on the evolution of virulence of HIV, and find that the topology of within-host adaptive landscape determines how virulence evolves at the epidemiological level. If viral replication rates increase significantly during the course of infection, the viral population will evolve a high level of virulence even though this will reduce the transmission potential of the virus. However, if replication rates increase more modestly, as data suggests, our model predicts that HIV virulence will be only marginally higher than the level which maximizes the transmission potential of the virus.

Session 2 THU MAX 415 25

Spatial constraints on public good production during biofilm development (51658)

Theresa Hölscher, Benjamin Bartels, Ramses Gallegos-Monterrosa, Akos T Kovacs.

Friedrich Schiller University Jena, Terrestrial Biofilms Group.

Biofilms are structurally complex bacterial communities, where the cells are enclosed in an extracellular matrix that mediates the attachment of cells to each other or to surfaces. While the biofilm matrix benefits the population, i.e. protection, attachment to a substratum or surface spreading, its production is costly for the individuals. Mutant strains of the Gram-positive bacterium, *Bacillus subtilis* lacking matrix production have a higher fitness under well mixed planktonic conditions. However, matrix producers have an advantage when

cultivated in spatially structured environment.

Two laboratory biofilm models of *B. subtilis*, surface colony biofilm and air liquid interface pellicle, are examined to understand how matrix producer cooperators gain advantage in a community. Strains lacking matrix production are excluded from a newly built pellicle, a developmental mechanism that selects for matrix producer cooperators. During colony development, spatial pattern formation facilitates cooperation in *B. subtilis* biofilms. The density of cells at the onset of biofilm growth affects pattern formation during biofilm growth. At low initial cell densities co-cultured strains strongly segregates in space, while at high initial cell densities they do not. EPS-producing cells have a competitive advantage over non-cooperative mutants at high assortment, while EPS-deficient cells have an advantage in mixed populations.

Session 2 THU MAX 415 25

Migrating together: how *Bacillus subtilis* uses division of labor to colonize surfaces. (52089)

Jordi van Gestel, Hera Vlamakis, Roberto Kolter.

University of Groningen; Harvard University.

Multicellular organization results from the interactions between cells. From cell-cell interactions collective properties can emerge that enable cells to face challenges that they separately cannot. One particularly important challenge for micro-organisms is migration. In this study, we show how migration depends on the division of labor between two cell types, which appear during *Bacillus subtilis* colony expansion. Cell collectives organize themselves into bundles that form filamentous loops at the colony edge. These loops exert a novel mechanism of migration by pushing themselves away from the colony. The formation of filamentous bundles depended critically on the synergistic interaction of two distinct cell types: surfactin-producing and matrix-producing cells. We propose that surfactin-producing cells reduce the friction between cells and their substrate, which allows matrix-producing cells to form bundles and migrate towards uncolonized regions of the plate where nutrients have yet to be depleted. Our study illustrates how simple organization of cells can yield a strong ecological advantage. This and similar types of ecological advantages are key for the numerous evolutionary transitions towards primitive and complex multicellular life.

Session 2 THU MAX 415 25

Experimental evolution of increased efficiency through serial propagation in emulsion (52948)

Iraes Rabbers, Frank Bruggeman, Herwig Bachmann, Bas Teusink.

VU University Amsterdam, dept. Systems Bioinformatics.

From an evolutionary perspective it is advantageous for single cells to grow fast -to outcompete competitors- and for microbial populations to use substrate efficiently -to make the most offspring-. Microbial cells are thought to be metabolically efficient when growing slow and inefficient when growing fast, giving rise to the concept “Tragedy of the commons”. There is experimental evidence for this yield/rate tradeoff in i.a. yeast, however these experiments employed culturing methods where the selection pressure is on growth rate (batch) or substrate affinity (chemostat) due to resource competition. A novel method has recently been introduced that compartmentalizes individual cells in a water-in-oil emulsion, thereby privatizing the resources and allowing for yield selection upon serial propagation. In this project we applied this method to *E. coli* wildtype for ~450 generations, leading to selection of mutants with increased cell number, exhibiting increased final optical density, total protein content and biomass. This yield increase appears to result from more efficient substrate usage, mainly the full depletion of pyruvate in contrast with the ancestral strain. Characterization of these strains is ongoing, and should reveal the genetic basis for the high yield phenotype and in addition allow more insight into the existence of a yield/rate tradeoff in *E. coli*.

Session 2 THU GEN B 35

Inference of past historical events using ABC and MCMC methods on population genetics data sets (52127)

Frederic Austerlitz.

Laboratoire EcoAnthropologie et Ethnobiologie.

New computer-intensive estimation techniques such as Approximate Bayesian Computation (ABC) and Monte Carlo Markov chains (MCMC) allows inferring unknown parts of the history of species from contemporary population genetics data. I will illustrate these possibilities with several examples. First, I will talk about a set of human populations from Western Central Africa. Using ABC, we could infer the history of splitting and admixture between these different groups. We could also identify sex-specific demographic processes. The second example that I will mention is the harbour porpoise (*Phocoena phocoena*) population from the Black Sea. Using again ABC techniques, we showed that this population underwent a strong expansion around 5000 years ago, probably as a result of the reconnection of the Black Sea with the Mediterranean Sea, but that it underwent also a drastic decline around 50 years ago. Finally I will talk about a study on worldwide human populations, in which by applying MCMC methods on a large set of populations with different lifestyles (farmers, herder and hunter-gatherers), we were able to show that these lifestyles strongly impacted the expansion patterns of these populations. These examples illustrate well how ABC and MCMC methods allow inferring precious information on the history of populations.

Session 2 THU GEN B 35

Unravelling the evolutionary history of the mosquito disease vector *Aedes aegypti*; lineage diversification and successful worldwide colonisation (52150)

Kelly Bennett.

University of Manchester.

The natural boundaries of populations are limited by their ability to disperse and competitively utilise novel habitats. What governs the success of colonising populations? The dengue disease vector *Aedes aegypti* has been particularly successful in expanding its geographic range from ancestral Africa. The dengue mosquito is also one of few mosquitoes which have acquired the ability to breed in domestic habitats and associate with man.

Studying the colonisation process of this mosquito could provide insight into the evolution of domesticity and factors contributing to the successful spread of disease vectors.

Previous studies based on microsatellite and SNP data suggest that domesticated populations outside of Africa represent a distinct genetic group different from populations found within Africa. On the other hand, mitochondrial studies find two genetic groups outside of Africa which may correspond to subspecies (associated with domestic and non-domestic habitats) or African geography (East and West Africa).

Findings from the present study suggest that divergent lineages within *A. aegypti* may have arisen through allopatric speciation during the Plio-Pleistocene. Divergent genetic lineages have undergone admixture associated with historical habitat change or human movement. I provide evidence that genetically heterogeneous populations of *A. aegypti* within Africa have contributed to the colonisation of new geographic areas outside of Africa.

Session 2 THU GEN B 35

Running faster or jumping further? Analysis of adaptive walks in various classes of fitness landscapes. (52502)

Barbora Trubenova, Tiago Paixao.

IST Austria.

In evolutionary biology it is often assumed that mutations are sufficiently rare and selection sufficiently strong to consider a population to be monomorphic at most of the time, 'jumping' between different genotypes. Analysis of adaptive walks in this regime have frequently resorted to simplifying assumptions about the fitness landscapes. In particular, they typically assume that selection coefficients are drawn from extreme-value distributions and that mutational neighbourhoods are not correlated.

This Strong Selection Weak Mutation (SSWM) model is closely analogous to (1+1) Evolutionary Algorithm (EA), used in computer science. The analysis of the performance of this algorithm have lead to tools that allow its analysis in classes of fitness functions, without disregarding their correlation structure. Making use of tools from computer science, we analyse several properties of adaptive walks in various classes of fitness landscapes, including average jump size, speed of adaptation and time until they reach the optimum.

Session 2 THU GEN B 35

The molecular mechanisms and reversibility of fisheries-induced evolution (52542)

Silva Uusi-Heikkilä, Tiina Sävilmä, Spiros Papakostas, Robert Arlinghaus, Craig Primmer.

University of Turku; Leibniz-Institute of Freshwater Ecology and Inland Fisheries.

Large shifts in phenotypic traits have been observed in exploited fish populations, which have not always fully recovered despite fishing has been ceased. Fisheries-induced evolution (FIE) can explain these potentially slowly reversible changes. However, detecting signals of FIE and its reversibility has proven difficult. We study the molecular mechanisms of FIE by sequencing the transcriptome of experimental fish (wild-origin zebrafish, *Danio rerio*) that have been harvested size selectively for five generations and then maintained under no-selection for six generations. We studied 1) what are the molecular mechanisms underlying FIE, 2) does intensive size-selective harvesting affect gene expression variation, and 3) whether the genetic changes caused by size-selective harvesting are reversible. Our results show that five generations of size selection induced substantial changes in gene expression. In addition to expression evolution, we found signals of sequence evolution: a large number of SNPs were candidates for being subject to selection. We further show that size-selective harvesting generally reduced gene expression variation. Harvest-induced changes in gene expression were eroded after cessation of size-selective harvesting but there was no clear sign of recovery at the sequence level. Similarly, gene expression variation did not rebound back to the initial levels.

Session 2 THU GEN B 35

Density dependence determines the role of extrinsic mortality in shaping life history traits (52318)

Maciej J. Dańko, Oskar Burger, Jan Kozłowski.

Max Planck Institute for Demographic Research; University of Kent School of Anthropology and Conservation (Canterbury, UK) ; Institute of Environmental Sciences, Jagiellonian University (Kraków, PL).

There is still debate about the role of extrinsic mortality in shaping life histories, especially the evolution of ageing. We show that the effect of extrinsic mortality depends on ecological conditions, particularly the effect of density dependence on population growth rate. We propose a novel method that combines the idea of the Evolutionary Unbeatable Strategy (EUS) with a projection matrix and resource allocation model. We consider three general classes of density dependence: acting on (i) mortality, (ii) fecundity or (iii) on resource acquisition rate. We extend previous research by allowing density effects in each of these cases to be constant or to vary with age or body mass. For each case we demonstrate the effects of density-independent extrinsic mortality on resource allocation strategies. We find that the effect of extrinsic mortality depends not only on the model of density dependence, but also on the strength of change in density dependent effects with age or size. For each scenario we compare EUS strategies with strategies resulting from maximization of more standard

measures of fitness (like r or R), and identify cases where neither of the standard measures provide correct predictions about the optimal allocation strategy.

Session 2 THU GEN B 35

Sex-specific evolution of learning performance, locomotion, reproduction and lifespan in an outcrossing nematode (51828)

Martyna Zwoinska, Martin Lind, Maria Cortazar, Mark Ramsden, Alexei Maklakov.

Evolutionary Biology Centre, Uppsala University.

Evolution of learning performance is constrained by trade-offs with life-history traits. Since male and female life-histories often diverge the costs and benefits of learning can differ between the sexes but intersexual genetic correlation will constrain the sexes from reaching their optimal trait values. We selected *Caenorhabditis remanei* nematode females for increased and decreased olfactory learning and measured learning performance, locomotory activity, reproductive performance and lifespan in virgin and mated males and females. While both sexes responded to selection, males performed better than females in two different learning assays. Downward-selected males showed higher locomotory activity and longer virgin lifespan yet sired fewer progeny than upward-selected males supporting the trade-off between learning and lifespan, and showing that increased reproduction and learning performance do not depend on increased activity. Strikingly, while we observed no effect of selection on female reproduction, virgin downward-selected females lived shorter than upward-selected females. Opposing effects of olfactory learning selection on lifespan evolution in the two sexes led to the reversal of sexual dimorphism in virgin lifespan in downward-selected lines, where virgin males outlived virgin females. Our results show that sex-specific genetic architecture results in the evolution of sexually dimorphic life-histories despite intersexual genetic correlation for learning performance.

Session 2 THU GEN B 35

A comprehensive phylogenetic study of mammalian embryology and skeletogenesis reveals the altricial life history of the placental ancestor, modularity and a brain-bone development link (51627)

Marcelo Sánchez-Villagra, Ingmar Werneburg, Michel Laurin, Daisuke Koyabu.

University of Zurich; University of Zurich; Muséum National d'Histoire Naturelle, Paris; University Museum, University of Tokyo.

We present the first comprehensive and phylogenetic study of mammalian organogenesis and skeletogenesis in all major clades. Our study is based on Museum specimens and non-invasive imaging and synthesis of embryological data. We coded the relative timing of discrete events, e.g. onset of ossification of all bones of the skeleton and major events in organogenesis and life history. Using heterochrony analyses, we reconstructed the ancestral

chronology of organogenesis and life-history modes. Placental altriciality is inherited from the last common ancestor of amniotes and the precocial lifestyle of many placentals was secondarily acquired. The last common ancestor of marsupials and placentals was intermediate in the altriciality-precocity gradient, but the newborn was anatomically more placental-like. Brain size evolution is related to the length of fetal development, the latter linked to the evolution of viviparity. The mode of ossification (dermal or endochondral) unites bones into integrated evolutionary modules visible through heterochrony and imposes evolutionary constraints. Ossification of the neurocranium occurred considerably earlier than other skull regions during mammalian origins and developmental timing of the skull roof bones and appear to be associated with brain size. We argue that cranial heterochrony in mammals occurred in concert with encephalization within a conserved modular organization.

Poster session A - POL 300

Evolutionary pattern of the phosphoproteome in 18 yeast species (53721)

Romain Studer, Judit Villen, Pedro Beltrao.

EMBL-EBI; Department of Genome Sciences, University of Washington.

Posttranslational modifications (PTM) have the ability to fine-tune the regulation of proteins. Phosphorylation, which consists in the addition of a phosphate group to a polar residues (serine, threonine or tyrosine), is one of the most common and studied PTMs. The advance of high-throughput mass spectrometry (MS) technology allows the rapid identification of phosphosites in a single proteome. Recent studies of the human phosphoproteome have identified approximately 200,000 phosphosites. However, only 10% of these sites have a described function. Phosphosite information has been used to investigate the turnover rate of phosphosites by comparing the phosphoproteomes of different organisms, such as human, mouse, claw frog, fly, yeast, plant or bacteria. However, these studies generally focused on only two or three phosphoproteomes at the same time, or using a very small subset of sites. This lack of resolution can impair the significance of the results. Two phosphosites might be conserved between two species, but might also be fast evolving and disappear in other close species. Here we report the phosphoproteomes of 18 yeast species. We identified a rapid turnover of phosphosites, as seen by the increase numbers in recent branches and species only. We also estimated that a shift in binding motif preference occurred in species that predates the whole-genome duplication in yeast. Finally, we observed that old phosphosites are more important than young phosphosites, in term of structural and phenotypic effects.

Poster session A - POL 300

Eusociality influence on the effective population size (52985)

Bruno Vieira, Yannick Wurm.

Queen Mary, University of London.

Social insects are the most successful animals on earth, with a combined biomass rivaling that of humans. Most of the research done has focused on their ecology, behavior, and morphology, while we still know relatively little about the effect that social evolution has on the genome evolution. In specific, how social evolution affects the contributions of selection and drift. Indeed, while each social insect colony includes up to hundreds of thousands of individuals, only a small percentage of those individuals (male and female) reproduces. Furthermore, social insects have a longer generation time than solitary insects. These two characteristics should result in a lower effective population size (N_e), which is an important measure of diversity that helps us understand the relative strength of selection and genetic drift. However, due to the difficulty of measuring N_e , a comparison between solitary and social insects has never been tested. Here we use an innovative approach, the Pairwise Sequentially Markov Coalescent (PSMC) method, to obtain the N_e history based on the distance of heterozygous regions in a single diploid genome sequence. To understand if the evolution of eusociality is associated with a reduction in N_e , we compared several social and solitary insect species.

Poster session A - POL 300

Diversity in the genus *Begonia* (52984)

Katie Emelianova.

Royal Botanic Gardens Edinburgh.

Begonia is one of the most speciose plant genera, comprising over 1,500 species. The genera's large size and diversification has been attributed to poor dispersal leading to low levels of drift, high endemism and extensive population differentiation. However, indications that the genus underwent a genome duplication early in its history has prompted investigation into the impact of this duplication on *Begonia* diversity.

The anthocyanin biosynthetic pathway is a preliminary focus of the project, based on the hypothesis that duplication of either regulators or biosynthetic enzymes facilitated the wide variation of anthocyanin pigmentation in *Begonia*.

Genomic resources developed for the genus include RNA-seq datasets from 6 tissues of two South American species, *B. conchifolia* and *B. plebeja*, and a draft genome of *B. conchifolia*. These resources will be used for expression, selection and copy number analysis in anthocyanin biosynthesis genes. Patterns showing differential duplication and expression and positive selection may support a hypothesis implying genome duplication as a key player in the diversification of *Begonia*.

Additionally, a bioinformatics pipeline designed for large-scale identification and analysis of gene families will be outlined. Further development of the pipeline will enable genome wide identification of candidate genes involved in diversification of *Begonia*.

Poster session A - POL 300

Improving contact prediction with direct coupling analysis using secondary structural information and amino acid properties (52973)

Guido Uguzzoni, Francesco Oteri, Marco Punta, Martin Weigt.

Laboratoire de Biologie Computationnelle et Quantitative; Laboratoire de Biologie Computationnelle et Quantitative; Laboratoire de Biologie Computationnelle et Quantitative; Laboratoire de Biologie Computationnelle et Quantitative.

Direct coupling analysis (DCA) is a global inference method based on the maximum entropy principle, which aims at predicting residue-residue contacts using the co of residues in multiple-sequence alignments of homologous proteins. DCA permits to disentangle direct and undirect correlation.

Previous works on a restricted number of bacterial PFAM families showed as DCA outperforms Mutual Information in terms of contact prediction, leading to accurate modelling of the 3D structures as well as detection of protein-protein interactions.

In this work, the performance of DCA has been evaluated over the whole PFAM 27 dataset. The behaviour has been characterised taking into account the physico-chemical properties of the residues as well as secondary structure elements of the proteins. The data shed light on different properties of the protein structure underling the correlation signals.

Exploiting this information we are able to improve the true positive rate of contract prediction. Complementing DCA with methods predicting different properties Secondary Structure, Solvent Accessible Surface) is discussed.

Poster session A - POL 300

Reconstructing past demography from population specific FSTs. (52959)

Jerome Goudet, Bruce Weir.

Dept Ecology and Evolution, University of Lausanne; Dept of Biostatistics, University of Washington.

Evolutionary biologists have a long standing interest in reconstructing the past demography of species using genetic data. The availability of large data sets and increased computer power have allowed very detailed inferences in several species, particularly in Homo sapiens. One key issue is which summary statistics to use in order to draw these inferences. Here, using simulated data sets as well as phase 3 of the 1000 human genomes project, we show that moment estimators of population specific FSTs are particularly well suited, in particular when used in conjunction with the Site Frequency Spectrum.

Poster session A - POL 300

A genomic perspective on locally adapted coastal cod populations (52958)

Julia M. I. Barth, Paul R. Berg, Bastiaan Star, Sara Bonanomi, Jakob Hemmer Hansen, Halvor Knutsen, Carl André, Nils Christian Stenseth, Sissel Jentoft.

Centre for Ecological and Evolutionary Synthesis, University of Oslo, Oslo, Norway; Section for Marine Living Resources, Technical University of Denmark, Silkeborg, Denmark; Institute of Marine Research (IMR), Arendal, Norway; Department of Biology and Environmental Sciences-Tjärnö, University of Gothenburg, Strömstad, Sweden.

Structured populations represent confined locally adapted interbreeding species units, which have long been assumed to be non-existent in open marine environments due to the lack of geographical barriers. However, this is increasingly disproved and populations with high levels of genetic differentiation important for adaptation to local environments are being documented at fine scales.

Since the 1970's, Atlantic cod (*Gadus morhua*) populations have been declining in the North Sea, leading to a near extinction of cod in the Norwegian and Swedish fjords. Whether cod in this area represents a large panmictic population where recruitment from offshore areas can substitute for local losses, or whether coastal areas and fjords are home to locally adapted populations is still an open question.

We used a large-scale genomic approach to genotype 500 individuals from 14 different locations at 10.000 single-nucleotide polymorphism (SNP) markers to answer the questions whether locally adapted coastal cod populations exist, which genes are ecologically relevant for adaptation, and to investigate connectivity and past demography of these populations in the light of climate change.

Our results will be highly relevant to provide a management strategy for the protection of locally adapted cod populations and the ecosystems they live in.

Poster session A - POL 300

Stability-activity tradeoffs constrain the adaptive evolution of RubisCO (52946)

Romain Studer, Pascal-Antoine Christin, Mark Williams, Christine Orengo.

EMBL-EBI; University of Sheffield; Birkbeck College; University College London.

The importance of the stability effect of mutations in protein evolution has been theorised and established in some single-case studies. When a change of function occurs, some mutations shift the stability outside the neutral range, thus they need other mutations after to compensate this difference. Ribulose-1,5-bisphosphate carboxylase (RubisCO) is the enzyme responsible for fixation of CO₂ during photosynthesis. In flowering plants, two forms exist, the C₃ and the C₄, the latter being faster in terms of catalytic activity. The C₄ form emerged by convergent evolution in multiple clades and was the result of a few amino acid substitutions under positive selection. We explored the impact of structural constraints on RubisCO evolution. We reconstructed in silico the ancestral sequences and their associated 3D structures. We were able to follow precisely the evolutionary path, by identifying each mutation on each branch. We found that there are more destabilising mutations at the base of C₄ clades, and that these mutations are then followed by other stabilising mutations. These results are consistent with a “stability-activity trade-off” model. These results demonstrated that the evolution of an enzyme can be under strong structural constraints and that adaptive mutations are balanced between stabilising and destabilising effects.

Demography and local adaptation of *Rana temporaria* across an environmental gradient (52945)

Alexandra Jansen van Rensburg, Josh Van Buskirk.

University of Zurich.

Understanding the genomics of local adaptation in natural populations currently suffers from confounding effects of demographic history, exacerbated by small sample sizes and sampling scheme limitations. These problems can be overcome by assessing signatures of adaptation across replicate environmental transects, where potential adaptive loci should be verified in parallel scenarios. Widespread species present an ideal opportunity to study local adaptation as they often occur across a range of environmental conditions, thus replicate transects can be sampled. Here we assess the use of reduced representation libraries to study the genomics of local adaptation in the common frog (*Rana temporaria*) across its range in Switzerland. Using a large and geographically extensive sampling scheme (1050 samples from 81 populations) across multiple parallel environmental gradients, we can infer fine-scale demographic history, as well as identify genomic regions important for local adaptation. Further, we use a modelling approach to assess the amount of gene flow and selection needed to maintain local adaptation at the range edge, given genomic architecture of the adaptively important trait.

Geographic variation in resistance of white spruce against spruce budworm (52939)

Genevieve J. Parent, Isabelle Giguère, John J. MacKay.

Centre d'Étude de la Forêt, Département des Sciences du Bois et de la Forêt, Université Laval; Institut de Biologie Intégrative et des Systèmes, Université Laval; Department of Plant Sciences, University of Oxford.

Variable in selective regimes within a distribution may cause local adaptation. Evidences for local adaptation in perennial species such as trees are sparse, which might be a consequence of variation in selective regimes through their life cycle. In white spruce (*Picea glauca*), a heritable mechanism of resistance against spruce budworm (*Choristoneura fumiferana*, SBW), the most damaging forest insect in eastern North America, was discovered for the first time. The PgβGLU-1 enzyme catalyzes the cleavage of acetophenone sugar conjugates to release the aglycons that are toxic for SBW. We investigated if patterns of geographic variations in resistance were present in the population. Levels of Pgβglu-1 transcripts and acetophenones varied widely in natural white spruce population, however putatively resistant trees were less frequent in the southern range of the distribution. Different factors such as temperature and insect feeding pressure are being tested to explain variable frequencies of resistant trees. These abiotic and biotic factors may help to explain the selective regimes exerted on white

spruce population. Furthermore, a genome wide association test is currently underway to identify genetic variants linked to resistance. These results may serve to predict the effects of future outbreaks of SBW in both managed and spruce natural population.

Poster session A - POL 300

Genetic diversity of European *Pinus sylvestris* populations studied with exome sequencing (52917)

Jaakko Tyrmi, Juan José Acosta, Zhen Li, Tanja Pyhäjärvi, Outi Savolainen.

Genetics & Physiology Unit, University of Oulu; Forest Genomics Labs, University of Florida; VIB Department of Plant Systems Biology, Ghent University.

Pine trees are key species in many ecosystems in Europe and North America also with significant economic value. Pines are also excellent species for studying molecular basis of local adaptation on natural populations because of their large native distribution ranges covering a diversity of environments and high levels of genetic and phenotypic variation. The genetic diversity of Pines have been studied in the past using a small number of candidate genes. The large and complex highly repetitive genomes still prevents whole genome resequencing, but here we have used targeted sequence capture. In several European populations, we have targeted some 10 000 genes. A first study was conducted using exome sequences of the related *Pinus taeda* to design the probes, a second set using *Pinus sylvestris* transcriptome derived sequences. We also have tried different options of mapping the captured sequences. Due to the repetitive genome, paralogous sequences need to be dealt with carefully. We examine genome-wide diversity, differentiation of populations, and the extent of genome-wide linkage disequilibrium. We then contrast our candidate locus variation for adaptive traits (cold tolerance, timing of budset) to the genome wide averages and examine them against predictions of selection models.

Poster session A - POL 300

Sifting through tangled trees: A particle-filtering method for Bayesian reconstruction of cophylogenies (52890)

Arman Bilge, Tim Vaughan, Alexei J Drummond.

The University of Auckland; Allan Wilson Centre for Molecular Ecology and Evolution.

Systems of interdependent evolutionary histories, often represented by cophylogenies, are important models for genome evolution (i.e., gene trees versus species trees) and the coevolution between a symbiont and its host organism. A cophylogeny consists of a "host" phylogeny, a "guest" phylogeny, and a reconciliation, the mapping of ancestral guests to their hosts, and is determined by a series of events, including cospeciation, duplication, loss, and host-switching/horizontal transfer. Existing methods for reconstructing cophylogenies generally assume that the host phylogeny is known and that its population dynamics are

deterministic and cannot consider uncertainties in dating and geographic location. We developed an approach that uses Bayesian Markov chain Monte Carlo to perform joint inference on the host and guest phylogenies, reconciliation, divergence dates, and event rates. Because the model complexity makes it impossible to compute analytically the likelihood of a cophylogeny, we employ a particle filtering method that uses piecewise simulation and resampling to approximate the likelihood. We implemented the sampler as a plugin for BEAST, an existing MCMC framework for Bayesian evolutionary analysis, and evaluated its performance on both simulated and real datasets. Furthermore, the use of simulation makes it straightforward to extend our code to consider more complex models.

Poster session A - POL 300

Phylogeography, population structure and phenotypic variation in the wing dimorphic grasshopper *Dichroplus vittatus* (Orthoptera: Acrididae). (52863)

Maria Remis.

Depto. Ecologia, Genetica y Evolucion, Facultad Ciencias Exactas y Naturales, Universidad Buenos Aires.

Dichroplus vittatus is a South American grasshopper that in field can display fully-winged (macropterous) or small-winged (brachypterous) morphs. In order to analyse the genetic and phenotypic differentiation, a fragment of 543bp of the mitochondrial COI gene and 5 body size related traits were studied in 7 populations from La Pampa and San Luis Provinces. We demonstrated a variable frequency in the percentage of brachypterous individuals, ranging from 100% to 25%. The MANOVA showed significant differences in body size among populations, between sexes with female-biased size and between wing morphs being the brachypterous morph the larger. Molecular studies detected 10 haplotypes from 5 polymorphic sites. Diversity indices were low, particularly in La Pampa populations with higher frequency of macropterous. The AMOVAs using F_{ST} showed significant heterogeneity among provinces, between populations and within populations. Haplotype network indicated a moderate component of geographical variation. Demographic indices and mismatch distribution revealed that one San Luis population fits a recent expansion model. Genetic and phenotypic analysis of populations studied here would indicate a relatively short evolutionary history. Consistent with a trade-off between flight capability and reproduction hypothesis our results suggest that La Pampa Province may be an unstable or less favourable environment for this specie.

Poster session A - POL 300

Reptilian Transcriptomes v2.0: an extensive resource for Sauropsida genomics and transcriptomics (52856)

Athanasia C. Tzika, Asier Ullate-Agote, Djordje Grbic, Michel C. Milinkovitch.

University of Geneva.

Despite the availability of deep-sequencing techniques, genomic and transcriptomic data remain unevenly distributed across phylogenetic groups. For example, reptiles are poorly represented in sequence databases, hindering functional evolutionary and developmental studies in these lineages substantially more diverse than mammals. Here, we present the 'Reptilian Transcriptomes Database 2.0' which provides extensive annotation of transcriptomes and genomes from species covering the major reptilian lineages. To this end, we sequenced normalized cDNA libraries of the leopard gecko and the corn snake and gathered published reptilian sequence datasets from representatives of the four extant orders of reptiles: Squamata, the tuatara, crocodiles, and turtles. LANE runner 2.0 was implemented to annotate all assemblies within a single integrated pipeline. We show that this approach increases the annotation completeness of the assembled transcriptomes/genomes. We then built large concatenated protein alignments of single-copy genes and inferred phylogenetic trees that support the positions of turtles and the tuatara as sister groups of Archosauria and Squamata, respectively. The 'Reptilian Transcriptomes Database 2.0' resource will be updated to include selected new datasets as they become available, thus making it a reference for differential expression studies, comparative genomics and transcriptomics, linkage mapping, molecular ecology and phylogenomic analyses involving reptiles.

Poster session A - POL 300

Morphological adaptation in a marine-freshwater habitat transition of Northern Neotropical Catfishes (52854)

Madlen Stange, Gabriel Aguirre, Walter Salzburger, Marcelo Sánchez.

University of Zürich, Palaeontological Institute; University of Basel, Zoological Institute.

The present study aims to disentangle the patterns of adaptation associated with a marine-freshwater habitat transition in the evolution of siluriform Ariidae (sea catfishes), and how those patterns are related to diversification. Successful habitat transitions require adaptation of populations with subsequent speciation. Such evolutionary habitat transitions are accompanied by morphological changes that in turn should leave signatures of adaptation. Ariidae contain mainly marine species, with some species inhabiting freshwater secondarily. All sister taxa but one inhabit fresh- or brackish water. That makes them the ideal study system to investigate the habitat transition from freshwater to marine and back to freshwater on morphological level. This study aims to assess and compare morphological disparity using 2D geometric morphometrics on opercula between and among freshwater and marine catfish species (Ariidae) and freshwater sister taxa. Opercula have been shown to be suitable structures to examine ecological adaptation as they have been shown to change when changing habitat from marine to freshwater habitat. Observed differences are determined whether they are the result of adaptation to marine or freshwater habitat, and/or phylogenetic signal. Opercula shape change among taxa and patterns of variation are visualised using CVA and PCA, respectively.

Poster session A - POL 300

Measuring constraints to cichlid diversification in small lakes (52852)

Florian N. Moser, Jacco C. Van Rijssel, Catherine E. Wagner, Ole Seehausen.

Institute of Ecology and Evolution, University of Bern, 3012 Bern, Switzerland; EAWAG Center for Ecology, Evolution and Biogeochemistry, 6047 Kastanienbaum, Switzerland.

Small lakes provide unique opportunities to study speciation in sympatry, as opportunity for geographical isolation within these environments is negligible. Cichlid fishes are famed examples of sympatric speciation due to instances of speciation in small lakes. However, cichlids occur in many other small lakes where they have not diversified. Although comparative studies reveal lake depth as an important predictor of cichlid diversification, and case studies show that natural and sexual selection operating along depth gradients can readily lead to speciation, the underlying microevolutionary processes which promote or constrain speciation along such depth gradients remain unclear. To investigate the constraints to diversification and differentiation, we studied haplochromines of two small lakes that differ greatly in depth, Lake Chala (90m) and Lake Babati (5m). Both lakes host only one known haplochromine species, *Astatotilapia* sp., which shows higher phenotypic variation in Lake Chala. We quantify phenotypic diversity and divergence in the two cichlid communities, and relate it to variation in fitness landscapes estimated from a fitness proxy, growth rate. We then investigate genetic differentiation using genome-wide SNP data. We discuss the environmental conditions under which phenotypic differentiation can evolve, and the cases in which it is associated with genetic divergence and speciation.

Poster session A - POL 300

Statistical physics of transcription-factor evolution: speciation with pleiotropic constraint (52846)

Alexander Tulchinsky, Normal Johnson, **Adam Porter**.

University of Massachusetts - Amherst.

Speciation can result from gene misregulation in hybrids when transcription factors (TF's) and their cis-regulatory targets differentially coevolve in separate populations. Pleiotropy should constrain the evolution of misregulation because multifunctional TF's should be less likely to diverge. How profound is this constraint?

We used a statistical physics model wherein fractional occupancy of a TF on its cis-regulated target determines gene expression, thus phenotype. TF concentration and free energy of association ($-\Delta G$) determined occupancy. Mutable bit strings represented alleles, and $-\Delta G$ depended on their match. Misregulation occurs when a phenotype differs from its environmentally determined optimum. The model can extend to any genetically determined, interacting molecules.

We simulated a pleiotropic regulatory pathway involving a conserved and a positively selected trait, sharing a TF, with two populations evolving in parallel to new optima. Pleiotropy shifted more of the response to the cis-site of the directionally selected trait, and compensatory evolution occurred at the cis-site of the conserved trait. Both traits contributed to misregulation of hybrids.

TF concentration and ΔG determined much of the evolutionary dynamics of speciation. Pleiotropy inhibited speciation when a mismatched bit changed occupancy too much; misregulation was negligible when a mismatch changed occupancy too little. Between, speciation occurred frequently.

Poster session A - POL 300

Genomics of adaptive life history variation in Atlantic salmon (52842)

Nicola J Barson, Tutku Aykanat, Kjetil Hindar, Matthew Baranski, Celeste Jacq, Sten Karlsson, Geir Bolstad, Matthew P Kent, Sigbjørn Lien, Craig R Primmer.

Norwegian University of Life Sciences; University of Turku; Norwegian Institute for Nature Research (NINA); NOFIMA.

Local adaptation often involves complex quantitative traits. However, when selection for local adaptation occurs with ongoing gene flow, control by a few loci of large effect is expected. This necessity can lead to constraints on the identity of loci and their position in regulatory networks and raises the possibility of a conserved genomic basis of adaptation across taxa.

Atlantic salmon exhibit extreme variation in age and size at maturity. Replicated divergence among populations in these key fitness related traits and ongoing gene flow make salmon an ideal organism in which to study the genomics of local adaptation. We present results of dense SNP genotyping (220k loci) of 1734 individuals from 57 wild populations, covering the coast of Norway, plus a Baltic outgroup. Populations are dominated by either large, late maturing (2-3 sea years), or small, early maturing (1 sea year) salmon. This sampling allowed analysis of genotype-phenotype associations (GWAS) and spatial variation in the genomics of adaptive responses. Our results suggest several major genes contribute to local adaptation, consistent with predictions under migration-selection balance, and a role for “master regulators”. Targeted re-sequencing enabled identification of locally adapted candidate gene variants, which will be discussed in a functional context.

Poster session A - POL 300

Chronology of fitness traits evolution to climate change over 100 years in the water flea *Daphnia magna* (52839)

Maria Cuenca Cambroner, Hollie Marshall, Hanna Tilley, Luisa Orsini.

Environmental Genomics Group, School of Biosciences, University of Birmingham .

The decline of water quality due to climate change and land use determined by the use of pesticides and leading to eutrophication is a recognized threat to ecosystem services and to the economy. However, the causes and effects of climate and land use changes occur over many decades, and are therefore difficult to measure. Critical for gauging the long term consequences of climatic change is the reconstruction of evolutionary dynamics over

extended time axes. Here, we reconstruct the evolution of fitness traits (mortality, fecundity and growth rate) to climatic change in *Daphnia magna* populations using animals resurrected from sediment biological archives with known history of eutrophication and temperature changes. Experimental evolution trials are used to measure fitness response of populations sampled across 80 years (1960-present) to the forecasted temperature increase for the upcoming century. In addition, we measure the evolution of fitness traits in response to the combined effect of temperature increase with pesticides and food quality changes. This study will identify fitness traits targets of natural selection and the long-term consequences of environmental stress in metazoan populations.

Poster session A - POL 300

Evolution of an endosymbiont genome associated with host dependency (52818)

Dré (A.A.) Kampfraath, Ken Kraaijeveld, Jacintha Ellers.

VU university.

Mutualistic relationships often result in the loss of traits that are being compensated for by the partner. Trait loss in endosymbionts is expected to be an ongoing process, but the rate and sequence in which traits are lost during the early stages of the interaction are poorly understood. *Wolbachia* is one of the most widespread endosymbionts infecting an estimated 40% of all terrestrial arthropod species. *Wolbachia* is known for manipulating the reproductive system of its hosts, but can also provide the host with benefits including defense against parasites. In some cases, the intimate relation between endosymbiont and host has resulted in host dependency. In the springtail *Folsomia candida*, eggs cleared from *Wolbachia* by heat or antibiotics don't hatch, showing that the host has become reliant on its *Wolbachia* endosymbiont for reproduction. Therefore, we sequenced and assembled the wFol genome. This is the first sequenced *Wolbachia* genome that is obligatory for its host. By comparing the wFol genome to 12 available *Wolbachia* genomes we test whether wFol strain (1) has a smaller genome size than other *Wolbachia*, and (2) has lost some otherwise essential genes that are compensated for by the host.

Poster session A - POL 300

Genetic architecture of morphological traits in the Mediterranean mussel *Mytilus galloprovincialis* (52816)

Dorotea Polović, Stuart Dennis, Anamaria Štambuk, Maja Šrut, Víctor Soria-Carrasco, Zachariah Gompert, Vid Baković, Goran Klobučar, Patrik Nosil.

Department of Biology, Faculty of Science, University of Zagreb; Department of Animal and Plant Sciences, University of Sheffield; Department of Biology, Utah State University.

The genetic architecture of phenotypic traits, including their heritability, numbers of loci involved, and effect sizes, are not well understood in bivalves. Anthropogenic pollution may create environmental differences that can alter mussel (*Mytilus galloprovincialis*) morphology through either genotypic or induced environmental effects. To assess the genetic architecture of morphology we measured 17 morphometric traits in over 1400 mussels from two populations inhabiting sites differing in pollution pressure. We used a genotype by sequencing approach to generate genomic data that allowed us to then describe the genetic architecture of these traits in a genome wide association study. Additionally, we estimated the genetic architecture of the same traits as well as proxies for fitness in an additional sample of 15 populations distributed across a pollution gradient using 20 mussels per population. The results thus characterise variation within and among populations in mussel morphology and assess the association between genotype, phenotype and environment.

Poster session A - POL 300

A case of rapid postglacial speciation in the songbird genus *Junco*: genome-wide divergence in SNP data suggests the role of multifarious selection (52810)

Guillermo Friis, Borja Milá.

National Museum of Natural Sciences (CSIC).

During early stages of ecological speciation, divergence may be driven by strong selection on a few loci, or alternatively through weaker multifarious selection acting on numerous loci across the genome. Cases of recent and rapid diversification provide the opportunity to examine the relative importance of these types of selection and their effect on genomic landscapes. The rapid postglacial radiation of the genus *Junco* in North America has given rise to a number of closely related yet phenotypically distinct forms within the last 10,000 years, as documented with mtDNA sequence data. A subset of several thousand high-FST SNPs obtained through Genotyping-by-Sequencing, reveals marked divergence between and even within junco morphs. This pattern is congruent with geographical and phenotypic structure and suggests restricted gene flow even among parapatric sister forms. Divergent SNP loci are spread across the entire genome despite the recent origin of the morphs, suggesting the role of selection acting on numerous loci across the genome from the early stages of the speciation process. This is consistent with preliminary data on the role of sexual selection and ecological niche divergence, suggesting that the diversification of junco forms is driven by a wide range of selective factors.

Poster session A - POL 300

Characterizing the architecture of gene expression regulation in the threespine stickleback, *Gasterosteus aculeatus*. (52801)

Victoria Pritchard, Juha Merilä, Mikko Nikinmaa, Craig Primmer, Heidi Viitaniemi, Erica Leder.

University of Turku, Finland; University of Helsinki, Finland.

It is increasingly clear that changes in the expression of genes play an important role in local adaptation. Thus, elucidating the genetic architecture of gene expression regulation is an important step to understanding how populations evolve in response to changing environments, and thus how adaptive divergence occurs. Here, we used an expression microarray, in combination with RAD-tag sequencing and a controlled cross, to characterize expression quantitative trait loci (eQTL) underlying variation in gene expression in the threespine stickleback (*Gasterosteus aculeatus*) - an important model in the study of adaptive radiation. We identified several thousand eQTL, of which >60% were cis acting. Trans acting eQTLs clustered into several putative 'eQTL' hotspots. We further discuss our results with respect to genes exhibiting expression variation between the sexes, and between different thermal treatments.

Poster session A - POL 300

Deciphering the molecular basis of a boreal adaptation: the transcriptional landscape of seasonal coat color change in two species of hares (52799)

Mafalda Sousa Ferreira, Paulo Célio Alves, Colin Callahan, L. Scott Mills, Jeffrey M. Good, José Melo-Ferreira.

CIBIO-InBIO, Centro de Investigação em Biodiversidade e Recursos Genéticos, Universidade do Porto; Departamento de Biologia, Faculdade de Ciências da Universidade do Porto, Porto, Portugal; Wildlife Biology, College of Forestry and Conservation, University of Montana, Missoula, MT, USA; Division of Biological Sciences, University of Montana, Missoula, MT, USA ; Department of Forestry and Environmental Resources, North Carolina State University, Raleigh, NC USA.

The effects of climate change in biodiversity are both a conservation problem and an opportunity to study the evolution of adaptive traits in response to the new environmental conditions. Seasonal coat color change, a remarkable adaptation of arctic and boreal species to their seasonally snow covered environment, is one of such traits. Global warming and the consequent decrease of the number of days with snow on the ground lead to increased periods of mismatch in crypsis, making these species highly conspicuous to predators. How will this phenotype respond to the new environmental conditions is now a pressing question. A crucial step to tackle this is to determine the molecular bases of seasonal coat color change to better understand how environmental cues act to time the production of two color phenotypes. In this work, we track the gene expression changes in the skin in the molting cycle of two distantly related species of hares, the snowshoe hare, *Lepus americanus*, and the mountain hare, *Lepus timidus*, using an RNA-sequencing approach. This will provide an unprecedented understanding of the genetic mechanisms underlying seasonal coat color molting and of the possibly independent evolutionary pathways of this phenotype in two distinct species.

Poster session A - POL 300

Genomic variation in the virilis group of *Drosophila* (52796)

Venera Tyukmaeva, Konrad Lohse, Ritchie Michael.

University of St Andrews; University of Edinburgh.

The *Drosophila virilis* group species show unique behaviours and adaptations and are an ideal model system to study speciation. The group has a long history of research on the evolution of mating behaviour, chromosome arrangements, adaptations and molecular evolution, however, the species phylogeny has many uncertainties and controversial points. We obtained 18 genome sequences for the species from the group (one fly individual per line, mostly two lines per species from different geographic locations) and adopted the likelihood framework developed by Lohse & Frantz (2014) to co-estimate species divergence times, ancestral population sizes and introgression parameters between closely related species using block-wise alignments sampled from the whole genome. Many species of the group occur both in allopatry and sympatry with their closest relative in North America which makes it possible to explicitly test for the effect of geography on species divergence and historical or on-going gene flow. At the same time the detailed sequence information from closely related species allows a detailed examination of the regions under positive selection between different species and help identifying the key genes involved in speciation.

Poster session A - POL 300

Evolution of tissue specificity of protein coding genes in vertebrates (52781)

Nadja Kryuchkova, Marc Robinson-Rechavi.

University of Lausanne; Swiss Institute of Bioinformatics.

One of the major properties of genes is their expression pattern. While there have been recent studies of the correlation of expression between species for a few tissues, little is known about the evolution of tissue-specificity itself. There are several methods to measure this tissue-specificity. In this study we compare available methods and use them to study evolution. More specifically, we inquire:

- Do tissue-specific genes evolve faster?
- Are there major differences between the evolution of tissue-specificity after duplication (paralogs) or without duplication (orthologs)?
- Could previous studies be biased, due to the bias in detecting low expressed genes?

Eight methods for tissue-specificity were analyzed on their robustness for choice and number of tissues and for data normalization. For RNA-seq, the results of most methods, established for ESTs and Microarrays, depend on the data pre-processing. Also tissue-specificity is better detected with RNA-seq than with Microarrays.

We show that new genes and genes with more paralogs tend to have more specific expression. Previous findings, that more broadly expressed genes evolve under stronger purifying selection, could be confirmed.

Genomic signature of local adaptation in *Populus tremula* (52780)

Jing Wang, Pär K. Ingvarsson.

Department of Ecology and Environmental Science, Umeå University; Department of Ecology and Environmental Science, Umeå University.

Identifying the signatures and targets of local adaptation is an increasingly important goal in ecology and evolutionary biology. With the advent of next generation sequencing (NGS) technologies, it has become feasible to perform genomics studies on ecologically and economically important non-model species. *Populus tremula*, European aspen, is a deciduous forest tree with a geographic distribution ranging throughout Eurasia, and thus, has normally adapted to a wide variety of environmental conditions. Using whole genome re-sequencing data from 85 *P. tremula* trees collected from twelve sites spanning latitudinal and longitudinal gradients throughout Sweden, we tested for evidence of local adaptation by using three different kinds of methods: (1) searching for elevated population differentiation using *F_{ST}*-based outlier analyses; (2) testing for significant associations between allele frequencies and environmental variables; (3) genome-wide association studies of two ecologically important traits (bud set and bud flush) associated with common garden experiments. In the end, we identified a set of candidate loci that have been subject to local adaptation. Our findings also provide insights into the relative contribution of new mutations and standing genetic variation to the evolution of local adaptation, as well as the genetic architecture of adaptive traits in *P. tremula*.

Evolution of convergent floral phenotypes during pollination shifts in Gesneriaceae: transcriptomic evidence (52775)

Martha Liliana Serrano-Serrano, Anna Marcionetti, Mathieu Perret, Alain Chautems, Nicolas Salamin.

University of Lausanne; Conservatoire et Jardin botaniques de la Ville de Genève.

Morphological changes have impacted the evolution of many groups in the tree of life, among those Angiosperms is an excellent case where evolutionary forces have shaped a great compendium of floral forms. Pollinator variation in the Gesneriaceae family has led to strong convergent floral phenotypes for different functional groups (insects, hummingbirds and bats). Further, Gesneriaceae has a labile pattern of plant-pollinator associations, with multiple changes within a single lineage. These pollinator shifts involve mainly changes in corolla shape and color, as well as, in the timing of anther dehiscence, nectar production, and sexual organ elongation. Here, we present the results from the transcriptomic data of six non-model plant species to investigate the differentiated loci during pollination shifts and their signatures of selection. We also profile the gene expression and regulation differences between the convergent floral phenotypes.

Local-scale genetics — genetic structure in natural *Pinus pinaster* populations at short spatial scales (52774)

Katharina B. Budde, Myriam Heuertz, Ana Hernández-Serrano, Felix Gugerli, Miguel Verdú, Juli G. Pausas, Santiago C. González-Martínez.

University of Copenhagen; CIFOR-INIA Forest Research Center, Madrid; INRA BIOGECO, Bordeaux; CIDE-CSIC/UV/GV Centro de Investigaciones sobre Desertificación, Valencia; WSL Swiss Federal Research Institute, Zürich.

Landscape genetics aims to disentangle which environmental factors shape the genetic structure of species or populations in the light of gene flow. Recent studies have determined environmental factors affecting neutral and adaptive genetic variation in plant species on regional to continental scale. However, selection is expected to be harder to detect over short distance, where extensive gene flow can exceed the migration–selection equilibrium. Here we tested the effect of topography, water availability and biotic indicators on the local genetic structure of maritime pine (*Pinus pinaster*) at single-nucleotide polymorphisms (SNPs) and adaptive phenotypes in eastern Spain. In one site, a 300 m altitudinal gradient significantly affected maritime pine local genetic structure and tree growth, while no environmental factor seemed strong enough to affect the genetic structure in other sites. Several environmental factors vary along (even short) altitudinal gradients, which could have led to divergent selection between upper and lower parts of slopes. Alternatively, adaptive and/or plastic responses in flowering phenology could have led to assortative mating and shaped the observed genetic structure. We conclude that neutral and adaptive processes at short spatial scales should be considered in landscape genetics studies aiming at understanding genetic structure within natural plant populations.

Selection pressures and recent adaptation in the genomes of invasive fire ants (52761)

Eyal Privman, Amir Cohanin, Yu-Ching Huang, John Wang, DeWayne Shoemaker, Laurent Keller.

University of Haifa; Academia Sinica; USDA; University of Lausanne.

Solenopsis fire ants evolved high invasiveness. A sub-clade of *Solenopsis* species have recently evolved a social polymorphism: a colony can either have one or many reproductive queens. This has been suggested to allow more efficient cooperation and faster population growth, which facilitate invasiveness. Therefore, we hypothesize that this transition was accompanied by positive selection on related adaptive traits. The social form is determined by the "social chromosome", a supergene containing over 600 genes. We set out to identify additional genes that contributed to this evolutionary innovation. We applied a population

genomic approach to infer selection pressures from RAD (Restriction site Associated DNA) sequencing and whole genome sequencing to achieve either high accuracy in allele frequency estimation or high resolution of SNPs, respectively. These data allow for high inference power in different types of tests for positive selection. We identified specific gene families and molecular functions under selection that could be implicated in social evolution. Furthermore, we identified loci with exceptionally high allelic variation, the hallmark of balancing selection. An extreme case is the recently discovered sex determination locus in *S. invicta*. These analyses provide for the first time a genomic view of selection pressures in an invasive social insect.

Poster session A - POL 300

Genomic consequences of hybridization and the loss of meiotic recombination in Root-knot nematodes (52760)

Laura Salazar-Jaramillo, Amir Stitzenberg, Dave Lunt, Mark Blaxter.

University of Edinburgh; University of Hull.

Root-knot nematodes (genus *Meloidogyne*) have undergone repeated transitions from sexual to asexual reproduction (besides obligatory sexual, they also exhibit both mitotic and meiotic parthenogenetic species). Transition from sexual reproduction to mitotic parthenogenesis involves the loss of meiotic recombination, which has been shown to result from interspecific hybridization events in some *Meloidogyne* species. Hybridization is expected to involve large genomic changes such as differences in the copy number of genes and chromosomes, which could result in major changes in biological function. At the same time, hybridization can potentially generate transgressive variation through the mixing of several parental genomes, while the resulting asexual reproduction is expected to limit genomic variation on the long run relative to sexual reproduction. Thus, by comparing the genomes of different root-knot nematode species, we investigate the genomic consequences of hybridization and the loss of meiotic recombination. Whole genome sequencing suggests that at least one of the most damaging asexual root-knot nematode species (*M. javanica*) is a triploid and shows a surprisingly high level of genomic variation. Such variation could help explain the great expansion of some *Meloidogyne* species in a wide range of agriculturally important crops.

Poster session A - POL 300

You are what you eat – Can selective advantages explain the AT-bias of endosymbiotic genomes? (52757)

Anne-Kathrin Dietel, Martin Kaltenpoth, Christian Kost.

Research Group Experimental Ecology and Evolution, Max-Planck-Institute for Chemical Ecology; Research Group Insect Symbiosis, Max-Planck-Institute for Chemical Ecology.

Endosymbionts are expected to evolve a reduced metabolic burden they impose on their host. Strikingly, both plasmids and intracellular bacterial symbionts generally exhibit a reduced GC-content relative to the host's chromosome. We hypothesize that competition among cytoplasmic elements for the hosts' nucleotides may explain this observation: Since dATP and dTTP are the most abundant nucleoside triphosphates in a cell, intracellular symbionts with lower GC-contents should be selectively favoured.

Here, we test this hypothesis by experimentally manipulating the GC-content of plasmids and analysing the fitness consequences for the bacterial host. Specifically, we introduced eight 1 kb sequences of eukaryotic DNA that were particularly AT- and GC-rich into two minimal plasmid backbones. Growth experiments with *Escherichia coli* revealed a significant fitness decrease of cells that harboured GC-rich plasmids as well as a reduced copy number of GC-rich plasmids, thus supporting the above hypothesis. Furthermore, externally supplying GC-nucleotides to plasmid-harboring cells caused a growth increase of cells containing GC-rich plasmids, while feeding of AT- nucleotides did not cause a similar effect. Our results demonstrate that by altering their base composition, plasmids can reduce the metabolic burden they impose on their bacterial host, which may explain the commonly observed GC-bias of endosymbionts.

Poster session A - POL 300

Spatial pattern of MHC diversity in barn owl (*Tyto alba*) (52741)

Arnaud Gaigher, Reto Burri, Walid Gharib, Pierre Taberlet, Alexandre Roulin, Luca Fumagalli.

Department of Ecology and Evolution, University of Lausanne, Biophore, 1015 Lausanne, Switzerland; Laboratory for Conservation Biology, University of Lausanne, Biophore, 1015 Lausanne, Switzerland; Department of Evolutionary Biology, Uppsala University, Norbyvägen 18D, SE-752 36 Uppsala, Sweden; Laboratoire d'Ecologie Alpine, CNRS UMR 5553, Université Joseph Fourier, 38041 Grenoble, France.

Major histocompatibility complex (MHC) genes play an essential role in the adaptive immune response and thus constitute a good model to study adaptive genetic variability. The extraordinary diversity exhibited by MHC genes is thought to be maintained by pathogen-driven selection. Because of the major role of MHC in pathogen defense, MHC genotypes can be expected to be locally adapted to pathogens, resulting in a more pronounced genetic structure in these genes compared to neutral expectations. Alternatively, balancing selection at the geographic scale can lead to a weaker genetic structure than compared to the neutral population structure, if for instance prevailing pathogens are the same over the whole study area. To distinguish between these two scenarios, we sequenced MHCII β and MHCI α loci with high-throughput sequencing technology in a large number of barn owls (*Tyto alba*) sampled throughout Europe (N=400). All samples were also genotyped with 22 neutral microsatellites markers used as a baseline to contrast with MHC diversity and genetic structure. Preliminary results suggest that MHC variation in Europe is a complex process, involving neutral and probably selective forces. Therefore, this study provides interesting perspectives for the understanding of MHC evolutionary ecology.

Assessing local adaptation in Aleppo pine by comparing molecular and phenotypic variation (52739)

Ruth Martín-Sanz, Stephen Cavers, Luis Santos-del-Blanco, Delphine Grivet, José Climent.

Forest Research Centre-INIA; Sustainable Forest Management Research Institute (UVA-INIA); Centre for Ecology and Hydrology-Edinburgh; Department of Ecology and Evolution, University of Lausanne.

The study of the existence of adaptive genetic variation has received substantial attention in short-lived species, but the knowledge in forest trees is still scarce. Mediterranean pines in particular show high adaptive variation demonstrated in different common garden experiments. The fact that some species have a strong geographic structure, deriving from different evolutionary processes makes these species a good model to compare selective and non-selective effects shaping the extant phenotypic variation in key life history traits like threshold size for reproduction, reproductive allocation and fire resilience traits. Our objective was to confirm that the clinal patterns found in such traits are due to selection in Aleppo pine (*Pinus halepensis*). We measured all traits in a common garden comprising 17 populations covering the species range. Patterns of genetic variation, assessed through quantitative traits and molecular markers (cSSRs and SNPs), were compared by two ways. Firstly by comparing QST and FST estimations and, secondly by extracting molecular variation from the ecotypic variation. Our analyses confirmed that selection has played a significant role in the current population differentiation in key fitness traits as female reproductive intensity and precocity in this species. These findings are relevant for the sustainable management and conservation of the genetic resources of Aleppo pine.

Dynamics of copy number variation in eight host races of the pea aphid species complex (52694)

Ludovic Duvaux, Quentin Geissmann, Karim Gharbi, Jing-Jiang Zhou, Julia Ferrari, Carole M. Smadja, Roger K. Butlin.

University of Sheffield; Imperial College, London; Edinburgh Genomics, University of Edinburgh; Rothamsted Research; University of York; ISEM, Université de Montpellier 2; University of Gothenburg.

Thanks to multiple divergent host races and a genome made of 35,000 genes, the pea aphid *Acyrtosiphon pisum* is a powerful system for studying the genome dynamics of copy number variation (CNV) and its role in host plant adaptation. Chemosensory multigene families, like gustatory and olfactory receptors (Grs and Ors, respectively), are well known to display large variation in gene content between species and recent studies have highlighted their importance in host race formation and speciation. Here, using targeted re-sequencing allowing a very high depth of sequencing, we contrasted the CNV dynamics of three multigene families with genes randomly sampled from the genome of the pea aphid (for a

total of 381 genes investigated in 104 individuals distributed across eight host races). We found that CNV was widespread, with higher occurrence in multigene families, especially in Ors. The probability of complete gene duplication or deletion (CDD) was shown to decrease with increasing coding sequence length. Genes with CDD variants were more polymorphic for copy number, especially in the P450 gene family where toxin resistance may be related to gene dosage. Finally, we found that Grs were over-represented among genes discriminating host races, as were CDD genes and pseudogenes.

Poster session A - POL 300

In search for selection signatures and footprints of local adaption in a rock ptarmigan population in Iceland (52691)

Kristinn P Magnusson, Máney Sveinsdóttir, Kristen Marie Westfall, Zophonías O Jónsson, Páll Melsted, Ólafur K Nielsen.

Icelandic Institute of Natural History, Akureyri, Iceland; Faculty of Natural Resource Sciences, University of Akureyri, Iceland; Life and Environmental Sciences, University of Iceland; Department of Computer Sciences, University of Iceland ; Icelandic Institute of Natural History, Garðabær, Iceland.

The latest NGS technology and efficient bioinformatics has enabled scientists to characterize genomes of non-model organisms. We have subjected two ptarmigan species, rock ptarmigan (*Lagopus muta*) and willow ptarmigan (*Lagopus lagopus*) to whole genome sequencing (WGS).

The study material was obtained from an ongoing longitudinal rock ptarmigan monitoring project in North-east Iceland. The Icelandic rock ptarmigan population cycles multi-annually, with peak numbers approximately 10 years apart where the difference in abundance between low and high numbers is 3–10 fold. The relationships among health, body condition and related parameters with respect to population cycling of the rock ptarmigan has been studied in detail.

Understanding the functional role of genetic variation in natural populations is crucial for applying genomic tools to investigate evolutionary processes and conservation issues, which are valuable for curbing the accelerating worldwide loss of biodiversity. Here we investigate the relationships among functional genomic variation, ecological, and physiological parameters associated with population cycling as part of this long-term study. We will present reduced genomic representation data generated with the ddRAD method, that has been shown to be capable of detecting selection signatures and footprints of local adaption.

Poster session A - POL 300

The evolution of untranslated regions of mRNAs in primates (52680)

Iris Finci, Anamaria Necsulea, Henrik Kaesmann.

University of Lausanne; École Polytechnique Fédérale de Lausanne (EPFL); Swiss Institute of Bioinformatics.

Untranslated regions (UTRs) of protein-coding mRNAs are important in many aspects of post-transcriptional regulation, such as translational control, mRNAs stability and mRNA subcellular localisation. However, functional roles and evolutionary dynamics of UTRs remain poorly understood, mainly due to incomplete UTR annotations in non-model organisms.

We use extensive RNA-sequencing (RNA-seq) data from 8 tissues across 6 primates (human, chimpanzee/bonobo, gorilla, orangutan, macaque and marmoset) to annotate UTRs and assess their functional evolution. We generated refined annotations for each species using RNA-seq data, adding thousands of new exons and extending known exon boundaries. We then classified exonic sequences as UTR or coding based on their evolutionary signatures, open reading frames and similarity to known proteins.

Using this comprehensive UTR dataset, we screened for differential UTR usage across tissues. Interestingly, we observed higher differential exon usage in UTRs compared to internal (coding) exons in primates, identifying many cases of tissue-specific and lineage-specific UTRs. Currently, we are trying to understand the functional relevance of these lineage-specific UTRs by analysing changes in miRNA binding potential and their nonsense-mediated decay susceptibility.

Besides providing novel insights into the functional evolution of UTRs, we believe our annotations and results will create a unique resource for future studies.

Poster session A - POL 300

Genome evolution during the radiation of *Timema* stick insects (52674)

Victor Soria-Carrasco, Moritz Muschick, Stuart R Dennis, Zachariah Gompert, Jeffrey L Feder, Aaron Comeault, Patrik Nosil.

University of Sheffield; Utah State University; University of Notre Dame.

Comparative genomics has grown to become a well-established and active field of research. Fueled by the continuous reduction in the cost of sequencing, the comparison of genomics features of a wide range of diverse organisms has greatly contributed to understand the mechanisms of evolution at the molecular level. However, the genomic changes taking place during the adaptive radiation of a group of closely related organisms from beginning to end are poorly understood. In this study, we have sequenced hundreds of genomes of individuals from multiple populations of several species of *Timema*, a 30-million-year-old genus of stick insects endemic to California adapted to a range of host plants. This data has allowed us to identify genomic regions of divergence across populations and species and to quantify the degree of genomic parallel evolution at different phylogenetic depths. In addition, using the annotations of the genome of one of the species, *T. cristinae*, we have tested whether such regions of divergence are preferentially located in coding regions and enriched in certain

functions. Our results contribute to the understanding of the evolution of genomes during adaptive radiations.

Poster session A - POL 300

Exploring the genome of Sparidae: linkage mapping in common pandora, *Pagellus erythrinus* (52667)

Tereza Manousaki, Alexandros Tsakogiannis, John B. Taggart, Christos Palaiokostas, Dimitris Tsaparis, Dimitris Chatziplis, Nikos Papandroulakis, Constantinos C. Mylonas, Costas S. Tsigenopoulos.

Institute of Marine Biology, Biotechnology and Aquaculture, Hellenic Centre for Marine Research; Department of Biology, University of Crete; Institute of Aquaculture, School of Natural Sciences, University of Stirling; Department of Agricultural Technology, Alexander Technological Educational Institute of Thessaloniki.

The teleost fishes of the family Sparidae are rising model species in the field of reproductive biology, mainly due to their diverse patterns of sex modes, ranging from hermaphroditism to gonochorism. Their economical importance for the aquaculture industry urges even more to explore the genome evolution of the group, as genomic information (e.g. genetic markers, linkage maps and QTL analyses) is increasingly being used to select for desirable production traits. Common pandora is a recently introduced species in Mediterranean aquaculture. We applied the ddRAD methodology on a full-sib family to identify polymorphic markers widely distributed in the unexplored genome of common pandora. Employing the Illumina technology, we sequenced a large genomic fraction in 99 individuals, which resulted in the discovery of nearly 1000 polymorphic loci. Downstream linkage mapping analysis led to the construction of 24 linkage groups representing the 24 chromosomes of the species. Common pandora linkage map showed a high degree of conserved synteny compared to other teleost genomes, suggesting a rather conserved genome structure. In conclusion, our work exploits the possibilities of RAD sequencing to gain insights regarding genome structure and evolution of the valuable but unexplored Sparidae species.

Poster session A - POL 300

Temporal and spatial variation in assortative mating: an example in Blue Tit Mediterranean populations (52661)

Amélie Fargevieille, Arnaud Grégoire, Anne Charmantier, Claire Doutrelant.

Centre d'Ecologie Evolutive et Fonctionnelle, CNRS UMR 5175 Montpellier; Université de Montpellier.

Assortative mating is a consequence of mate choice, particularly mutual mate choice, in which partners choose each other over the same criteria. Several studies in Blue Tits (*Cyanistes caeruleus*) suggest the importance of two color patches in female and male

preferences, the blue crown and the yellow breast, but a recent meta-analysis challenges these results. The aim of our study is to test the existence of a pattern of assortative mating for those patches. We also cross variables of the color patches to see if preference is based on different criteria in males and females. The strength of our study lies in our database; which includes information on feather colorations for these patches and individual life-history traits for more than 1500 pairs over three populations and ten years. Therefore, additionally to testing for a potential pattern of assortative mating or mutual mate choice, we test the variation in space and time for this pattern. Our results confirm that the patterns of color assortative mating in the blue tit can vary substantially, over years and through populations, shedding a new light on the processes of sexual selection and evolution of ornaments in a metapopulation context.

Poster session A - POL 300

GENOME EVOLUTION OF BURKHOLDERIA LEAF NODULE SYMBIONTS (52659)

Marta Pinto-Carbó, Leo Eberl, Aurélien Carlier.

Department of Microbiology, Institute of Plant Biology, University of Zurich.

Bacteria of the genus *Burkholderia* establish an intimate association with plant species of the Rubiaceae family. This symbiosis is unique among other plant-microbe interactions. The bacteria are housed within the leaves, and the symbiosis is obligate for both partners. Little is known about the molecular nature and genome evolution of the leaf nodule symbionts. We sequenced the genomes of eight leaf nodule symbionts and found that they exhibit features consistent with recently evolved symbionts. They also shared some commonalities with more ancient symbionts such as a reduction in their genome. However the decay in the genome size is heterogeneous among the different leaf nodule symbionts and is not as dramatic as in long-term symbiosis. Strict phylogenetic congruence between partners was not observed, indicating possible events of host switching. We also identified genes possibly acquired through horizontal gene transfer events that could potentially play a role in the establishment of the symbiosis. These genes, conserved only in leaf nodule symbionts, may be involved in the biosynthesis of secondary metabolites. The genomic analysis of leaf nodule symbionts gives, for the first time, new insights in the genome evolution of obligate symbionts in their early stages of the association with plants.

Poster session A - POL 300

Convergent evolution story of β -lactamase enzyme (52657)

VIVEK KESHRI, Pierre Pontarotti, Jean-Marc Rolain, Didier Raoult.

Aix-Marseille Université, I2M UMR-CNRS 7373, Evolution Biologique et Modélisation; Unité de Recherche sur les Maladies Infectieuses et Tropicales Emergentes (URMITE) UM63 CNRS 7278; URMITE CNRS IRD UMR 6236, IHU Méditerranée Infection, Faculté de Médecine et de Pharmacie.

Extensive and irresponsible use of β -lactam antibiotics has contributed to the widespread dissemination of antibiotic-resistance bacteria. These bacteria have evolved three strategies (alteration of target, reduction of drug permeation in membrane and production of β -lactamase enzyme) to escape the activity of β -lactam antibiotics. The β -lactamase enzymes inactivate β -lactam antibiotics by hydrolyzing the four-membered β -lactam ring. Currently, more than 1300 naturally β -lactamase enzyme have been reported which have classified into four different molecular classes (Class A, B, C and D) and functional group. The aim of this study is to explore the evolutionary history of β -lactamase enzyme followed by investigate the correlation with hydrolyzing properties (function).

MIC is generally regarded as the most basic laboratory measurement of the activity of an antimicrobial agent. Therefore, we have started this study with extraction of MIC value of 1161 β -lactamase enzyme. After collection of MIC's, followed by filtration of unwanted data only 220 enzymes were shortlisted for evolutionary analysis. The phylogenetic analysis were carried out followed by tree were annotated based on hydrolytic properties (MIC) with respect to different β -lactam antibiotic. The detailed phylogenetic analysis of this study reveals the story of functional convergent evolution of β -lactamase enzymes.

Poster session A - POL 300

Linkage disequilibrium network analysis (LDna) – an unsupervised approach to study genomic signatures of local adaptation (52655)

Petri Kemppainen, Catherine Walton, Christopher Knight.

Centre for Biodiversity Dynamics, Department of Biology; Computational and Evolutionary Biology, University of Manchester.

Loci similarly affected by selection are expected to be non-randomly associated with each other i.e. in linkage disequilibrium (LD). LD can therefore be highly informative about processes involved in local adaptation. To access such information, we developed LD network analysis (LDna), an unsupervised approach to detect clusters of loci connected by high LD. Each cluster represents a sub-set of loci that bear a distinct evolutionary genetic signal. In data from three-spined sticklebacks we successfully identified LD clusters associated with local adaptation, inversions and geographic structure. Downstream analysis of these loci identified that most differentiation between freshwater and marine ecotypes was found within the Pacific Ocean rather than between the ecotypes from the Pacific and Atlantic Oceans pooled. This represents a more nuanced view of local adaptation in this species compared to previous supervised approaches (where groups between which differences are sought need to be defined a priori).

Our network analytical approach to studying LD enables a novel global view of all evolutionary processes that result in high LD among multiple loci in a data set. It does not require a linkage map or reference genome, so is applicable to any population-genomic dataset, making it especially valuable for non-model species.

Poster session A - POL 300

Genome-wide patterns of selection in the nematode *Pristionchus pacificus* (52647)

Christian Rödelisperger, Angela McGaughran, Eduardo Moreno, Katy Morgan, Jan Meyer, Dominik Grimm, Karsten Borgwardt, Mark Leaver, Ralf Sommer.

Max Planck Institute for Developmental Biology, Dept. for Evolutionary Biology; Max Planck Institute for Intelligent Systems; Max Planck Institute of Molecular Cell Biology and Genetics.

The nematode *Pristionchus pacificus* has been established as a satellite model to *Caenorhabditis elegans* for comparative studies in developmental biology, ecology, and population genetics. Based on whole-genome sequencing of hundred globally sampled isolates, we have previously identified background selection as a major factor shaping genetic diversity.

In this study, we investigate selective processes that act on top of background selection. To this end, we sequenced genomes of 218 isolates from the island la Reunion, which was previously identified as a hotspot of *P. pacificus* diversity. On this geographically diverse island, we identified several distinct *P. pacificus* populations (defined by location) that group into four evolutionary lineages. Despite the fact, that strains of distinct evolutionary lineages can be successfully crossed in the lab, there is almost no evidence for outcrossing across lineage borders in the wild. Focusing on population comparisons within lineages, we identified numerous genomic loci with almost complete differentiation between populations. These candidate loci for adaptation harbor several genes that were previously described as playing a role in chemosensation and pathogen resistance. In addition, we identified highly polymorphic variants near immune response related genes, that suggest the action of frequency dependent selection.

Poster session A - POL 300

Exchange of Genetic Material between Non-Recombining Sequences on a Genomic Scale (52644)

Claus Vogl.

Inst Animal Breeding and Genetics.

Only the pseudo-autosomal regions of the mammalian sex-chromosomes recombine. But obviously Y-chromosomal genes outside this region also exchange genetic information with the homologous X-chromosomal genes. Similarly, in many allopolyploid species inheritance is disomic, i.e., the homoiologous chromosomes do not recombine. Nevertheless, genetic exchange among homoiologous genes has been observed. Technically, it is difficult to discover such, especially on the genomic scale. The specific molecular and computational methods are presented and discussed. Exchange of genetic materials between non-

recombining regions may thus go undetected and may have a much higher impact on genome evolution than generally believed, which will also be discussed.

Poster session A - POL 300

Selectome, a database of positive selection (52640)

Sébastien Moretti, Marc Robinson-Rechavi.

UNIL DEE / SIB Swiss Institute of bioinformatics.

Selectome (<http://selectome.unil.ch/>) is a database of positive selection, based on a branch-site likelihood test. This model estimates the number of non-synonymous substitutions (dN) and synonymous substitutions (dS) to evaluate the variation in selective pressure (dN/dS ratio) over branches and over sites. Special care is taken to minimize false positives, with a thorough quality control procedure on multiple sequence alignments. The Web interface presents results mapped both onto phylogenetic trees and onto protein alignments. It allows rapid access to results by keyword, gene name, gene ontology term, or taxonomy based queries. Selectome covers most gene trees from vertebrates and *Drosophila*.

Proux et al 2009 Nucl. Acids Res. 37: D404-D407

Moretti et al 2014 Nucl. Acids Res. 42: D917-D921

Poster session A - POL 300

Bgee, a database for the study of gene expression evolution (52639)

Frederic B Bastian, Anne Niknejad, Julien Roux, Marta Rosikiewicz, Sebastien Moretti,
Marc Robinson-Rechavi.

University of Lausanne; Swiss Institute of Bioinformatics.

Gene expression patterns (where and when genes are expressed) are a key feature in understanding gene function and evolution. To apply compare results between different model organisms and human, or to study gene expression evolution, a comparative approach must be used, but no tools allow to easily compare gene expression across species.

We have thus developed Bgee (Base for Gene Expression Evolution), a database designed to automatically compare expression patterns between animals. This is achieved by i) the aggregation and curation of expression data from different types and sources, to map them to formal representations of anatomies and developments of different species; Bgee release 13 contains curated and quality controlled data for RNA-seq libraries, Affymetrix chips, EST libraries and in situ hybridizations. ii) The analysis of these data by dedicated statistical tests to define high confidence gene expression patterns. iii) The definition of comparison criteria between anatomies of different species; Bgee curators have designed homology relationships between across all Bilateria, which are integrated into the multi-species anatomical ontology Uberon. Bgee 13 includes 17 species, with a focus on vertebrates, but also *D. melanogaster*

and *C. elegans*.
Bgee is available at: <http://bgee.org/>

Poster session A - POL 300

An experiment in the wild to test if stickleback males adapt their colour to the ambient light environment (52624)

Thor Veen, Chad Brock, Diana Rennison, Dan Bolnick.

University of Texas at Austin; University of British Columbia.

Many organism show spatial variation in phenotypic traits correlated with environmental characteristics, some on very small scales. For example colouration of nesting male three-spined stickleback consistently varies with the ambient light along a two-meter depth gradient in multiple populations. An earlier experiment showed that male colour changed predictably after nesting males were transplanted to either deep or shallow enclosures. We set out to test the hypothesis that change in male colour is driven by changes in the ambient light environment. This change is predicted because different colours are required at different depths to maximize contrast (and hence visibility to females). 40 cages were constructed in shallow parts of a freshwater lake in British Columbia and divided into light treatment pairs. Two natural light environments were mimicked by wrapping sheets of light filter around and over each cage, this changed the sunlight to represent the sidewelling irradiance at a depth of 0.5 m and 1.8 m, respectively. To assess the magnitude of the colour adaptation we measured the change of male colouration between the start of the experiment (which depends on natural nesting depth) and the end, and the colour differences between males of the two treatment groups.

Poster session A - POL 300

THREE-DIMENSIONAL POST-GLACIAL EXPANSION AND DIVERSIFICATION OF AN EXPLOITED OCEANIC FISH (52603)

Peter Shum, Christophe Pampoulie, Ronald Douglas, Rachel Brenchley, Kristján Kristinsson, Stefano Mariani.

School of Environment & Life Sciences, University of Salford, Salford M5 4WT, UK; Marine Research Institute, Skúlagata 4, 101 Reykjavík, Iceland; Department of Optometry and Visual Science, The City University, London EC1V 7DD, U.K..

Despite the striking physical and environmental gradients associated with depth variation in the oceans, relatively little is known about their impact on population diversification, adaptation and speciation. The pelagic redfish, *Sebastes mentella*, exhibits depth-associated patterns of substructure in the central North Atlantic, with a widely distributed shallow-pelagic population inhabiting waters between 250 and 550m depth and a deep-pelagic population dwelling between 550 and 800m.

By sequencing and genotyping *S. mentella* samples caught between 2006 and 2013, at different depths, across the North Atlantic, we show the existence of two strongly divergent evolutionary lineages, with significantly different distribution patterns and dwelling at different depth layers. We then carried out de novo RNA-seq of retina transcriptome from a subset of “shallow” and “deep” individuals, in order to characterise differential expression and polymorphisms of candidate genes involved in sensory reception in organisms adapted to different depths. Overall, we cast new light on the role of depth in generating biodiversity in the oceans, and consider the practical implications of such findings.

Poster session A - POL 300

From positive selection in songbird MHC genes to binding properties of songbird MHC proteins. (52591)

Helena Westerdahl, Elna Follin, Michael Rasmusson, Soren Buus, Maria Strandh, Morten Nielsen, Kajsa Paulsson.

Biology, Lund; Experimental Medical Science, Lund; Experimental Immunology, Denmark; Center for Biological Sequence Analysis, Denmark.

Hosts cannot predict which pathogens they may encounter in the future but vertebrates have evolved an adaptive immune system that can handle an enormous variety of pathogens. This pathogen recognition is created by random by somatic recombination in B- and T-cell receptors, uniquely so in every individual. Major Histocompatibility Complex (MHC) molecules then enable immunological tolerance so that only ‘non-self’ cells are attacked. MHC genes are highly polymorphic and a classical example of genes subjected to balancing selection. However, to understand the standing genetic variation in host MHC genes the functional aspect, binding properties of MHC molecules, must be considered. Most songbirds have a larger number of MHC genes than other animals: What is the functional relevance of all these gene copies? Does it give songbirds an advantage in handling pathogens? We have taken a functional approach to determine binding properties of songbird MHC molecules and compared them with human MHC molecules. Using two recombinant songbird MHC proteins we were able to generate unique peptide-binding motifs. The preferred peptide length was similar to human MHC molecules though the binding repertoires of songbird MHC molecules were quite different, suggesting that we cannot extrapolate binding repertoires across very distantly related species.

Poster session A - POL 300

Ecologically driven divergence between multiple populations of the marine snail *Littorina fabalis* (52583)

Rui Faria, João Carvalho, Juan Galindo, Graciela Sotelo, **Diana Costa**.

CIBIO/InBIO, Centro de Investigação em Biodiversidade e Recursos Genéticos, Univ. Porto, Portugal ; Depart. de Bioquímica, Xenética e Inmunoloxía, Facultade de Bioloxía,

Universidade de Vigo, Spain; IBE, Institute of Evolutionary Biology (UPF-CSIC), Universitat Pompeu Fabra, PRBB, Barcelona, Spain.

Speciation is often a continuous process, with different mechanisms interacting during the buildup of barriers to gene flow. It is well established that ecology can play a critical role in population divergence and ultimately in speciation. Nonetheless, our understanding of how it occurs is still scarce. Characterized by abrupt changes in the environmental conditions over a narrow spatial scale, the marine intertidal is an ideal system to provide valuable insights into ecological speciation. We focus on ecotypes of the flat periwinkle *Littorina fabalis* from the NE Atlantic to explore to what extent adaptation and genetic divergence are promoted by contrasting wave exposure intensities and other associated factors. We analysed phenotypic differentiation (shell morphology) using geometric-morphometrics, and performed a genomic scan based on AFLPs to estimate divergence between sheltered and exposed populations at different geographic scales (<100 Km and >1000 Km) and to identify putative loci under disruptive selection among ecotypes in a repetitive manner along the species range. Some overlap between outliers was observed at both scales, even among populations from the Iberian Peninsula and Scandinavia. Various hypotheses to explain this pattern will be discussed to shed light on how repeatable (parallel) is divergent evolution in *L. fabalis*.

Poster session A - POL 300

An unexpected oviposition preference of the common bush brown (*Bicyclus safitza*) may help to explain butterfly-host plant coevolution (52556)

Ossi Nokelainen, Brad Ripley, Colin Osborne, Erik van Bergen, Paul Brakefield.

University of Cambridge; Rhodes University; University of Sheffield.

Butterfly oviposition behaviour is a crucial determinant of offspring success. Thus, the decision about choice of substrate on which a female lays an egg will strongly determine the hatching larva's chance of establishment on a food plant. The oviposition decision often follows female scouting in suitable habitat and localisation of a host plant. Individual data on variation in female preference and its consequences for hatchlings, however, remain scarce. We examined oviposition behaviour of the common bush brown (*Bicyclus safitza*) on ecologically relevant host plants in South Africa. Specifically, we studied whether individual female butterflies preferred species of local grasses with C3 or C4 photosynthetic pathway and that grow in open or shaded habitats. We predicted that C3 grasses would be preferred over C4 grasses due to a generally higher palatability, and shade grasses over open grasses, as the butterfly is typically associated with shaded-habitats. We found a strong interaction between habitat and photosynthetic pathway of the plants. Unexpectedly, females preferred C4 shade grasses, followed by C3 shade over C3 open grasses; they particularly tended to avoid C4 grasses from open habitats. We discuss this pattern of oviposition behaviour in relation to how it relates to co-evolutionary relationships in plant-herbivore interactions.

Poster session A - POL 300

Reconstructing metal specificity-evolution in ribonucleotide reductases (52526)

Daniel Lundin, Gustav Berggren, Britt-Marie Sjöberg.

Stockholm University.

The radical generating subunit (NrdB) of class I ribonucleotide reductases typically harbours a diiron site that is able to initiate a radical on a neighbouring tyrosine residue. In the subclass Ic, the tyrosine is replaced by a phenylalanine and the relevant metal centre is a heterodinuclear iron/manganese centre. Metal specificity in subclass Ic is high, with manganese occupying site 1 and iron occupying site 2 almost exclusively. How the specificity is achieved remains an enigma since the metal-binding site is very similar between diiron and iron/manganese enzymes. Mutagenesis of metal ligands and residues in their vicinity aiming to turn an iron/manganese enzyme to a diiron has not been able to resurrect diiron specificity, suggesting that substitutions in other parts of the protein play a role in selectivity. We have phylogenetically identified a group of diiron NrdBs closely related to the iron/manganese enzymes. This provides us with the opportunity to complement earlier mutagenesis experiments with experiments going in the other direction, trying to convert a diiron enzyme to an iron/manganese one, and to reconstruct ancestral enzymes. Here, we report preliminary data on resurrected proteins as well as a structural analysis of important substitutions.

Poster session A - POL 300

Carry-over effects of the social environment on future divorce probability in great tits (52520)

Antica Culina, Ben Sheldon, Camilla Hinde, **Reinder Radersma**.

Oxford University; Wageningen University; Edward Grey Institute of Field Ornithology, Department of Zoology, University of Oxford, UK.

Suboptimal partnerships can appear when the initial mate choice was constrained by the social environment. To correct for such suboptimal partnerships, individuals of socially monogamous species may adopt secondary mating strategies (infidelity and divorce). In this study we aim to better understand the influence of the social environment in which a pair has formed on later divorce. Using detailed data on social networks of tagged Great tits over four winters we found that males with a higher proportion of female associates, and males whose partner ranked lower amongst these, were more likely to divorce after breeding. We found no evidence that a female's social environment influenced divorce probability. Our study demonstrates that divorce in monogamous species might not only be affected by the social environment to which existing pairs are exposed, but also by the social environment in which pairs have formed (and which is likely to constrain the initial choice). Second, our results indicate that this might be more driven by the male's social environment and preference for a partner. Further exploration of these carry-over effects of the social environment, and how they differ between sexes, may give new valuable insights into processes of mate choice, population dynamics, and sexual selection.

The consequences of mating system and population dynamics on genome evolution: a comparative study of inbreeding and outcrossing sister species of the spider genus *Stegodyphus* (52483)

Virginia Settepani, Jesper Bechsgaard, Mads F. Schou, Michelle Greve, Lena Grinsted, Trine Bilde.

Department of Bioscience, Aarhus University; Department of Plant Science, University of Pretoria; School of Life Sciences, University of Sussex.

Regular inbreeding results in reduced effective population size, which reinforces genetic drift and accelerates loss of genetic diversity. These processes act to decrease the efficacy of selection causing a build-up of the genetic load, ultimately impairing the potential of populations to respond to environmental change. Social spiders live in communal nests where they cooperate in prey capture and brood care. Phylogenetic analyses show multiple independent origins of sociality from solitary ancestors, and the transition to permanent group living is associated with a strictly inbreeding mating system. Furthermore, strong metapopulation dynamics of social spiders and frequent extinction events acts to homogenise genetic structure. We performed RAD-sequencing in a comparative population genomic approach to examine the effects of inbreeding and outcrossing mating systems on genetic diversity, population structure, and genome evolution. We included independent sister species pairs of social inbreeding and solitary outcrossing spiders of the genus *Stegodyphus* that were extensively sampled over a large geographical range. This approach provides extraordinary high power to gain insights into the consequences of mating system and population dynamics on genome evolution in non-model wild species.

Can fluctuating selection explain levels of variation in natural populations? (52478)

Sebastian Novak, Srdjan Sarikas, Nick Barton.

IST Austria.

Natural environments are never constant but vary in time and space. Furthermore, from the point of view of a single locus, there is background selection on multiple other loci, possibly for a plethora of traits that are influenced pleiotropically. To what extent can this combination of external and internal factors be described by a scheme of randomly fluctuating selection? What pattern of fluctuations can we expect to be experienced by a single locus? Continuing from there, we can venture forth trying to explain the observed levels of variation in natural populations that could so far not be reproduced convincingly by quantitative trait models of constant selection. Can fluctuating selection models unveil the missing variability?

Speciation history of Atlantic eels and its genomic footprints (52477)

Magnus W. Jacobsen, José Martin Pujolar, Shenglin Liu, Kasper Munch, Louis Bernatchez, M. Thomas P. Gilbert, José Victor Moreno-Mayar, Thomas D. Als, Michael M. Hansen.

Department of Bioscience, Aarhus University ; Bioinformatics Research Centre (BiRC), Aarhus University; Département de Biologie, Institut de Biologie Intégrative et des Systèmes (IBIS), Laval University ; Centre of Geogenetics, Natural History Museum of Denmark, University of Copenhagen; Department of Biomedicine - Human Genetics, Aarhus University.

Speciation-with-gene flow scenarios are increasingly appreciated. Yet, the specific processes and the resulting genomic footprints of selection are subject to much discussion. To elucidate the genomic mechanisms underlying speciation-with-gene flow, accurate knowledge is needed, not only of the genomic patterns of selection but also the demographic history of the species. Here we present the results of several studies on the European and American eel (*Anguilla anguilla* and *A. rostrata*), two panmictic and sympatrically spawning sister-species. Hybrids are known to occur and low but biologically significant gene flow takes place. We employed mitogenome sequencing of 106 individuals in order to test hypotheses about the demographic processes linked to their speciation, including divergence time and the possibility of allopatric periods during the speciation process. Furthermore, RAD sequencing of 60 individuals and alignment of reads to the European eel draft genome was used for analyzing genome-wide linkage disequilibrium, genomic footprints of diversifying selection, divergence time and demographic history. Our results demonstrate that demography has a major effect on genomic footprints. Very high effective population sizes of the two species lead to minimal background genetic differentiation, interrupted by numerous smaller regions of strong differentiation that mark interspecific diversifying selection.

Landscape genomics of oaks (*Quercus* spp.): Adaptive genetic variation in candidate genes in respect to present and future climatic conditions (52457)

Christian Rellstab, Lorenz Walthert, Christoph Sperisen, Catherine Bodénès, Isabelle Lésur, Andrea R. Pluess, Antoine Kremer, Felix Gugerli.

WSL Swiss Federal Research Institute, Birmensdorf, Switzerland; INRA Pierroton, Cestas, France; University of Bordeaux, Pessac, France; HelixVenture, Mérignac, France; ETH, Zürich, Switzerland.

Testing whether and how populations are adapted to their local environment, and predicting their response to future habitat alterations is of key importance in the face of climate change. A powerful approach to investigate such processes is landscape genomics, which identifies genes and environmental factors involved in local adaptation. We investigated whether the three common oak species in Switzerland (*Quercus petraea*, *Q. pubescens*, *Q. robur*) are

adapted to their present and future environmental conditions. In a pooled amplicon sequencing approach of 95 genes in 71 oak populations, we identified over 3'500 SNPs, many being private to populations and species. We tested if these SNPs show an association to abiotic factors related to local topography, climate and soil. We found genes that are putatively involved in adaptation to the present environment and tested whether these loci were congruent among all species and defined seed zones. We then used allele frequency distributions of candidate SNPs along environmental gradients to test the adaptedness of populations and species for simulated future climatic conditions. Our results help assessing the classification scheme of the seed zones in an evolutionary perspective, since afforestations that intend matching future environmental conditions are likely to increase in the future.

Poster session A - POL 300

Genomic response to rapid convergent evolution in wild crickets (52456)

Sonia Pascoal, Timothee Cezard, Xuan Liu, Karim Gharbi, Urmi Trivedi, Sam Haldenby, Marlene Zuk, Michael G. Ritchie, Nathan W. Bailey.

University of St Andrews; University of Edinburgh; University of Liverpool; University of Minnesota.

The initial stages of convergence provide insight into the genomic dynamics of adaptive evolution in the wild. A rapidly-evolving mutation, flatwing, silences male crickets in Hawaii by altering their wings, but it persists because of natural selection arising from an acoustically-orienting parasitoid fly. Despite appearing only a decade ago, silent males now occur on two islands and have distinct forms on each. Mutants on Kauai have wings that are almost completely feminized, whereas Oahu flatwings retain a larger portion of the secondary wing venation typical of normal males. Nevertheless, both are silent and share the same mode of inheritance, i.e. the phenotype segregates as a sex-linked, sex-limited Mendelian trait in both populations. I will present results from a combination of complementation crosses and Bulk Segregant Analysis using RAD-markers to provide evidence that the male-silencing wing morph has arisen twice, independently, on different islands, but spread under similar selection. Furthermore, I will illustrate how gene expression profiling using RNA-seq along with RAD-mapping and QTL analysis elucidates the early genome response to this dramatic recent wing adaptation and associated effects of its spread. The results provide unprecedented insights into the adaptive evolution of convergent phenotypes, in real time, in the wild.

Poster session A - POL 300

The Evolution and Divergence of the Special Homeobox Genes in *Pararge aegeria* (52454)

Luca Livraghi, Peter W. Holland, Leonardo Dapporto, Roger Vila, Melanie Gibbs, Casper J. Breuker.

Oxford Brookes University; Zoology Department, Oxford University, South Parks Road, Oxford UK; Institut de Biologia Evolutiva, Pg. Marítim de la Barceloneta 37, Barcelona Spain; Centre for Ecology and Hydrology, Benson Ln, Wallingford UK.

Paralogs arise through gene duplications and their subsequent divergence provides the raw material for functional innovation. Although this has been inferred from studies on interspecific sequence variation in paralogs, not much is known about standing intraspecific paralog variation and associated phenotypic variability. Paralogs in the Hox cluster are rare, but the so called paralogy group 3 (PG3) has undergone independent tandem duplications in several insect clades. Within the ditrysia, a derived clade of the Lepidoptera, duplications in the ancestral PG3 gene *zerknüllt* (*zen*) resulted in 4 so-called special homeobox genes (*Shx*). It has recently been shown that there is significant interspecific variation in these *Shx* paralogous genes. Sequencing of the *Shx* genes within my model species, the Speckled Wood butterfly *Pararge aegeria*, has revealed that although intraspecific variation is lower than interspecific variation, it is very high for a Hox (-derived) gene. To investigate this in more depth, I sequenced the four *Shx* genes, *zen*, *wingless* and the cytochrome oxidase I subunit in 25 populations of *P. aegeria* spanning from N. Africa to Scandinavia. Preliminary results show the presence of population specific variants, even within the highly conserved homeobox region of one of the *Shx* paralogs. This suggests possible local adaptation events in response to different selection pressures.

Poster session A - POL 300

Local adaptation of reproductive traits (52433)

Charlotta Kvarnemo, Erica Leder, Jonathan Havenhand, Kai Lindström, Topi Lehtonen, Ola Svensson.

University of Gothenburg, Sweden; University of Turku, Finland; Åbo Akademi University, Finland.

The distribution of animals is not only determined by which environment adults can tolerate, but in which environment they can reproduce. Based on experiments on the sand goby, *Pomatoschistus minutus* aimed at understanding local adaptation of reproductive traits, we found that males have difficulties to reproduce outside their native salinity. This is likely to be caused by local adaptation of their gametes, as our study using sperm from males that originate from high vs. low salinity areas, shows that sperm perform poorly in non-native salinity. The two salinities also differ regarding risk of fungus infection of eggs, affecting both paternal care and mate choice behaviours. We also investigated protein and mRNA expression in testes, and found differences in both, when comparing pairs of males of high and low salinity origin. We argue that reproductive traits per se are under divergent selection and that non-random mating and reduced gene flow arise as a bi-product. This is important because local adaptation – and in its extension speciation – can only evolve if the strength of selection overrides the effect of gene flow. Our studies provide new insights into the evolutionary processes and the mechanisms behind geographic distributions of species.

Adaptive genetic diversity of *Apis mellifera* populations using whole-genome sequence data (52425)

Melanie Parejo, Peter Neumann, Laurent Gauthier, Markus Neuditschko.

Institute of Bee Health, Vetsuisse Faculty, University of Bern; Swiss Bee Research Center, Agroscope.

The original distribution of the honey bee *Apis mellifera* ranges from Europe, Africa and the Middle East, encompassing a large native range with diverse environmental conditions. There are >29 *Apis mellifera* subspecies differing in phenotypic traits such as morphology, behavior and resistance to disease and which cluster into four major geographically and genetically different lineages. This evolutionary history offers a great model system to study molecular diversity of local adaptations in geographic range expansions.

The native honey bee of Northern Europe *A. m. mellifera* is adapted to short foraging seasons and comparatively long winters through, for instance, the ability to form winter clusters. Global trade of this important pollinator for commercial operations in combination with the particular polyandrous mating system pose a risk on the genetic integrity of locally adapted ecotypes through introgression, potentially resulting in the loss of valuable local adaptations shaped by natural selection.

We will present insights into the adaptive genetic diversity of Swiss *A. mellifera* populations from different lineages by comparing neutral vs. adaptive molecular markers inferred from whole-genome next-generation sequencing data. A special focus will be given on the diversity and conservation of the native European subspecies *A. m. mellifera*.

How to estimate selection from evolve and resequence experiments (52418)

Katarina Bodova, Srdjan Sarikas, Nick Barton.

IST Austria.

With more data available from evolution experiments on sexual populations in the laboratory, it is now plausible to detect candidates for selected regions in the genome. This, however, brings several challenges. First, it is difficult to distinguish effects of random drift from selection: many candidates may be false positives. Second, various patterns of selection may act, and it is useful to know which properties of selection can be inferred in general. Third, recombination and epistasis influence evolution, and further distort effects of selection. We address the above challenges and provide insight into how to efficiently design an evolutionary experiment.

Genetic basis of eye and face shape differences in *Drosophila mauritiana* and *Drosophila simulans* (52353)

Michaela Holzem, Kentaro M. Tanaka, David L. Stern, Maria D. S. Nunes, Alistair P. McGregor.

University of Konstanz; Oxford Brookes University; Princeton University.

Differences in head shape between closely related *Drosophila* subgroups were often described. Still underlying genetic differences in evolution of organ size and shape involved in head development remain unclear. Head shape is mostly maintained by the negative correlated shape and size of compound eyes and face width. The occurrence of heritable variation suggests it might be possible to map underlying genes. We selected extreme backcross individuals of “eye-face trade-off” distribution and performed multiplexed shotgun genotyping. QTL analysis of this data suggested a QTL for shape difference between *D. simulans* and *D. mauritiana* at 11.5 Mb on chromosome 3L. To validate the QTL position and narrow down the mapped region we performed independent introgressions of this region from *D. mauritiana* into *D. simulans* and further analysed those using geometric morphometrics. We found two regions for face and one for eye shape, this one detected directly at 11.5 Mb. Thus, it was possible to narrow the QTL down and proof that the position at 11.5 Mb is responsible for shape differences between the strains. These regions will be analysed for interesting genes involved in development of eye and face. Overall, this will lead to better understanding of evolutionary and developmental differences in head shape formation.

Poster session A - POL 300

Genome-wide genetic variation in populations of *Calanus finmarchicus* and *C. glacialis* across their distributional ranges (52351)

Irina Smolina, Marvin Choquet, Martina Kopp, Ann Bucklin, Janne Søreide, **Galice Hoarau**.

University of Nordland; University of Connecticut; The University Centre in Svalbard.

Calanus finmarchicus and *C. glacialis* are the keystone zooplankton species in subarctic and arctic marine food webs respectively. However, as a response to ocean warming, *C. finmarchicus* is showing a consistent northward shift increasing the competition with *C. glacialis* that may influence the arctic ecosystems. To understand the ecological and evolutionary potential and functioning of the two species, an ocean-basin-scale analysis of *C. finmarchicus* and *C. glacialis* is required. Genome-wide genetic variation was accessed from 10 locations per species encompassing their whole distributional range. Forty females of genetically identified *C. finmarchicus* and *C. glacialis* per location were pooled equally and sequenced on Illumina MiSeq platform using restriction site-associated DNA (RAD)-sequencing. SNPs were used to assess genetic differentiation between species populations and possible adaptive polymorphisms across environmental conditions of species distribution. We compared both species in terms of population genetic structure and genetic diversity. The whole transcriptome profiling of both species under thermal stresses was also used to investigate their acclimatory potential to ocean warming.

Parallel or convergent evolution in human population genomic data revealed by genotype networks (52346)

Ali R. Vahdati, Andreas Wagner.

University of Zurich.

A genotype network is a graph whose nodes are genotypes (DNA sequences) with the same broadly defined phenotype. Two nodes are connected if they differ in some minimal way, e.g., in a single nucleotide. Here we analyze human genome variation data from the 1000 genomes project, and construct haploid genotype (haplotype) networks for 12235 protein coding genes. The structure of these networks varies widely among genes, indicating different patterns of variation despite their shared evolutionary history. We focus on those genes whose genotype networks show many cycles, which can indicate homoplasy, i.e., parallel or convergent evolution, on the sequence level. We show that in 47 genes the observed number of cycles is so large that it cannot be explained by either chance homoplasy or recombination. In some of these 47 genes, positive or balancing selection may be responsible for the great abundance of cycles. Genotype networks are representations of genetic variation data that facilitate analyzing unusual patterns of inheritance or variation not easily captured in phylogenetic trees.

Long-term fitness consequences of a prenatal maternal effect and their impacts on evolutionary dynamics (52328)

Joel Luke Pick, Barbara Tschirren.

Institute of Evolutionary Biology and Environmental Studies.

The prenatal environment can have important and long-lasting consequences on offspring morphology, physiology, behaviour, and ultimately fitness. Mothers are in a unique place to alter this environment and so the future phenotype of their offspring, through a process known as maternal effects. Although theoretical work has shown that maternal effects may play an important role in influencing evolutionary dynamics, by affecting how traits respond to selection, there is a lack of empirical work supporting these models. In birds, many of these prenatal maternal effects are mediated through differential allocation of resources into the egg. Despite a considerable amount of data showing investment into the egg has large consequences on early life traits, there is only equivocal evidence of long term effects, and in particular on reproductive performance. Through the use of repeated divergent selection lines for prenatal maternal investment, we investigate how egg size influences both body size and reproductive investment of the offspring. We show that egg size has pronounced effects on

offspring phenotype throughout its life, most notably on egg size itself. This has important consequences for the strength and predictability with which egg size can respond to selection.

Poster session A - POL 300

Evolution of dominance in trait under balancing selection: polymorphic mimicry as a case-study (52323)

Violaine Llaurens, Yann Le Poul, Monica Arias, Mathieu Chouteau, Sylvain Billiard, Mathieu Joron.

CNRS - National Museum of Natural History; University of Lille 1.

Spatial heterogeneity promotes fixation of locally adaptive alleles but can lead to the persistence of polymorphism within population depending on migration. Such balancing selection might shape the genetic architecture of adaptive trait. Since heterozygotes are frequent in such polymorphic loci, dominance among adaptive alleles can evolve in response to natural selection. Here we used the evolutionary convergence of warning signal in toxic species, i.e. Müllerian mimicry, as an example of local selection. Most species involved in Müllerian mimicry display a single warning signal within population because of selection exerted by predators, fixing the most common signal. However, in the toxic butterfly *Heliconius numata*, several warning patterns are maintained within localities, and each displays high resemblance with distasteful species from different communities. These variations in warning pattern are controlled by a supergene in which each allele encodes for a different mimetic pattern. Heterozygotes might display an intermediate, non-mimetic phenotype, depending on the dominance among alleles. Using experiment in natural populations, we showed a significant selection acting on dominance. We then performed theoretical simulations describing the condition of invasion of dominance modifiers. Finally, we investigated variations of dominance in natural populations to understand the molecular mechanisms shaping dominance in polymorphic adaptive loci.

Poster session A - POL 300

Heterozygote deficit through time in a gene (MC1R) encoding melanin-based color morphs involved in predator-prey relationships (52291)

Valérie Ducret, Jérôme Goudet, Alexandre Roulin.

Department of ecology and evolution, university of Lausanne, Lausanne, Switzerland.

Despite numerous theoretical and empirical studies on geographic phenotypic variation, the relative contribution of selection and gene flow in shaping clines remains largely unknown. In this context, the barn owl (*Tyto alba*) is a promising study system because its coloration varies clinally with owls being white in southern Europe and darker reddish towards north-eastern Europe, a cline maintained by natural selection. Pheomelanin-based reddish coloration is explained by a mutation of the MC1R gene and its frequency increases from 0.9% in southern

Europe to 60.3% in north-eastern Europe. We studied a Swiss population located in the centre of the pronounced color cline and hence should undergo gene flow from southern and northern owls. Using 10 microsatellite markers we tested for non-random departure from Hardy-Weinberg Equilibrium (HWE) of the MC1R gene during a period of 15 years. We found a deficit of MC1R heterozygotes through time for cohorts but no deviation in neutral genetic markers. In-depth analyses show that temporal variation in assortative mating and transmission ratio distortion are responsible for this deficit. This study highlights the importance of considering populations along phenotypic clines to understand the evolution of phenotypic diversity and its role in reproduction isolation.

Poster session A - POL 300

Environment-dependent patterns of phenotypic integration in Aleppo pine. (52267)

José Climent, Jordi Voltas, Rafael Zas, Ruth Martín-Sanz, Pitter Ferrio, Eduardo Notivol, Luis Sampedro.

Forest Research Centre-INIA; Univ. of Lleida; UMG-CSIC; CITA.

Global Change imposes new challenges to many ecosystems, and among these Mediterranean forests are particularly sensitive due to combined drought, wildfires and biotic stressors. Mediterranean forest populations are expected to harbour high adaptive genetic diversity, but we know too little on their ability to respond to multiple challenges. Precisely, life history theory postulates that adaptive evolution implies optimizing resource investment to growth and maintenance, reproduction and defence to maximize fitness under a given environment. Our objectives were first, to determine the genetic differentiation among populations in key adaptive traits considering their correlations and second, to confirm differences in key trade-offs among a high-stress and a low-stress environment. We measured a wide set of traits in a replicated common garden of *Pinus halepensis* at two sites. Traits related to growth and maintenance, reproduction, constitutive and induced defences and water and carbon acquisition and storage. While population differentiation was significant for most traits, differences were environment-specific. As expected, key trade-offs were neatly different among the two sites indicating differently plastic strategies of resource usage. These findings may improve our understanding of the real adaptive value of a single trait and how resource shortening can modify it in long-lived woody plants.

Poster session A - POL 300

Environment-dependent sexual selection: Bateman's parameters under varying levels of food availability (52265)

Elodie Chapuis, Patrice David, Tim Janicke.

IRD; CNRS.

Sexual selection is considered as a potent evolutionary force that has been shown to vary in strength and direction depending on demographic factors such as density and sex ratio. However, the effect of other environmental factors on the mode of sexual selection remains largely unexplored. Here we tested experimentally how food restriction affects the potential for sexual selection in the male and female sex function of the simultaneously hermaphroditic freshwater snail *Physa acuta*. We manipulated food availability and compared Bateman's metrics of sexual selection between groups of five well-fed and five food-restricted snails. Our results indicate that food-restricted snails had a reduced female reproductive output suggesting that we successfully manipulated the reproductive resources. Importantly, food restriction reduced the male opportunity for sexual selection (in terms of a lowered variance in male mating success) and lead to diminishing returns of mating in both sexes (in terms of non-significant Bateman gradients). Furthermore, we observed significant changes in the relative contribution of different fitness components suggesting stronger post-copulatory selection in the male and stronger fecundity selection in the female sex role under restricted food conditions. This study highlights the need to incorporate ecological factors to better understand how sexual selection operates in the wild.

Poster session A - POL 300

Searching for signatures of selection in Iberian honey bee (*Apis mellifera iberiensis*) using whole genome sequences (52236)

Dora Sofia Martins Henriques, Andreas Wallberg, Chavéz-Galarza Julio, Costa F., Rufino José, Webster Mathew, Pinto M.Alice.

Centro de Investigação de Montanha (CIMO), Instituto Politécnico de Bragança; Centro de Biologia Molecular e Ambiental (CBMA), Universidade do Minho; Department of Medical Biochemistry and Microbiology, Science for Life Laboratory, Uppsala University; Instituto Politécnico de Bragança; Laboratório de Instrumentação e Física Experimental de Partículas, Campus de Gualtar.

The Iberian Peninsula comprises a diverse set of habitats. It was an important glacial refugium during the Pleistocene and has served as a bridge for populations migrating between Africa and Europe, resulting in a complex mix of ancestry and diversity. The Iberian honey bee (*A. m. iberiensis*) is no exception and has been the subject of numerous incongruent population genetic surveys. Recent mtDNA and SNP analyses indicate a steep northeastern-southwestern cline of African ancestry along the peninsula, which has been explained by selection. Advances in DNA sequencing technology and computational tools provide unprecedented opportunities to study demography, search for signatures of selection across the genome and illuminate its role in shaping genomic diversity. We used Illumina technology to sequence the whole genomes of 86 Iberian honeybees, collected across three longitudinal transects in the Iberian Peninsula and spanning semi-arid climates in the southeastern peninsula to oceanic in the North-West. The dataset was first analyzed for FST-outliers, CLR (composite-likelihood ratio) and EHH (Extended Haplotype Homozygosity) methods were further deployed to evaluate polymorphisms implicated in local adaptation and possibly in the response to human-mediated environmental changes, including known and novel variants in genes related to behavior, vision, xenobiotic detoxification and immune response.

The evolutionary challenge of climate change : adaptive processes in the Mediterranean red coral (52229)

Marine Pratlong, Anne Haguénauer, Olivier Chabrol, Pierre Pontarotti, Didier Aurelle.

Aix Marseille Université, CNRS IMBE UMR 7263, IRD UMR 237 Station Marine d'Endoume; Aix Marseille Université, CNRS UMR 7373, I2M Équipe Evolution Biologique et Modélisation.

The on-going climate change should have major impacts on the different components of biodiversity, from genes to ecosystems. Mediterranean marine species are already suffering from climate change, as shown by mortality events linked with thermal anomalies. These events highlighted a diversity of thermotolerance levels in the temperate red coral (*Corallium rubrum*). The main objective of this work was to understand the origin of these differences and to search for local adaptation of the red coral to thermal conditions. This species is present in very contrasted ecological conditions which correspond to genetically differentiated populations. Moreover, colonies from different regions, depths but also from the same site present thermotolerance differences. These differences might be linked to the individual history through acclimatization or to population level through genetic adaptation. Two complementary approaches were developed to study these mechanisms: i. Transcriptomic (gene expression and polymorphism) basis of thermotolerance differences. ii. Genomic study of local adaptation. We looked for genetic-environment associations through the identification of outlier loci with particular patterns of genetic differentiation using RAD-sequencing (Restriction site Associated DNA sequencing). For this purpose we chose to compare populations from above the thermocline which deal with high thermal variations to population from a more thermal stable zone below the thermocline.

Harvest induced phenotypic selection in an island moose *Alces alces* population (52227)

Thomas Kvalnes, Bernt-Erik Sæther, Hallvard Haanes, Steinar Engen, Erling J. Solberg.

Centre for Biodiversity Dynamics (CBD), Dep. of Biology, NTNU, Trondheim, Norway; Norwegian Radiation Protection Authority, Østerås, Norway; Centre for Biodiversity Dynamics (CBD), Dep. of Mathematical Sciences, NTNU, Trondheim, Norway; Norwegian Institute for Nature Research (NINA), Trondheim, Norway.

Human exploitation has frequently led to evolutionary changes in wild populations. These changes are generally rapid and observable within ecological time scales, often within a few generations. Here we demonstrate selection for later birth dates in males and reduced yearling body mass in females induced by phenotype-based selective harvest in an moose population. We apply a recently developed framework combining population dynamics and quantitative

genetics theory to data from a 20-year study of a wild population, where genetic pedigrees has been established tracing back to founders. During the study birth date has advanced by 0.75 days per year for both sexes, while no significant changes has occurred in body mass. Both traits harboured significant additive genetic variance, with heritabilities of 11 % for body mass and 22 % for birth date, though the evolvability for body mass was only 0.16 %. Following standard quantitative genetics theory propagating uncertainty in estimates parameters we predicted a response to selection corresponding to the direction of observed changes for birth date. While body mass did not respond to selection during the study period the predicted phenotypic changes will generally not be fully transferred until lifetime reproduction is achieved.

Poster session A - POL 300

Detection of locus under selection from temporal samples of partial-selfing populations (52220)

Arnaud Becheler, Renaud Vitalis, Miguel Navascués.

INRA, UMR CBGP Montpellier; IRD, UMR LEGS Gif-sut-Yvette.

In a single isolated populations, allele frequencies will change through time subject to the processes of selection (acting on specific loci) and genetic drift (acting on the whole genome). Genetic data collected at different times can be used to make inferences on the effective population size (i.e. strength of drift) and to detect outlier loci, whose changes in allele frequencies are unlikely to be only the product of the inferred demography. However, the presence of self-fertilization may pose a problem for the detection of loci under selection. Selfing reduces the effective size of populations and the effective recombination among loci (promoting hitch-hiking). We investigated the effect of the presence of partial selfing reproduction in the power and false discovery rate for the detection of selected loci. In addition, we characterized the footprint of selection along the chromosome containing the selected site.

Poster session A - POL 300

Genomic changes during adaptation to a common environment in initially differentiated *Drosophila subobscura* populations (52205)

Sofia G. Seabra, Inês Fragata, Pedro Simões, Gonçalo S. Faria, Marta A. Santos, Miguel Lopes-Cunha, Margarida Matos.

CE3C - Faculdade de Ciências, Universidade de Lisboa.

Real-time evolution studies of laboratory populations of *Drosophila subobscura* founded from wild collections in contrasting European latitudes have previously revealed fast convergence at phenotypic traits. In contrast, though there were also significant temporal changes in chromosomal inversion frequencies, populations remained differentiated across generations.

We are now performing genome-wide analysis in two foundations derived from the extremes of the European cline, characterizing both the initial genomic differentiation, as well as the temporal changes during laboratory adaptation. We also aim at characterizing genomic content within and outside inversions in order to understand the mechanisms of evolution of inversions. Three different approaches for genome-wide analysis are taken: 1) Genome resequencing of pools of individuals (three replicates from each population) from four different generations; 2) Restriction site associated DNA (RAD) sequencing of individual larvae with known karyotype from two different generations; 3) Genome resequencing of pools of individuals of homokaryotypic lines for two chromosomal inversions in the O chromosome (OST and O3+4) to characterize SNP variation within and outside these inversions. The combination of these approaches will allow us to address the impact of history, chance and selection in genomic variation and evolution, and further the knowledge of the genomic impact of chromosomal inversions.

Poster session A - POL 300

Weak conservation of pathways in mouse and human aging tissues (52196)

Andrea Komljenovic, Marc Robinson-Rechavi.

Department of Ecology and Evolution; Swiss Institute of Bioinformatics, Lausanne, Switzerland.

Despite different experimental designs and different data available to study aging, the mechanisms of aging are still poorly understood. To tackle this, we are interested in evolutionarily conserved marks associated with aging that are different from those eventually specific to long lived species, such as human. We retrieved publicly available aging datasets diverse in species and tissues to analyze the gene expression differences during aging. Using modularization algorithm, we characterized co-modules showing the level of gene expression conservation between mouse and human tissues. Meta-analysis across different tissues in mouse and human shows overall down-regulation of age-related gene expression profiles. Since physiological changes that occur during aging in skeletal muscle and brain are striking, we identified the biological processes using gene set enrichment analysis and found that changes associated with age-related gene expression in skeletal muscle and brain are involved in the mitochondrion pathways and inflammatory response, respectively. However, there is a weak positive correlation between aging effects in the human and mouse brain, and in human and mouse skeletal muscle. The co-module identification showed connection to immune response process in brain tissue between human and mouse. Our study provides a statistical framework for comparative analysis in aging across different species.

Poster session A - POL 300

Phenotypic population divergence of the common frog across an elevational gradient in the Swiss Alps (52184)

Judith C. Bachmann, Josh Van Buskirk.

Species are distributed across varying environments which leads to variation in fitness and (genetic and phenotypic) divergence between populations, but all species ranges occur within limits. As populations along a species distribution encounter different habitats, natural selection should favor phenotypic traits beneficial in the local environment. Local adaptation is counteracted by gene flow reducing divergence among populations. Species distributions along an elevational gradient encounter environmental changes that happen on a small spatial scale compared to dispersal distances of many species. We study the elevational range of the common frog (*Rana temporaria*) in the Swiss Alps (200 m – 2775 m a.s.l.). Tadpoles from twelve populations from the elevational distribution were raised until metamorphosis in common conditions manipulating temperature and exposure to predation. Countergradient variation in development time and body mass was found. Populations diverge in larval life-history traits but not as strong as on the latitudinal gradient, suggesting that (potentially) high gene flow reduces phenotypic differentiation between populations. Future work will focus on limits to adaptation at the edge of the elevational distribution by genetic correlations.

Poster session A - POL 300

Analysis of mtDNA heteroplasmy in hermaphroditic mussels. First case of doubly uniparental inheritance without dioecy? (52163)

Aleksandra Przyłucka, Beata Śmietanka, Marek Lubośny, Artur Burzyński.

IO PAN.

In bivalves having doubly uniparental inheritance (DUI) males are heteroplasmic because they transmit one of their mtDNAs (M-type) to sons. Females have only one mtDNA (F-type), inherited in a regular way. Evolution and mechanism of DUI, despite years of investigations, still remains unclear but it is believed, that it does not occur in hermaphrodites. Furthermore, it has been shown, that sex determination and mitochondrial inheritance are quite closely linked in some bivalves (Unionidae). The very taxonomic distribution of DUI across bivalves remains obscured, largely due to technical difficulties. To overcome these we applied a novel gonadal transcriptome screening approach in hope to easily identify candidate DUI species. The approach was rather successful and here we report, for the first time, a case of a hermaphroditic bivalve with two divergent mitochondrial genomes, indicative of a working DUI. The sequencing of gonadal transcriptomes revealed the presence of two sets of mitochondrial transcripts. Observed high sequence divergence as well as a distinct pattern of amplification from generative tissues tentatively confirm this as a DUI case. We believe that this discovery will require deep revision of our understanding of the relationship between DUI, sex determination and evolution of reproductive strategies, at least in bivalves.

Poster session A - POL 300

Mussels from the Chilean Pacific coast: preliminary transcriptomic data (52155)

Marek Lubośny, Beata Śmietanka, Aleksandra Przyłucka, Artur Burzyński.

Institute of oceanology PAN.

Over the last 20 years, since sequencing of the first bacterial genome in 1995 through the sequencing of the first eukaryote in 1996, and human genome in 2001 till present day, sequencing research and technologies have made a great leap forward. It takes much less time, money and effort to obtain more, longer genomic sequences of higher quality. Organisms with sequenced genomes stand for only a very small percentage of all living beings on Earth. Most of currently available genome sequences (Ensembl database) comes from model organisms. However, much less data is available for marine organisms. In particular, there are only two genomes from phylum mollusca currently available in the database. In contrast to the costly genomic projects, RNA sequencing constitutes a viable alternative of obtaining large amounts of representative sequence data for a reasonable price. Here we present the results of a small transcriptomic survey performed on mussels from Chilean Pacific coast. Total RNA was isolated from generative tissues of several bivalves, subject to library construction and Miseq (Illumina) sequencing. After assembly, the obtained contigs were analyzed using a set of bioinformatic tools. This gave us a first glimpse at the bivalvian transcriptome, illustrating the productivity of this approach.

Poster session A - POL 300

How much can History constrain adaptive evolution? The two sides of a story. (52153)

Inês Fragata, Pedro Simões, Margarida Bárbaro, Bárbara Kellen, Josiane Santos, Marta A. Santos, Gonçalo S. Faria, Mauro Santos, Margarida Matos.

CE3C - Faculdade de Ciências, Universidade de Lisboa; Departament de Genètica i de Microbiologia, Universitat Autònoma de Barcelona.

The ability to adapt to environmental changes is of utmost importance for species survival. Insights on the mechanisms and forces underlying this ability can be obtained from studying species that present a wide geographical distribution. However, few studies have examined how history affects the adaptive dynamics of such species, at several levels of organization. In order to test the impact of historical differentiation during adaptation, we followed the real-time evolutionary dynamics of phenotypic traits and chromosomal inversion frequencies in replicated *Drosophila subobscura* populations. These populations were derived from the 3 locations along the European latitudinal cline and introduced in a new (laboratorial) common environment. Initially populations were highly differentiated for all traits. However, pervasive phenotypic convergence was achieved after only few generations in the laboratory. A different story was told at the karyotypic level, with selection shaping the evolutionary dynamics of inversion frequencies, but doing so within the constraints imposed by previous history. The signature of history and its impact on the evolutionary dynamics may thus have different outcomes depending on the level of observation. Given that similar phenotypic optima were reached through different genetic routes, this suggests that history plays an important role but does not constrain adaptive evolution.

MICROGEOGRAPHIC VARIATION IN TROPICAL TREES: SELECTION SHAPES INTRA-POPULATION DIVERGENCE AT HUNDREDS OF LOCI (52143)

Louise Brousseau, Ivan Scotti.

INRA - URFM; CNR - IBBR; INRA - ECOFOG.

Tree species harbour high levels of within-population genetic diversity, generally explained away based on purely neutral processes. Nevertheless, within-population environmental gradients and mosaics and variable selective pressure suggest that part of the variation may be maintained by Darwinian processes.

To test this hypothesis, we have analysed genome-wide patterns of polymorphism in two adult stands of the tropical tree, *Eperua falcata* Aubl. (Fabaceae), occupying areas where starkly contrasted habitats can coexist at very short distances. We have assembled a draft containing roughly one fourth of the total genome. After filtering for quality, approximately seventy-thousand SNP loci were retained for further analyses.

One of us (LB) has developed a Bayesian framework to analyse population-specific and locus-specific divergence in nested sampling schemes and we have also applied Nielsen's (2009) G2D test to detect sequences under directional selection.

Approximately 1% of the loci is subject to either stabilising or directional/divergent selection, which is probably an underestimate, because we partitioned our samples based on only one gradient. It is likely that the inclusion of other environmental axes will lead to the detection of further adaptive loci. These results are consistent with a substantial role of Darwinian selection in the shaping of within-population genetic diversity.

Genome-wide screen for adaptive divergence between freshwater and brackish-water ecotypes of prickly sculpin (*Cottus asper*) (52141)

Stefan Dennenmoser, Arne W Nolte, Steven M Vamosi, Sean M Rogers.

Max-Planck Institute for Evolutionary Biology; University of Calgary.

Understanding the genomic basis of adaptive divergence in the presence of gene flow remains a major challenge in evolutionary biology. In prickly sculpin (*Cottus asper*), high genetic connectivity exists among estuarine habitats of coastal rivers and nearby tributaries, but apparently does not preclude the emergence of genetically differentiated life history ecotypes. It is unclear whether this is driven by adaptive evolution. We predicted that adaptation to brackish-water and freshwater habitats manifests as increased genetic differentiation at candidate genes underlying salinity tolerance and osmoregulation in teleosts. The high similarity to the genome of the stickleback allowed us to approximate the position of *Cottus* genomic sequences along the stickleback chromosomes and to explore their gene content.

This permitted sequencing of genomic DNA pools representing two estuarine and two freshwater habitats in the lower Fraser River system (southwestern British Columbia, Canada) to explore genetic differentiation across the genome. Among 36 predicted candidate genes, sodium/potassium ATPase and Na⁺Cl⁻ co-transporter showed strong signals of differentiation among habitats, indicating their potential role in local adaptation to different osmotic niches. Overall, the presence of both parallel and non-parallel signatures of differentiation across many loci scattered throughout the genome suggests polygenic adaptation that varies among local populations.

Poster session A - POL 300

How much is adaptive evolution contingent on space and time? A meta-analysis in *Drosophila subobscura* (52135)

Pedro Simões, Inês Fragata, Sofia G. Seabra, Gonçalo S. Faria, Marta A. Santos, Margarida Matos.

CE3C-FCUL.

Environmental changes across space and time as well as stochastic events can shape genetic backgrounds and thus affect evolutionary responses and potential. Here we address experimentally these effects on the initial performance of populations and their evolutionary changes in fecundity, physiological traits and inversion polymorphisms during short-term adaptation to a new environment. We use two sets of two laboratory foundations of *Drosophila subobscura*, sampled 3 years apart, from the same contrasting European locations (Portugal vs. Netherlands). We found initial differentiation between foundations from different locations, consistent in both years, for most traits. Early differences between years were found only for age of first reproduction and male starvation resistance. Concerning the evolutionary rate, starvation resistance showed significant variation across locations and years. As for chromosomal inversion frequencies, these differed initially across locations but not years. Differences between locations remained significant after 6/8 generations. Inversion frequency changes during that period were minor. Altogether, our findings indicate that spatial rather than temporal variation in source natural populations is more likely to produce disparate starting points for evolution. Also, it seems that the evolution of traits more loosely related to fitness (e.g. starvation resistance) is more contingent on location and time of natural collections.

Poster session A - POL 300

Latitudinal variation in temperature-stress resistance and tolerance in *Arabidopsis lyrata* (52133)

Guillaume Wos, Yvonne Willi.

University of Neuchâtel.

Numerous species tend to have distribution boundaries that coincide with thermal isoclines. What limits thermal adaptation? We hypothesized that resistance and tolerance to extreme temperatures cannot be maximized because of genetic trade-offs. We conducted an experiment on eight populations of *Arabidopsis lyrata* collected along a latitudinal temperature gradient in North America and repeatedly exposed plants to either frost or heat stress. We measured resistance and tolerance to frost and heat using electrolyte leakage and growth data, respectively, and tested whether they (a) co-vary with latitude, (b) are genetically negatively correlated and (c) are costly. Plants from high latitude populations grew to a larger size and were more frost resistant, while those from low latitudes were more heat resistant and heat tolerant. Surprisingly, populations from the north were less frost tolerant, probably because frost tolerance was genetically correlated with small size. We found no indication that trade-offs between resistance and tolerance to the same or different thermal stresses limit adaptation to frost and heat. However, the results suggest that the cost of frost tolerance could be an important constraint to adaptation at the northern distribution boundary.

Poster session A - POL 300

The role of sexual selection on a threshold trait in the black scavenger fly *Sepsis thoracica* (52126)

Juan Pablo Busso, Wolf U. Blanckenhorn.

IEU- University of Zürich.

Sexual selection is an important force shaping phenotypic diversity within a species and can ultimately contribute to the evolution of reproductive isolation and sympatric speciation. To analyze the divergent role of sexual selection we focused on *Sepsis thoracica* (Diptera: Sepsidae), a black scavenger fly that presents a sigmoid relationship between body size and coloration resulting in two condition dependent male morphs: a smaller black and a larger yellow morph. Competitive matings between the two morphs showed that copulation success was greater for larger black males and smaller yellow males. This special type of stabilizing sexual selection should result in a narrower distribution peaking at intermediate male sizes. However, *S. thoracica* presents a bimodal male size distribution with little overlap between morphs. Since there was no assortative mating within either morph, but there was assortative mating across morphs, this antagonistic selection could not only strengthen the sigmoid relationship between body size and coloration, but also lead to divergence between the morphs. Further experiments varying the strength of sexual selection (different sex ratios) should confirm its role on shaping the particular body size-coloration relationship in this species.

Poster session A - POL 300

Effects of temperature dependent survival during early development on adult fitness traits (52119)

Martin A. Schäfer.

University of Zurich.

Differential survival during early development may play an important, but neglected, role in shaping allelic variation encoding for traits exposed to natural or sexual selection at later life stages. Using a fine-grained temperature gradient at the upper margin of the thermal tolerance curve, I explored sex-specific selection during development in the dung fly *Scathophaga stercoraria* by comparing the size of non-hatched and hatched pupae. In female pupae and adult flies I further quantified the development of an additional, fourth spermatheca, which is rarely expressed in the field and entails fitness costs at the adult stage. Males had lower temperature-survival thresholds, but survival was not related to body size within both sexes, indicating no physiological costs of growing large in a species with male-biased size dimorphism. In females high temperatures induced the expression of the additional spermatheca as a correlated side effect of fast extrinsic (environmental) and/or intrinsic (genetic) growth. Interestingly, females that survived the pupal stage expressed the naturally rare phenotype more frequently, implying that antagonistic pleiotropy across developmental stages can contribute to the evolutionary diversification of female sperm storage morphology.

Poster session A - POL 300

Evolution of canalization in gene regulatory networks (52110)

Estelle Rünneburger

Laboratoire Evolution, Génomes, Comportement, Ecologie.

The genetic architecture of complex traits involves numerous interacting genes as well as environmental effects. To study the influence of genetic architectures on the evolution of phenotypes and gene networks themselves, we surveyed through in-silico individual-based simulations how quantitative measurements of evolvability and robustness change in time under natural selection. Our main model features gene regulatory networks, in which the evolution of complex phenotypes (gene expression patterns) depends on the evolution of a regulation matrix. We also considered simpler alternative settings, such as the epistatic multilinear model.

It is generally acknowledged that stabilizing selection tends to promote genetic canalization in epistatic architectures. We investigated the influence of various properties of gene networks on this evolution towards low evolvability, focusing on parameters related with the network topology (number of genes, connectivity, ...). Simulation results show that robustness to mutations tends to evolve faster in networks of intermediate complexity, suggesting that evolution of evolvability could be constrained by the size of the underlying gene networks.

Poster session A - POL 300

Evolution of bow-tie architectures in biology (52101)

Tamar Friedlander, Avraham E. Mayo, Tsvi Tlusty, Uri Alon.

IST Austria; Weizmann Institute of Science; Institute for Advanced Study, Princeton.

Bow-tie or hourglass structure is a common architectural feature found in many biological systems. A bow-tie in a multi-layered structure occurs when intermediate layers have much fewer components than the input and output layers. Examples include metabolism where a handful of building blocks mediate between multiple input nutrients and multiple output biomass components, and signaling networks where information from numerous receptor types passes through a small set of signaling pathways to regulate multiple output genes. Little is known, however, about how bow-tie architectures evolve. Here, we address the evolution of bow-tie architectures using simulations of multi-layered systems evolving to fulfill a given input-output goal. We find that bow-ties spontaneously evolve when the information in the evolutionary goal can be compressed. The maximal compression possible determines the size of the narrowest part of the network - that is the bow-tie. A further requirement is that a process is active to reduce the number of links in the network, such as product-rule mutations, otherwise a non-bow-tie solution is found in the evolutionary simulations. This offers a mechanism to understand a common architectural principle of biological systems, and a way to quantitate the effective rank of the goals under which they evolved.

Poster session A - POL 300

Geographically limited selection at the blood group-related gene B4galnt2 in house mice is associated with gastrointestinal pathogens (52095)

Marie Vallier, Miriam Linnenbrink, Philip Rausch, Guntram Grassl, John Baines.

Max Planck Institute for Evolutionary Biology, Ploen, Germany; Christian-Albrechts-University of Kiel, Germany.

B4galnt2 is a blood group-related glycosyltransferase whose two murine alleles (driving gastrointestinal- and vascular expression) are maintained by balancing selection in house mice and their relatives. The vascular allele induces a defect in coagulation and subsequent bleeding phenotype, suggesting that this fitness cost may be offset by other unknown benefits. Interestingly, despite its overall long-term maintenance, the vascular allele is absent in wild mouse populations from Germany and Northeast France, but recently increased in Southwest France as evidenced by a partial selective sweep. This suggests that geographic-dependent selective forces may be operating. Given other examples of blood group-related glycosyltransferase variation in humans, we hypothesize that resistance to pathogen(s) may mediate selection operating on B4galnt2 over space and time. Indeed, experiments in lab mice show that the presence/absence of B4galnt2 expression in the gastrointestinal tract influences the response to Salmonella infection. By applying metagenomic approaches in a wild mouse population displaying evidence of recent selection (i.e. a partial selective sweep), we found that B4galnt2 genotype correlates with differences in intestinal inflammation and the presence of candidate pathogens that could drive selection at B4galnt2. We thus suggest the limited dispersal of pathogens to be a potentially potent source of variation in selection.

Opposite forces of selection modify local life history adaptations in insects (52084)

Panu Välimäki, Netta Keret, Sami M. Kivelä, Markku Orell, Toomas Tammaru.

University of Oulu; Stockholm University; University of Tartu.

Increasing body size is favored by fecundity selection among income breeders. In seasonal environments, larval development time is a key life history trait because individuals have to reach a diapause stage before winter. Theory assumes that large size can be achieved only by a prolonged development time. This may hold true at the phenotypic level, but the evolutionary consequences lie in the genetic level. Genetic correlation of the traits may vary spatially depending on variance in growth rate. We studied quantitative genetics of development time and body size in a laboratory experiment in four latitudinal populations of *Chiasmia clathrata* (Geometridae). Development time and body size expressed high additive variance at national scale but not at local scale. In univoltines, development time was highly heritable, whereas body size appeared almost a fixed trait, the two being negatively correlated at the genetic level. In bivoltines, opposite pattern emerged but the traits were uncorrelated at the genetic level. This implies that fecundity selection is strong in less time-constrained univoltine populations. In the strongly time-constrained populations short development time is selected for instead. Either compensating (bivoltines) or over-compensating (univoltines) growth rate may break down development time vs. body size trade-off in an adaptive manner.

Spatial Variation in Natural Selection Determines Patterns of Divergence in an Adaptive Radiation (52057)

Greg M Walter, Melanie Wilkinson, David Aquirre, Daniel Ortiz-Barrientos.

University of Queensland; Massey University.

A group of organisms that colonise a heterogeneous landscape are exposed to spatial variation in natural selection, facilitating adaptation and diversification possibly leading to adaptive radiation. Divergence during adaptive radiation is potentially driven by adaptation and divergence at a local scale. Although studies of local adaptation are common, particularly in plants, few of them have addressed the role of natural selection in driving population and ecotypic divergence across multiple environments. Here, we use reciprocal transplant experiments of ecotypes and select hybrids to investigate how selection is currently shaping population and ecotype divergence in a widely distributed wildflower. Local populations performed better in their local environment and better than foreign ecotypes. Additionally, populations of the same ecotype exhibited some level of local adaptation themselves. The similarity of the environmental conditions between their native environment and the transplant environment determined the fitness of a population in any given locality. However, despite a strong signature of local adaptation F1 hybrids displayed heterosis while backcrosses and F2's exhibited hybrid breakdown. We provide experimental evidence for

environmentally driven diversification that has resulted in local adaptation on a wide spatial and historical scale across contrasting environments.

Poster session A - POL 300

Looking for Ecologically dependent reproductive barriers and intrinsic genetic incompatibility between ecotypes of *Senecio lautus* (52055)

Tom Richards, Daniel Ortiz-Barrientos, Katrina McGuigan.

University of Queensland.

Ecologically dependent reproductive isolation is a process fundamental to the model of ecological speciation, although evidence of it is relatively limited. A fundamental test is whether barriers to gene flow between divergent wild populations are due to intrinsic genetic incompatibilities or ecologically dependent fitness reductions in hybrids. *Senecio lautus* is a species complex where these predictions can be tested; there are several ecologically divergent ecotypes however they retain the ability to produce viable crosses when grown in a common environment. In this work, we use a field based reciprocal transplant experiment using parental and hybrid (F1, F2 & Backcross) genotypes from three coastal ecotypes of *Senecio lautus* to ascertain the relative importance of ecologically-dependent and intrinsic-genetic barriers to gene flow. We find that there is evidence for local adaptation, with reduced fitness seen in some hybrid genotypes and immigrant parentals, and that there is some ecological dependence, as fitness decreases proportionately with the presence of immigrant genes present in the cross. We find some evidence for ecologically dependent isolation, however, support is not as clear as theory would predict, suggesting the existence of other factors.

Poster session A - POL 300

Divergent ecology causes within generation polygenic selection and ecotypic differences in American Eel (*Anguilla rostrata*). (52039)

Louis Bernatchez, Scott Pavey, Jérémy Gaudin, Céline Audet.

Université Laval; ISMER.

The two primary ways that species cope with heterogeneous environments is through local adaptation and phenotypic plasticity. American Eel presents a paradox; despite inhabiting drastically different environments, the species is panmictic and long-term local adaptation is impossible. All spawning takes place in the southern Sargasso Sea. Then, the planktonic larvae disperse to rearing locations from Cuba to Greenland and juveniles colonize either freshwater or brackish/saltwater habitats, where they spend 3-25 years before returning to the Sargasso Sea to spawn as a panmictic species. Depending on rearing habitat, individuals exhibit drastically different phenotypes. The hypothesis that phenotypic plasticity alone can account for the differences has been disproven. In this study, we present a genome-wide

association study that demonstrates a genetic basis for the drastic phenotypic differences that is the likely result of within-generation selection. We found that 331 loci out of 42,424 initially considered were most associated with the divergent ecotypes. These 331 loci are within 101 genes that represent vascular and morphological development, calcium ion regulation, growth and transcription factors, and olfactory receptors. Our results demonstrate that divergent natural selection of phenotypes can have a subtle polygenic genomic signal, occur within a single generation, and manifest in divergent ecotypes, despite panmixia.

Poster session A - POL 300

The genomic basis of colour dimorphism and cold adaptations in a seabird. (52036)

Anna Tigano, Tone Reiertsen, Kjell Einer Erikstad, Vicki Friesen.

Queen's University; Norwegian Institute for Nature Research - NINA.

In the North Atlantic, common guillemots (*Uria aalge*) are located from arctic to temperate waters and include two morphs: unbridled birds have a completely black or dark brown head, and bridled birds are characterized by a white eye-ring and auricular groove. Mating between the two morphs is random and the dimorphism is based on simple Mendelian inheritance of an autosomal gene, where bridling is recessive. Several lines of evidence suggest that bridled guillemots are more adapted to colder temperatures than are unbridled ones and the frequencies of the two morphs across their range may be the result of fluctuating selection. To designate a trait as 'adaptive' connections between genotype, phenotype and fitness must be made. The correlation between phenotype and fitness has been documented, but genetic characterization of phenotypic variation and genomic signature of selection are needed to close the circle. We are using whole genome resequencing data from bridled and unbridled common guillemots to investigate the genomic basis of bridling and associated cold adaptations. This system allows us not only to characterize the basis of the phenotypic traits of interest, but also to investigate the genomic architecture of adaptation.

Poster session A - POL 300

Empirical insights of the effects of pollen flow on the adaptive potential of *Fagus sylvatica* populations (52030)

Julie GAUZERE, Etienne KLEIN, Sylvie ODDOU-MURATORIO.

CEFE CNRS; BioSP INRA; URFM INRA.

In temporally variable environments, gene flow is expected to facilitate the adaptive response of populations by spreading pre-adapted genes in the landscape and increasing the genetic variance available for the response to selection. However we still lack empirical evidence of these beneficial effects of gene flow.

Here, we investigate the effects of gene flow on the adaptive potential of three populations of *Fagus sylvatica* along an altitudinal gradient using direct gene flow estimate based on paternity analyses. We measured eleven ecophysiological traits on 60 maternal families. Genetic data were used to assign the offspring to two categories, “migrant” or “local”, according to the origin of their fathers. We first show that pollen immigration rates were high (56% on average) and that 6 traits genetically diverged along the gradient. Our results overall fail to demonstrate significant effect of pollen flow on trait mean or variation within population. Only for the population at the intermediate altitudinal level, we found that immigrant pollen increase the genetic variances of two traits (timing of budburst and diameter growth). This may be due to a weak power to detect gene flow effect in weakly differentiated populations. A better characterization of the pollen origin may help to reveal the effects of pollen flow on adaptive potential.

Poster session A - POL 300

The genome sequence of the corn snake (*Pantherophis guttatus*), a valuable resource for EvoDevo studies in squamates (52025)

Asier Ullate Agote, Michel C. Milinkovitch, Athanasia C. Tzika.

Laboratory of Artificial & Natural Evolution (LANE); SIB Swiss Institute of Bioinformatics; Institute of Genetics and Genomics of Geneva (iGE3).

Squamates exhibit a striking variety of phenotypes, with little known on their generative mechanisms. Studies aiming to understand the genetic basis of this diversity in morphology, physiology and ecology will greatly benefit from whole genome sequencing initiatives, as they provide the foundation for comparative analyses and improve our understanding on the evolution, development and diversification of traits. Here, we present the first draft genome of the corn snake *Pantherophis guttatus*, an oviparous snake that we promote as an appropriate model species for evolutionary developmental studies in squamates. We sequenced 100-bases paired-end reads from multiple individuals of a single family that produced a genome assembly of 1.53 Gb, roughly covering 75% of the expected genome size, and 297,768 scaffolds >1Kb. We were able to retrieve 192 of the 248 CEGMA core genes, indicating that high genome completeness was achieved. Using MAKER2, we annotated 10,917 genes with high confidence. Numerous colour and colour pattern morphs exist in *P. guttatus*, making it an ideal model to study the genetic determinism, development, and evolution of adaptive colour traits in reptiles. Using our draft genome and a SNP calling approach, we located the interval with the causative mutation for the amelanistic phenotype.

Poster session A - POL 300

Genomic footprint of local climate adaptation (52021)

Ann-Marie Oppold, Markus Pfenninger, Simit Patel.

Local adaptation is a common observation in species with a wide distribution range. However, little is known about its underlying genomic basis and therefore the molecular mechanisms driving this adaptation. Especially for ectothermic organisms, as is our non-model organism *Chironomus riparius*, the ambient temperature is a crucial environmental factor. We analysed *C. riparius* populations along a climatic gradient across Europe by the integration of genome-scans and common garden experiments.

Common garden experiments at three different temperatures (14, 20, and 26 °C) revealed local climate adaptation in six natural populations. Differences in the population growth rate showed temperature-dependent effects on fitness of the populations. We applied the Pool-Seq method to scan the population genomes and found more than 2.5 million SNPs among six natural populations. Based on F_{ST} -analyses more than 2000 highly differentiated SNPs were identified and annotated. We further associated the identified SNPs to environmental variables and found significant correlations. To also account for patterns of polygenic adaptation and not merely focus on outlier loci, we further aimed to perform gene-set enrichment analyses.

Our results give insight in the complexity of the genome-wide distribution of adaptive genetic variation in natural populations.

Poster session A - POL 300

An approximate Bayesian estimator of allele age and selection strength (52020)

Louise ORMOND, Gregory Ewing, Matthieu Foll, Jeffrey D Jensen.

EPFL; WHO.

Single Nucleotide Polymorphism (SNP) data can be used to infer both the age of a beneficial allele and the strength of selection acting upon it. These estimates can outline variation in selection over time and space, offering important implications regarding the mode and tempo of adaptation. Although new time-sampled methods have been developed, there remains significant scope for improvement in the single time point inference of selection parameters. Here, we first apply forward and backward simulations investigating a range of parameters, including effective population size (N_e), mutation rate (μ), recombination rate (r), the strength of selection (s) and allele age (T_s) to generate summary statistics. We then use an approximate Bayesian (ABC) approach to generate the posterior distribution of s and T_s . Second, we replicate previous results for the Bayesian inference of T_s (Przeworski 2002) and develop an improved single-time point Bayesian estimator for the joint inference of these parameters. We then incorporate demographic scenarios and explore the relative gains in performance from using single- versus multiple-time points. This approach improves on existing methodology through the incorporation of several informative summaries, including data from linked neutral sites, and through the computational efficiency and speed afforded by ABC-based approaches.

EVOLUTION IN SPATIOTEMPORAL VARIABLE METAPOPOPULATIONS FACILITATES PERFORMANCE IN NOVEL CHALLENGING CONDITIONS (52006)

Dries Bonte.

Ghent University.

Human-induced changes of the landscape often lead to the fragmentation or reduction of quality of habitat and forces many organisms to live in a heterogeneous landscape. The landscape structure affects local and metapopulation dynamics which are in turn expected to impact life history evolution.

By means of experimental evolution using the spider mite *Tetranychus urticae* as a model we demonstrate that spatiotemporal variation in habitat availability affects metapopulation dynamics and that these changes induce evolutionary divergence in life history, physiological endpoints and gene expression. The induced metapopulation-level selection pre-adapts the mites towards an enhanced performance on novel challenging hosts.

Our integrated approach highlights the linkage between spatial structure, local demography and trait evolution. The multivariate responses point towards general adaptations in stress resistance pathways and are suggested to be driven by metapopulation-level variation in competition and patch extinction rates.

Poster session A - POL 300

Detecting signals of strain-specific selection in genomic sequences of *Staphylococcus aureus* (52001)

Chieh-Hsi Wu, Daniel Wilson.

University of Oxford.

There are myriad examples of bacterial populations rapidly adapting in response to selection pressure imposed by antibiotics, often within individual patients. Selection is therefore pervasive in bacterial evolution. Many species such as the common pathogen *Staphylococcus aureus* exhibit strong strain structuring – such that the level of diversity among strains is much higher than within – but low geographic structuring, with local sampling capturing global diversity. These observations indicate that strain structuring is maintained by selection, and that patterns of variation cannot be well explained by classical selective sweeps. Strain structure may hinder attempts to discover genomic signatures of selection based on models of selective sweeps. To address this, we extended a recently proposed Bayesian statistical method based on the chromosome painting technique to detect partial selective sweeps. The extension adapts the original method to suit prokaryotic mechanisms of homologous recombination, which differ to those in eukaryotes. Our extension also accommodates recombination rate variation along the genomic sequences. We have applied our method to a

dataset of 100 *S. aureus* genomes sampled from Oxfordshire, England, to search for strain-specific adaptation that may explain the long-term coexistence of diverse strains.

Poster session A - POL 300

Evolutionary analysis linked to epigenetic modifications in the largest transcription factor family of humans. (51985)

Adamandia KAPOPOULOU, Lisha MATHEW, Didier TRONO, Jeffrey D. JENSEN.

EPFL; SIB.

The KRAB-containing zinc finger (KRAB-ZNF) genes represent the biggest family of transcription factors in humans, yet for the great majority, their function and specific genomic target remains unknown. However, it has been shown that a large fraction of these genes arose from segmental duplications, and that they have expanded in gene and zinc finger number throughout vertebrate evolution. To determine whether this expansion is linked to selective pressures acting on different domains, we have manually annotated all KRAB-ZNF genes present in the human genome and assessed the evolutionary forces acting at the sequence level as well as on the epigenome. When compared across primates and across tissues, KRAB-ZNFs demonstrate species-specific expression rather than tissue-specific expression. Interestingly, those carrying a nonsynonymous SNP in their DNA-contacting amino acids exhibit significantly reduced expression in all tissues accompanied by repressive histone marks; these KRAB-ZNF genes also seem to be less strongly constrained than those without such polymorphism. This work represents the first large-scale effort to characterize selective effects on KRAB-ZNFs and to correlate those effects with epigenetic modifications and population genetic data.

Poster session A - POL 300

The ADiv Project (Analyzing Diversification in the Agaricales, 2013-2017): Analyzing patterns of diversification in the largest group of mushroom-forming basidiomycetous fungi (51981)

János Gergő Szarkándi, Bálint Dima, Sándor Kocsubé, Csilla Szebenyi, Nikolett Rác, Tamás Papp, Csaba Vágvolgyi, László G Nagy.

Department of Microbiology, University of Szeged; Fungal Genomics and Evolution Lab, Biological Research Center of the Hungarian Academy of Sciences .

The ADiv project aims to investigate patterns in the rates of evolution in the Agaricales. The Agaricales is the largest group of mushroom-forming fungi with ca. 14,000 described species. The driving forces underlying taxonomic diversification in these mushrooms are poorly known and are among the most important challenges in mycology. To address these questions, we will use phylogenetic comparative analyses on a new two-gene dataset (the diversity dataset) for ca. 3,000 species. We selected the nLSU and RPB2

loci, which are known to provide sufficient phylogenetic information for relationships at the infrageneric level. We have already sequenced the nLSU gene in 1,500 species from 2,200 specimens. In addition, a phylogenomic dataset is also being produced from publicly accessible genomes of Agaricales, meaning about 60 to 100 species. These two datasets will be used to examine general patterns of speciation and extinction and to identify shifts in diversification rates. Sampling efforts have been concentrated on regions with poor phylogenetic coverage, e.g. the southern hemisphere (Australia, New Zealand). Currently we are experimenting with different primer sets for the amplification of the RPB2 gene and further sequencing of the LSU gene is in progress.

This study was supported by the grant OTKA NN106394.

Poster session A - POL 300

The role of habitat dynamics in driving diversification (51968)

Thijs Janzen.

Max Planck Institute for Evolutionary Biology.

It is commonly accepted that geographical isolation can play an important role in speciation. Geographic isolation is often assumed to slowly increase over time, for instance through the formation of rivers or mountains. Cyclic changes in connectivity between areas might occur however when water levels fluctuate in a large lake, or when changes in sea level changes the connectivity between islands. These habitat dynamics may act as a driver of allopatric speciation and propel local diversity. Here we present a basic model of this interaction between changes in the environment and speciation. We model fluctuations in water level and compare results of our model with a published phylogeny of cichlid fish from Lake Tanganyika where such cyclic changes have occurred. When confronting our model to the phylogeny of cichlid fish from Lake Tanganyika, we do not find evidence for water level changes and associated allopatric speciation. This suggests that large-scale water level fluctuations have had little impact on the current diversity of cichlids in Lake Tanganyika. However, we argue that the Yule tree model prior used to reconstruct the phylogeny may have biased our results, and therefore advocate the incorporation of more complex tree model priors that take into account habitat dynamics.

Poster session A - POL 300

Detecting selection with haplotype-based methods: benchmarking and application to tropical butterflies (51966)

Angeles de Cara, Annabel Whibley, Marianne Elias, Mathieu Joron, Frederic Austerlitz.

Lab d'Ecoanthropologie et Ethnobiologie, Museum National d'Histoire Naturelle, Paris (France); John Innes Centre, Norwich (UK); Museum National d'Histoire Naturelle, Paris (France).

The vast amount of genome-wide polymorphism data available has led to considerable efforts to develop methods to detect natural selection at the molecular level. Finding regions under selection is one of the first steps towards understanding the processes of adaptation and speciation. Our ability to detect selection depends critically on the data available and on the robustness of the methods to the underlying assumptions. Several commonly used methods look for F_{ST} outlier loci. However, these methods sometimes fail to identify loci under weak selection. Conversely, some neutral markers can be inferred to be under selection. Alternatively, we can use haplotype-based methods to infer selection within populations. These methods rely on the idea that positive selection on a position in the genome will create a region of extended homozygosity. We study here the efficiency of three such methods (iHS, nSL and H12) in simulated data obtained by performing artificial selection on a polygenic trait. We show that these methods work mainly when selection is strong and the traits are only mildly polygenic. Furthermore, we analyse sets of individuals of the tropical butterflies *Heliconius* and *Ithomiini* of different species and morphs, to test the power of these methods on known regions under selection and to infer new candidates of selection.

Poster session A - POL 300

Genomic insights into the transition from oviparity to viviparity: the case of the reproductively bimodal lizard *Zootoca vivipara* (51962)

Luca Cornetti, Alex Panziera, Andrea Benazzo, Mike W. Bruford, Cristiano Vernesi, Giorgio Bertorelle.

Department of Biodiversity and Molecular Ecology, Research and Innovation Center, Fondazione Edmund M; Dipartimento di Scienze della Vita e Biotecnologie, University of Ferrara, Ferrara, Italy; Cardiff School of Biosciences, Cardiff University, Wales, UK.

Squamate reptiles provide a unique model for gaining crucial information about the evolutionary transition from oviparity to viviparity in vertebrates. The lizard *Zootoca vivipara* is one of the few species with distinct reproductive modalities in different subspecies; in detail *Z. v. carniolica* (European Alps) and *Z. v. louisianzi* (Pyrenees) are egg-laying lizards, while *Z. v. vivipara* (Central Western Europe) is a live-bearing one, with *carniolica* and *vivipara* that overlap their distributional ranges in the Alps. This provides an interesting natural setting for studying the evolutionary consequences of the shift from oviparity to viviparity and investigating possible evidence of hybridization between individuals with different reproductive modes.

We used a genomic approach (RAD sequencing), for isolating and analysing about 85 thousand of SNPs that allowed to explore both neutral and adaptive variation. Population genomics analyses indicated that hybridization between egg-laying and live-bearing lizards is unlikely to happen and that oviparous and viviparous populations experienced different demographic dynamics. Additionally, mapping of coding sequences containing polymorphisms with high and significant differences in allele frequencies between oviparous and viviparous populations on *Anolis carolinensis* genome allowed to highlight genes related to physiological pathways involved in the mode of reproduction.

Ecological genomics of *Betula nana* and *Fraxinus excelsior* in Europe (51961)

James Borrell, Elizabeth Sollars, Bernardo Clavijo, Laura Kelly, William Bodles, Steve Lee, Richard Nichols, Sarah Ayling, Richard Buggs.

Queen Mary University of London; Qiagen, Aarhus; The Genome Analysis Centre, Norwich; Highland Birchwoods, Munlochy; Forest Research, Roslin.

We present genome-wide polymorphism data for two tree species in Europe, analysed in an ecological and evolutionary contexts. *Betula nana* is common in boreal environments, and rare in the UK. We present RAD-seq and microsatellite data for 28 populations in the UK and 10 populations in Finland, showing contrasting patterns of genetic structure and allele distribution. *Fraxinus excelsior* is widespread in Europe and of ecological and economical importance, but threatened by ash dieback and the emerald ash borer. We present a reference genome sequence for *F. excelsior* and whole genome re-sequence data for 39 populations throughout Europe.

Recombination hotspots and genomic patterns of horizontal gene transfer in bacteria (51960)

Sarah Earle, Martin Maiden, Derrick Crook, Daniel Wilson.

University of Oxford.

Bacteria reproduce clonally, but recombination is critical to accelerating adaptive response, both in the core and accessory genome. This research investigates signatures of core genome recombination using ClonalFrameML in the species *Mycobacterium tuberculosis*, *Clostridium difficile*, *Escherichia coli*, *Klebsiella pneumoniae*, *Campylobacter jejuni*, *Campylobacter coli*, and *Neisseria meningitidis*, which range from genetically monomorphic to highly transformable. One hundred whole genome sequences of each species were analysed, either from mapped or core-genome MLST data, taken to represent species-level diversity. Recombination was estimated both by using a model with a single set of recombination parameters estimated for all branches, and by estimating different parameters per branch. ClonalFrameML estimates the relative probabilities that a nucleotide is changed as the result of recombination relative to point mutation (r/m), which is a direct measure of the relative impact of recombination on evolutionary change, giving a general indication of homologous recombination rates which can be directly compared across the species. We examine the frequency, distribution and local genomic context of recombination in the core genome, discovering various hotspots and coldspots, and find that HGT of very large regions is common to many species, indicating that this is an important process in bacterial evolution.

Inference and misinference under models of Background Selection. (51952)

Gregory Ewing, Jeffrey Jensen.

EPFL.

Background selection (BGS), the process where unavoidable deleterious mutations are constantly removed from the population, is widely accepted to have a significant effect on patterns of genetic diversity and the efficiency of selection via linkage. Despite this, it is rarely taken into account in current studies due to the practical difficulties of doing so. This includes availability of adequate simulation software, their performance, tractability of current models and the difficulty of applying theory to real data.

We have developed an efficient coalescent based simulation method, that permits BGS models with arbitrary Distributions of Fitness Effects (DFE) in nonequilibrium populations, to address these issues. Due to the high performance Approximate Bayesian Computation for direct inference from suitable data is practical. We explore estimation of parameters under non trivial demographic models with and without BGS. We find that when BGS is present but not accounted for positively misleading inference are possible. Further we present results of directly inferring the DFE from data.

Poster session A - POL 300

Genomic signatures of adaptation in sticklebacks: convergent or not? (51950)

Philine Feulner.

Eawag.

After the last glaciation, marine three-spined sticklebacks colonized various newly available freshwater habitats. Comparing populations across a salinity gradient, genome scans have identified convergent genomic regions showing signatures of adaptation. However, when comparing sticklebacks from distinct freshwater habitats such as lakes and rivers hardly any convergent genomic regions have been identified. Here, I will argue that this not due to different approaches, sampling strategies, or genomic data. Utilizing whole genome resequencing data from 66 individuals from 11 populations, I will demonstrate that known candidate regions for the adaptation to freshwater can be readily identified while the same data and approach does not detect convergent adaptation between lake and river sticklebacks. I will discuss potential reasons for these differences and provide further evidence utilizing alternative approaches such as hierarchical models and exploration of polygenic signatures of local adaptation.

Poster session A - POL 300

The genome of *Gonium pectorale* reveals early genetic co-option during the evolution of multicellularity (51924)

Erik Hanschen, Bradley Olson.

University of Arizona; Kansas State University.

The evolution of multicellularity is a major evolutionary transition which has occurred numerous times throughout all domains of life, yet the evolutionary history of the basis of this transition is unknown. The volvocine green algae, including *Chlamydomonas* and *Gonium*, and *Volvox*, are a common model for evolution of multicellularity. Previous genomics revealed few differences attributed to *Volvox* morphology and development. Using the undifferentiated multicellular *Gonium pectorale*, we investigated when the genetic changes associated with the evolution of multicellularity evolved. Expanded or modified pathways shared in *Gonium* and *Volvox* include a retinoblastoma cell cycle regulator, cyclinD cell cycle regulators, transcription factors, and predicted gene families. Cell differentiation transcription factors are not expanded, and we demonstrate these genes evolved shortly after the speciation of *Gonium*. These data suggest that genes important for multicellularity were co-opted early during the evolution of multicellularity. Using multiple lines of evidence, we find the genetic changes associated with multicellularity evolved early during the evolution of multicellularity, which is consistent with other multicellular evolutions, including plants and animals.

Poster session A - POL 300

Genomic signatures of contrasting adaptation in cork oak populations across the species' range (51917)

Octávio Paulo, Pina-Martins Francisco, Modesto Inês, Ribeiro Carla, Costa Joana, Miguel Célia, Batista Dora.

CE3C – Centre for Ecology, Evolution and Environmental Changes. Universidade Lisboa. Portugal ; Instituto de Tecnologia Química e Biológica (ITQB), Universidade Nova de Lisboa, Portugal; RAIZ – Instituto de Investigação da Floresta e Papel. Herdade de Espirra, 2985-270 Pegões, Portugal; Instituto de Biologia Experimental (IBET), Oeiras, Portugal; Instituto de Investigação Científica Tropical, Oeiras, Portugal.

How natural populations adapt to contrasting environments and which genomics signatures can be detected associated with this process is one of the most challenging question in current evolutionary biology. These questions are particular complex for West-Mediterranean tree species showing both long distance gene flow and evolutionary and demographic histories influenced by Pleistocene glaciation or even older geological events.

Cork Oak populations were sampled and genotyped across the species' range and 21 environmental variables were used. Several types of genetic and genomic data (e.g.: MassArray and GBS) were used to gather a total of approximately 1300 SNPs. The results from traditional molecular markers and NGS based genome scans show the complexity of the evolutionary process and the interplay between structure, adaptation and gene flow. Furthermore, genomic signatures of positive and balancing selection were unravelled and their potential role in local adaptation through associations with environmental variables was explored under several scenarios and methodologies.

These results reinforce previous work (Modesto et al. 2014) emphasising the role of selection

and gene flow, rather than history and drift as the main driving forces in shaping the pattern of genetic diversity and local adaptation in this species. The implications of contrasting adaptation in the species response to rapid climate change will be discussed.

Poster session A - POL 300

Cryptic species within a cardinalfish: evidence for ecological speciation in the coral reef (51900)

Gabriele Gerlach, Jelle Atema, Michael Raupach, Michael J. Kingsford.

Carl von Ossietzky University Oldenburg; Boston University; Senckenberg am Meer, German Center of Marine Biodiversity Research; Centre of Excellence for Coral Reef Studies and School of Marine, James Cook University.

Evolutionary theory requires understanding of mechanisms that drive microevolution and maintain population divergence. Isolation of marine populations caused by large-scale geographic barriers cannot alone explain the high speciation rates and biodiversity of coral reef fishes with their larval dispersal that would predict genetic homogeneity. We searched for other isolating mechanisms starting at small spatial scales that drive microevolution despite gene flow.

We show that incipient speciation can be observed on the spatial scale of meters to few kilometers. Genetic analysis of the cardinalfish *Ostorhinchus doederleini* over ten generations at the Capricorn-Bunker group in the Great Barrier Reef, Australia, revealed five overlapping, phenotypically indistinguishable clades that can be considered different species inhabiting two different ecological niches: coral reef lagoons and coral reef slopes. Sequence data of two mitochondrial gene fragments as well as microsatellite markers indicated almost complete genetic isolation; but hybrids exist.

Our data provide evidence that shortly after hatching larvae imprint on olfactory cues of their natal environment including their own population. Orientation behavior, divergent selection between ecological niches and population recognition contributes to natal recruitment and genetic divergence that can persist despite gene flow.

Poster session A - POL 300

Asymmetric gene flow between populations of the marine crab *Liocarcinus depurator* (51879)

Francesc Mestres, Víctor Ojeda, Pere Abelló, Marta Pascual, Teresa García.

Universitat de Barcelona; Universitat de Barcelona; Institut de Ciències del Mar. Barcelona; Universitat de Barcelona; Centro Oceanográfico de Málaga.

In marine species, oceanographic discontinuities may be permanent and asymmetric, allowing mostly unidirectional gene flow. Nonetheless, even so-called permanent fronts can fluctuate, allowing for changes in migrant direction. We analyzed spatial genetic differentiation in the

crab *Liocarcinus depurator* across the three main oceanographic discontinuities found along the western Mediterranean: Gibraltar Strait, Almeria-Oran Front and Ibiza Channel. A partial fragment of the cytochrome oxidase I gene was sequenced in more than 400 individuals collected in five localities during four different time periods, so that genetic changes could be estimated across space and time. The intensity of interannual differences varied among populations, probably due to local shifts in circulation patterns modifying the asymmetric flow. The discrepancies previously reported on the effect of oceanographic discontinuities over multiple species could result from time-space interactions on the distribution of genetic variation. The present study highlights the importance of temporal replicates to better understand the spatial genetic structure of marine species and implement better management strategies for their conservation.

Poster session A - POL 300

Dominance genetic variance for traits under directional selection in *Drosophila serrata* (51860)

Jacqueline Sztepanacz, Mark W. Blows.

University of Queensland.

In contrast to our growing understanding for patterns of additive genetic variance in single and multi-trait combinations, the relative contribution of non-additive genetic variance, particularly dominance variance, to multivariate phenotypes is largely unknown. While mechanisms for the evolution of dominance variance have been, and to some degree remain, subject to debate, the pervasiveness of dominance is widely recognized, and may play a key role in several evolutionary processes. Theoretical and empirical evidence suggests that the contribution of dominance variance to phenotypic variance may increase with the correlation between a trait and fitness; however, direct tests of this hypothesis are few. Using a multigenerational breeding design in an unmanipulated population of *Drosophila serrata*, we estimated additive and dominance covariance matrices for multivariate wing shape phenotypes, together with a comprehensive measure of fitness, to determine whether there is an association between directional selection and dominance variance. Fitness, a trait unequivocally under directional selection, had no detectable additive genetic variance, but significant dominance genetic variance. For single and multivariate morphological traits, however, no relationship was observed between trait-fitness correlations and dominance variance. These data suggest that for many fitness components a positive association between directional selection and dominance variance may not be expected.

Poster session A - POL 300

The genome-wide landscape of population genetic variation in brown rat (*Rattus norvegicus*) populations. (51839)

Martha Gavan, Alex Douglas, Andy Black, Darren Christie, Sally Poncet, Martin Collins, Stuart Piertney.

University of Aberdeen; University of Aberdeen; Government of South Georgia & South Sandwich Islands; Government of South Georgia & South Sandwich Islands; Government of South Georgia & South Sandwich Islands; Government of South Georgia & South Sandwich Islands; University of Aberdeen.

Demographic perturbations such as founder effects can often create small, isolated populations that are at risk of becoming genetically depauperate due to the effects of random genetic drift. However, it has previously been demonstrated that even in small populations, selection can oppose drift to maintain variation at adaptive loci. Understanding the extent to which genetic diversity at immunologically important genes is affected by demographic perturbations is essential for the effective management of genetic resources in natural populations. Here we utilise next-generation sequencing techniques, specifically genotyping-by-sequencing (GBS), to identify genome-wide variation across ten isolated populations stemming from two separate founder events of brown rats (*R. norvegicus*) at the island of South Georgia in the southern Atlantic. GBS target sequences are assembled and mapped to the rat reference genome using a low density linkage map. SNP calls and estimated allele frequencies are used to characterise the patterns of genetic structure across samples, and pinpoint the regions of the genome that are displaying significantly higher sequence diversity than predicted by the genomic background. These “diversity islands” will highlight the genomic regions that are acting in a non-neutral way, and comparison across populations provides insight into the extent to which parallel or convergent responses occur.

Poster session A - POL 300

Hidden giant viruses in the public databases. (51837)

Vikas Sharma, Philippe Colson, Pierre Pontarotti, Didier Raoult.

Evolution Biologique et Modélisation.

Nucleocytoplasmic large DNA viruses (NCLDV), or proposed order Megavirales, belong to families of giant viruses that infect a broad range of eukaryotic hosts. Environmental metagenomic studies show that there is a “dark matter”, composed of sequences not linked to any known organism, as determined mainly using ribosomal DNA (rDNA) sequences, which therefore ignore giant viruses. Large scale phylogenetic analysis were performed, where we found few universally conserved genes were able to delineate Megavirales as separate clade which strongly suggest them as distinct biological entity compared to cellular organisms. Among these genes, DNA-dependent RNA polymerase (RNAP) is universally conserved in microbes and as well as in giant viruses. While phylogenetic reconstruction using RNAP gene, we found that three giant virus that have been mis annotated as as *Hydra magnipapillata*, *Marine group II Euryarcheota* and *Phytophthora parasitica*, additionally new viral clades have been detected from environmental database (Sharma et al., 2014)□. Our analysis suggest that RNAP as well as few other genes is a critical marker to detect hidden microbes and dark matter which may replace rDNA to delineate the four branches of life, Archaea, Bacteria, Eukarya and “Megavirales”.

Variation in the strength and shape of natural selection across three centuries of human civilisation (51832)

Erik Postma, Dominique Waldvogel.

University of Zurich.

Although natural selection is ubiquitous in plant and non-human animals, the question how selection is acting in human populations remains controversial. Indeed, it has been argued that with the introduction of birth control and dramatic improvements in medical care, selection has become negligible, and human evolution has come to a halt. However, this idea appears to be at odds with reality, with recent studies showing substantial amounts of variation in fitness, and strong selection on a range of human traits. As of yet we know very little about the generality of these findings, as they are based on a few populations and relatively short time periods. Here we will present an analysis of a uniquely detailed, longitudinal and individual-based human dataset, covering a period of three centuries. We will show how the distribution of lifetime reproductive success and its relationship with reproductive timing and lifespan has changed during this period, and how these have been shaped by culture, demography and the environment. Thereby we will provide one of the most complete investigations of variation in selection in our own species, and a fascinating glimpse into life as we know it.

Reference genome, population genetics and population genomics of wild falcons (51822)

Xiangjiang Zhan, Michael Bruford.

Institute of Zoology, Chinese Academy of Sciences, China; School of Biosciences, Cardiff University, UK.

Using the next generation sequencing technology, we have sequenced the genome of saker falcons (Zhan et al., 2013). The genome was about 1.2 Gb in length, from which we have annotated 16,204 genes. Falcon genomes were found to have consistent signatures of rapid evolution but less olfactory receptor genes. Compared with its relative species, peregrine falcons, the saker living in the arid environments seems to have evolved a robust gene repertoire to conserve more water and secrete more sodium. Then, we used the candidate gene approach referencing the draft genome to study the population genetics of sakers across Eurasia, and we found that exonic SNPs were key to resolving genetic differentiation between the QTP and non-QTP sakers, and were able to infer five SNPs as being subject to directional selection (Zhan et al., 2015). Now we are at the stage of taking our research from candidate genes and the reference genome to a population genomics level.

Comparative transcriptomics reveals the modular organisation of ant phenotypic traits (51818)

Claire Morandin, Morten Schiøtt, Liselotte Sundström, Jes Søe Pedersen, **Heikki Helanterä**, Alexander S. Mikheyev.

Centre of Excellence in Biological Interactions, Helsinki University; Centre for Social Evolution, University of Copenhagen; Okinawa Institute of Science and Technology.

Alternative phenotypes may be the results of genomic novelty or gene network interactions co-opted via natural selection. Reproductive division of labor in eusocial insects represents a major transition in evolution, and is a striking example of the same genetic background giving rise to alternative phenotypes, namely queen and worker castes. The extent to which caste-associated regulatory architecture is preserved across taxa remains unexplored. Applying weighted gene co-expression network analysis to transcriptomic data from 17 ant species, we show that most genes participate in conserved co-expression modules of functionally related transcripts. Furthermore, selection operating on these genes is heavily influenced by the co-expression network properties. Surprisingly, in addition to playing a role in caste differentiation, module expression levels were associated with other important traits, such as the evolution of worker sterility, caste dimorphism, polygyny and even invasiveness. These results provide insights into the complex structure of social insect transcriptional architecture, and identify functionally important units that serve as building blocks of phenotypic innovation. This study gives novel insights into the molecular interactions responsible for outstanding characteristics of eusocial insects, which would not be achieved by analyzing data from a single species.

Poster session A - POL 300

Estimating Selection of Skull Shape using Geometric Morphometrics (51796)

Elis Damasceno, Chris Klingenberg.

University of Manchester.

Natural selection is the evolutionary theory's centrepiece, and therefore it has drawn the interest of many researchers since its discovery. Although a very sought-after subject, selection gradients are not easily estimated, since it requires a measurement of fitness in addition to the quantitative data throughout several generations. Fitness and cross-generational data are even harder to obtain in wild populations, making such studies quite scarce in the literature. The Soay sheep of St. Kilda is one of the few wild populations in which such data is available, seeing that the population has been closely monitored since 1985. In this study, I used geometric morphometrics to estimate selection on skull shape. I digitized 1,527 Soay sheep skulls, that are stored at the National Museum of Scotland in Edinburgh. Using geometric morphometrics to estimate selection is particularly useful since not only do we get the strength of selection, but we can also visualize exactly how each trait is being selected. Given that skulls are very complex, multi-dimensional structures, it gives an enormous advantage when compared to traditional measurements.

The evolution of genomes and fitness traits in response to environmental change in the emerging model system *Daphnia* (51784)

Luisa Orsini, Anurag Chaturvedi, Craig Jackson, Nathan Keight, Omid Shams Solari, James Brown, Michael Pfrender, Kelley Thomas, Luc De Meester.

University of Birmingham, UK; University of Leuven, Belgium; Indiana University Bloomington, USA; University of California Berkeley, USA; Notre Dame University, IN, USA; University of New Hampshire, USA.

Understanding evolutionary adaptive responses of natural populations to environmental stress is challenging, owing in part to the complexity of natural environments. The waterflea *Daphnia magna* is a keystone species in aquatic ecosystems, a sentinel for water quality, and a model organism for eco-evolutionary genomics. It also creates dormant populations that accumulate in layered sediments of lakes and ponds – which can be resuscitated centuries later – thereby showing clear adaptive responses to environmental changes. Capitalizing on this unique ecological system, we present a complete analysis of genome structural variation and evolution of fitness traits in response to a suite of environmental stressors (parasites, land use, and fish predation) across a complex landscape of shallow ponds. We further validate these findings in time in populations resurrected from sediment cores with known histories for the same stressors. In our analysis of structural variation we link candidate gene networks and CNV genes to fitness traits using statistical tools optimized by the ENCODE consortium, unraveling the genetics of complex traits. We identify the mechanisms of evolution underlying responses to both natural and anthropogenic stressors and assess repeatability of evolutionary adaptive processes in nature.

Rapid morphological evolution related to male-male combat of invasive green anole in Ogasawara Islands, Japan. (51769)

Wataru Anzai, Hiroo Takahashi, Mitsuhiko Toda, Hideki Endo.

The University of Tokyo; Japan Wildlife Research Center.

Introduced species have been noted to be model organisms which can be observed rapid evolution. We report that two populations of invasive green anole lizard (*Anolis carolinensis*) in Chichi-Jima Island and Haha-Jima Island show different morphological traits although it has been only thirty years since invasion of these lizards. By comparison of body size and head size between two populations of islands and sexes, males of Haha-Jima populations showed significant larger body and head considered to be advantageous for territorial combat though females indicated no significant differences between islands. Because of diverse results between sexes, it is considered that these traits are affected by not only ecological factors common to sexes such as prey animals or vegetation but also male-specific factors

such as territorial combat between individuals. Addition, as a result of the comparison of mass of limb muscles between populations, heavier humeral adductor muscles of lizards in Chichi-Jima than in Haha-Jima were shown only in males. Our results demonstrate that green anole have occurred morphological differences between island populations for only fifty years, and suggest the differences have evolved through sexual selection such as male-male combat.

Poster session A - POL 300

Investigation of selection patterns across the New Zealand Giant Weta genome, using comparative transcriptomics (51766)

Victoria Twort, Richard Newcomb, Howard Ross, Thomas Buckley.

Landcare Research; The Univerisy of Auckland; Allan Wilson Centre; The New Zealand Institute of Plant and Food Research Ltd.

Giant Weta are among the largest extant insects on earth, and are an iconic part of the New Zealand biota. However, a number of these species are endangered. The Poor Knight Giant Weta (*Deinacrida fallai*, Orthoptera) is one such species, and is restricted to a small offshore island. Our aim is to construct a comparative genomic dataset that will be used to investigate various aspects of molecular evolution and evolutionary relationships of this endemic New Zealand insect. The *D. fallai* genome is larger (approximately 8.5 GB) than the only other published Orthoperan genome (*Locusta migratoria*), with the current draft assembly being generated with SOAPdenovo2. Transcriptome data has been obtained to identify unigenes involved in reproduction, glycolysis and sensory processes in order to study rates and patterns of molecular evolution among species. RNA-seq data has also been generated for a number of Tree and other Giant Weta species, resulting in an average of 190,943 contigs per species, and an average N50 of 875 bp. This current dataset is being combined with Genotyping-By-Sequencing data to investigate various conservation genetics issues, in order to better inform current and future conservation efforts.

Poster session A - POL 300

Evaluation of adaptive potential of the European eel population suggests a recovery of its genetic status (51762)

Miguel Baltazar-Soares, Seraina E. Bracamonte, Till Bayer, Frédéric J.J. Chain, Reinhold Hanel, Chris Harrod, Christophe Eizaguirre.

Helmholtz Center for Ocean Research (GEOMAR); Department of Biology, McGill University, Canada; Thunen-Institute of Fisheries Ecology, Germany; Universidad de Antofagasta, Chile; School of Biological and Chemical Sciences, Queen Mary University of London, UK.

The integration of evolutionary theory in conservation programs provides a framework that has greatly improved our ability to protect endangered species. However, it is only seldom

applied to the management of marine living resources. One of the most staggering examples is that of the European eel, the only critically endangered species in the World whose exploitation is still legal. The recruitment of this species has suffered a sudden collapse in the beginning of the 1980s. By 2011, it remained as low as 1% of the values preceding the 1980s period. Surprisingly, conservation measures are limited to the translocation of juveniles and implementation of fishing quotas. Here we present the first study assessing the evolutionary potential of the European eel. We compared the neutral genetic diversity - microsatellites and mtDNA - and the adaptive genetic diversity - the Major Histocompatibility Complex (MHC) - of two distinct generations of eels. The evolution of MHC genes is particularly relevant as the European eel faces a parasitic threat by a recently introduced nematode. Our results show that both the recruitment collapse and the parasite introduction have left signatures of a genetic bottleneck event. However, results also suggested an ongoing recovery positively affecting estimates of genetic diversity - critical for the adaptive potential of the species

Poster session A - POL 300

Catch me if you can: Adaptation from standing genetic variation to a moving phenotypic optimum (51748)

Sebastian Matuszewski, Joachim Hermisson, Michael Kopp.

University of Vienna; Max F. Perutz Laboratories; Aix Marseille Université.

Natural populations are constantly faced with environmental changes that force them to either adapt or go extinct. Therefore, increasing our understanding of the adaptive process is important for both basic and applied research. Accordingly, numerous studies have tried to provide a formal framework for the description of the adaptive process. Out of these, two complementary modeling approaches have emerged: While so-called adaptive-walk models consider adaptation from the successive fixation of de-novo mutations only, quantitative genetic models, on the other hand, assume that adaptation proceeds exclusively from pre-existing standing genetic variation. The latter approach, however, has focused on short-term evolution of population means and variances rather than on the statistical properties of adaptive substitutions. Thus, I will here address what has been described as "the most obvious theoretical limitation when describing the adaptive process," and propose an analytical framework for the genetic basis of adaptation from standing genetic variation in terms of the effect-size distribution of individual alleles. This approach addresses one of the central questions in this context: From the multitude of standing genetic variants segregating in a population, which are the ones that ultimately become fixed and contribute to adaptation, and how does their distribution differ from that of de-novo mutations?

Poster session A - POL 300

Why no stabilizing selection (in damselflies)? (51742)

John Waller.

Lund University.

Several published reviews of selection gradients that have been estimated field populations have failed to show that stabilizing selection is the predominant mode of selection on microevolutionary time scales. Instead these reviews have shown that stabilizing and disruptive selection are equally common in nature. Two major explanations have been put forward to resolve this apparent discrepancy between these selection gradients on microevolutionary time scales, and the macroevolutionary assumption that stabilizing selection should predominate and lead to evolutionary stasis: (1) Low statistical power (2) and fluctuating selection. However, few studies have been replicated over several generations and with high sample sizes, and even fewer have attempted to verify that stabilizing selection is indeed operating on macroevolutionary time scales. Here we will present the results of a multi-season selection study of two congeneric damselfly species (“demoiselles”; *Calopteryx splendens* and *C. virgo*), using large sample sizes and replicated estimates across years and populations. Additionally, macroevolutionary trends on body size within the suborder Zygoptera (damselflies) will be presented and compared to the patterns of selection in extant populations. Finally, I will address other sources of low power within selection studies, namely low recapture probabilities can affect the results of natural selection studies in field populations.

Poster session A - POL 300

Sex in space: what changes? (51738)

Hanna Kokko, Anna Harts, Luke Holman, Lisa Schwanz.

University of Zurich; Australian National University; University of New South Wales.

No-one who travelled from afar to the ESEB disputes that environments vary spatially. Still, many topics in evolutionary ecology are modelled assuming one panmictic population. I will discuss two cases where this tradition can make us miss intriguing and important phenomena. The first question considers spatial variation with dispersal in the context of the lek paradox. A spatial selection mosaic is sometimes seen to be ‘bad’ and sometimes ‘good’ for female choice for genetic benefits: bad because it disrupts signal reliability; good because it prevents female choice from being too efficient for its own good (by depleting variation). We will show the need to proceed beyond simplistically discrete GxE worlds to find out how often “good > bad” in this context. The second question: is there an a priori reason to expect that alleles that benefit one particular sex are favoured when there is sexual antagonism? One might think ‘no’ in diploid species because approximately ½ of gene flow operates through males, the other ½ through females. Our modelling shows, however, that a fundamental asymmetry between female and male importance as determinants of demography can change this conclusion – but only when there is spatial variation in habitat quality.

Poster session A - POL 300

Using a landscape genomic analysis to detect selection by climate in natural populations of a Mexican endemic oak, *Quercus rugosa* (51733)

Karina Martins, Paul Gugger, Jesus Llanderal Mendoza, Antonio Gonzalez-Rodrigues, Ken Oyama, Victoria Sork.

Ecology and Evolutionary Biology, University of California; Department of Biology, Federal University of São Carlos; Centro de Investigaciones en Ecosistemas, UNAM; Institute of the Environment and Sustainability, University of California.

Climate places strong selective pressure on local populations. In tree species with extensive gene flow, it is not clear the extent to which climate creates locally adapted populations. By using a landscape genomics analysis of geographic patterns of genome-wide single nucleotide polymorphisms (SNPs), DNA sequence data can be used to test the hypothesis that tree populations are locally adapted to climate. Our goal to find evidence of local adaptation to climate and identify specific loci under selection by surveying DNA fragments spread throughout the genome of *Quercus rugosa*. We sampled adult leaf tissue from 105 trees in 17 localities across Mexico, extracted DNA, and used the genotyping-by-sequencing (GBS) method to generate SNPs from thousands of “random” 100-bp fragments. We controlled for background demographic history using covariance matrices and then correlated individual SNP genotypes with specific climate variables using the Bayesian approach implemented in Bayenv2. After aligning our fragments to a *Quercus lobata* reference draft genome, we generated 8,383 SNPs. Several SNPs were correlated with climate variables, usually variables associated with precipitation. We conclude that landscape genomics provides an effective tool to find evidence for selection in natural populations of nonmodel species, and for providing excellent information about the genome-wide genetic structure.

Poster session A - POL 300

The evolutionary history of *Cochlearia* (Brassicaceae) in Central Europe: Population- and phylogenomics of a cold relic in a warming world (51728)

Marcus Koch, Eva Wolf.

COS Heidelberg, Heidelberg University.

The genus *Cochlearia* represents an isolated evolutionary lineage that diverged from its Mediterranean sister clade during the Miocene and since that did not underwent any significant speciation until Pleistocene glaciation and deglaciation cycles. During the Pleistocene approximately 20 taxa evolved within a polyploid complex, with most of the species closely associated with cold-characterized habitats. Similar eco- and phenotypes of varying ploidy levels emerged and are scarcely distributed all over Europe and the Circumarctic. One sub-group of species is occurring mostly along coastal lines and a second sub-group is highly restricted to mountain and high elevation/altitude regions. The proposed project aims to unravel the evolutionary history of the various species, subspecies and cytotypes on a high-resolution-scale in space and time. The resulting evolutionary-systematic framework will lay the ground to study in particular hypotheses on parallel evolution and

adaptation to cold environments with its respective characteristics and types of habitats (e.g. bedrock types, elevation, etc.).

Poster session A - POL 300

Effects of environmental heterogeneity on phenotypic and genetic variance components in a tree swallow population (51696)

Audrey Bourret, Dany Garant.

Université de Sherbrooke.

Despite numerous reports of selection on heritable traits in wild populations, expected evolutionary responses are often absent. Different causes for this stasis are suggested, including undescribed fluctuating selection and unstudied factors influencing phenotypic/genetic variance components. Heterogeneous environmental conditions, in space and/or in time, can affect both selective pressures and trait heritabilities in wild populations and thus reduce our capacity to predict evolutionary changes. Here, we will use data from a long-term study of Tree swallow (*Tachycineta bicolor*) in southern Québec (Canada) to assess the effects of environmental heterogeneity on phenotypic and genetic variance components of several traits. This study system, followed since 2004, is composed of 400 nest boxes equally distributed within 40 farms in a highly heterogeneous agricultural landscape. Previous studies in this population reported patterns of fluctuating selection in direction and/or strength for morphological and reproductive traits over space and time. Our analyses will assess the importance of phenotypic and genetic variance components across these scales and provide predictions on the evolutionary potential of these traits in this population. Our results will thus contribute to a better understanding of the environmental effects on evolutionary processes in the wild.

Poster session A - POL 300

Evolutionary Origin of Antimicrobial Peptide (AMP) Resistance in Firmicutes Bacteria (51678)

Sonja Grath, Helge Feddersen, Susanne Gebhard.

*Department of Biology II, University of Munich (LMU), Planegg-Martinsried, Germany ;
Department of Biology and Biochemistry, University of Bath, United Kingdom.*

To combat the alarming rate of antibiotic resistance, antimicrobial peptides (AMPs) are seen as promising new drugs. However, AMP resistance already exists in many bacteria, including important pathogens. We focus on BceAB-like transport systems, which mediate AMP resistance in a wide range of Gram-positive bacteria. Here, we present a highly interdisciplinary approach that combines bioinformatic analyses of the evolutionary origin of BceAB-like transporters with experimental work on the structure and function of these proteins. Protein domains – the evolutionary, functional and structural building blocks of

proteins – are the modules on which evolution acts. Bce-like transporters possess two FtsX domains of unknown function, which also occur in other resistance transporters found in most bacterial phyla. To gain insights into the relationship and evolution of the diverse group of FtsX-domain transporters, we studied their domain arrangements. Computational analyses of FtsX domains showed that the two domains in BceAB-like transporter have diverged from one another, which is a good indication of the evolution of separate functions. Our approach is aimed to gain insights that can ultimately lead to the development of new stochastic models for the evolution of antibiotic resistance in general or of new drugs that counteract this resistance.

Poster session A - POL 300

Domestication of Lima bean (*Phaseolus lunatus* L.) and its adaptation (51660)

Maria Chacon, Jaime Martinez-Castillo.

Universidad Nacional de Colombia; Centro de Investigación Científica de Yucatán.

Lima bean is an ancient crop widely distributed in Mesoamerica and the Andes. Three wild gene pools with disjunct distributions are recognized: the Andean one distributed on the western slope of the Andes in Ecuador and northern Peru, the Mesoamerican I located in central-western Mexico, and the Mesoamerican II distributed from southern Mexico to northern Argentina, always on the eastern slope of the Andes. Humans domesticated Lima beans in at least two separate events: once in Mexico from wild populations of the gene pool MI, and a second event in the Andes of Ecuador-northern Peru. Both domestication events resulted in strong founder effects and in a group of landraces that although share many domestication traits, also differ in many morphological characteristics and in their adaptation to diverse agroecological conditions. In this study, we applied Genotyping by Sequencing in a set of wild and domesticated individuals of Lima bean representative of its geographical distribution in the Americas for two purposes: identify genomic regions associated with climate adaptation and with the adaptive syndrome of domestication. The present results contribute to our understanding of the adaptation processes of wild species to new environments during domestication and the origin of traits of agricultural importance.

Poster session A - POL 300

Genetic structure and signature of selection in a cyanobacterial lichen symbiosis (51646)

Silke Werth, Hörður Guðmundsson, Zophonías Oddur Jónsson, Ólafur Sigmar Andrésón.

Institute of Plant Sciences, University of Graz, Austria; Life and Environmental Sciences, University of Iceland, Iceland.

Lichens represent a textbook example of mutualistic symbiosis. For green-algal lichens, evidence is mounting that the ecological niche of the lichen-forming fungi is shaped by

associations with green-algal strains that are locally adapted to specific ecological and climatic conditions. These green-algal associations are frequently highly specific, with lichen-forming fungi associating with one or few green-algal taxa. Cyanobacterial symbioses represent about 10% of the lichens. Cyanobacterial lichen symbioses frequently show low specificity, with local strains being present in a lichen that are frequently more closely related to free-living or bryophyte-associated cyanobacteria than to the cyanobacterial strains occurring in the same lichen, collected from another site. Here, we compare the genetic structure among *P. membranacea* and its *Nostoc* photobiont based on ddRAD tag sequences. We found differences in genetic structure among lichen symbionts, with the fungus showing less isolation by distance than its associated cyanobacteria. Finally, we detect outlier RAD tag loci in both symbionts and relate these to the bioclimatic factors and environmental conditions of the sites to evaluate whether either one of the partners exhibits signatures of selection.

Poster session A - POL 300

Long term sperm competition radically alters male success (51630)

Tom Price, Paulina Giraldo-Perez, Paul Herrera, Nina Wedell.

University of Liverpool; University of Vienna; University of Exeter.

Competition between sperm from more than one male within females has major evolutionary impacts. However, research has typically focused on females that store sperm for a short time. In nature, females from many insects and reptiles store sperm overwinter or summer, and some may store sperm for decades. Here we investigate sperm competition in the fruit fly *Drosophila pseudoobscura*. We show that sperm competition that occurs over winter has radically different outcomes to the short term sperm competition seen in the summer. Moreover, overwintering duration greatly increases the cost of carrying an ejaculate, with high death rates among females that have mated with particular male genotypes. We suggest that many of the puzzles of reproductive physiology may turn out to be adaptations to long term sperm storage and competition.

Poster session A - GEN 2000

Resistance and tolerance towards parasites in a polymorphic insect (51645)

Beatriz Willink, Erik I. Svensson.

Lund University.

The role on biotic conflicts promoting the buildup of distinct genetic clusters is widely appreciated in evolutionary biology. Evolutionary arms races propelled by parasitism and sexual conflict can be driven to a halt through the evolution of alternative phenotypic strategies governed by or linked to a few major loci. In the pond damselfly *Ischnura elegans* (Common Bluetail) sexual conflict over mating rates is involved in the maintenance of female genetic colour morphs via frequency-dependent male-mating harassment. However, several

other traits differ between these discrete morphs. These damselflies are parasitized by water mites (*Arrenurus* spp.) whose abundance and pathogenicity may vary largely across populations and years. We analyzed how parasite loads effected female fecundities over a decade and across a dozen populations in southern Sweden. Resistance and tolerance are integrated differently in the two most common morphs: male coloured females suffered from higher parasitism but their egg production was largely insensitive to mites, whereas the other morph carried fewer parasites but their fecundity was more severely affected by the parasite loads. Our results are in line with the theoretical tenet that negative correlational selection operates to couple resistance and tolerance, resulting in alternative adaptive peaks of these sympatric morphs.

Poster session A - GEN 2000

Evolutionary Potential of Ectoparasitism by Mites (51750)

Michal Polak, Joshua Benoit.

University of Cincinnati.

Knowledge of the fitness costs of parasitism and the genetic basis of host defensive traits are critical components of our ability to predict evolutionary response to parasitism. We studied the evolutionary potential of ectoparasitism by mites in two species of *Drosophila* hosts, *D. nigrospiracula* and *D. melanogaster*, which occur naturally in the North American Sonoran Desert and in Taiwan, respectively. We demonstrate significant fitness costs of ectoparasitism, including damage to host lifespan and reproduction. Both host species responded to laboratory artificial selection for increased resistance, demonstrating significant additive genetic variation for defense. Flies resistant to one species of mite exhibited cross-resistance to the other, indicating that resistance may be a broad-based multiple-parasite defensive phenotype, as seen in certain other animal, plant and microbial systems. We performed RNA-seq analyses to characterize acute responses to ectoparasitism. Parasitized flies exhibited over 600 genes with differential expression compared to controls. Among flies exposed to mites but that evaded parasitism, 13 genes were upregulated while 27 were downregulated. Among upregulated genes, some are involved in gluconeogenesis and amino acid metabolism, suggesting shifts in metabolic processes resulting from defensive activities. This transcriptional characterization identifies potentially variable genes serving as substrate for evolutionary response under parasite-mediated selection.

Poster session A - GEN 2000

Coevolution between the red flour beetle and *Bacillus thuringiensis* bacteria: transcriptome analysis of host defence after experimental evolution (51782)

Barbara Milutinovic, Jennifer Greenwood, Kevin Knoblich, Philip Rosenstiel, Daniela Esser, Hinrich Schulenburg, Joachim Kurtz.

Institute of Science and Technology Austria; Insitute for Evolution and Biodiversity (University of Münster); Institute of Clinical Molecular Biology (CAU Kiel); Zoological Institute (CAU Kiel).

Host-parasite interactions are ideal systems for studying fast coevolutionary processes. We performed a laboratory evolution experiment using an oral infection system of the red flour beetle *Tribolium castaneum* and the entomopathogenic bacterium *Bacillus thuringiensis*. We were specifically interested in distinguishing coevolution-specific patterns from patterns resulting from the adaptation to a non-changing antagonist. For this, we used such an experimental design where the antagonists were either adapting reciprocally to each other ('coevolution' treatment), or to a non-changing, ancestral parasite or host genotype, respectively ('evolution' treatments). We found that after only seven host generations, parasite virulence was increased in the 'coevolution' treatment, but not in the parasite 'evolution' treatment, where some replicate lines of the parasite even showed reduced virulence. By contrast, the hosts evolved to increased resistance in both 'coevolution' and 'evolution' treatments. Using RNA sequencing, we studied the transcriptomes of the evolved hosts upon infection to find out to what extent differences in the regulation of host defences might be responsible for the fast (co-) evolutionary responses of the hosts. To detect evolved differences in host defences shaped by the differing selection pressures we compared transcriptome responses of the selected hosts upon infection and will report our first results.

Poster session A - GEN 2000

Contemporary evolution of immunity in invasive species: the case of the domestic mouse (*Mus musculus domesticus*) and of the black rat (*Rattus rattus*) in Senegal. (51810)

Christophe Diagne, Khalilou Bâ, Carine Brouat, Nathalie Charbonnel, Ambroise Dalecky, Mamoudou Diallo, Emmanuelle Gilot-Fromont, Laëtitia Husse.

Centre de Biologie pour la Gestion des Populations (CBGP) Montpellier, FRANCE; IRD-BIOPASS/CBGP (Dakar, SENEGAL); Département de Biologie animale (FST/UCAD, Dakar, SENEGAL); LPED UMR 151 IRD, Marseille FRANCE; VetAgroSup / LBBE (Lyon, FRANCE).

Biological invasions provide unique opportunity for studying adaptive evolution over contemporary time scales. The recently refined “evolution of increased competitive ability” (EICA) theory predicts that invasive populations are likely to favour less expensive antibody-mediated immunity at the expense of costly cell-mediated one, what would increase their competitive ability.

We tested this hypothesis by comparing immune responses of invasive (*Mus musculus domesticus*, *Rattus rattus*) and native (*Mastomys erythroleucus*) rodents along invasion routes in Senegal. We estimated several components of immunity, including humoral pathways (natural antibodies and complement) and inflammation (haptoglobin).

We found significant differences in immune investment between native and invasive rodents, as well as between anciently established and wave-front populations of invasive species. Surprisingly, inflammatory responses were found to increase in wave-front populations of both invaders, whereas an increase in humoral responses was only detected in *M. m.*

domesticus. These results are compatible with some patterns observed when studying parasite communities (helminths, bacteria) along invasion routes, which highlighted higher infection risks for invasive hosts in wave-front populations. Experimental immune challenges are in progress to decipher whether these changes in immune investments may be explained by selection or plasticity.

Poster session A - GEN 2000

A targeted proactive response to prevent disease outbreaks in ant societies (51870)

Christopher D Pull, Simon Tragust, Mark JF Brown, Sylvia Cremer.

IST Austria; University of Regensburg, 93040 Regensburg, Germany; Current address: University of Bayreuth, 95447 Bayreuth, Germany ; Royal Holloway University of London, Egham, Surrey, TW20 0EX, UK.

Infectious diseases will have represented a major challenge during the evolution of sociality, given that close contact with conspecifics is a key transmission route for many pathogens. To prevent epidemics, societies have evolved mechanisms to reduce pathogen exposure, and to prevent transmission when infections do occur. The most efficient way to block transmission is to break the infectious cycle of the pathogen.

Here we show how ants alter their behavioural response, from the initial intensive care of pathogen-exposed colony members, to a colony-level disease-containment strategy, when an individual becomes fatally infected. Crucially, we found that the ants responded proactively towards infected colony members, inhibiting pathogen replication early during the infection cycle, before they became a source of infection to others. The ants achieved this through the very early detection of sick individuals, before they displayed outward signs of disease, followed by destructive mechanical and chemical disinfection, which inhibits pathogen growth.

Thus, although this defensive strategy does not cure the sick colony member, it has a beneficial effect at the colony level, avoiding further infections that may otherwise lead to an epizootic.

Poster session A - GEN 2000

Parasitism as a driver of age-specific mortality in Asian Elephants (*Elephas maximus*) (51896)

Carly Lynsdale, Hannah Mumby, Khyne U Mar, Virpi Lummaa.

University of Sheffield.

Parasitism has long been proposed to drive trade-offs between host investment in reproduction and survival. In natural populations, hosts vary in their ability to resist or succumb to parasite infection and the extent to which such infection impacts upon host health and reproductive fitness. Determining the causes of variation in resistance and the consequences of infection for different individual hosts is key in understanding host-parasite evolution.

We investigated the effect of parasitism as a driver of age specific mortality in a population of semi-captive Asian elephants (*Elephas maximus*) employed in logging camps across Myanmar. First, using a longitudinal database encompassing elephant life-history, health and reproductive data (n= ~2,350), we determined variation in causes of host mortality across different ages and any sex differences therein. Second, we linked parasite-caused mortality at different ages to individual reproductive history across previous life.

This research highlights the importance of host variation in parasitic resistance and susceptibility, providing data on effects of parasitism on elephant mortality and reproduction across a lifetime. Through determining individuals for which infection may be a particular risk, we provide important insights for the conservation, welfare and management practices of Asian elephants.

Poster session A - GEN 2000

Protein evolution of Toll-like receptors 4, 5 and 7 within Galloanserae birds (51898)

Michal Vinkler, Hana Bainova, Josef Bryja.

Department of Zoology, Charles University in Prague; Institute of Vertebrate Biology, Academy of Sciences of the Czech Republic.

Toll-like receptors (TLRs) belong among essential activators of vertebrate immunity. We analysed interspecific variability in coding sequences of three TLRs (bacterial-sensing: TLR4, TLR5 and viral-sensing: TLR7) within the Galloanserae bird clade (13 species). The investigated TLRs are interspecifically invariant in their tertiary structures but vary in some of their physiochemical properties, mainly in the predicted surface electrostatic potential distribution. The predicted ligand-binding features of avian proteins (mainly TLR4 and TLR5) were distinct from their fish and mammalian counterparts and variable within the Galloanserae clade. We have identified 20 positively selected sites and 79 evolutionarily non-conservative sites, several of which were located in close topological proximity to the ligand-binding sites reported for mammalian and fish TLRs. Most of these functionally relevant positively selected sites were found in TLR5. In viral-sensing TLR7 the variability seems to be functionally far more conservative than the variability in the bacterial-sensing TLRs. Our results suggest that avian TLRs might be differentially adapted to pathogen-derived ligand recognition than the corresponding TLRs in mammals and we have found signatures of positive selection even within the Galloanserae lineage itself.

Individual multilocus heterozygosity at immune gene loci but not microsatellites influences roe deer natal dispersal (51957)

Cécile Vanpé, Lucie Debeffe, Maxime Galan, Mark Hewison, Jean-Michel Gaillard, Emmanuelle Gilot-Fromont, Nicolas Morellet, Erwan Quéméré.

LBBE - CNRS; CEFS - INRA; CBGP - INRA; VetAgro-sup - Université Lyon 1.

Most previous studies on immune genes have focused on immunological defence, pathogen resistance, mate preference, or kin recognition. Although both immune function and pathogen infestation, which are associated with immune gene diversity, have been found to influence dispersal decisions, no study has yet investigated the influence of immune genes on dispersal. Here, we filled the gap by investigating the effect of individual heterozygosity at five immune gene loci (from the Major Histocompatibility Complex and encoding Toll-Like Receptors) on roe deer natal dispersal. We showed that dispersal propensity was affected by immune gene diversity, with a body-mass dependent effect likely linked to pathogen-mediated selection through over-dominance, whereas individual multilocus heterozygosity at 12 putatively neutral microsatellite markers did not affect natal dispersal. Overall, in support of the body-condition dependent dispersal hypothesis, dispersal propensity increased with both body mass and immune gene diversity. However, very light roe deer with low immune gene diversity dispersed much more than expected from their size. We suggest these poor quality individuals exhibited an emergency life-history tactic to escape a heavily infested environment associated with poor fitness prospects. Our results have potentially important consequences in terms of population genetics and demography, and improve our knowledge of host-pathogen evolution.

The QRS (Quantification of Representative Sequences) pipeline for amplicon sequencing: Case study on within population ITS1 sequence variation in a microparasite infecting *Daphnia*. (51964)

Enrique Gonzalez Tortuero, Jakub Rusek, Adam Petrusek, Sabine Giessler, Dimitrios Lyras, Sonja Grath, Federico Castro Monzon, Justyna Wolinska.

Department of Ecosystem Research, Leibniz-Institute of Freshwater Ecology and Inland Fisheries (IGB); Berlin Centre for Genomics in Biodiversity Research (BeGenDiv); Department of Biology II, Ludwig Maximilians University, Munich; Department of Ecology, Faculty of Sciences, Charles University in Prague.

Next Generation Sequencing (NGS) platforms are replacing traditional molecular biology protocols like cloning and Sanger sequencing. However, accuracy of NGS platforms has rarely been measured when quantifying relative frequencies of genotypes or taxa within populations. Here, we compared results generated by 454 amplicon sequencing with the results obtained from Sanger sequencing of cloned PCR products. Specifically, we focused on sequence variation of the first internal transcribed spacer (ITS1) region of the nuclear ribosomal DNA of the ichthyosporean *Caullerya mesnili*, a microparasite that commonly

infects water fleas (*Daphnia*). *Caullerya* samples were obtained from seven spatially isolated host populations, some of which were sampled across different years (16 population samples altogether). In order to analyse 454-generated sequence data, we developed a bioinformatic pipeline – Quantification of Representative Sequences (QRS) – that clusters slightly varying sequences into representative variants and determines the frequency of these variants per population sample. Overall, there was a good correspondence in absolute frequencies of ITS1 variants obtained from Sanger and NGS sequencing; consequently, the respective analyses of molecular variance (AMOVA) resulted in similar amounts of genetic variance partitioned across spatial and temporal components. Our results support the usefulness of amplicon sequencing data for studies of within-population structure.

Poster session A - GEN 2000

Variation of vector competence in *Culicoides sonorensis* (51979)

Ramiro Morales-Hojas, Rhiannon Silk, Malcolm Hinsley, Irina Armean, Paul Kersey, Simon Carpenter, Mark Fife.

The Pirbright Institute; European Bioinformatics Institute.

Culicoides species include major vectors of livestock disease agents such as Bluetongue (BTV), Schmallenberg and African Horse sickness viruses. Understanding the genetics of virus transmission is a fundamental step towards controlling these diseases. As in the case for other vector-borne diseases, this task can be greatly facilitated by the availability of a genome sequence, however the closest phylogenetic species to the biting midges for which complete annotated genomes are available are the mosquitoes, which have a divergence of more than 200 million years. With the aim of understanding the genetic basis of vector competence in *C. sonorensis*, the North American vector of BTV, we have de novo sequenced the first genome for this group of vector species. Using this genome as reference, we have studied the differences in gene expression between individuals that are susceptible to virus infection and are, thus, vector competent, and those that are refractory to infection and are not capable of BTV transmission. The differences observed will help understanding the evolution of *Culicoides*-BTV interactions and the relevance of genetic variation in vector species for arbovirus transmission. This information will be central to control BTV transmission and its range expansion.

Poster session A - GEN 2000

Why Sexually Transmitted Bacteria Tend to Cause Infertility: An Evolutionary Hypothesis (51988)

Péter Apari, Joao Dinis De Sousa, Viktor Müller.

Eötvös Loránd University; Katholieke Universiteit Leuven.

Extending earlier work we argue that the tendency of sexually transmitted infections (STIs) to cause infertility is likely to reflect an evolutionary adaptation of the pathogens. We use an evolutionary perspective to understand how STI pathogens may benefit from reducing fertility in the host, and what clues the mechanisms of pathogenesis can offer to the evolution of this ability.

We survey three lines of evidence. First, we present a compilation of recent epidemiological and clinical data to illustrate the breadth and magnitude of the problem; second, we draw on sociological and behavioural data to argue that infertility can destabilize partnerships and thereby increase promiscuity—which facilitates the transmission of STI pathogens; and third, we review the pathomechanisms of STI induced infertility, and demonstrate that most of these mechanisms have a specific targeted effect on fertility, which is strong indication that the mechanisms have evolved specifically for their role in infertility.

Our evolutionary framework also provides clues to why STI induced infertility tends to affect female host more than male hosts, and suggests specific medical interventions.

Poster session A - GEN 2000

Ants do drugs to fight disease (51990)

Nick Bos, Liselotte Sundström, Siiri Fuchs, Dalial Freitak.

Centre of Excellence in Biological Interactions, University of Helsinki and University of Jyväskylä; Centre of Excellence in Biological Interactions, University of Helsinki.

Parasites are everywhere, and if anything in life is certain, it is that at one point, you are going to get infected. One way to fight infection is self-medication, which occurs when an organism consumes biologically active compounds to clear or inhibit an infection. Self-medication can either be therapeutic or prophylactic, depending on the health status of the organism when it consumes the biologically active compounds. Here, we show for the first time that ants selectively consume harmful substances (Reactive Oxygen Species, ROS) upon exposure to a fungal pathogen *Beauveria bassiana*, yet avoid these in the absence of infection. This increased intake of ROS, while harmful to healthy ants, leads to higher survival of infected ants. The fact that ingestion of this medicine carries a fitness cost in the absence of pathogens rules out compensatory diet choice as the mechanism, and provides the first conclusive evidence that social insects engage in therapeutic self-medication. They have a sense of what they eat, and can modulate their choice of food in response to environmental challenges such as pathogens, resulting in a fine-tuned interaction between pathogens and host.

Poster session A - GEN 2000

Steady state and induced immunity among castes of *Formica exsecta* (52105)

Dimitri Stucki, Liselotte Sundström, Dalial Freitak.

Centre of Excellence in Biological Interactions / Department of Biosciences; University of Helsinki; Tvärminne Zoological Station, University of Helsinki; Centre of Excellence in Biological Interactions, University of Jyväskylä.

Probably the most striking feature of eusocial insects is the separation into distinct castes, each of which specialize in different aspects of colonial performance. As a consequence gynes, males and workers which perform different tasks follow different life history trajectories. While the short-lived males and long-lived gynes only leave the colony for reproduction, workers experience frequent contact with the surrounding environment. In addition, depending on their task some workers stay closer around the nest (nurses) or spread further outdoors (foragers). Thus, each caste and worker class encounters pathogens at a different frequency, which might influence demands on individual immune defenses. We examined the differences in steady state immunity and expression of immunity after challenge with *Beauveria bassiana* in males, gynes and two worker classes of *Formica exsecta*. Using gene expression data for ten genes we found a clear separation between castes in steady state gene expression patterns. The response in gene expression to infection with *B. bassiana* was distinct between gynes and males but not between nurses and foragers or sexuals and workers in general.

Poster session A - GEN 2000

The Impact of Parasite Mediated Selection on the Host's Genetic and Phenotypic Diversity at the Metapopulation Level (52123)

Andrea P. Kaufmann, Ebert Dieter.

University of Basel; 2Tvärminne Zoological Station, Hanko, Finland.

Theory suggests that parasite mediated selection varying in space and time is capable of maintaining diversity in disease related traits. Studying parasite mediated dynamics in natural populations has proven challenging because it is difficult to disentangle the relative roles of natural selection, migration, drift and mutation in shaping the genetic structure of a subdivided population. In this project we aim to uncover signatures of spatially fluctuating, parasite mediated selection in a natural metapopulation of *Daphnia magna*. We hypothesize that the polymorphism in disease related traits of the host can be explained by the dynamic metapopulation structure of the host and the parasite. The spatial variation in the presence and absence of a microsporidian parasites leads to fluctuating selection for and against (if there is a cost of resistance) resistance, respectively. As a consequence hosts evolve specific adaptation to the parasites, which is costly and hence lost in uninfected populations. To test this hypothesis we compare among population variation in neutral marker allele frequencies and quantitative trait divergence and correlate the infection status of local populations (infected or uninfected) with the measured phenotypes to infer local adaptation of the host to the parasite, simultaneously inferring a measure of the cost of resistance.

Poster session A - GEN 2000

Use, effectiveness and variability of external immune defense in ants (52148)

Simon Tragust.

University of Bayreuth.

Antimicrobial secretions delivered to the environment play a major role in several host-parasite interactions. Although they are generally not viewed as an integral part of the immune system of an organism, these compounds improve an organism's survival and manipulate the microbial community surrounding the organism. It has recently been proposed to that these secretions play an underappreciated selective force in shaping the evolution of insect immune systems. However variability in the susceptibility of different pathogen strains to antimicrobial secretions as well as variability in the effectiveness of antimicrobial secretions within and among species has seldom been shown, despite the fact that it represents the raw material for (co)evolution and might shed new light on the evolution of virulence. Using the recently described external immune defense trait of formic acid as cleaning agent against entomopathogenic fungi I will investigate the universality and variability of this cleaning agent within the formic acid carrying ant subfamily Formicidae as well as the possibility of entomopathogenic fungi to adapt to formic acid.

Poster session A - GEN 2000

MULTIDIMENSIONAL MANIPULATION OF HOST BEHAVIOUR EXPLAINS THE ECOLOGICAL SUCCESS OF A SOCIAL PARASITE (52149)

Evelien Jongepier, Isabelle Kleeberg, **Susanne Foitzik.**

Johannes Gutenberg University Mainz.

Manipulative parasites influence interspecific interactions and thereby the composition of communities. Yet, how evolutionary dynamics govern the ecological success of these parasites is still poorly understood. Manipulative parasites frequently alter multiple host traits and here we test the hypothesis that variation in host resistance to this multidimensional manipulation drives the parasites' ecological success. We quantified parasite-induced behavioural alterations in 16 populations of two hosts of the social parasitic ant *Protomognathus americanus*. We thereby covered the entire range of these *Temnothorax* ants, including non-parasitized populations. We demonstrate that the parasite can manipulate its hosts along two, interrelated behavioural axes, and that these manipulations promote parasite survival and prevalence. Hence, the multidimensional manipulation can explain the parasite's ecological success, whereas initial variation in the host's constitutive defences, which are target of the manipulation, cannot. Our findings underline the importance of host manipulation for the ecological and evolutionary dynamics between hosts and parasites.

Poster session A - GEN 2000

Host age modulates parasite within-host competition (52190)

Rony Izhar, Frida Ben-Ami.

Tel Aviv University.

Among the most striking differences among hosts within most populations is host age, which is a key epidemiological factor, but there is very little data on how age-dependent effects impact ecological and evolutionary dynamics of host and parasite populations. Using two clones of the water flea *Daphnia magna* and two clones of its bacterial parasite *Pasteuria ramosa*, we examined how host age at exposure interacts with multiple infections to influence the expression of parasite virulence and lifetime transmission potential. We further analyzed the competitive outcome of multiple infections in different host age groups. We found that multiply-infected hosts were more susceptible to infection and suffered higher mortality than singly-infected hosts. As host age increased competition shifted from coinfection, where both parasite clones succeeded in producing transmission stages, to superinfection, where one of the parasite clones was excluded. Thus, the host population age structure could serve as a limiting factor for parasite strain coexistence. Our results emphasize that the outcome of within-host competition is influenced by the complex interplay between host demography and the ecology of host and parasite populations, and present a call for incorporating age-dependent epidemiological parameters into stage-structured theory and virulence modeling.

Poster session A - GEN 2000

Local adaptation between malaria and its bird hosts: an experimental approach (52242)

Tania Jenkins, Jessica Delhay, Philippe Christe.

Dept Ecology and Evolution.

The virulence and dynamics of malaria parasites can depend on whether they coevolve with their vertebrate hosts. Previous studies have investigated the spatial and genetic patterns of malaria and have suggested that coevolution is likely. However, experimental data demonstrating local adaptation, a signature of coevolution, is needed in order to confirm this hypothesis. We tested for local adaptation between the great tit, *Parus major*, and its malaria parasites by conducting a reciprocal transplant experiment in the field, where we exposed individuals from two populations of great tit to *Plasmodium* parasites. We were therefore able to assess the extent of host adaptation to their local parasites. We present three main findings: i) there was low support for local adaptation. However, the direction of the effect was more consistent with one of host adaptation and hosts appeared better able to resist foreign parasites; ii) there were site-specific effects of malaria infection on the hosts and iii) there was a sex-bias in infection success. These data represent one of the few experimental studies of parasite-host local adaptation using a natural malaria system. These results may have consequences on the ecology and evolution of vector-transmitted parasites and on the evolution of host defense traits.

Variation in Toll-like receptor 4 in closely related passerine species adapted for different environments (52243)

Tereza Králová, Michal Vinkler, Hana Bainová, Arild Johnsen, Jan T. Lifjeld, Josef Bryja, Tomáš Albrecht.

Institute of Vertebrate Biology, The Czech Academy of Sciences, Brno, Czech Republic; Department of Botany and Zoology, Faculty of Science, Masaryk University, Brno, Czech Republic; Department of Zoology, Faculty of Science, Charles University in Prague, Prague, Czech Republic; National Centre for Biosystematics, Natural History Museum, University of Oslo, Oslo, Norway.

Toll-like receptors (TLRs) are designed to optimally bind conservative microbe-associated molecular patterns (MAMPs). These proteins, therefore, evolve under strong diversifying selection. It has been repeatedly shown that even MAMPs are structurally variable and this may be particularly true for structures originating from pathogens occurring at different latitudes. According to one of the hypothesis, tropical and migratory birds are exposed to higher pathogen diversity than their closely related sedentary species, and thus they may also be expected to exhibit higher variability in immune receptors. In this contribution we focused on genetic variability in Toll-like receptor 4 (TLR4) which binds, amongst other ligands, lipopolysaccharides from outer membranes of Gram-negative bacteria to trigger the immune response. Here, we present our result on intra- and interspecific comparison of TLR4 ligand-binding region sequence variation in closely related passerine species from tropical (Cameroon, Nigeria) and temperate zone (Czech Republic, Norway). We assessed 15 unrelated individuals per species to evaluate the differences in TLR4 variability and ongoing selection using 46 species from 26 passerine families. The acquired information provides us with unique insight into the evolutionary effects acting on this genes in different environments.

The Genetic Basis of Behavioral Coevolution: Adaptations in Socially Parasitic Slavemakers and Their Hosts (52258)

Austin Alleman, Barbara Feldmeyer, Daniel Elsner, Susanne Foitzik.

Johannes Gutenberg-Universität Mainz.

In the ant genus *Temnothorax*, socially parasitic, slavemaking behavior has evolved multiple times independently. Results of phenotypic studies suggest that slavemakers and hosts, which tend to be closely related species, engage in evolutionary arms races, coevolving through reciprocal adaptations. Aside from morphological differences, the behavior and activity patterns vary markedly between slavemaker and host workers. Slavemaker workers do not participate in normal worker chores and display raiding activity only during a few weeks in summer. Conversely, host workers carry out a number of different tasks, including brood care, foraging, and, during slavemaker raiding season, nest defense. However, the genetic basis of

raiding and defensive behavior, including the primary genes involved in the ongoing coadaptation of these systems, remains unknown. Through transcriptome analysis of three host and three slavemaker species, we will investigate three primary objectives: a) to elucidate the genetic basis of differential behavior patterns within a species, b) the general evolution of slavemaker raiding and host defensive behavior, and c) search for selective signatures involved in parasite-host differentiation. We will report on genes and functional groups responsible for a specific behavioral pattern, their consistency across species, as well as selective signatures of parasite-host coevolution.

Poster session A - GEN 2000

MIXED DIETS – THE KEY TO A HEALTHY LIFE? (52263)

Franziska Dickel, Johanna Mappes, Dalial Freitak.

Centre of Excellence in Biological Interactions, University of Jyväskylä; Centre of Excellence in Biological Interactions, University of Jyväskylä; Centre of Excellence in Biological Interactions, University of Jyväskylä and University of Helsinki.

The uptake of secondary metabolites can increase the ability to combat an infection. Therapeutic self-medication describes the insect's ability to actively change their diet, ingesting possibly toxic plants after encountering an infection. Most of the studies so far have focused on the short term effect of a single diet post infection, rather than looking at the mixed food in long term. Also, even if the consumption of a harmful substance is increasing the probability to survive an infection, how is this affecting the long-term fitness of the insect?

To test this we used larvae of the polyphagous Wood tiger moth, *Parasemia plantaginis*, fed them with three different food plants (*Plantago major*, *Taraxacum sect. ruderalia*, *Lactuca sativa*) and infected them with a bacterial pathogen, *Serratia marcescens*. We found that a combination of diet 1- harmful plant and diet 2- nutrient rich plant provides the highest medication effect and furthermore guarantees a normal larval development. Steady state immunity is upregulated in response to the most harmful plant. This indicates that the change of food plants is essential in increasing the ability to survive bacterial infections, but also the combination of several diets is the key for long-term fitness.

Poster session A - GEN 2000

Evolution of immune responses and parasitoid virulence in a spatial context (52273)

Peter Hambäck, Lisa Fors, Ulrich Theopold, Robert Markus.

Dept Ecol. Env. and Plant Science, Stockholm university; Dept of Molecular Life Sciences, Stockholm university.

In polyphagous parasitoid species, the ability to successfully parasitize hosts may vary between host species and depending on community context, potentially causing population divergence and speciation. Causes for host race formation and speciation are however poorly understood in parasitoid species and deserves further attention. In a system with a eulophid parasitoid (*Asecodes parviclava*) and three leaf beetle species (*Galerucella* sp), we found that hosts vary in their ability to encapsulate parasitoid eggs from weak encapsulation (*G. calmariensis*) to efficient encapsulation (*G. pusilla*). Encapsulation was shown to involve at least three cell types in the hemolymph and particularly one type was differentially induced among host species. We also found differences among parasitoid populations in parasitism success. Parasitoids hatching from *G. pusilla* had much higher success rate than parasitoids hatching from *G. calmariensis* when attacking *G. pusilla* larvae. This ability was particularly obvious when using parasitoids from some localities, suggesting local adaptation in parasitoid virulence. The differences in parasitoid success rate was also apparent in cytological studies, where induction in several cell types was suppressed when parasitized by a highly virulent parasitoid. We believe that this system is at an early stage of speciation, conclusions that are also supported by genetic studies.

Poster session A - GEN 2000

How are coevolutionary trajectories affected by variable environments? (52275)

Franziska Brunner, Jaime Anaya-Rojas, Blake Matthews, Christophe Eizaguirre.

Queen Mary University of London; Swiss Federal Institute of Aquatic Research and Technology .

Host-parasite interactions are strongly affected by their environmental context. Differences in such context dependence between populations can occur in two different ways: differences in molecular host responses between populations reflect adaptation to a local optimum whereas different patterns of variation within populations can reveal different levels of genetic diversity and/or how phenotypic plasticity has evolved in each of them.

Using experiments performed with different three-spined stickleback ecotypes and their monogenean parasite *Gyrodactylus gasterostei* we examined how eutrophication – a major environmental factor affecting stickleback habitat – alters parasite success and molecular host responses on the gene expression level. We found that eutrophication has opposite effects on parasite success between host ecotypes. We also show that host gene expression response to eutrophication is population specific in both mean expression levels and variation within ecotypes. Together, these findings show that ecological conditions can rapidly alter both directional selection and plasticity within a host-parasite system. Both aspects can have an important impact on coevolutionary trajectories.

Poster session A - GEN 2000

Uncovering host defense strategies: bacterial infection in *Drosophila melanogaster* (52283)

Megan A. M. Kutzer, Sophie A. O. Armitage.

Institute for Evolution and Biodiversity, Westfälische Wilhelms-Universität Münster.

In principle hosts can employ two strategies to limit parasite load. Resistance, a host's ability to limit pathogen load, has been well studied. While tolerance, a host's ability to limit damage caused by a parasite, a phenomenon well documented in the plant literature, is less well understood in animals. Previous work on resistance and tolerance in animals focuses primarily on host survival or health rather than on fitness measures or life history traits like fecundity. Reproduction for insects like *Drosophila melanogaster* is costly, so it is reasonable to predict a tradeoff in egg and offspring production in response to bacterial infection, depending on the defense strategy employed by the host. Here we aimed to assay resistance and tolerance in response to dietary restriction by limiting protein intake and to characterize bacterial infection pathology at the individual level. Because infectious diseases are not always lethal we chose to test the effect of two non-lethal, persistent bacteria. A low protein diet translated into lower egg production and decreased resistance, but tolerance was unaffected. We uncovered considerable individual variation in resistance despite controlled conditions. Future experiments will reveal the long-term impacts of infection and the underlying causes of individual variation.

Poster session A - GEN 2000

The relationship between host oxidative stress and *Plasmodium* infection in the canary, *Serinus canaria* (52320)

Jessica Delhaye, Fabrice Lalubin, Philippe Christe.

Inter-individual variation in parasite susceptibility exists among hosts. However, the underlying mechanisms driving these inequalities are still poorly understood. The release of pro-oxidants is known to play a key role in the fight against pathogens with potential harmful side-effects for hosts in terms of oxidative stress. Pro-oxidant and antioxidant compounds have been shown to affect *Plasmodium* development. In this study, we experimentally infected canaries, *Serinus canaria* with two *Plasmodium* strains, *P. relictum* and *P. polare* to investigate the link between *Plasmodium* infection and host oxidative stress. We monitored the infection dynamic in terms of changes in parasite intensity and host oxidative stress, measuring both pro-oxidant production and antioxidant defence traits. We looked at the effect of oxidative stress prior to infection on subsequent *Plasmodium* development as well as the effect of infection on oxidative stress. One component of oxidative stress prior to infection affected subsequent *Plasmodium* development. We further found that infection status, parasitaemia and *Plasmodium* strain affected oxidative stress during the course of infection. These results support that initial oxidative stress can play a role in affecting host susceptibility and that *Plasmodium* infection can also impose a further physiological stress on the host.

Poster session A - GEN 2000

Coinvasion and Coinfection: evolution and adaptation in two invasive parasites infecting blue mussels (52369)

Marieke E. Feis, K. Mathias Wegner.

Alfred Wegener Institute; Alfred Wegener Institute.

Biological invasions of parasites offer ideal opportunities to study coevolution in nature – especially when hosts are faced with repeated invasions of parasites. Such coinvasions not only lead to selection on the host but also to selection on parasites arising from direct competition. Here, we present data from a crossed coinfection experiment using two closely related copepod parasites that have invaded the Eastern Atlantic, infecting mussels. One is the specialist *Mytilicola intestinalis* that invaded from the Mediterranean Sea in the 1930ies and the other one is the generalist *Mytilicola orientalis* that invaded from Japan in the 1990ies. This system thus offers the opportunity to study host-parasite interactions along a gradient of different coevolutionary timescales and host specificity. Here we report the first results of this experiment on the phenotypic level focussing on the balance and trade-offs between host and parasite traits, i.e. infectivity – virulence for parasites and virulence - tolerance for hosts. We find different interactions along these trade-offs between both interactions. We also find that the generalist new invader is outcompeting the old invader.

Poster session A - GEN 2000

Gene diversity of Major histocompatibility complex (MHC) class II β alleles of Scandinavian anuran species (52376)

***Maria Cortazar Chinarro**, Ella Z. Lattenkamp, Yvonne Meyer-lucht, Anssi Laurila, Jacob Höglund.

Uppsala University. Animal Ecology Department.

Gene diversity of Major histocompatibility complex (MHC) class II β alleles of Scandinavian anuran species.

Amphibian populations face a multitude of threats, including habitat degradation, environmental change and infectious disease such as those caused by the chytrid fungus *Batrachochytrium dendrobatidis* (Bd) or Ranavirus, among others. Major histocompatibility complex (MHC) class II genes play key roles in the vertebrate immune system response. MHC loci are the most polymorphic genes ever reported which are used by vertebrates to withstand newly emerging diseases. The proposed mechanism for why MHC is so polymorphic is balancing selection ultimately caused by parasites and pathogens. MHC Class II molecules bind to chopped up particles of bacteria and macroparasites that have been engulfed by macrophages. When MHC molecules present these particles on the cell surface of the macrophages, antibody production against the disease is induced. Using the Miseq sequencing platform and 10 different microsatellites markers, we investigated the patterns of genetic diversity and differentiation of five species of frogs along a latitudinal gradient in Sweden. For one species, the moor frog (*Rana arvalis*), preliminary results show low gene

diversity at northern and southern latitudes and high gene diversity at intermediate latitudes.

Poster session A - GEN 2000

Disentangling genetic and parental effects in determining immune function in a simultaneously hermaphroditic snail (52420)

Otto Seppälä, Laura Langeloh.

Eawag / ETH Zürich.

Parasites are an ubiquitous selective force in natural populations. Evolutionary change in defence traits, such as immune function, requires additive genetic variance in them. However, also parental (especially maternal) effects can be important in determining the strength of immune function, which could affect their evolution by altering the phenotypes on which selection can act. Therefore, understanding the relative role of genetic background and parental effects in determining expression of immune traits is highly important. We investigated variation in constitutive immune defence traits in a simultaneously hermaphroditic snail *Lymnaea stagnalis*. We compared phenoloxidase-like and antibacterial activity of snail haemolymph across pairs of full-sib families, each pair sharing the same two parents (i.e. same genetic background) but in reversed sex roles. We found that the variation in immune defence traits was largely dependent on the genetic background of snails (i.e. families sharing the same genetic background were often similar, but differed from families with different genetic backgrounds). However, also parental effects played a role indicated by differences between families in some of the family pairs. This suggests that parental effects (possibly due to immune priming) can add to evolution of defence traits against parasites.

Poster session A - GEN 2000

Microbiota plays a role in oral immune priming in *Tribolium castaneum* (52476)

Momir Futo, Joachim Kurtz.

Institute for Evolution and Biodiversity.

Animals are inhabited by a diverse community of microorganisms. The relevance of such microbiota is increasingly being recognised in a broad spectrum of species, ranging from sponges to primates, revealing various beneficial roles microbes can play. The red flour beetle *Tribolium castaneum* represents a well-established experimental model organism for studying questions in ecology and evolution, however, the relevance of its microbial community is still largely unknown. *T. castaneum* larvae orally exposed to inactivated bacterial components of the entomopathogen *Bacillus thuringiensis tenebrionis* showed increased survival upon a subsequent challenge with this bacterium. We explored the role of microbiota for oral immune priming in this species. To investigate whether *T. castaneum* microbiota plays a role

in this phenomenon, we established a protocol for raising germ-free larvae and subsequently tested whether they differ in their ability to mount such a priming response. Here we demonstrate that larvae, which lack their microbiota, show decreased survival upon secondary challenge with bacterial spores, compared to animals which still had, or were allowed to regain their microbiota before priming. Although the exact mechanism of oral immune priming is still unclear, we here suggest that the microbiota plays a crucial role in oral immune priming in this species.

Poster session A - GEN 2000

Not all MHC alleles are equal: different characteristics of MHC Class I alleles among song birds (52497)

Emily O'Connor, Maria Strandh, Jan-Åke Nilsson, Dennis Hasselquist, Helena Westerdahl.

Lund University.

Molecules of the Major Histocompatibility Complex (MHC) play a key role in protecting animals against infection by helping to determine which pathogens can be presented to the immune system for elimination. Song birds (i.e., passerines) appear to possess a larger number of MHC genes than most other animals. However, very little is currently known about potential differences in characteristics and functions among these gene copies which could influence the number of pathogens they recognise.

We have used next generation amplicon sequencing to investigate MHC class I alleles for 12 candidate songbird species spanning the passerine radiation from each of the following families: Passeridae, Muscicapidae, Acrocephalidae, Sylviidae, Phylloscopidae and Paridae. We found three different MHC allele lengths with a strong phylogenetic signature in the distribution of these sequences among species. In some species these length differences were associated with evidence for different selection pressure. Furthermore, in species from Passeridae, Acrocephalidae and Paridae there were groups of alleles with strikingly little variation. This is counter to expectations for classical MHC genes where selection from a diverse pathogen fauna is expected to generate high allelic polymorphism.

Potential implications for pathogen recognition of the observed differences in allele characteristics among species will be discussed.

Poster session A - GEN 2000

Use of Concanavalin A in skin-swelling test of immune responsiveness facilitates interpretation of the measurement in rodents (52532)

Barbora Bílková, Tomáš Albrecht, Milada Chudíčková, Vladimír Holáň, Jaroslav Piálek, Michal Vinkler.

Department of Zoology, Faculty of Science, Charles University; Institute of Vertebrate Biology, Academy of Sciences of the Czech Republic, v.v.i., Květná 8, 603 65; Institute of Experimental Medicine, Academy of Sciences of the Czech Republic, v.v.i., Videňská 1083.

Skin-swelling test is a widely used method to quantify immune responsiveness of free-living animals in immunoecological studies. This test is based on measuring magnitude of tissue swelling in the time after injection of an artificial inflammatory stimulant, most commonly phytohaemagglutinin (PHA). However, given the complexity of the immune response, interpretation of the test results is not completely clear. The aim of our study was to improve the test protocol to facilitate interpretation of the skin-swelling data. In mice, we compared cellular immune response to PHA and an alternative pro-inflammatory stimulant Concanavalin A (ConA). We measured magnitude of the tissue swelling and compared it with intensity of infiltration of blood cells into the tissue in a 72-hour time frame. Our results show that the response to ConA and PHA differs in time. ConA induces greater swelling with greater cellular activity and higher pro-inflammatory cytokine expression than PHA. Furthermore, after ConA injection, the magnitude of the swelling is positively associated with the cellular activity. Considering also the molecular binding specificity of the two lectins, we conclude that ConA is a more suitable stimulant for the skin-swelling test in rodents than PHA.

Poster session A - GEN 2000

Evolution of specific resistance against bacterial infection: Based on genetically hard-wired or phenotypically plastic defences? (52582)

Kevin Knoblich, Robert Peuß, Joachim Kurtz.

University of Münster.

Insect immune systems can provide their host with pathogen-specific protection, either via genetically hard-coded or acquired responses (genetic and phenotypic specificity, respectively). So far the evolution of phenotypic specificity is not well understood, in particular during the process of genetic adaption to a pathogen. Therefore, we experimentally selected the Coleoptera *Tribolium castaneum* for its ability to survive an infection with either one of four closely related strains of *Bacillus thuringiensis* or one of the two Gram-negative bacteria *Lactococcus lactis* and *Pseudomonas fluorescens*. Selection regimes consisted of immune priming (using heat-killed bacteria) followed by septic challenge (with the same bacteria as for priming, but alive). After 11 generations, we performed a full-factorial priming and challenge experiment to discriminate whether genetically hard-wired or phenotypically plastic immune specificity responded to selection. We found that the beetles evolved a slightly increased resistance for five out of the six bacteria species or strains. Resistance was specific for the bacterial species and even strain, i.e. there was no cross-resistance towards the other bacteria. Survival of the infection was not strongly affected by the priming treatment. This suggests that in this host-pathogen system, resistance evolution might mostly rely on genetically hard-wired rather than acquired defence components.

Poster session A - GEN 2000

Host-mutualist and host-parasite coevolution in tripartite interactions (52586)

Charlotte Rafaluk, Kayla King.

University of Oxford.

Host-parasite coevolution can drive rapid reciprocal adaptation. Several host-parasite coevolution experiments have been carried out to date demonstrating reciprocal coevolutionary change under laboratory conditions. In nature, however, hosts and parasites coexist in complex ecological communities, with different kinds of interaction taking place between different species pairs within the community. In communities where hosts and their parasites coexist, species that decrease the negative impacts caused by parasites to hosts, termed defensive mutualists, may have important effects on the dynamics of host-parasite coevolution. Additionally, coevolution is also likely to occur between the defensive mutualist and the host which may feedback in turn to effect host-parasite coevolution. In order to test whether host-parasite coevolutionary dynamics differ when a protective mutualist is present and to assess how hosts and mutualists coevolve, we are carrying out a coevolution experiment with: 1) treatments allowing a host species, *Caenorhabditis elegans* to coevolve with a parasite species, *Staphylococcus aureus*, in the presence and absence of an evolutionarily static defensive mutualist, *Enterococcus faecalis*; and 2) treatments allowing *C. elegans* to coevolve with a defensive mutualist, *E. faecalis*, in the presence and absence of an evolutionarily-static parasite, *S. aureus*.

Poster session A - GEN 2000

Differential expression of MHC genes in three species of sparrows indicates conserved functional differences (52589)

Anna Drews, Maria Strandh, Lars Råberg, Helena Westerdahl.

Lund University.

The Major Histocompatibility Complex, MHC, is an important component of the vertebrate immune system. MHC enables recognition of foreign antigens which triggers an immune response. MHC genes are highly variable and this variation is thought to be maintained by host-parasite interactions. Songbirds have a larger number of MHC genes than most vertebrates. However the individual function of these multiple copies are to a large extent unknown. We have therefore studied gene expression of different MHC gene copies, as a first estimate of their relative importance in the immune system, in three species of sparrows; house sparrows, tree sparrows and Spanish sparrows. All three species had a similar MHC organization containing MHC alleles with low variability. This group of alleles was significantly separated from all the remaining MHC alleles which were highly variable. We hypothesized that these alleles with low variability would be expressed to a lower degree than the other alleles. We used massively parallel amplicon sequencing to determine relative expression of the alleles. Not all alleles were expressed equally; the low variability alleles were expressed to a significantly lower degree. This conserved differential gene expression pattern among species suggests that there are MHC genes of different functions in sparrows.

Interactions among co-infecting bacterial strains and fluke genotypes shape disease virulence (52654)

Katja-Riikka Louhi, Lotta-Riina Sundberg, Jukka Jokela, Anssi Karvonen.

University of Jyväskylä, Department of Biological and Environmental Science, Jyväskylä, Finland. ; Eawag, Swiss Federal Institute of Aquatic Science and Technology, Dübendorf, Switzerland.; ETH Zurich, Institute of Integrative Biology, Zürich, Switzerland..

It is common that several parasite or pathogen genotypes of the same or different species co infect a single host individual. Such co infection can intensify competition for host resources, favoring more competitive strains that are more virulent to the host. Here, we present the first evidence that the genetic identity of the co- infecting partners largely determines the virulence of co infections between bacterial strains and parasitic fluke genotypes, to a degree that the outcome cannot be predicted from the virulence of respective single infections. By measuring the overall disease virulence of single bacterial strains, single fluke genotypes, and combinations of reciprocal co infections, we demonstrate that co infection caused higher than predicted virulence and infection intensity in most strain genotype combinations, but not in all. We conclude that predicting the overall disease virulence may be much more complex than previously acknowledged, making it necessary to consider how genetic interactions among co infecting parasites affect disease dynamics and host health in different host parasite systems.

Acquired host responses erode advantages of co-infection by multiple parasite genotypes (52658)

Ines Klemme, Katja-Riikka Louhi, Anssi Karvonen.

University of Jyväskylä.

Co-infections by multiple parasite genotypes or species are common and have important implications for host-parasite evolution through within-host interactions. Typically, these infections take place sequentially and thus, co-infection dynamics may be shaped by host immune responses targeted against previous infections. However, our understanding of these processes is limited. Here, we investigated whether acquired host resistance affects interactions between co-infecting parasite genotypes of the trematode eye-fluke *Diplostomum pseudospathaceum*, infecting one of its intermediate hosts, the rainbow trout *Oncorhynchus mykiss*. We show that simultaneous attack of two genotypes facilitates parasite establishment in immunologically naïve hosts, which is in accordance with previous results. More importantly, we show that sequential infection and immune priming of the host erode this facilitation in infection, thus significantly altering the interactions between co-infecting

genotypes. Our results may have significant implications for the evolution of co-infections and parasite transmission strategies.

Poster session A - GEN 2000

Defence by AMP synergies against variable parasites (52677)

Monika Marxer, Paul Schmid-Hempel.

ETH Zurich; ETH Zurich.

In the model system of the bumblebee, *Bombus terrestris* and its trypanosome parasite, *Crithidia bombi*, parasite populations are highly variable. We studied how hosts can defend themselves despite having genetically fixed immune repertoires. We show experimentally that variation in the concentrations of the expressed genes for anti-microbial peptides (AMPs) can keep different strains of the parasites specifically in check. This defence by “synergistic cocktails” is an efficient and flexible strategy of defence against variable and quickly changing parasites. Some evolutionary implications are discussed.

Poster session A - GEN 2000

MHC and *Borrelia* in bank voles: Divergent allele advantage (52732)

Kristin Scherman, Martin Andersson, Helena Westerdahl, Lars Råberg.

Department of Biology, Lund University.

Parasite-mediated selection is generally invoked to explain the extreme allelic diversity found in the vertebrate Major Histocompatibility Complex (MHC). Balancing selection may operate either in the form of heterozygote advantage, or through the interaction of pathogens and specific MHC alleles. Moreover, heterozygotes with minimal overlap in antigen recognition should be selected for according to the divergent allele advantage hypothesis. Selection for divergence can also work on multiple genes favouring individuals that recognise a wider range of antigens. We surveyed allelic polymorphism at the MHC class II DQB gene in wild bank voles (*Myodes glareolus*) hosting *Borrelia afzelii*, a multi-strain infection causing Lyme disease in humans. Screening more than 500 individuals and a subset of families on DQB made it possible to group alleles from four loci in a haplotypic framework. We tested 12 different DQB haplotypes for associations with *Borrelia*. We found two significant associations between DQB haplotype and infection prevalence: one associated with resistance and the other with susceptibility. We found no evidence for heterozygote advantage but the average pairwise amino acid divergence (p-distance) was higher for voles with the protective haplotype than other voles. Conversely, voles with the susceptible haplotype had less divergent genotypes than other voles.

Transcriptomic response to pathogen challenges in leaf-cutting ants (52737)

Morten Schiøtt, Sze Huei Yek, Jacobus J. Boomsma.

University of Copenhagen.

Social insects can be expected to experience a high selection pressure on their immune system, as their social lifestyle is prone to ease the spread of diseases. This is especially true for leaf-cutting ants due to their large colony size and the monoclonality of their fungal symbiont. Paradoxically genome sequencing projects have revealed that social hymenopterans such as the honey bee have fewer known immune genes than e.g. fruit flies, which may be attributed to social immunity of social insect colonies. Alternatively social insects may have evolved immune genes not known from insect model species. We examined the behavioural and gene expression (using RNA-seq) response in leaf-cutting ants after challenging both the ants and their fungal symbiont with either an ant pathogen (*Metarhizium brunneum*) or a fungus-garden pathogen (*Escovopsis weberi*). While the behavioural response by the ants was largely independent of pathogen identity, the gene expression response showed clear differences, and only inoculations with *Metarhizium* caused a large increase in the expression of known immune genes. Inoculations with *Metarhizium* also caused a pronounced upregulation of several genes of unknown function. These putative immune genes are currently being functionally analysed using RNAi knock-down methods and immune assays of heterologously expressed proteins.

Distribution of protective symbiont in natural populations (52749)

Mélanie LECLAIR, Jean-Christophe SIMON, Yannick OUTREMAN.

Université Rennes 1; INRA; Agrocampus-Ouest.

A majority of species maintains associations with symbiotic microorganisms. They can change the ecology and evolution of their hosts by inducing a variety of effects on phenotype. Symbionts are most often heritable; phenotypes induced by symbiotic associations can be transmitted to subsequent generations. The obtained phenotypes can appear very beneficial for the host: some microbial symbionts allow their host to access a new food resource or be protected against their natural enemies. Although very beneficial, these symbiotic associations are sometimes poorly represented or absent in some natural populations. Our goal is to understand why a beneficial trait conferred by a symbiotic association is not spread in all host populations.

To answer this question, the biological model used was the pea aphid and its optional bacterial symbiont leading to many phenotypic effects including protection against natural enemies. The distribution of these symbionts in different specialized populations of aphids was analyzed via numerous field surveys. Two major effects on the distribution of the symbionts, a priori beneficial, were tested: interactions between symbionts and properties of the host environment as pressure of natural enemies.

Our study reveals that distribution of the symbionts in natural populations is affected by many ecological and evolutionary factors and doesn't respond to a simple relationship 'profit-fixing'.

Poster session A - GEN 2000

Is There An Association Between Haemosporidian Parasite Infection And Toll-Like Receptor (TLR) Genotype? (52759)

Haslina Razali, Shinichi Nakagawa, Terry Burke.

University of Sheffield; University of Otago.

There is an enormous advantage to being polymorphic in the immune genes such as the major histocompatibility complex and toll-like receptors (TLRs) loci because this increases the chance of combating multiple pathogens. TLRs are part of the first line of defence in the immune system. In humans, TLR4 and TLR7 have been found to be associated with malaria. We tested whether TLR polymorphism in house sparrows (*Passer domesticus*) has been shaped by local pathogenic pressure. We hypothesized that different malaria strains exert different selection pressures on the TLRs. Testing for infection with haemosporidian parasites, such as malaria, may result in false negatives, especially using PCR detection methods. The advent of next-generation sequencing enables more accurate detection and identification of haemosporidian parasites. Initial analyses detected two major malarial strains in the north and south islands of New Zealand. We screened seven TLR loci in this house sparrow population and report our results on their association with malaria infection.

Poster session A - GEN 2000

Superinfection and the coevolution of parasite virulence and host recovery (52802)

Sara Kada, Sébastien Lion.

CEFE, UMR 5175 CNRS, 1919 route de Mende, 34293 Montpellier Cedex 5 France; Université de Montpellier 2.

Parasite strategies of host exploitation may be affected by host defence strategies and multiple infections. In particular, within-host competition between multiple parasite strains has been shown to lead to higher virulence. However, little is known on how multiple infections could affect the coevolution between host recovery and parasite virulence. Here, we extend a coevolutionary model introduced by van Baalen [1] to account for superinfection. When the susceptibility to superinfection is low, we recover van Baalen's results and show that there are two potential evolutionary endpoints: one with avirulent parasites and poorly defended hosts, and another one with high virulence and high recovery. However, when the susceptibility to superinfection is above a threshold, only the outcome where both virulence and defence are high remains. We discuss how different parasite and host strategies (facilitation, competitive

exclusion) as well as demographic and environmental parameters, such as host fecundity or various costs of defence, may affect the interplay between multiple infections and host-parasite coevolution.

Poster session A - GEN 2000

An examination of Dscam1 in the light of immunity, fecundity and behaviour (52864)

Robert Peuß, Kristina U. Wensing, Luisa Woestmann, Hendrik Eggert, Barbara Milutinović, Marlene Sroka, Jörn P. Scharsack, Joachim Kurtz, Sophie A.O. Armitage.

Institute for Evolution and Biodiversity, University of Münster; Department of Biosciences, Faculty of Biological and Environmental Sciences, University of Helsinki; : Institute of Science and Technology Austria.

Dscam1 (Down syndrome cell adhesion molecule 1), has important neuronal functions and seems to play a role in immunity as well, which is however less well understood. We took an integrative approach to understand more about the roles that Dscam1 plays in fitness-related contexts in *Drosophila melanogaster* and *Tribolium castaneum*. At present there is a lack of consensus on the conditions under which Dscam1 expression changes after exposure to pathogens. We therefore tested whether exposure to the same bacteria species affects Dscam1 expression in two model insect species in a similar way. We found no short-term modulation of Dscam1 expression after septic or oral bacteria exposure. Furthermore we hypothesized, if Dscam1 is involved in immunity, RNAi-mediated knockdown and subsequent bacterial exposure might result in reduced *T. castaneum* survival, but this was also not the case. Since Dscam1 is vital for nervous system development and is also expressed in the reproductive system we predicted that there may be a behaviour and fecundity cost to the knockdown. Indeed, Dscam1 knockdown as larvae resulted in significant changes in adult behaviour and fecundity-related traits. Our results take a step towards understanding more about the role of Dscam1 in immunity, fecundity and behaviour.

Poster session A - GEN 2000

Ecological factors dictate the degeneration of induced immunity in the spider mite *Tetranychus urticae* (52886)

Gonçalo Matos, Nicky Wybouw, Nelson E. Martins, Maria Riga, John Vontas, Miodrag Grbic, Thomas van Leewen, Sara Magalhães, Élio Sucena.

Instituto Gulbenkian de Ciência, Oeiras, Portugal; CE3C, Faculdade de Ciências, Universidade de Lisboa, Lisbon, Portugal; Laboratory of Agrozoology, Faculty of Bioscience Engineering, Ghent, Belgium; Faculty of Applied Biotechnology and Biology, University of Crete, Crete, Greece; Department of Biology University of Western Ontario, Canada; IBED,

University of Amsterdam, Amsterdam, The Netherlands; Departamento de Biologia Animal, Faculdade de Ciências, Universidade de Lisboa, Lisbon, Portugal.

The genome of the spider mite *Tetranychus urticae*, is missing important elements of the canonical *Drosophila* immune pathways necessary to fight bacterial infections. Thus, the spider mite may rely on different mechanisms to mount an immune response or may have lost this response to pathogen aggression.

We compared the consequences of bacterial infection in the spider mite that feeds on virtually aseptically plant cell contents, to infection in *Sancassania berlesei*, a litter-dwelling mite. Whereas in *S. berlesei* infections are kept under control, *T. urticae* does not mount a response and dies from uncontrolled bacterial proliferation. Furthermore, in accordance with their different ecologies, spider mites harbour three orders of magnitude fewer commensal bacteria than *S. berlesei*.

We postulate that life-history has driven the loss of induced immune responses in *T. urticae* and is convergent with other arthropods with which it shares ecological conditions.

Poster session A - GEN 2000

Endosymbiont-mediated immune protection in a novel host species (52915)

Tânia Paulo, Vitor G. Faria, Alexandre B. Leitão, Élio Sucena.

Instituto Gulbenkian de Ciência; Universidade de Lisboa, Faculdade de Ciências, Departamento de Biologia Animal, Lisbon, Portugal.

Host-symbiont relations are a key class of interactions present in natural populations. *Drosophila melanogaster* hosts several species of symbionts, such as *Wolbachia*, a gram-negative endosymbiont of arthropods, known to manipulate the host's reproductive system for its own advantage. Yet, beneficial effects of *Wolbachia* infection have been unveiled also, namely that it confers protection to viral infection in *D. melanogaster*.

Our first objective is to determine whether the viral protection conferred by the *Wolbachia* strain carried by *Drosophila* would operate in a novel host, the parasitoid wasp *Leptopilina boulardi*. Secondly, we wish to determine whether this protection can occur upon horizontal transmission from a *Wolbachia*-infected *D. melanogaster* host to the wasp host.

We screened parasitoid wasps for horizontal transmission of one of two *Wolbachia* strains (wMel-like and wMel_CS) and infected them with *Drosophila C Virus* through systemic and oral routes. We estimate the maintenance of the distinct protective effects of different *Wolbachia* strains in its novel host. We will also determine if wasps can act as viral vectors between *Drosophila* hosts.

In sum, this work will highlight the immediate ecological and evolutionary consequences that *Wolbachia* presence may confer to a novel host upon a naturally occurring event of horizontal transmission.

Poster session A - GEN 2000

Local specialists and global generalists : understanding parasite diversification patterns within host communities at different spatial scales. (51657)

Karen McCoy.

CNRS.

The parasitic environment is often both strongly spatially-structured and highly heterogeneous, and particularly so when parasites exploit a wide range of host species within local communities. At the scale of their global distribution, such parasites are often classified as host generalists, only to find that they are in fact composed of a series of local host specialists. Such is the case for the cosmopolitan seabird tick, *Ixodes uriae*. This ectoparasite commonly exploits colonial seabirds across the temperate and polar regions of both hemispheres. Host race formation has occurred multiple times across its worldwide distribution, with clear signatures of local adaptation to different host types within the local seabird community. Here, we use genetic markers and simulation modeling to explore the relative roles of selection and drift in the diversification process by retracing host colonization patterns at regional scales. We quantify both the frequency and direction of local host divergence events at the within-colony scale in three isolated regions of its distribution and place our results within the context of its historical phylogeography. Our results illustrate how understanding the origin of parasite diversity at different spatial scales can help us predict the evolution patterns in a changing world.

Poster session A - GEN 2000

Linking morphologic and genetic divergence with host use in the tropical tick complex, *Ornithodoros capensis sensu lato*. (51659)

Marlene Dupraz, Céline Toty, Valérie Noël, Jean-Pierre Dujardin, Thierry Boulonier, Karen McCoy.

Université Montpellier; IRD; CNRS.

Vector-borne diseases are often the result of a complex transmission cycle where a vector transmits a pathogen through numerous reservoir host species; the epidemiology of the pathogen being a consequence of host use by the vector. Vector-host interactions can be intense and host use by the vector is not always directly related to host availability. In order to understand pathogen transmission cycles, it is therefore essential to understand the local structure of vector populations within host communities. Soft ticks of the *Ornithodoros capensis* complex exploit colonial seabirds in tropical-subtropical areas across the globe. Morphological resemblances among species and a lack of genetic data have limited our ability to clarify the local and global phylogenetic positions of the species of this complex. Here, we link phenotypic and genetic data to understand geographical distributions and host relationships within this complex. We test whether host use is always accompanied by the same phenotypic changes and, if these changes are associated with patterns of genetic divergence. We find that strong host associations, closely linked to genetic structure, exist across the complex suggesting that speciation in the group has been strongly shaped by host adaptation and that geography plays only a secondary role.

Phylogenetic patterns in species diversity (51760)

Eric Lewitus, Helene Morlon.

Institut de Biologie, Ecole Normale Supérieure.

Our understanding of any biological phenomena is guided by our ability to identify what is universal and what is specific. In the particular case of species diversity, identifying features of diversification universal to all clades and specific to certain clades could allow us to derive a general model of the evolution of species richness. Here, we introduce a method based on phylogenetic trees — trees defining species relationships over evolutionary time — that allows such an identification. We treat phylogenies as graphs and characterize them by the spectrum of the graph Laplacian. This allows us to quantitatively and visually compare phylogenies both across and within clades and to identify features of diversification universal to all clades and specific to certain clades. Because biological systems are most aptly explained by the distribution of their parts, graph theory is, in general, well suited for deciphering the organization of biological networks. The spectrum of the graph Laplacian is shown here, in its application to phylogenetic trees, to be particularly useful in identifying evolutionary patterns in species diversity. We illustrate our approach with birds and mammals.

Resistance to invasive congener's pollen in Japanese dandelion: reproductive character displacement in response to biological invasion? (51761)

Daisuke Kyogoku.

Kyoto University.

Japanese dandelion, *Taraxacum japonicum*, has declined in abundance in the last several decades due to the invasion of common dandelion, *T. officinale*. The decline is thought to be due to reproductive interference; seed production of *T. japonicum*, which is self-incompatible, is reduced by *T. officinale* pollen even when sufficient amount of compatible pollen is pollinated. However, recently I found a place where *T. japonicum* is apparently recovering from population decline. The recovery of *T. japonicum* population suggests the evolution of resistance to *T. officinale* pollen. In a preliminary experiment, I found that the seed production of *T. japonicum* in that population was not affected by *T. officinale* pollen, a consistent result with my prediction. *T. japonicum* may be being evolutionarily rescued by the evolution of resistance to heterospecific pollen. To make the hypothesis testing vigorous, the same experiment needs to be performed in other sites both where *T. japonicum* population is recovering and where it is not.

Correlation of the intraspecific diversity patterns of benthic invertebrates with the microbial community functioning (51843)

Katerina Vasileiadou, Christina Pavloudi, Anastasis Oulas, Giorgos Kotoulas, Christos Arvanitidis.

IMBBC-HCMR; Biology Department, University of Patras; Department of Biology, Faculty of Sciences, University of Ghent; Department of Microbial Ecophysiology, Faculty of Biology, University of Bremen.

Transitional water ecosystems host a number of habitats with temporally and spatially variable conditions, thus they can be very useful in understanding the mechanisms affecting population establishment. Samples were collected from lagoons located in Amvrakikos Gulf (Western Greece). These ecosystems are characterized by increased hypoxia and high concentrations of hydrogen sulfide, which is produced by sulfate-reducing bacteria. It has been suggested that burrowing polychaetes may cause substantial changes in oxygenation and redox potential of surficial and burrow-lining sediments, that may have a significant effect on the bacterial assemblages. The polychaete *Nephtys hombergii* is one of the most abundant species found in the lagoons. A fragment of the mitochondrial DNA (COI gene) was analyzed from this species. Sediment DNA was extracted and processed through next generation sequencing of a region of the dissimilatory sulfite reductase (dsr) gene, which is found in sulfate reducing bacteria.

The C-score index was used to quantify patterns of taxa co-occurrence. The observed values for this index were significantly different from that of simulated assemblages suggesting that the patterns of species co-occurrence do not arise by chance and that the genetic diversity of benthic assemblages may be driven by the microbial community functions.

Interlopers or welcome guests? The role of non-protective invertebrates in an ant-plant mutualism (52066)

Joyshree Chanam, MS Sheshshayee, Srinivasan Kasinathan, Amaraja Jagdeesh, Kanchan A. Joshi, Renee M. Borges.

National Centre for Biological Sciences, Bangalore; University of Agricultural Sciences, GKVK, Bangalore; Indian Institute of Science, Bangalore.

How a symbiosis originates and is maintained is an important evolutionary question. Symbioses in myrmecophytes (plants providing shelter for ants) are believed to be maintained by protection and nutrition provided by specialist plant-ants in exchange for nesting spaces (domatia) and nourishment offered by ant-plants. In the unspecialised ant-plant *Humboldtia brunonis* (Fabaceae), which offers extrafloral nectar to ants, only some plants have domatia. These domatia are occupied mostly by non-protective ants and invertebrates, especially

arboreal earthworms; protection mutualism with ants is restricted to a small part of the plant's geographical range. Stable isotope analysis showed that 8% (earthworms) to 17% (protective or non-protective ants) of nitrogen of plant tissue nearest the domatium came from domatia-inhabitants. ¹⁵N-enriched feeding experiments with domatia-inhabitant ants demonstrated nutrient flux from domatia-inhabitants to nearby plant modules from domatia-bearing branches. This study is the first to demonstrate nutritive role of non-protective ants and non-ant invertebrates, hitherto referred to as interlopers, in an unspecialised myrmecophyte. This suggests that even in the absence of specialised ant–plant protection mutualism, nutritional benefits conferred by domatia-inhabitants can explain fitness benefits of bearing domatia, and thus might have had a role in the origin and maintenance of this symbiosis.

Poster session A - GEN 2000

Interspecific interactions influence contrasting spatial genetic structures in two closely related damselfly species (52112)

Aapo Kahilainen, Inka Keränen, Katja Kuitunen, Janne S. Kotiaho, K. Emily Knott.

Department of Biological and Environmental Science, University of Jyväskylä; Department of Mathematical Information Technology, University of Jyväskylä; Natural History Museum, University of Jyväskylä.

Spatial genetic structure (SGS) is largely determined by colonization history, landscape and ecological characteristics of the species. Therefore, sympatric and ecologically similar species should exhibit similar SGSs, potentially enabling prediction of the SGS of one species from that of another. On the other hand, due to interspecific interactions, ecologically similar species could have different SGSs. We explored the SGSs of the closely related *Calopteryx splendens* and *Calopteryx virgo* within Finland and related the genetic patterns to characteristics of the sampling localities. We observed different SGSs for the two species. Genetic differentiation within short distances in *C. splendens* suggests genetic drift as an important driver. However, we also observed indication of previous gene flow (revealed by a negative relationship between genetic differentiation and increasing potential connectivity of the landscape). Interestingly, genetic diversity of *C. splendens* was negatively related to density of *C. virgo*, suggesting that interspecific interactions influence the SGS of *C. splendens*. In contrast, genetic differentiation between *C. virgo* subpopulations was low and only exhibited relationships with latitude, suggesting high gene flow, colonization history and range margin effects as the drivers of SGS. The different SGSs of the two species caution indirect inferences of SGS based on ecologically similar surrogate species.

Poster session A - GEN 2000

Invasion triggers rapid phenotypic evolution in a native freshwater snail species (52277)

Elodie Chapuis, Thomas Lamy, Jean-Pierre Pointier, Philippe Jarne, Patrice David.

IRD; EPHE; CNRS.

A successful invasive species and a closely related native species occupying similar niches may coexist in a community through niche or character displacement. We here evaluate whether the invasion of the metacommunity of freshwater snails from Guadeloupe (Lesser Antilles) by *Physa acuta* is associated with a modification in life-history traits in the related species *Aplexa marmorata*, or in the invader itself. We study 21 populations of *A. marmorata* and 16 of *P. acuta*, which have been in contact with the other species from zero to eleven years. Reproduction, growth and survival were measured under common garden conditions. Our analyses show that several traits have changed in the native species as a result of fast evolution while the invasive species was hardly affected. Our analysis also indicates that local changes in the environment or in the snail community do not explain these modifications. These results therefore show that bioinvasions may trigger fast phenotypic evolution. They also are of interest for theories of species interaction and community assembly.

Poster session A - GEN 2000

Spatial genetic structures of strongly interacting species at different trophic levels in a fragmented landscape (52426)

Abhilash Nair, Christelle Couchoux, Saskya van Nouhuys.

University of Helsinki; Cornell University.

The genetic structures of species that interact trophically are interrelated, and differ depending on resource specialization and dispersal behaviour. The Glanville fritillary butterfly, *Melitaea cinxia*, lives as a metapopulation in the Åland islands, Finland. The butterfly hosts multiple parasitoid species at different trophic levels. Its caterpillars are parasitized by a specialist parasitoid wasp, *Hyposoter horticola*, which itself is parasitized by the specialist hyperparasitoid wasp, *Mesochorus stigmaticus*. Studying the genetic differentiation of these strongly interacting species helps us to understand the influence of landscape fragmentation on demographic histories and evolution of spatial genetic structure in multitrophic communities. The host butterfly populations are highly differentiated spatially and genetically in this fragmented landscape, with a high number of genetic clusters ($n=27$). In contrast, the parasitoids, which depend on the host butterfly and inhabit the same landscape, have weak spatial genetic structure ($F_{ST} = 0.02-0.06$) and fewer genetic clusters ($n=3-8$), with the hyperparasitoid having less structure than the primary parasitoid. This is expected because the parasitoids are much more dispersive than the host butterfly, resulting in weaker spatial genetic differentiation. They are however, constrained by the population dynamics and dispersal limitation of the host butterfly in the fragmented landscape

Poster session A - GEN 2000

Viral diversity in ant communities (52459)

Matthias, Alois Fürst, Thomas Eder, Thomas Rattei, Sylvia Cremer.

IST Austria; University of Vienna; University of Vienna; IST Austria.

Viruses are important infectious pathogens, regularly causing epidemics in societies, whether human or social insect. While research has made considerable progress in understanding viral infections in vertebrate societies, our knowledge in social insects is nearly exclusive to honey bees as important pollinators and fire ants, a serious pest species. Almost all studies available focus on single viral infections rather than multiple viruses present in a host population, taking the pathogen community into account. In this study we explore the natural viral component communities, different virus species populating a single host species, of three host ant species from three different subfamilies across various sampling sites. Next generation sequencing allows us to catch the whole viral diversity within the sampled host populations. We will highlight conserved viral community patterns within single host species across our sampling sites. For a deeper understanding of natural host pathogen systems the new techniques at hand offer valuable insights into complex ecological communities like multi-host multi-pathogen systems.

Poster session A - GEN 2000

From mutualism to parasitism: variation of toxicity in communities of mimetic butterflies (52547)

Mónica Arias, Johanna Mappes, Bastien Nay, Marianne Elias, Marc Théry, Violaine Llaurens.

UMR 7205. CNRS-MNHN. Institut de Systématique, Evolution et Biodiversité. Batiment d'entomologie. 45; University of Jyväskylä. Department of Biological and Environmental Science P.O. Box 35 FI-40014 Uni; UMR 7245. CNRS-MNHN. Molécules de Communication et Adaptation des Micro-organismes, 57 rue Cuvier; UMR 7179. CNRS-MNHN. MECADEV 1 avenue du petit château 91800 Brunoy (France).

Müllerian mimicry is the evolutionary convergence of several toxic species towards common warning signals and an example of mutualistic interactions driving species assemblage. Common local warning signals allow toxic species to share predator learning costs. However, such signals vary within natural communities, perhaps due to toxicity levels variation. Less defended species might weaken the protection brought by the shared signals, promoting new warning signals and associated mimetic communities. To investigate the role of toxicity variation in the warning signal diversity of the mimetic communities, we focused on toxic and brightly coloured neotropical butterflies from the genus *Heliconius* and a distantly related tribe, *Ithomiini*. Several mimetic communities include several species from one or both clades. The *Heliconius* butterflies' toxicity relies on cyanogenic compounds, whereas *Ithomiini* butterflies present pyrrolizidine alkaloids. A characterization of the compounds found in both clades and a dosage analysis were done, providing information about the toxicity levels variation among various phylogenetic distance species. Additionally, the toxicity variation effect on the rejection of different butterflies by predators, was tested through behavioural experiments with insectivorous wild caught birds (*Parus major*). Our results provide new insights on the effect of toxicity variation on species and colour pattern diversity of mimetic communities.

Ploidy level and genome size influence angiosperm species distributions under different nutrient conditions. (52623)

Maite Guignard, Ilia Leitch, Richard Nichols, Rob Knell, Catalina-Andreea Romila, Andy MacDonald, Mark Trimmer, Andrew Leitch.

Queen Mary University of London; 2Jodrell Laboratory, Royal Botanic Gardens, Kew; Queen Mary University of London; Queen Mary University of London; Queen Mary University of London; Rothamsted Research; Queen Mary University of London; Queen Mary University of London.

Angiosperm species display a 2400-fold wide range in genome size and ploidy levels as high as 38 are estimated. Focusing on nitrogen (N) and phosphorus (P) availability, we hypothesise that ploidy and genome size influence angiosperm distributions and abundance under different nutrient regimes. Angiosperm genomes are strongly skewed towards small values, suggesting selection for small genomes. A potential source of selection is N and P availability, since large genomes are more costly in terms of the N and P needed to make nucleic acids. We analysed the impact of fertilizer treatments on angiosperm species with different genome sizes, ploidy levels, and Grime's C-S-R plant strategies, growing in the world's longest running ecological experiment, Park Grass (Rothamsted, UK).

Genome sizes of species growing on plots with N+P fertilizer were significantly higher than plants growing on control plots and plots with either N or P. Polyploids also increased most significantly with N+P fertilizer, in particular polyploids with a strong C (competitor) strategy. These results are consistent with the hypothesized influence of large genome size on plant abundance under macronutrient limitation. They also suggest that ploidy and genome size are functional traits which contribute to plant distributions, community composition, and plant responses under different nutrient conditions.

Unraveling the role of host traits in predicting host parasite assemblages (52635)

Alexander Hayward, Masahito Tsuboi, Christian Owusu, Alexander Kotrschal, Josefina Zidar, Hanne Løvlie, Niclas Kolm.

Stockholm University; Uppsala University; Linköping University.

Parasites are common and abundant members of ecological communities. Additionally, parasites impose a range of host impacts, leading to major influences on community composition and function. However, despite their widely appreciated ecological and evolutionary significance, little is known about the factors that determine the great variation in parasite load observed among host species. Specifically, understanding remains lacking regarding the influence of host species traits, such as diet, body size, habitat usage, phylogeny

and mating system, on the abundance and diversity of parasites. To address this question, we sampled a wide range of Lake Tanganyika cichlid fishes, a model system in speciation research, and their gut macroparasites. This powerful approach, combining an extensive field sample with comparative evolutionary analysis, permits us to tease apart the relative influence of a large set of host traits on the abundance, diversity, prevalence and spread of parasites. Our findings suggest that the species richness of hosts occupying a habitat is the dominant factor in dictating differences in parasite diversity, abundance, and prevalence, while mating system explains skew in the distribution of parasites across individuals within a species. Our results provide unique new insights into the factors that govern variation in parasite assemblages across host species.

Poster session A - GEN 2000

The distribution and phylogeography of an important pollinator parasite (52665)

Regula Schmid-Hempel, Paul Schmid-Hempel.

ETH Zürich.

Crithidia spp, especially *C. bombi*, are important parasites of bumblebees; in turn, bumblebees are key pollinators in temperate and cold areas. Work over the last decade has shown that Crithidia are more diverse than realized before and that they occur in most of the areas so far investigated, forming communities of co-shared parasites. Here, we report on the worldwide distribution and communities of these parasites. The findings have implications of the study of host invasions into different areas, e.g. South America, as well as for the problem of possible parasite spillovers as has been reported for several cases.

Poster session A - GEN 2000

Rapid evolution alters natural microbial community structure (52683)

Pedro Gómez, K. McElroy, L. Xuan, S. Paterson, M.D. Sharma, A. Buckling.

Biosciences, University of Exeter, Penryn Campus. TR109FE, UK; Centre for Marine Bio-Innovation and School of Biotechnology and Biomolecular Sciences, UNSW, AUS; Institute of Integrative Biology, University of Liverpool, Liverpool L69 7ZB, UK.

There is growing acceptance of the key role that evolution occurring over ecological time scales plays in shaping the structure and function of communities. However, while there are numerous demonstrations in laboratory settings, studies in natural communities have only reported effects when evolutionary change, although rapid, occurred over much longer time scales than the ecological time scales of the experiments. We determine whether and how rapid evolution of a single resident species affects the structure of a soil microbial community, where evolutionary and ecological changes occur over comparable time scales. We compared how the presence of ancestral or pre-adapted (for 48 days) populations of the soil bacterium

Pseudomonas fluorescens SBW25 affected the natural microbial community structure in soil-compost over 2 months. The pre-adapted *P. fluorescens* bacteria both reduced the density and altered the composition of the resident community, a key feature of the latter being a large reduction in the proportion of resident *Pseudomonads* – the species most related to the pre-adapted focal species. Our results show that evolution of a single microbial species over ecological time scales predictably alters natural community structure by outcompeting genetically (and presumably ecologically) similar species.

Poster session A - GEN 2000

Agricultural landscapes influence the repartition of traits on carabid beetles. (52748)

Alexia Marie, Manuel Plantegenest.

Agrocampus-ouest.

The intensification of agriculture and its consequences on landscapes are considered as a major cause of biodiversity decline. The composition of landscape affects diversity of arthropods in particular through the diversity of available habitats. Indeed, a general trend that landscape heterogeneity is positively correlated with specific richness is well documented. On an applied point of view, this loss of biodiversity affects ecosystem services that it provided, especially, pest regulation service provided by natural enemies' diversity.

However, an approach based on species traits at the community level can highlight strategies that allow species to settle and to maintain themselves in an environment, and in the same time, identify filters that favor benefic traits for biological control.

During this study, we focused on carabid beetles which are considered as good natural enemies on several pests. The work consisted in finding links between landscape composition and traits at the community level. The beetles were trapped on 57 fields spread on 3 different regions of West of France. An analysis on fields according to their landscape characteristics showed an opposition between two agricultural systems: cereals farms and breeding farms. For each system, particular traits were found, showing an opposition between two strategies.

Poster session A - GEN 2000

Phylogeography and taxonomy of *Arabidopsis halleri* across its distributional range (52786)

Gabriela Fuxová, Eliška Závěská, Filip Kolář, Magdalena Lučanová, Stanislav Španiel, Karol Marhold.

Department of Botany, Faculty of Science, Charles University in Prague, Prague, Czech Republic; Institute of Botany, University of Innsbruck, Innsbruck, Austria; Natural History Museum, University of Oslo, Oslo, Norway; Institute of Botany, Academy of Sciences of the Czech Republic, Průhonice, Czech Republic; Institute of Botany, Slovak Academy of Sciences, Bratislava, Slovak Republic.

Arabidopsis halleri comprises about five subspecies and represents an important model species for the study of heavy metal tolerance and phytoremediation. Nevertheless, the so far unclear evolutionary history and provisional taxonomy may hamper correct interpretation on the evolution of these important traits within the species.

A. halleri is a perennial, clonal and self-incompatible plant. Four subspecies tentatively recognised (*A. halleri* subsp. *halleri*, subsp. *dacica*, subsp. *ovirensis*, subsp. *tatica*) are centred in Central Europe, while the last one, *A. halleri* subsp. *gemmifera* occurs in Japan and the Far East. Despite representatives of *A. halleri* are purely diploid ($2n=16$), a high morphological variation combined with geographic differentiation stand behind complex and still unresolved taxonomy of the group.

Using six microsatellite loci and AFLP's we aimed to reveal phylogeographic structure of this lineage and to find correlations with the results of morphological analyses. We collected 450 samples from 40 populations across its whole European range in the Carpathian Mountains, the Dinaric and Balkan Mountains, the Bohemian Massif, the Alps and comparative material of *A. halleri* subsp. *gemmifera* from Japan. Our results indicate simpler genetic structure with three main groups within the European area generally correlated with geographical distribution, not with the current taxonomic concept.

Poster session A - GEN 2000

Evolution of a community of a multiple-strain tick-borne pathogen during 11 years: Is fitness a good predictor? (52836)

Jonas Durand, Maarten Voordouw.

Laboratory of Ecology and Evolution of Parasites, University of Neuchâtel.

Borrelia afzelii is a tick-borne spirochete that causes Lyme disease in humans. The polymorphic *ospC* gene of *B. afzelii* codes for the immunodominant outer surface protein C and is a useful strain-specific marker. Previous genetic studies on the *ospC* gene found a pattern of balancing selection. One explanation is that the host immune system targets common *ospC* groups, thereby reducing their frequency over time.

We examined the diversity of *ospC* groups in a local population of *Ixodes ricinus* ticks infected by *B. afzelii* ($n=196$) over 11 years (2000-2010). We used 454-sequencing to characterize the *ospC* community in each tick. We also used experimental infections of mice to estimate the intrinsic fitness of six *B. afzelii* *ospC* strains in the lab.

We found that the frequency distribution of the *B. afzelii* *ospC* groups was stable over the duration of the study. Our laboratory estimates of strain fitness explained over 65% of the variation in the strain-specific frequencies in the field. The pattern of genetic variation at the *ospC* locus suggested there was strong selection against intermediately divergent *ospC* alleles. Our results are consistent with theoretical models on how acquired immunity structures multi-strain pathogen populations.

Poster session A - GEN 2000

The Role of Plant-Microbe-Insect interactions in driving rapid evolution using *Medicago polymorpha* as an experimental system (52990)

Chandra Jack, Maren Friesen.

Michigan State University.

Invasive plant species leave behind coevolved herbivores and competitors when they invade novel environments. In these new environments, they face new biotic conditions that they must adapt to in order to become established. This includes multitrophic interactions with microbes and insects. Historically, these interactions were studied in two group interactions (plant-microbe or plant-insect) (Biere and Tack 2013). Yet, evidence suggests that these interactions are driven either directly or indirectly by a third party and can alter ecological and evolutionary outcomes (Heath and Lau, 2011). Our work explores the role of simultaneously interacting with beneficial microbes and insect herbivores in the evolution of *Medicago polymorpha*, a small invasive legume, in novel environments to determine the importance of multitrophic level interactions on rapid evolution and the success of invasive species as they enter new territories.

Poster session A - GEN 2000

Host-microbiota interactions during adaptation to different nutritional conditions in *Drosophila melanogaster* (51830)

Berra Erkosar, Sylvain Kolly, Jan Roelof van der Meer, Tadeusz Kawecki.

DEE-UNIL; DMF-UNIL.

In the last decade, *Drosophila* emerged as a model to study host-microbiota interactions. Compared to mammals, *Drosophila* has a relatively simple microbiota that is mainly composed of aero-tolerant species, belonging to Lactobacillales and Acetobacteraceae families, which were previously shown to influence host digestive function and/or metabolism, that in turn impacts hormonal pathways and juvenile growth. Our major aim is to identify the role of gut microbiota during evolutionary adaptation to different nutritional conditions. To do this, we use experimentally evolved *Drosophila* populations that are maintained in distinct diets over numerous generations. During this period, fly populations got adapted to their nutritive regime causing remarkable phenotypes in terms of life history traits. By performing microbiota transplants among populations that are kept in distinct nutritional regimes, we aim to understand better how microbiota evolves on different food sources and how it contributes to host phenotypes that emerged upon adaptation.

Poster session A - GEN 2000

Can different biocontrol agents be combined to develop evolutionary-proof biocontrol method against *Ralstonia solanacearum* plant pathogen? (51897)

Zhong Wei, Xiaofang Wang, Ville Petri Friman, Yangchun Xu, Qirong Shen, Alexandre Jousset.

Nanjing Agricultural University; UK-based University of York; Utrecht University.

Ralstonia solanacearum (RS) is a notorious soilborne plant pathogen. It has been demonstrated that many biocontrol methods including interference competition and parasitic phages might efficiently suppress RS disease. However, the long-term effectiveness or combinatory effects of different biocontrol methods have been less studied. For example, it is possible that RS could rapidly evolve resistance to single biocontrolling bacteria or phages. However, it is less likely that RS would evolve resistance simultaneously to different biocontrol agents. Here we tested this directly in realtime co-evolution experiments where we cultured RS bacterium with antagonistic antibiotic-producing *Bacillus amyloliquefaciens* T-5 strain and RS-specific phage pQL2014 alone or in combination. Besides tracking population dynamics, we also measured RS resistance evolution against different biocontrol agents. Our results show that *B. amyloliquefaciens* T-5 strain offered relatively more long-term protection against RS, while bacteria evolved resistance to phage pQL2014 within 4 days. Surprisingly, phage selection constrained the inhibitory effect of *B. amyloliquefaciens* T-5 strain. Using multiple biocontrol agents simultaneously could thus potentially reduce the effectiveness of each single biocontrol agent. Applying different biocontrol agents sequentially will be discussed. This work provides an important step toward understanding the resistance evolution of *R. solanacearum* against different biocontrol agents.

Poster session A - GEN 2000

More than just density: different paths to the evolution of larval competitive ability (51908)

Manaswini Sarangi.

JNCASR.

In *D. melanogaster*, series of studies on adaptation to larval crowding has led to an understanding about enhanced competitive ability being strongly correlated with increase in feeding rate and waste tolerance. This has been shown to be at the expense of lowered food to biomass conversion efficiency. More recent studies from our laboratory suggest that there are alternative routes to the evolution of adaptation to larval crowding in *Drosophila* populations. We show that populations of *D. melanogaster* when subjected to extreme larval crowding evolve greater competitive ability by a combination of different suite of traits which includes faster egg to adult development and greater food to biomass conversion efficiency. This is in contrast to what had been seen earlier in similar selection experiments, that there was neither elevated feeding rate nor enhanced tolerance to nitrogenous waste in the culture. We did certain experiments in which we observed subtle changes in the ecology of laboratory-adapted *Drosophila* populations under slightly different maintenance regimes can potentially affect the suite of traits that evolve in response to chronic larval crowding. We discuss the findings in the perspective of how the balance of food availability and build-up of nitrogenous waste can potentially affect the fitness of different traits underlying competitive ability.

Shape matters: lifecycle of cooperative patches promotes cooperation in bulky populations (51977)

Dusan Misevic, Antoine Frénoy, Ariel B. Lindner, François Taddei.

INSERM U1001, University Paris Descartes, Sorbonne Paris Cité.

Natural cooperative systems take many forms, ranging from one-dimensional cyanobacteria arrays to fractal-like biofilms. We use in silico experimental systems to study a previously overlooked factor in the evolution of cooperation, physical shape of the population. We compare the emergence and maintenance of cooperation in populations of digital organisms that inhabit bulky (100x100 cells) or slender (4x2500) toroidal grids. Although more isolated sub-populations of secretors in a slender population could be expected to favor cooperation, we find the opposite: secretion evolves to higher levels in bulky populations. We identify the mechanistic explanation for the shape effect by analyzing the lifecycle and dynamics of cooperator patches, from their emergence and growth, to invasion by non-cooperators and extinction. Because they are constrained by the population shape, the cooperator patches expand less in slender than in bulky populations, leading to fewer cooperators, less public good secretion, and generally lower cooperation. The patch dynamics and mechanisms of shape effect are robust across several digital cooperation systems and independent of the underlying basis for cooperation (public good secretion or a cooperation game). Our results urge for a greater consideration of population shape in study of the evolution of cooperation across experimental and modeling systems.

Co-evolutionary constraint after the true domestication of fungal crops by attine ants (51980)

Jonathan Z. Shik, Ernesto Gomez, William T. Wcislo, Jacobus J. Boomsma.

Centre for Social Evolution, University of Copenhagen; Smithsonian Tropical Research Institute, Apartado 0843-03092, Balboa, Ancon, Republic of Panama; Smithsonian Tropical Research Institute, Apartado 0843-03092, Balboa, Ancon, Republic of Panama; Centre for Social Evolution, University of Copenhagen.

Unlike humans, attine ants receive all of their nutrition from a single food crop, obligately farming fungus for over 50 million years. Around 20 MYA, the attines domesticated a specialized fungal lineage capable of concentrating nutrients in special organs (staphylae with gongylidia). Despite this innovation, attine colony-farms remained small (100 workers) until 12 MYA when the genus *Atta* began using fresh-cut leaves as compost to produce massive fungus gardens sustaining millions of ants. Towards explaining this transition, we used geometric framework experiments to compare the nutritional ecology of two Panamanian rainforest attines: *Atta colombica* (industrial-scale farmer) and *Trachymyrmex cornetzi*

(small-scale sister lineage). We found that *A. colombica* produces faster-growing fungus that is more robust to nutritionally imbalanced compost. In contrast, *T. cornetzi* workers are extremely averse to harvesting substrate with excess protein because this induces fungus-garden collapse and constrains colony growth. Moreover, *T. cornetzi* (but not *A. colombica*) faces nutritional compromises between maximizing fungus growth (fueled by carbohydrates) and staphylae production (fueled by protein). Our results shed new light on how nutritional adaptations helped leaf-cutting ants overcome co-evolutionary constraints in selection for crop improvement and achieve symbiotic complementarity that gave rise to the most advanced societies of farming ants.

Poster session A - GEN 2000

The simplicity and complexity of the attine ant gut microbiota: living within a symbiotic network (52071)

Panagiotis Sapountzis, Mariya Zhukova, Lars H. Hansen, Søren J. Sørensen, Morten Schiøtt, Jacobus J. Boomsma.

Centre for Social Evolution, Department of Biology, University of Copenhagen; Institute of Cytology and Genetics, Siberian Branch of the Russian Academy of Sciences, Novosibirsk,; Molecular Microbial Ecology Group, Department of Biology, University of Copenhagen.

The attine fungus-growing ants are a monophyletic group that switched to an almost exclusive fungal diet ca. 50 MYA. They are a model of complex symbiosis and have several fungal and bacterial symbionts. We obtained comparative and functional gut-microbiome data for 19 Panamanian species, representing 8 genera, which are dominated by few bacterial species belonging mostly to the Alpha-Proteobacteria and Mollicutes. These bacteria are located in specific gut tissues with some being found intracellularly. Rhizobiales species were among the most abundant gut bacteria and mediated the acquisition of nitrogen via the expression of NifH proteins in the hindgut where they form a biofilm. Guts and surrounding organs of higher attine, and particularly leaf-cutting, ants harbor most of these bacteria, consistent with the symbiosis being protein-limited in spite of increasing specialization of the crop fungus over evolutionary time. The composition of the gut microbiota appears to be correlated with the presence or absence of a cuticular microbiome of actinomycete bacteria: attine species that maintain cuticular actinomycetes had more stable gut microbiomes, possibly because the antibiotics produced by these bacteria protect gut microbiomes against invasion by non-symbiotic bacteria.

Poster session A - GEN 2000

Host genotype × environment interaction change the microbial community of *Daphnia* (52177)

Karen Sullam, **Samuel Pichon**, Tobias Schär, Dieter Ebert.

University of Basel.

The environmental conditions and genetic background are believed to shape the composition of host-associated microbiota. It is unclear if the environment or the host genotype has the predominant role in shaping the microbiota of the host and whether they interact in doing so. We evaluated the effect of environment (temperature), host genotype, and their interaction on the composition of microbiota by using the cyclic parthenogenetic freshwater crustacean *Daphnia magna*. We used 21 different clones of *D. magna* from a wide geographic range, reared at 20 and 28 °C, to focus on microbial diversity and the abundance of indicator taxa under different environmental conditions. Our analysis reveals strong genetic, temperature and G x E interaction effects on the microbiota of *D. magna*, including a shift in overall community structure. Additionally, the abundance of certain microbial constituents shift consistently at higher temperatures across clones, while others exhibit clone-specific characteristics and change minimally across temperature conditions. The disparity in reactions of microbes to different temperatures and clones highlights their complex interactions with the environment and their host. This work enables a better understanding of the genotypic and environmental controls and selective forces that shape the variation found within a host's microbiota.

Poster session A - GEN 2000

Chemical warfare no solution against parasite attack: *Tribolium castaneum* vs. *Beauveria bassiana* (52199)

Gerrit Joop, Charlotte Rafaluk, Yang Wentao, Andreas Mitschke, Philip Rostenstiel, Hinrich Schulenburg.

University of Giessen; University of Oxford; University of Kiel.

The beetle *Tribolium castaneum* disposes an extended external immune defence, in addition to the classical invertebrate immune defence, coming with broad antimicrobial properties. Here, we wanted to gain a better understanding of if and how this external defence responds upon contact with a parasite and how the two interact.

We conducted a coevolution experiment with the entomopathogenic fungus *Beauveria bassiana*, taking the host and the parasite perspective. In the host we measured levels of internal and external immune traits throughout the experiment and survival as a proxy of resistance against the fungus. In the parasite, we tested for fungal virulence towards the host as well as for potential resistance against the host's external secretion, combined with a transcriptomics approach.

While no obvious change in host external immunity or survival was observed as a consequence of host-parasite coevolution, we were able to show that *B. bassiana* increased in virulence during the course of coevolution, based on the fungal isolates evolving resistance to the external immune defences of *T. castaneum*.

Results present a rare example of an experimentally coevolved increase in virulence, where the exact barrier of host immune defence overcome by the parasite has been described, the external secretion of quinones.

Poster session A - GEN 2000

Heterosis in yeast increases with parental divergence and environmental stress (52247)

Joana Bernardes.

Max Planck Institute for Evolutionary Biology.

Reproduction between genetically different parents often leads to F1 offspring with enhanced traits, a concept known as heterosis. While the phenomenon itself can be easily described using familiar genetic concepts (dominance, over-dominance and epistasis), the underlying molecular mechanisms for heterosis are still unknown. We tested the genetic and environmental factors that influence the strength of heterosis, using a set of sequenced and phenotyped yeast strains. We accurately measured heterosis in 45 heterozygous F1 hybrids, by competing them with their homozygous parental strains. F1 hybrids were on average 4% fitter than their mean parent. Interspecific crosses were significantly fitter than the intraspecific crosses, thus genetic distance was positive correlated with the strength of heterosis. We then tested a representative interspecific F1 hybrid under a range of extreme environmental conditions to measure how the strength of heterosis was affected. We found an increase of heterosis under stress. Next we will use transcriptome data to test if there is a general molecular mechanism underlying heterosis at a multigenic level. For this, we will test if the hybrids may be able to preferential express certain alleles for a specific environment.

Poster session A - GEN 2000

Stability and variation in the gut and fungus comb microbial communities in fungus-growing termites (52287)

Saria Otani, Michael Poulsen.

University of Copenhagen.

The higher termite subfamily, Macrotermitinae, domesticated a plant-degrading fungus, *Termitomyces*, 30MYA. The adoption of *Termitomyces* has shaped fungus-growing termite gut microbiotas to become different from those of other termites and predicts that the external fungus combs could inhabit specialised bacteria communities. Using 16S rRNA high-throughput sequencing, we investigated the bacterial community compositions in fungus-growing termites by analysing guts of nine termite species from the Ivory Coast, 33 different fungus combs from four termite species and four sites in South Africa over two years, and 134 gut samples from worker and soldier castes from four South African Macrotermitinae species. Forty-two bacteria form a core community in Macrotermitinae guts and this core is more similar to cockroach microbiotas than those of other termites, with signals of termite phylogenetic ancestry. Comb communities were non-random, more variable than gut microbiotas, and shaped by gut content and time, likely due to environmental fluctuations. Gut microbiotas are expected to be shaped by caste more than species or colony, as gut communities are influenced by caste-specific functions. These results imply the uniqueness of fungus-growing termite microbiotas; both in guts and fungus combs, and that variation exist among castes and different genera as finer adaptations to specific lifestyles.

Eco-evolutionary dynamics of a predator-prey system provide insight into the paradox of enrichment (52416)

Gökçe Ayan, Lutz Becks.

Max Planck Institute for Evolutionary Biology.

Resource enrichment might cause destabilization of a predator-prey system. However, it might stabilize the system by accelerating coevolutionary dynamics and diversification due to increased population sizes of interacting species. Coexistence of different prey types might also stabilize the system via preventing the predator to overexploit a specific prey type. Here, we combine these aspects in ciliate-bacteria (predator-prey) microcosm experiments to test for coevolution with resource enrichment in homogeneous and heterogeneous environments. We followed the population dynamics, measured the diversification in the prey as well as important traits such as the prey's grazing resistance, and the predator's counter adaptation over time. We found that with resource enrichment the extinction of predator occurred when there was no diversification in the prey (i.e. in homogeneous environments), whereas coexistence of predator and prey lasted 60 days in heterogeneous environments. We also showed that the frequency of defended prey increased with increasing resource levels. All these suggest that selection by predator and diversity in prey populations affect the coexistence of the predator-prey and matter for stabilization of the interaction. Thus, an eco-evolutionary approach is needed to understand the role of resource enrichment and the importance of rapid evolution for resolving the paradox of enrichment.

Predation and the evolution of multicellular groups in algae (52512)

Stefania Kapsetaki.

University of Oxford.

The major evolutionary transition from unicellular to multicellular life and, in particular, social group formation is a puzzling question in biological research. Why do single cells form a group? Defence against predation has been proposed to drive social group formation mainly on the basis of predators being unable to engulf large sized entities. However cells in some species remain in their unicellular state upon encounter with a predator, implying that there are also fitness costs to forming groups. We investigated how widespread predation pressure is as a driving force towards colony formation by using *Ochromonas* spp., *Tetrahymena thermophila* and *Daphnia* as predators and the algae *Chlorella sorokiniana*, *Chlorella vulgaris* and *Scenedesmus obliquus* as prey, giving rise to a total of nine different predator-prey combinations. Our results showed that in all combinations, apart from two cases, *Ochromonas* spp.-*S.obliquus* and *T.thermophila*-*S.obliquus*, the prey species formed colonies, though the hypothesis of there being a size advantage in forming a colony was only confirmed in the case

of *T.thermophila*-*C.sorokiniana*. Overall, in seven combinations we observed that predation pressure causes colony formation in the prey and potentially, ensuring high relatedness, can favour multicellularity.

Poster session A - GEN 2000

Insects' detoxification mechanisms as target for antagonistic filamentous fungi? (52649)

Monika Trienens, Joachim Kurtz, Bregje Wertheim.

Institute for Evolution and Biodiversity, University of Münster DE; Evolutionary Genetics, University of Groningen NL.

Insects and microorganisms co-inhabit resources for feeding and development. Microorganisms often excrete detrimental substances, i.e. mycotoxins and antibiotics, into these resources, and co-occupants need to cope with these substances. To study the evolution of such coping mechanisms in insect-fungus interactions, we combined experimental evolution and transcriptomics.

We mimic co-infestation, using breeding sites of fruitflies, *Drosophila melanogaster*, and inoculate these with filamentous fungi, *Aspergillus nidulans*. To disentangle the fruitfly responses to the mere presence of fungi (e.g., alterations in substrate pH-level, amino acid import) from responses caused by mycotoxins, we forced fruitfly populations to develop in the presence of wild type fungus, toxin-impaired fungus, a pure mycotoxin or under control conditions. After several generations, the wild-type and mycotoxin-selected populations survived subsequent confrontations significantly better, while the mycotoxin-selected fruitflies did not show increased survival when confronted with wild-type fungus.

RNA-seq analysis of *D. melanogaster* larvae during confrontation revealed a small set of genes in first and second line detoxification mechanisms that were induced during mycotoxin confrontation, whereas exactly these mechanisms were down-regulated in both fungal strain confrontations. Mycotoxins elicit selection in insect-fungus interaction, yet are they the key mechanism?

Poster session A - GEN 2000

The genotypic view of social interactions in multispecies microbial communities (52660)

Sara Mitri, Kevin Foster.

University of Lausanne; University of Oxford.

Microbes live in dense communities composed of different strains and species, where cells can affect the growth and survival of their neighbours both positively and negatively.

Disentangling these social interactions is central to understanding the stability and productivity of these microbial communities that are ubiquitous in our lives. By combining

ecological and evolutionary theory, we have recently proposed a general null model, which we call the genotypic view. This states that cooperation will be under positive selection when cells are surrounded by identical genotypes at the loci that drive interactions, whereas different genotypes will typically compete, leading to the evolution of antagonistic phenotypes or spatial separation. I will begin by presenting the logic of the genotypic view, supported by a mathematical model. I will then discuss various theoretical and experimental methods we are currently developing to test these ideas within two relatively simple communities composed of five to seven microbial species. These include approaches to disentangle existing social interactions, and later to follow their evolutionary trajectory over larger time-scales.

Poster session A - GEN 2000

Eco-evolutionary dynamics of Pepino mosaic virus (52679)

Pedro Gómez, M. Juárez, M.A. Sánchez-Pina, C. Alcaide, M.A. Aranda.

CEBAS- CSIC, Dpto Patología Vegetal, Murcia, Spain; Escuela Politécnica Superior de Orihuela, Universidad Miguel Hernández, Alicante, Spain.

While individual plants are often infected in nature with more than one related or unrelated virus, the extent to which mixed infections can modulate the evolutionary dynamics of these viruses is unclear. Pepino mosaic virus (PepMV) is an emerging RNA virus known to be one of the most important tomato pathogens worldwide. Phylogenetic analyses have shown that PepMV populations in Spain are composed of isolates of two types (PepMV-CH2 and PepMV-EU) that appear to be still co-circulating after 10 years from their first detection. This study addressed how viral interactions among both PepMV types and also with other tomato RNA virus (Cucumber mosaic virus; CMV) could affect their evolutionary dynamics. Combining a population genetics approach with biological analyses of these viruses in planta, our results showed that an antagonistic interaction between both PepMV types was host-nonspecific, as patterns of RNA viral accumulation in single and mixed infections in different hosts were similar, and neither was affected by the presence of CMV. Furthermore, microscopy preliminary results show that these viruses are able to infect the same cell types, and ultra-structural analysis by electron microscopy will reveal whether they are infecting the same cell, and therefore, competing for the same plant and/or viral resources.

Poster session A - GEN 2000

The role of parasitisms and environmental change in ecosystems during sticklebacks adaptive radiations (52735)

Jaime M. Anaya-Rojas, Franziska Brunner, Christophe Eizaguirre, Ole Seehausen, Blake Matthews.

Swiss Federal Institute of Aquatic Science and Technology ; University of Bern; Queen Mary University London and Ewag.

Ecosystems can be affected by both ecological and evolutionary changes, for instance, through changes in the nutrient levels or indirect trait-mediated effects. Theory suggests that different phenotypes have different effects on the environment, however, less is known about the role of other relevant ecological factors such as parasitism. In a large scale mesocosm experiment, we studied how parasite exposure and contrasting nutrient levels affect (1) the diet of a recently divergent lake-stream pair of sticklebacks and (2) prey-community structure and ecosystem dynamics. Parasites had strong effects on fish diet, particularly for lake fish. The ecosystem effects of parasites were weaker. At the prey-community and ecosystem processes level (e.g., nutrients concentration, and primary productivity) interactive effects were statistically significant. We concluded that parasites can affect ecosystem processes through changes in feeding behavior of sticklebacks (e.g. prey-preferences or feeding performance) in different ways depending on the nutrient level of the environment.

Poster session A - GEN 2000

Genome streamlining in bacteria evolving under high predation pressure (52804)

Michael Baumgartner, Stefan Roffler, Thomas Wicker, Judith Blom, Jakob Pernthaler.

University of Zurich, Limnological Station; University of Zurich, Institute of plant biology.

Predation by eukaryotic protists is a major mortality source for aquatic bacteria. Consequently, many species have developed phenotypic antipredator strategies to cope with this threat. Such mechanisms are costly in terms of resource allocation or cause other competitive disadvantages, and therefore, are expected to be under strong selection pressure. We set up a long-term predator-prey experiment with a bacterial freshwater isolate, *Sphingobium* sp. Z007 and the bacterivorous flagellate *Potamochochromonas* sp.. The prey bacterium forms increased proportions of inedible cell aggregates in the presence of the predator. Bacteria in pure culture and a bacteria-predator co-culture were maintained in oligotrophic medium and regular propagations for 200 days. In both treatments, bacteria exhibited a rapid phenotypic adaptation to the presence or absence of flagellates. Strains under continuous predation pressure showed higher proportions of aggregates, and this phenotype was also maintained when grown in the absence of a predator. Bacteria in pure culture lost their ability to form aggregates but showed higher efficiency in substrate usage. Three independent evolutionary lineages of strains exposed to predation showed pronounced genome streamlining, whereas this was never observed in the evolved pure cultures. We hypothesize that this adaptation helped the evolved strains to increase their growth efficiency despite the resource investment in predator defence.

Poster session A - GEN 2000

The genomic basis of phenotype variation in social myxobacteria isolated from nature (52889)

Sébastien Wielgoss, Gregory Velicer.

Analyzing genetic variation in nature is mandatory for better understanding the processes governing the evolution of phenotypes in natural populations. For microbes, however, data on how natural genetic diversity relates to phenotypic divergence are sparse, including the remarkably sophisticated social traits exhibited by the myxobacteria. For example, members of this bacterial cooperate upon starvation to engage in the formation of fruiting bodies within which only a small fraction of cells form stress-resistant spores. Fruiting bodies of the model organism *Myxococcus xanthus* harvested from soil are composed of clones among that are highly genetically related and harbor a surprisingly high degree of diversity in social phenotypes. However, the molecular basis of this extremely fine-scale social diversity is unknown. Here, by applying whole genome sequencing to dozens of clones derived from individual fruiting bodies from nature, we shed light on the genomic basis of natural social diversity. Based on experiments, we then set out to pinpoint the evolutionary forces that could explain the particular genetic and phenotypic variation within groups. We conclude that fruiting bodies could be viewed as natural analogs to laboratory colonies in experimental evolution settings in which individuals share a single recent common ancestor but have undergone micro-diversification.

Poster session A - GEN 2000

The outcomes of bacteriophage selection on the evolution of virulence in *Klebsiella pneumoniae* (52911)

Anni-Maria Örmälä-Odegrip, Harald Eriksson, Lauri Mikonranta, Pilvi Ruotsalainen, Sari Mattila, Ville Hoikkala, Anders Nilsson, Jaana Bamford, Jouni Laakso.

University of Jyväskylä; Stockholm University; University of Helsinki.

Bacterial viruses or bacteriophages are ubiquitous bacterial parasites that impose a strong selection pressure for bacterial phage-resistance. Phage-resistance is often associated with fitness costs on bacterial traits such as virulence in multicellular hosts. We studied whether there were associated costs for resistance against single or multiple phages on bacterial virulence, growth ability and biofilm formation in a clinical isolate of *Klebsiella pneumoniae*. We found that resistance against multiple phages was in general associated with lowered virulence, when measured in vivo with *Galleria mellonella* wax moth larvae. However, selection by two phages alone led to increased virulence, coupled with an increased growth rate in bacteria. Biofilm production was negatively correlated with virulence, whereas growth rate had a positive correlation with bacterial virulence across all treatments. Our findings suggest that the presence of multiple phages could select for bacterial virulence, possibly due to a trade-off between phage resistance and rate of replication. However, this is dependent on the identity of phages. This is the first study to report increased bacterial virulence associated with exposure to lytic bacteriophages. Our findings are of practical importance when developing phage therapy, the use of bacterial viruses in treating bacterial infections that are resistant to conventional antibiotics.

ACQUIRED IMMUNITY AND CROSS-IMMUNITY EFFECTS ON SYSTEMIC AND CO-FEEDING TRANSMISSION OF A MULTI-STRAIN TICK-BORNE PATHOGEN. (52968)

Maxime Jacquet, Maarten Voordouw.

Université de Neuchâtel.

Tick-borne pathogens have multiple modes of transmission including systemic (host-to-tick) and co-feeding transmission. Co-feeding transmission can occur when ticks exchange pathogens by feeding at the same time on the same host. We tested whether *Borrelia afzelii*, which causes Lyme disease in Europe, can use co-feeding transmission to escape the acquired immune response in the vertebrate host, and how cross-immunity influences the fitness of cross-reactive strains.

Outer surface protein C (OspC) is a single-copy, polymorphic antigen of *B. afzelii* that induces a strong immune response in the vertebrate host. Mice were immunized with one of two variants of the OspC antigen: A3 or YU then challenged with the homologous or heterologous *B. afzelii* ospC strain via tick bite. Mice were infested with larval ticks to measure co-feeding and systemic transmission. Ticks were tested for infection prevalence and bacterial load using qPCR.

Acquired immunity against the rOspC antigens blocked both co-feeding and systemic transmission of the homologous but not the heterologous strains. Cross-immunity had no effect on transmission but reduced the spirochete load in the tick vector. Acquired immunity and cross-immunity against the immunodominant OspC antigen have important consequences for the fitness and evolution of multi-strain *Borrelia* populations.

Evolution of male and female choice in promiscuous mating systems (51788)

Mikael Puurtinen, Lutz Fromhage.

University of Jyväskylä; Centre of Excellence in Biological Interactions.

While empirical studies have revealed that both males and females often exercise mate choice, theoretical understanding of systems where both sexes can evolve mate choice is limited. We studied the evolution mate choice in a system where females vary in fecundity and males in sperm production. Additionally, sperm availability limits female fertility, and ejaculate size affects males' success in sperm competition. The probability with which opposite sex individuals are accepted as mating partners is a freely evolving parameter for each sex. Both sexes can also evolve choosiness, the cost of which increases with increasing discrimination between individuals of different quality. We solve the model for evolutionarily stable combinations of male and female mate acceptance strategies, varying the costs of mating and choosiness. Results of the model show that while highest quality males and females mate most often, these patterns mostly result from lower mating activity and higher choosiness of low quality males who have less sperm and evolve to use it more prudently.

These results highlight the need for explicit evaluation of mate acceptance criteria of both sexes in empirical mating system studies, and caution against making unsubstantiated conclusions about the mechanisms underlying mating patterns.

Poster session A - GEN 2000

Disassortative mating in plants: paternity analysis of floral morphs within experimental populations (51831)

Violeta I. Simón-Porcar, Thomas R. Meagher, Juan Arroyo.

University of Stirling; University of St. Andrews; University of Seville.

Heterostyly enhances disassortative pollination between floral morphs through reciprocal placement of stigmas and anthers, and through a physiological heteromorphic incompatibility system which impedes within-morph fertilization. Which of these mechanisms is the main driver of disassortative mating in this polymorphism is object of debate. Styler-dimorphism lacks reciprocal anther placement and hence disassortative mating could be compromised, particularly when there is not intra-morph incompatibility. Variable rates of disassortative mating along with differential female fecundity or siring success among floral morphs could lead to variation in morph ratio in this polymorphism.

We investigated mating patterns in *Narcissus papyraceus*, an intra-morph compatible species with dimorphic (long- and short-styled) and monomorphic (long-styled) populations in central and north regions of its range, respectively. We established experimental populations in both regions and exposed them to ambient pollinators. Using paternity analysis, we found high disassortative mating in most populations. Female fecundity of morphs was similar in all populations.

Our results provided evidence for the evolutionary stability of styler dimorphism in *N. papyraceus* and reveal the central role of morphological reciprocity of sexual organs in promoting disassortative pollination, even when such reciprocity is imperfect. However, it is unclear what forces lead to complete loss of one of the morphs in some natural populations.

Poster session A - GEN 2000

A novel cost to sex allocation in the mostly monandrous wasp, *Nasonia vitripennis* (51840)

Rebecca Boulton, David Shuker.

University of St Andrews.

The near-ubiquity of polyandry is a crucial component of mating system evolution, yet there is much we still do not understand about the economics of polyandry. Females of the parasitoid wasp *Nasonia vitripennis* are “mostly monandrous” in the wild, but become increasingly polyandrous under laboratory culture. They have also been well-studied in terms of sex allocation, producing female-biased sex ratios in line with the predictions of local mate

competition (LMC) theory. Here we present the results of a series of experiments showing that the costs and benefits of multiple mating in this species are contingent on sex allocation under LMC. We show that harassment and multiple mating during oviposition results in the increased production of sons under conditions that instead favour female-biased sex ratios. We also find evidence that mating multiply with virgin but not with previously-mated males increases female fecundity. In the laboratory, LMC is low compared to the wild, increasing the abundance of virgin males and perhaps relaxing the sex allocation cost of harassment and mating. We discuss the relevance of these findings with regards to the laboratory evolution of polyandry, and the evolution of polyandry more generally.

Poster session A - GEN 2000

Paradox of high outcrossing and no selfing syndrome despite no inbreeding depression after a loss of self-incompatibility (51884)

Marie Voillemot, John R. Pannell.

Unil; Unil.

Evolution toward selfing is one of the most frequent transitions to have occurred in flowering plants, and its causes, mechanisms and consequences continue to pose puzzles. Species that vary in their mating systems among populations offer ideal material to test hypotheses for the transition. A strong prediction is the evolution of high selfing rates and a syndrome of self-fertilization (low attraction to pollinator attraction and reward) in populations that evolve low inbreeding depression. The toadflax species, *Linaria cavanillesii* (Scrophulariaceae), which is endemic to south-eastern Spain, exhibits variation in self-incompatibility (SI) among populations, with some populations being SI and others having lost this outcrossing mechanism to become self-compatible (SC). Surprisingly, populations with SC individuals appear to maintain a high outcrossing rate, and their flowers do not show the typical evolution toward a full selfing syndrome. We present results of an inbreeding depression experiment that further shows that SC individuals display much lower inbreeding depression than their SI counterparts. We discuss the reasons for the combination of low selfing rates and low inbreeding depression despite the loss of SI.

Poster session A - GEN 2000

Beauty in the eyes of the beholders: Color vision is tuned to mate preference in the Trinidadian guppy (*Poecilia reticulata*) (51886)

Ben Sandkam, C. Megan Young, Felix Breden.

Simon Fraser University.

A broad range of animals use visual signals to assess potential mates, and the theory of sensory exploitation suggests variation in visual systems drives mate preference due to sensory bias. Trinidadian guppies (*Poecilia reticulata*), a classic system for studying mate

choice evolution, provide a unique opportunity to test this theory by looking for co-variation in visual tuning, light environment, and mate preferences. Female preference co-evolves with male coloration, such that guppy females from 'low predation' environments have stronger preferences for males with more orange/red coloration than do females from 'high predation' environments. We found color vision also varies across populations, 'low' predation guppies invest more of their color vision to detect red/orange coloration. In independently colonized watersheds, guppies expressed higher levels of both LWS-1 and LWS-3 (the most abundant LWS opsins) in 'low predation' versus 'high predation' populations at a time that corresponds to differences in cone cell abundance. We also observed differences in the frequency of a coding polymorphism between high and low predation populations. Together this shows the variation underlying preference could be explained by simple changes in expression and coding of opsins, providing important candidate genes to investigate the genetic basis of variation in this model system.

Poster session A - GEN 2000

The repeatability of mating failure in a polyandrous insect (51919)

Ginny Greenway, David Shuker.

University of St Andrews.

Sexually-selected post-copulatory traits combined with well-documented costs of mating would be expected to maximise fertilisation success, yet high rates of mating failure (the lack of production of offspring following copulation) are observed across multiple taxa. However the mechanisms and causes of mating failure are not easy to isolate, typically being hard to directly observe. For example, it is unclear if failures are stochastic occurrences between incompatible mating partners or represent a persistent, meaningful phenotype on the part of one or other sex. Here we test this in the seed bug *Lygaeus simulans*, by sequentially mating families of males with randomly-allocated unrelated females and calculating the repeatability of mating outcome for each individual male and family. Mating outcome was found to be significantly repeatable within individual males but far less so between full-sib brothers. Furthermore approximately a quarter of experimental males failed to father any offspring given multiple opportunities to do so. We infer from the observed low levels of between-sib repeatability that mating failure, in this species at least, represents a commonly occurring male-associated and environmentally-influenced phenotype with low heritability. This may be key to unravelling the evolution of polyandrous mating systems in both this species and more generally.

Poster session A - GEN 2000

Evolution of female multiple mating and sperm competition: co-evolutionary feed-backs between female and male traits (51963)

Greta Bocedi, Jane M. Reid.

University of Aberdeen.

Explaining the evolution of costly polyandry remains a major challenge in evolutionary biology. Polyandry creates sperm competition, exerting strong selection on male allocation to sperm traits. Such male allocation may simultaneously affect female fitness, thereby imposing positive or negative selection on polyandry. However, the degree to which female polyandry and male allocation to sperm traits can drive co-evolution of both sexes' strategies has not been explicitly modelled and clear, empirically testable predictions are lacking. We used a genetically-explicit individual-based model to test the "sexually-selected sperm" (SSS) hypothesis, that polyandry evolves due to indirect selection stemming from positive genetic covariance with male sperm competitiveness. We show that the SSS process is unlikely to generally explain the evolution of costly polyandry. We then used a multi-trait model that allows simultaneous evolution of female mating interval and male allocation to sperm number versus longevity to test the hypothesis that co-evolutionary feed-backs between female mating interval and male sperm allocation can drive the evolution of costly polyandry assuming female sperm limitation. We demonstrate that depending on the cost of sperm and the degree of sperm limitation, sperm allocation driven by sperm competition can prevent males from overcoming sperm limitation, thereby driving evolution of polyandry.

Poster session A - GEN 2000

The impact of cuticular hydrocarbon profiles on mate attraction and reproductive isolation in two grasshopper species (*Chorthippus biguttulus* and *C. mollis*) (51970)

Jonas Finck, Sven Geiselhardt, Janine Kuntze, Monika Hilker, Bernhard Ronacher.

Humboldt-Universität zu Berlin; Freie Universität Berlin.

The attraction and identification of mating partners are major tasks in animals' lives. Many species uses multiple signals to increase reproductive success and to sustain reproductive isolation. Sympatrically occurring grasshoppers' species (genus *Chorthippus*) are morphologically and genetically similar. Acoustic signals serve as pre-zygotic barrier and are under sexual selection. On a close range scale, however, the acoustic signal has only a minor impact on the fertilization rate of *Chorthippus* females, suggesting that additional hybridization barriers exist, probably based on chemical cues. A GCMS analysis provided evidence that the cuticular hydrocarbon profiles of *C. biguttulus* and *C. mollis* exhibit species- and sex-specific differences. Behavioral tests demonstrated that males of *C. biguttulus* respond with a calling song to the odor of conspecific females but not to odors of heterospecific females. This behavior could be reproduced with males of the sibling species (*C. mollis*). Therefore, we conclude that grasshoppers use chemical signals to identify mating partners and that multiple hybridization barriers evolved to prevent gene exchange.

Poster session A - GEN 2000

Are females always better? Sex ratio variation and population genetic diversity affect the female advantage in gynodioecious *Plantago coronopus* (51973)

Sascha van der Meer, Thomas Sebrechts, Nicholas Lund, Hans Jacquemyn.

KU Leuven.

Gynodioecy is a reproductive system in which hermaphrodites and females co-occur within a population. Theoretically this polymorphism can only be maintained when females have a reproductive advantage over hermaphrodites.

In this study, we examined how sex ratio variation and population genetic diversity affected the female advantage in 27 populations of *Plantago coronopus*. We hypothesized that: 1) females produce more seeds than hermaphrodites and seed production is related to population sex ratio, 2) seeds of females have higher germination rates, 3) females are genetically more diverse than hermaphrodites and therefore have a higher chance of establishing in stressful environments.

The studied populations showed large variation in sex ratios from 2 to 60% females. In contrast to our hypothesis, females had, on average, a reproductive disadvantage in terms of seed production (FA: 0.91), but this diminished when the percentage of females in the population was low. On the other hand, seeds of females were heavier and germinated better, most likely reflecting a trade-off between seed production and seed weight. Genetic analysis showed that females were genetically more diverse than hermaphrodites, suggesting that inbreeding avoidance as well as frequency dependent processes explain the occurrence and size of the female advantage in *P. coronopus*.

Poster session A - GEN 2000

Selection and differentially expressed genes governing mixed mating in a plant (52003)

Maria Strandh, Jane Jönsson, William B. Walker III, Bengt Hansson, Josefin Madjidian, Mattias C. Larsson, Åsa Lankinen.

Lund University, Sweden; Swedish University of Agricultural Sciences (SLU) Alnarp, Sweden.

The evolutionary processes governing the large variation in mating system found in flowering plants are unclear. Using mixed-mating *Collinsia heterophylla* as a model we investigated population selfing rate variation in relation to environmental and floral trait variation and whether selection or genetic drift determine floral trait variation. Population selfing rates varied substantially. The best predictor of selfing rate was a negative association with dichogamy, 'stage of stigma receptivity'. Floral trait differentiation (PST) was substantially higher than neutral genetic differentiation (FST) in four estimated traits, suggesting that variation in floral traits is shaped by natural selection. Moreover, we report differential gene expression in self- vs outcross pollinations. The association between stage of stigma receptivity and selfing rate in *C. heterophylla* indicates that this floral trait is strongly linked with the mating system. The detected effect of natural selection acting on this trait and three additional mating-system related traits suggests that variability in mating system is not only

determined by genetic drift or by direct abiotic or biotic environmental factors. Determining the evolutionary processes influencing levels of mixed mating and associated floral traits, as well as mining the transcriptomes expressed in these pollinations provide important insights to mating system function and evolution.

Poster session A - GEN 2000

Molecular evolution of freshwater snails with contrasted mating systems (52046)

Concetta Burgarella, Philippe Gayral, Marion Ballenghien, Aurélien Bernard, Patrice David, Philippe Jarne, Sylvie Hurtrez, Nicolas Galtier, Sylvain Glémin.

Institut des Sciences de l'Evolution, UMR CNRS 5554, Université Montpellier II; Institut de Recherche sur la Biologie de l'Insecte, UMR 7261, CNRS, Univ. François-Rabelais, Tours; CEFÉ/CNRS, Montpellier.

Selfing recurrently evolved from outcrossing in many groups, especially in flowering plants. However, selfing species are of recent origin and less numerous than outcrossing ones. Despite short-term advantages, selfing is supposed to be an evolutionary dead-end strategy: selfing species experience reduced effective population size and recombination rates, which decrease the efficacy of natural selection. Selfing species should thus go through higher extinction rates because of reduced adaptive potential and/or genomic accumulation of deleterious mutations. However, empirical evidences are only partly congruent with theoretical expectations. Here we analyze coding sequence polymorphism, divergence and expression levels of two groups of freshwater snails in which mating systems have been stable for several millions of years. We report strongly reduced genetic diversity, decreased efficacy of purifying selection, slower rate of adaptive evolution and weakened codon usage bias/GC-biased gene conversion in the selfer *Galba* compared to the outcrosser *Physa*, in full agreement with theoretical expectations. Our results demonstrate that self-fertilization, when effective in the long run, is a major driver of population genomic and molecular evolutionary processes. We also suggest that the particular ecology of *Galba truncatula* may buffer the consequences of the genetic load, shedding new light on the dead-end hypothesis.

Poster session A - GEN 2000

The role of geographical and demographic factors in shaping floral morph frequencies in the tristylous *Lythrum salicaria* at the southern edge of distribution (52087)

Joana Costa, Sílvia Castro, João Loureiro, Spencer CH Barrett.

CFE, Centre for Functional Ecology and Department of Life Sciences, University of Coimbra; Department of Ecology and Evolutionary Biology, University of Toronto.

Style morph frequencies in heterostylous populations are largely determined by a balance between stochastic forces and negative frequency-dependent selection. Investigation of morph frequencies at geographical range limits can provide new insights on the forces maintaining the floral polymorphism and the factors causing biased morph ratios. The aim of our study was to investigate floral morph frequencies at the southern European range of the tristylous self-incompatible perennial *Lythrum salicaria* L. (Lythraceae). Floral morph composition was assessed in 101 localities along a latitudinal transect from Galicia to Andalusia, Iberian Peninsula. Population size and morph frequencies were recorded for each population. Most populations of *L. salicaria* were trimorphic (90.10%) and isoplethic (68.75%). No consistent bias in floral morph frequencies across the sampled area was found. Population size was positively associated with latitude, i.e., smaller populations occurring towards the southern range limit. Despite the greatest variance in morph frequencies detected for smaller populations, a positive relation between population size and morph evenness was found. Our results provide evidence for the abundant centre distribution model and highlight the influence of finite population size and genetic drift on morph frequencies in a tristylous species which seems to be quite resilient to changes to the polymorphism.

Poster session A - GEN 2000

The evolution of reproductive isolation between two hybridizing dungfly species *Sepsis cynipsea* and *S. neocynipsea* (Diptera: Sepsidae) (52111)

Athene Giesen, Martin A Schäfer, Wolf U Blanckenhorn.

Institute of Evolutionary Biology and Environmental Studies.

Identifying traits contributing to reproductive isolation among species and their evolution challenges biological research. The evolution of sexual traits for mating and fertilization is interesting due to their role in the establishment of reproductive barriers to gene flow. It is necessary to characterize phenotypic differentiation, evolutionary and genetic processes underlying trait diversification that contributes to reproductive isolation. Only then we can understand the mechanisms of speciation, driven by pre- and postzygotic reproductive isolation.

To understand the underlying processes of speciation in two closely related, allopatrically and sympatrically occurring sister species *Sepsis cynipsea* and *S. neocynipsea* (genetic distance at COI gene < 2%), we investigated mating behavior and fitness measures (fecundity, hatching success) of hybrid offspring as an indicator of pre- and postzygotic barriers. We show successful hybridization, with lower hybridization rates between sympatric than between allopatric populations. Our data reveal prezygotic isolation with females discriminating more strongly against hetero-specific males in geographic areas of co-occurrence. These results indicate that this female resistance can be due to species recognition. Further we show greatly decreased copulation success for pure hybrid crosses and backcrosses, with male hybrid offspring being more sterile than females, indicating postzygotic isolation in accordance with Haldane's rule.

Polyandry rates and reproductive success in a nuptial gift-giving dance fly *Rhamphomyia longicauda* (52115)

Elizabeth J. Herridge, Rosalind L. Murray, Deborah A. Dawson, Gavin J. Horsburgh, Terry Burke, Andre Gilburn, Darryl T. Gwynne, Luc F. Bussière.

University of Stirling; University of Sheffield; University of Toronto at Mississauga.

Females are rarely monogamous, but the processes that explain variation in polyandry are little understood, in part because few studies have measured selection on female mating frequency in the wild. In many species of dance fly, females obtain protein-rich nuptial gifts from males during courtship, and in many cases competition for these gifts involves elaborate female ornamentation which challenges theoretical arguments for the rarity and modesty of female ornaments. We use molecular markers to assess mating frequency among wild female long-tailed dance flies (*Rhamphomyia longicauda*) by probabilistically estimating the likeliest number of males contributing to the allele profiles of stored sperm. We compared mating frequency estimates to reproductive success as indicated by developing egg number and egg size. We consider how mating frequency, the proportion of multiply mated females, and egg maturation changes over the season, and use these measures to quantify how mating success mediates fecundity selection on ornamentation in the long tailed dance fly.

Artificial selection in the context of contrasted mating system (52172)

Elsa Noël, Philippe Jarne, Violette Sarda, Sylvain Glémin, Patrice David.

CEFE ; ISEM ; .

Autogamous species are thought to adapt more slowly than allogamous ones and to go extinct more easily, for several reasons. (i) Self-fertilization leads to homozygosity and inefficient recombination. (ii) Self-fertilizing species have a lower effective population size and are more sensible to drift. (iii) Because of the magnitude of inbreeding depression, numerous families (and then genomes) are lost, by purge of the lethal genes they carry. The consequences are that they are suspected to have less standing variation and then a lower adaptive potential than outcrossing species.

In the lab, we have experimental lines of *Physa acuta*, a preferential outcrossing freshwater snail, able to self-fertilize if partners are missing. Two types of lines are evolving under two different mating systems, since around 30 generations: one "Control" line where the individuals reproduce in random mass mating (a proxy of panmixy), and one "Lack of partners" line, where individuals are isolated and forced to self-fertilize frequently. We decided to apply artificial selection on one morphological trait of those snails, in two contrasted mating systems treatments: (i) self-fertilization and (ii) random mass mating. The aim of this experiment is to see whether the response to selection differs between these two types of lines and these two reproduction treatments.

Bottom-up effects of selection locally on outcross siring success shape the regional population genetic structure of an annual plant (52176)

Luis Santos del Blanco, John Pannell.

University of Lausanne.

In outcrossing plant populations, selection on siring success is expected to lead to the evolution of traits that enhance the production and effective dispersal of pollen locally. Indeed, such selection is probably the ultimate cause of a great many floral and inflorescence traits in angiosperms, including genetic polymorphisms such as dioecy and distyly. Importantly, local selection for siring success can have strong implications for population structure, because traits selected for high dispersal locally can also reduce genetic differentiation among population regionally. In the wind-pollinated plant *Mercurialis annua*, selection for enhanced siring success is probably responsible for the maintenance of males with females or hermaphrodites, whereas hermaphrodites are probably maintained by selection for self-fertilization when population densities are low. Here we show that variation in the maintenance of males among local populations strongly impacts on the regional genetic structure of the metapopulations to which they belong. Although metapopulation dynamics likely contribute to the population structure observed, we argue that competition for siring success locally has important knock-on effects on the metapopulation, too. Our study points to the possibility that the distribution of long-distance dispersal events may be shaped by the outcome of selection principally dispersal over short-distances.

Frequency and life-history consequences of mixed mating in the freshwater snail *Radix balthica* (52185)

Anja Bürkli, Kirstin Kopp, Jukka Jokela.

EAWAG, Swiss Federal Institute of Aquatic Science and Technology & ETH Zurich.

Mixed mating describes the coexistence of self-fertilization (henceforth selfing) and outcrossing within individuals or populations, and might occur in almost half of the animals capable of selfing. Yet, our understanding of mixed mating is surprisingly limited.

To document the frequency of mixed mating and its importance for reproductive fitness in the freshwater snail *Radix balthica*, I estimated within- and among-individual variation in selfing rates using microsatellite progeny arrays for both lab-laid and field-collected clutches. As selfing rates might show seasonality, e.g. driven by changes in mate availability, field clutches were obtained throughout reproductive season.

I then investigated the consequences of being selfed on life-history traits and parasite

infection rate in a large-scale field experiment. I placed selfed and outcrossed juveniles sharing the same mother in cages, either at the site of their grandparents or in a nearby deep-water habitat. After ten weeks, surviving snails were counted, measured, and screened for parasite infections. First results suggest that inbreeding depression in survival was considerable in both habitats, but not intensified in deep water where overall mortality was higher.

These rare datasets on mixed mating in a free-living population will help to understand the ecological and evolutionary consequences of this fascinating mating system.

Poster session A - GEN 2000

Inbreeding depression and selective history in *Noccaea caerulea* (52285)

Mathilde Mousset, Agnès Mignot, Ophélie Ronce, Christophe Petit, Marine Second, Pierre-Olivier Cheptou.

Institut des Sciences de l'Evolution de Montpellier; Centre d'Ecologie Fonctionnelle et Evolutive.

Inbreeding depression, a key driver of self-fertilization evolution, varies among species and populations, and can increase or decrease under stressful conditions. Few studies have attempted to disentangle the effects of stressful environmental conditions from those of selective history and adaptation to these conditions on the variation in inbreeding depression magnitude.

We here test whether adaptive history affects inbreeding depression in stressing conditions using the self-compatible and heavy-metal tolerant herb *Noccaea caerulea*. This species harbors two ecotypes with different adaptation history to soil pollution: the non-metallicolous ecotype grows on regular soils whereas the metallicolous ecotype thrives on contaminated soils such as mine wastes. Metallicolous and non-metallicolous plants originating from outbred and inbred crosses from nine populations were grown in controlled conditions on contaminated and non-contaminated soils. Inbreeding depression was measured on vegetative and reproductive traits along the life cycle. We found that metallicolous plants often suffer from greater inbreeding depression than non metallicolous plants. Early survival of inbred progeny is greater than that of outbred progeny in most non-metallicolous populations on both soil contamination levels, revealing outbreeding depression within-populations. These findings are discussed in the context of variation of self-fertilization rate and adaptation history of the different ecotypes.

Poster session A - GEN 2000

Female mate sampling strategy based on acoustic signals of a field cricket: implications for sexual selection (52333)

Diptarup Nandi, Rohini Balakrishnan.

Centre for Ecological Sciences, Indian Institute of Science.

Empirical studies on sexual selection in orthopterans and anurans have generally focused on measuring male mating success based on their acoustic signals by quantifying the variation in their signal components and by studying female preferences for the different signal components. However, little is known about how females in natural choruses sample males based on their acoustic signals in the process of choosing mates. Theoretical models of mate sampling have demonstrated significant differences in individual fitness returns for different sampling strategies. Moreover, studies on mate sampling strategies can further elucidate the relative importance of the two mechanisms of sexual selection: male-male competition and female mate choice. Thus, in this study we empirically investigated female mate sampling based on acoustic signals of males in a wild population of the field cricket species *Plebeiogryllus guttiventris*. We then used simulations to generate estimates of male mating success based on male trait distribution and their relative spacing in natural choruses, for the observed female mate sampling strategy and also for the different theoretical sampling strategies. We finally compared male mating success between the observed and the theoretical sampling strategies to infer the mechanisms of sexual selection acting on these acoustic signals.

Poster session A - GEN 2000

To each according to her... colour? Non-random male courtship effort in a viviparous fish with traditional sexual roles (52383)

Marcela Méndez-Janovitz, Constantino Macías García.

Instituto de Ecología, Universidad Nacional Autónoma de México.

Lower potential re-mating rates of females than of males lead to female mating selectivity, often based on male badges of quality. By definition such male displays are costly, and if they make every mating attempt too costly, males may also become selective, preferentially directing their mating efforts towards females with high reproductive value. We evaluated this possibility in *Girardinichthys viviparus* (Goodeidae), a matrotrophic fish whose stringent female mate choice is associated with costly male courtship. We found that males exposed to pairs of females devoted more courtship effort to the female whose flank had a more orange chroma, and to the one with wider abdominal distension -a direct indication of fecundity- even if this was the smaller of the pair. As we expected, male *G. viviparus* did not devote their courtship efforts randomly, but rather concentrated them on certain females; those with attributes that appear to indicate reproductive value. Yet males seemed to neglect the most obvious correlate of fecundity in viviparous fish; female size. This is probably because the mechanics of Goodeidae copulation promote size-assortative mating, thus variance in the size of available females is small for any given male, promoting the use of other indices of female quality.

Poster session A - GEN 2000

Measuring sexual selection: a more holistic model of reproductive life histories (52434)

Jonathan Henshaw, Karoline Fritzsche, Andrew Kahn.

The Australian National University; Uppsala University.

Sexual selection drives the evolution of some of nature's most spectacular traits, yet its measurement has proved difficult and controversial. Empirical studies are plagued by the problem of choosing appropriate target traits. Theoretical studies, on the other hand, have concentrated on a relatively narrow subset of naturally occurring patterns of sexual selection. This makes it difficult to draw general conclusions about how sexual selection covaries with mating system, sex roles, and other aspects of an organism's reproductive life history. We present a mathematical model that mirrors patterns of sexual selection across a wide range of biologically realistic life histories, incorporating variation in mating system, parental investment, mate choice and competition. We determine what common measures of sexual selection, such as the opportunity for sexual selection and the Bateman gradient, can tell us about the underlying biology and discuss their limitations. A recently defined measure, the 'maximum intensity of precopulatory sexual selection' s'_{\max} , performs better than other measures at tracking the actual strength of sexual selection across populations. We compare the predictions of our model to published empirical studies. Our study aims to synthesise insights from recent debates over measures of sexual selection.

Poster session A - GEN 2000

Experimental evolution under manipulated sex ratios alters mating behaviour in two sex role reversed beetle species (52546)

Karoline Fritzsche, Isobel Booksmythe, Göran Arnqvist.

Uppsala University.

We examined how two beetle species with sex role reversed mating systems evolved in response to experimentally induced differences in sex ratio and food availability. In both species males transfer a large nutritious ejaculate during mating. Females actively court males for this direct benefit and males are choosy about whom they mate with. We let both species evolve under either male biased (125M:25F) or female biased (25M:125F) adult sex ratios and with either high or no food resources during adulthood. After 20 generations of evolution the two species showed very different adaptations. In one species males responded to elevated male-male competition under male-biased sex ratios by transferring more ejaculate per mating. In the other species, males surprisingly showed no measurable response to evolution. Females however responded to female-biased sex ratios by initiating courtship sooner and were more successful in gaining matings. Females of the second species that evolved under high food availability also increased their turning rates (a form of courtship effort). Our study provides direct evidence that closely related species can show very different evolutionary responses to the same selection pressures.

Reproduction in social insects: what can superorganisms teach us about mating system evolution? (52548)

Heikki Helanterä.

University of Helsinki.

Social insect colonies have been for a long time likened to individual organisms or "superorganisms", and thus considered a prime example of a major transition in evolution, or a transition in individuality. However, this metaphor has not been exploited to its full potential, but has mainly been used as a mechanistic description of colony function. But what kind of organisms are they? Could superorganisms and their diversity allow testing evolutionary hypotheses about sex and reproduction in a novel way? In this work, I present an evolutionary framework in which to employ social insect diversity in novel independent tests of evolution of mating systems. I will discuss cases like evolution of anisogamy, evolution of separate sexes, and evolution of gamete dispersal. This approach will aim for a more thorough understanding of the general principles on the one hand, and idiosyncratic determinants on the other, of mating system evolution.

A Drosophila-based screen for genes important to reproductive regulation in social insects (52613)

Graham Thompson, Alison Camiletti.

Western University.

For 50 years kin theory has provided a gene-based explanation for sociality, but for the most part we have yet to identify these genes. The burgeoning field of sociogenomics is bridging this gap between theory and discovery, but is limited by the genomic tools available for all but a few social insects. Here we show that we can use queen honeybee pheromone to 'trick' female *Drosophila* into a state of worker-like sterility. This remarkable observation potentially enables a *Drosophila*-based screen of mutant and transgenic lines responsive to queen pheromone. Preliminary screens reveal that the pseudo-social response from flies is mediated by mutations at the foraging locus as well as other loci previously implicated in honey bee worker sterility. Our results suggest deeply conserved elements of reproductive regulation in social and non-social insects. We further nominate new loci that seem to affect the fly's worker-like response to bee pheromone, including Or83b that is essential to insect olfaction and has a clear bee orthologue. Beyond screens, our novel *Drosophila*-based assay provides a framework for testing social gene function in situ using RNAi targeted knockdowns. We highlight the potential and limits for adopting non-social *Drosophila* as a model of social gene discovery.

Contrasting patterns of inbreeding depression and hybrid vigor between small and large populations of *Daphnia magna* (52637)

Christoph Haag, Jennifer Lohr, Barbara Walser.

CNRS Montpellier, France; Univ. Hamburg, Germany; Univ. Fribourg, Switzerland.

The freshwater crustacean *Daphnia magna* shows a wide array of different breeding systems, including partially genetic sex determination, which favours outcrossing and which is found only in some populations. One factor that is thought to play a major role in determining the advantage of outcrossing is population size through its predicted effect on the magnitude of inbreeding depression. Here we test these predictions empirically and show that, among eight populations of *Daphnia magna* that strongly differ in size, strong inbreeding depression is consistently found for a number of life-history traits in large populations. Small populations, on the other hand, show only low or no inbreeding depression, suggesting that the load of deleterious mutations has either been purged or become fixed. To test for fixed load, we crossed individuals among nearby populations of similar size and found that outcrossing resulted in strong hybrid vigour in crosses between small, but not between large populations. This confirms the presence of fixed load in small populations. Overall, our results show that the fitness benefits of obligate outcrossing strongly depend on population size, suggesting that the amount of genetic drift is an important modulator of costs and benefits in breeding system evolution.

Paternal care and paternity revisited (52738)

Julia Schroeder, Yu-Hsun Hsu, Isabel Winney, Mirre Simons, Shinichi Nakagawa, Terry Burke.

Max Planck Institute for Ornithology; University of Otago; University of Sheffield.

Whether and why male parents should adjust the amount of care they provide to young if the female partner is unfaithful has been discussed for more than two decades. While there is general agreement that such a relationship exists across species, empirical results for within-population effects are ambiguous. The problem partially lies in the difficulty to disentangle between-individual from within-individual processes. We use an exceptionally well-suited dataset on wild house sparrows (*Passer domesticus*) to revisit this problem. Females were repeatable in the proportion of extra-pair offspring they produced per brood, however, the repeatability was higher when they stayed with the same male. Individual males phenotypically adjusted paternal care to paternity only when they changed mates. We found no support for an association of this adjustment within pair bonds. The within-male paternal adjustment between-pairs was not affected by male age, offspring relatedness to the caring male, seasonality or the brood order. However, the paternal care adjustment was negatively associated with the number of annual extra-pair paternities the male gained with other

females. Our results support that social feedback may be driving paternity-parental care dynamics, allowing a better understanding of evolution female polygamy.

Poster session A - GEN 2000

A protected polymorphism for shell colour in a natural population of a marine snail (52778)

Daniel Estévez, Emilio Rolán-Alvarez, Juan Galindo.

University of Vigo.

A well-established population of *Littorina fabalis* has been monitored since 1990, showing an apparently stable shell colour polymorphism. The analysis of mating pairs captured in the field across several years revealed a significant negative assortative mating ($I_{PSI} = -0.4$) for shell colour. This pattern could be produced by a mechanism of, negative frequency-dependent sexual selection based in shell colour. In order to test this prediction we estimated colour fitness with two alternative methods: by using 1) sexual selection plus viability estimates, and 2) inter-annual total fitness estimates. Both types of fitness estimates presented a significant (negative) correlation with colour frequency across samples of different years, providing a clear evidence for the polymorphism being maintained by frequency-dependent natural selection presumably caused by strong negative assortative mating. The evolutionary mechanisms (inbreeding avoidance or apostatic selection) able to cause the origin and maintenance of strong negative assortative mating are discussed.

Poster session A - GEN 2000

Condition-dependent outcrossing in the filamentous fungus *Aspergillus nidulans* (52861)

Nicolas O. Rode, Sijmen Schoustra, Devin Arbuthnott, Rees Kassen, Howard Rundle.

INRA-Montpellier; University of Wageningen; Univeristy of Washington; Univeristy of Ottawa.

Recent theoretical models predict that facultatively sexual organisms should reproduce clonally when their fitness is high, but sexually when their fitness is low (condition-dependent sex).

Most empirical studies have been hampered by the difficulty of measuring simultaneously fitness along with sexual and asexual reproduction. For example, male fitness is notoriously difficult to estimate in most species. In facultatively sexual organisms, sexual reproduction virtually always produces sexual structures involved in spatial (or temporal) dispersal. Hence, disentangling condition-dependent sex from condition-dependent dispersal is almost impossible in most organisms.

In homothallic haploid organisms, selfed spores are genetically identical to asexual spores. We investigated condition-dependent outcrossing in the filamentous fungus *Aspergillus*

nidulans, where sexual spores (both selfed and outcrossed) are enclosed within the same structures. This property allows ruling out condition-dependent dispersal as a possible alternative to condition-dependent outcrossing.

We competed different wild and lab strains in a single environment. We measured the investment in asexual reproduction, self-fertilization and outcrossing, along with absolute and relative fitness. Our results unravel the complex interactions between resource allocation to these different modes of reproduction and fitness.

Poster session A - GEN 2000

Does self-fertilization enhance or reduce response to selection ? Empirical test in a freshwater snail. (52924)

Marie-Agnès Coutellec, Marc Collinet, Maïra Coke, Patrice David.

INRA, UMR ESE 0985; INRA, U3E; CNRS, CEFÉ.

Selfing as an evolutionary dead-end is a longstanding hypothesis, based on two main tenets: unidirectional evolution towards selfing through a purge process of the genetic load, and increased extinction rate due to low adaptive potential associated with selective interference in highly homozygous lineages. Although ancient, this hypothesis has been only recently started to be tested empirically. As a contribution to this endeavour, the present study focuses on the expected relative adaptability of selfing and outcrossing lines of an animal hermaphrodite (gastropod, *Lymnaea stagnalis*). The short-term response to selection was compared between enforced selfing and outcrossing, using lines set up from various natural populations and a pesticide as selective pressure vs benign conditions. In preferentially outcrossing species such as *L. stagnalis*, selfing is expected to lower the response to selection, due to high inbreeding depression. However, this species exhibits moderate inbreeding depression, which suggests a possible purge of part of the genetic load. Therefore, selfing may actually facilitate the response to selection. Nevertheless, after two generations, selfing lines are clearly more sensitive than outcrossing ones to the pesticide (weaker response to selection). Third-generation performances and subsequent inbreeding depression will be compared between selection regimes to get a more comprehensive picture (ongoing experiment).

Poster session A - GEN 2000

Cooperative blood-feeding explains feeding aggregations in Phlebotomine Sandflies (51797)

Frederic Tripet, Simon Clegg, Dia-Eldin Elnaiem, Richard Ward.

School of Life Sciences, Keele University, United Kingdom; LMVR/NIAID/NIH, Twinbrook Parkway, Rockville, MD, USA.

Given the importance that the evolution of cooperation bears in evolutionary biology and social sciences, extensive theoretical work has focused on identifying conditions that promote cooperation among unrelated individuals despite potential cheating individuals. In insects, cooperative interactions typically occur amongst related individuals and are explained by kin selection. Here we provide evidence that in *Lutzomyia longipalpis*, a small biting fly vector of leishmaniasis in the New world, cooperative bloodfeeding in groups of unrelated individuals results in a strong decrease in saliva expenditure. Feeding in groups significantly affected the timing and duration of the flies' bloodmeal and resulted in greatly enhanced egg production. The benefits of feeding aggregations were particularly strong when flies fed on older hosts suggesting that flies were able to overcome the stronger immune response of pre-sensitized hosts. Our results demonstrate that, in *Lutzomyia longipalpis*, feeding cooperatively maximizes the effects of salivary components injected into hosts to facilitate blood intake and to counteract the host immune response. As a result, cooperating sandflies enjoy enormous fitness gains. This constitutes the first functional explanation for feeding aggregations in hematophagous insects and a rare example of cooperation in a non-social insects species. The evolution of cooperative group feeding in sandflies may have important implications for the epidemiology of leishmaniasis.

Poster session A - GEN 2000

Transitioning from pathogen to mutualist: the evolution of vertical transmission (51855)

Devin Drown, Michael Wade.

University of Alaska Fairbanks; Indiana University.

We investigate the coevolution of transmission mode and virulence in host-symbiont interactions using population genetic models. Vertical transmission enhances the genetic fidelity of the host-symbiont interaction and directly affects the efficiency of selection on host-symbiont gene combinations (inter-genomic epistasis). We find that the interaction between virulence and population genetic structure determines the evolutionary balance between a host-symbiont arms race and host-mutualist coevolution. It is well known from models of the evolution of sex that, with horizontal transmission, evolution drives an arms race, wherein hosts adapt to escape virulent pathogens and pathogens adapt toward discovering susceptible hosts. Conversely, with vertical transmission, the more likely host-symbiont mutualistic coevolution becomes with an attendant reduction in symbiont virulence. We find that, when mutation generates inter-genomic epistasis, modifiers increasing the degree of vertical transmission can hitchhike to fixation. Once an intermediate level of vertical transmission is established, mutualistic coevolution or 'symbiont capture' predominates. That is, the evolutionary stable state is mutualistic symbiosis rather than an escalating host-pathogen arms race.

Poster session A - GEN 2000

Tripartite network of an ant host, transposable elements and intracellular bacteria. (51987)

Antonia Klein, Lukas Schrader, Jan Oettler.

University Regensburg, Germany.

The evolution of eukaryotic organisms is often influenced by transposable elements (TEs) and microbial symbionts that confer novel traits to their hosts. Here I will describe the tripartite system of a *Cardiocondyla obscurior* ant host, associated (TEs) and intracellular endosymbionts which likely play a significant role in the invasive success of the host. On the one hand TEs contribute to high rates of genomic novelty as precursor for adaptive variation (Schrader et al 2014). On the other hand the newly described gut-associated endosymbiont ‘*Candidatus Westeberhardia cardiocondylae*’ might facilitate development under poor nutritional regimes. I will discuss these findings from a holistic perspective of an extended genotype of egalitarian cooperation partners in changing environments. Contrary to common belief, environmentally initiated novelties by “selfish” intragenomic or intracellular interaction partners may have great evolutionary potential, strongly advising against a simplified view of organismal evolution.

Poster session A - GEN 2000

Co-evolution with natural enemies promotes probiotic activity in a plant-associated bacterium (52075)

Erqin Li, Peter Bakker, Alexandre Jousset.

Utrecht University; Utrecht University; Utrecht University.

Plants roots are colonized by mutualistic, free living microbes that provide essential functions such as antibiosis that inhibits pathogens. However, this system cannot be evolutionarily stable if the host plant only feeds the microbes, but does not dispose of mechanisms for specifically rewarding cooperators or punishing defectors. As a result, mutualistic bacteria rapidly lose their ability to produce antibiotics and turn into free-riders consuming host resources without providing services in return. However, thanks to a functional overlap between disease suppression and antipredator defense, presence of predators (protozoa) may prevent the decay of plant-microbe mutualism by counter-selecting defectors. Here we co-evolve *Pseudomonas protegens* CHA0, a model mutualistic bacterium inhibiting several plant diseases, in presence of ciliated protozoa. We show that co-evolution with protozoa not only prevents the apparition of defectors but also results in an enhanced expression of the traits linked to pathogen suppression. Our results reveal that natural enemies may be essential to maintain host-microbe mutualism and that a multitrophic evolutionary framework should be used to assess the costs and benefits of interkingdom cooperation.

Poster session A - GEN 2000

Can Altruism Evolve Between Species? (52138)

Christopher Quickfall.

University of Sheffield.

Multi-species associations, involving co-adapted species, are widespread in nature; examples include multi-species biofilms, plant-pollinator associations, and associations between algae and fungi to form lichens. Hamilton showed how altruism can evolve between members of the same species, due to genetic relatedness. However, the literature is much less clear on whether altruistic acts can evolve between species, whereby a member of one species reduces their reproductive success to benefit other species, without a direct or indirect fitness return. One potential problem is that genetic relatedness between species appears to be ill-defined and thus might normally be assumed to be zero. These arguments bear on the fundamentals of social evolution theory.

We clarify these issues, using simple models to define the evolutionary conditions favouring costly donation between species without immediate return benefits. In particular, we examine inter-species models that are intended to represent, as much as possible, Hamilton's scenario for altruism within species. Results are found both analytically, and through deterministic and stochastic simulation. We find that costly donation between species can evolve with a specific type of whole-genome assortment between species, but argue that it is explained by indirect fitness benefits within the donating species, using partner species as vectors for altruism.

Poster session A - GEN 2000

Diversity of moral strategies in human reputation-based cooperation (52206)

Martijn Egas, Violet Swakman, Lucas Molleman, Aljaz Ule.

Institute for Biodiversity and Ecosystem Dynamics (IBED), University of Amsterdam (UvA); The Centre for Decision Research and Experimental Economics (CeDEx), University of Nottingham; Center for Research on Experimental Economics and political Decision-making (CREED), UvA.

The question why humans often help others without selfish material interest intrigues many scientists. In theory such human reciprocal cooperation can be explained when helping is directed to individuals with a good reputation of helping others. Evolutionary models predict stable cooperation when reputations are based on moral assessment rules incorporating whether helping someone is justified, which requires information on the behavior of the person to be judged but also of the persons (s)he interacted with. Here, we provide first empirical evidence that such information indeed affects cooperative decision making: more help is provided to people who helped cooperative players and refused to help uncooperative players. A detailed analysis of individual strategies reveals that many subjects base their decisions solely on their recipients' past behavior. Some classify as unconditional cooperators or defectors, and a few as maintaining a fixed level of helpfulness. Importantly, however, a substantial proportion of individuals consistently consider the motivations behind behaviors. Our results provide strong empirical support for the use of moral strategies that theoretically

underpin reputation-based cooperation, but also challenges theory by highlighting the existence of pronounced individual variation in human cooperative strategies.

Poster session A - GEN 2000

Pattern and process in the evolutionary history of the mycorrhizal symbiosis (52299)

Hafiz Maherali.

University of Guelph.

The vast majority of plants form symbioses with mycorrhizal fungi, which provide them with soil nutrients in return for sugars from photosynthesis. The high frequency of the mycorrhizal symbiosis in plants could be explained by two non-mutually exclusive hypotheses. First, the symbiosis may be adaptive in many different plant lineages, leading to convergent evolution. Second, possessing the symbiosis may cause higher speciation and lower extinction rates, leading to higher net diversification in mycorrhizal relative to non-mycorrhizal lineages over evolutionary time. To test these hypotheses, we reconstructed the evolution of the symbiosis using maximum likelihood based multiple state speciation and extinction models (MuSSE) applied to a ~3000 taxon mycorrhizal state database matched with a fossil calibrated molecular phylogeny. Results supported the first hypothesis but not the second hypothesis. Transition rates to the mycorrhizal symbiosis from the non-mycorrhizal state were an order of magnitude more frequent than losses, and the mycorrhizal state was much more stable over time than the non-mycorrhizal state. By contrast, net diversification rates were lower in mycorrhizal than non-mycorrhizal plant lineages. The high frequency with which the mycorrhizal symbiosis evolves from non-mycorrhizal ancestors suggests that there is strong selection to form the symbiosis in one or both partners.

Poster session A - GEN 2000

Birds of almost the same feather flock together: phenotypic clumping characterises the composition of mixed-species bird flocks, worldwide (52410)

Hari Sridhar, Umesh Srinivasan, Robert Askins, Julio Cesar Canales-Delgadillo, Chao-Chieh Chen, David Ewert, George Gale, Eben Goodale, Wendy Gram.

Centre for Ecological Sciences, Indian Institute of Science, Bangalore, India; National Centre for Biological Sciences, Bangalore, India; Department of Biology, Connecticut College, New London, Connecticut, USA; Department of Behavioral Biology, University of Osnabrück, Osnabrück, Germany; Department of Biomedical Science and Environmental Biology, Kaohsiung Medical University, Kaohsiung; The Nature Conservancy, Lansing, Michigan, USA; School of Bioresources and Technology, King Mongkut's University of Technology, Bangkok, Thailand; Division of Biological Sciences, University of California, San Diego, California, USA; National Ecological Observatory Network, Boulder, Colorado, USA.

Our current understanding of animal sociality comes, mainly, from an intraspecific context. Heterospecific sociality, although widely prevalent, finds little mention in theories and discussion on group-living. This could be because heterospecific sociality is thought to be qualitatively different, i.e., while single-species groups are based on cooperation among ecologically-similar individuals, heterospecific association is believed to be for obtaining benefits from ecologically-dissimilar individuals. While this is certainly true for some of the most striking heterospecific associations known (e.g., grouper-moray eel; babbler-drongo), whether it is also true for larger multi-species groups is unclear.

Using a multi-continent dataset on mixed-species bird flock composition (55 presence-absence matrices, 2421 flocks), we find that flocks are, largely, groupings of ecologically-similar species. Null model-randomization approach, followed by meta-analysis, revealed that body-size similarity, foraging behaviour similarity and taxonomic relatedness in flocks is higher than expected at random, in most locations. These results suggest that benefits in multi-species groups might, in fact, be qualitatively similar to single-species groups, and highlight the need to think of sociality along a continuum from conspecifics to heterospecifics. We discuss conditions that might promote grouping with heterospecifics over conspecifics, especially in relation to competition and conspecific availability.

Poster session A - GEN 2000

The implications of *Termitomyces* domestication for gut microbiome function in fungus-growing termites (52663)

Michael Poulsen, Haofu Hu, Cai Li, Duur K. Aanen, Jacobus J. Boomsma, Guojie Zhang.

University of Copenhagen; BGI Shenzhen; University of Copenhagen, BGI Shenzhen; Wageningen University; University of Copenhagen; University of Copenhagen, BGI Shenzhen.

Thirty MYA, the ancestors of the higher termite sub-family Macrotermitinae and the basidiomycete fungus *Termitomyces* joined forces in what was to become one of the most sophisticated plant biomass decomposition symbioses on Earth. The degree to which the innovation of fungiculture induced a functional shift in the gut microbiota has remained unclear. We used 16S rRNA 454 pyro-sequencing to portray the community composition of the core gut microbiota associated with the Macrotermitinae and Illumina sequencing to obtain metagenome insight into the functional gut community roles. Focusing on carbohydrate-active enzymes encoded by *Termitomyces* and gut microbes from the termite *Macrotermes natalensis*, we found that gut bacteria primarily contribute enzymes for final digestion after *Termitomyces* has degraded the most complex carbohydrates. We also pursued comparative analyses of fungal-cell-wall-degrading enzymes in gut bacteria associated with *M. natalensis* and *Odontotermes yunnanensis*. These gut communities share remarkably similar enzyme profiles and the bacteria producing these enzymes are generally over-represented in fungus-growing termites relative to termites that rely on cellulolytic gut microbes. The shift in gut metagenome function after *Termitomyces* domestication thus appears to have involved both complementary division of labour and targeted digestion of the novel food offered by *Termitomyces*.

The bacterial network: Cooperative nutrient exchange via nanotubes (52763)

Samay Pande, **Shraddha Shitut**, Lisa Freund, Martin Westermann, Felix Bertels, Claudia Colesie, Ilka Bischofs, Christian Kost.

Experimental Ecology and Evolution group, MPI for Chemical Ecology, Jena; The Evolutionary biology group, ETH Zurich; Centre for Electron Microscopy, Jena University Hospital, Friedrich Schiller University of Jena; Department of Plant Ecology and Systematics, University of Kaiserslautern; Zentrum für Molekulare Biologie der Universität Heidelberg (ZMBH); Center for Quantitative Analysis of Molecular and Cellular Biosystems (BioQuant), Heidelberg.

Bacterial interactions frequently involve an exchange of essential metabolites. However, it remains unclear whether such cross-feeding relies exclusively on diffusion of metabolites through the cell-external environment, or if bacteria also utilize contact-dependent mechanisms to directly transfer metabolites between cells. To test this, we have synthetically generated interactions within and between *Escherichia coli* and *Acinetobacter baylyi*, in which both species reciprocally exchanged essential amino acids. Our results show that the two distantly related bacterial species can exchange cytoplasmic amino acids and protein by connecting to each other through membrane-derived nanotubes. The inter-cellular connections seem to be induced by the amino acid auxotrophy mutations introduced into the organism. The nutrient exchange was dependent on the nutritional status of the cell, thus indicating that the exchange may primarily serve to satisfy the metabolic requirements of nanotube-forming cells. Altogether, our findings show for the first time that bacteria can use direct cell-to-cell connections to exchange essential metabolites. The possibility that by connecting via nanotubes two or more bacterial cells can extend their biochemical repertoire without the need for genetic change, suggests that bacteria may function as multicellular, interconnected entities rather than as individual, physiologically autonomous units

Negotiation and appeasement are more effective drivers of sociality than kin selection (52769)

Andres Quiñones, Ido Pen, Sander van Doorn, Franjo Weissing, Michael Taborsky.

University of Groningen; University of Bern.

Conflicts of interest are common in group-living organisms, since behaviour that maximizes an individual's reproductive success often compromises that of other group members. One way to prevent such conflicts from undermining sociality is to restrict group membership to genetically related individuals. Alternatively, unrelated individuals can prevent being exploited by utilizing a conditional strategy, enabling two pro-social partners to negotiate a mutually beneficial outcome by responding to each other's previous actions. How these two processes – kin selection and negotiation – interact in the evolution of sociality remains an open question. Here we show, using a mathematical model inspired by cooperatively breeding

fish with dominant breeders and subordinate helpers, that negotiation can be more effective than kin selection at resolving social conflict and promoting high levels of help. When the two processes act in concert, evolving populations can reach two alternative equilibria. In the first, negotiation drives subordinates to appease dominants, resulting in high levels of help and low levels of aggression. In the alternative equilibrium, which evolves by kin selection, subordinates help their kin unconditionally. Our model demonstrates that negotiation and kin selection do not necessarily interact synergistically and that kin structure can hamper rather than facilitate the evolution of efficient cooperation.

Poster session A - GEN 2000

Insights into the asymmetrical nature of nursery pollination mutualisms: the *Trollius*-*Chiastocheta* interaction as a case study (52962)

Tomasz Suchan, Nadir Alvarez.

University of Lausanne, Dept. of Ecology and Evolution; University of Lausanne, Dept. of Ecology and Evolution.

The nursery pollination interaction between the European globeflower *Trollius europaeus* and *Chiastocheta* flies is often cited as an example of a specific and obligate mutualism — the flies pollinate the plant and their larvae eat a fraction of developing seeds. We tested this hypothesis by examining seed set and traits related to offspring fitness in isolated *Trollius* populations, some in which *Chiastocheta* communities went extinct. We found that despite a significant drop in the seed set, the seeds produced in the absence of flies were larger and showed higher germination rate, a result compatible with the resource allocation hypothesis. Therefore, relative fitness in the populations without flies was similar to those with flies, a result of the tradeoff between the number of seeds produced and their germination rate. This outcome highlights the role of *Chiastocheta* flies as seed parasites, and the asymmetry of their interaction with *Trollius* — while the flies need the plant to reproduce, the opposite is not true.

Poster session A - MAX 412

Genital form and the evolution of reinforcement in Littorininae (51576)

Johan Hollander.

Lund University.

Speciation requires reproductive isolation and biologists have examined multiple different processes of lineage splitting by which it could evolve. Within this range, reinforcement is recognised as having a special position as the only process in which natural selection directly favours an increase in reproductive isolation. Similarly, a role for genital form influencing copulatory and post-copulatory components of reproductive isolation has long been suspected because, among animals with internal fertilization, male genitalia demonstrate rapid divergent

evolution and species-specific forms. However, reinforcement and genital form have virtually always been studied separately. In order to increase our understanding of how genital form may influence the evolution of reinforcement, I will present a comparative analysis (on an unusually large and complete phylogeny of the marine gastropod subfamily Littorininae 147 species, 97% complete) which show a strong signal of greater genital divergence in sister-species pairs with overlapping ranges than in those with allopatric ranges, providing a prima facie case for widespread reinforcement, suggesting that diversification and genital evolution are intimately linked. These results are combined with a detailed experiment, between a specific Littorininae sister-species pair from Australia, confirming reinforcement in mating behaviour.

Poster session A - MAX 412

Edaphic adaptation in *Arabidopsis*: a genomic perspective on the calcicole-calcifuge problem (51582)

Alessia Guggisberg, Xuanyu Liu, Léonie Suter, Alex Widmer.

Institute of Integrative Biology, ETH Zürich, Universitätsstrasse 16, CH-8092 Zürich.

It remains unclear what type of factors drives edaphic adaptation in plant communities occupying either calcareous or siliceous bedrocks, advocating for comparative genomic studies on calcicole-calcifuge vicariants, i.e. sister taxa that grow on either calcareous or siliceous substrates. We study the genetic basis of edaphic adaptation in two diploid species of *Arabidopsis* (*A. lyrata* and *A. arenosa*, Brassicaceae) that grow on both soil types, using whole-genome re-sequencing data obtained from both individual and pooled DNA libraries. We have identified hundreds of loci that carry a clear signature of divergent selection. These loci are enriched for genes involved in ion transport, and do sometimes overlap with soil-specific tandem duplications. Yet, balancing selection may also contribute to the maintenance of adaptive genetic variation in mixed habitats. Overall, our results suggest that chemical soil composition constitutes the main cause of ecological differentiation in these species, and that *A. lyrata* and *A. arenosa* underwent parallel edaphic evolution at the biochemical, genic and sometimes even SNP level.

Poster session A - MAX 412

Genetics of Jaw Divergence in a Trophically Polymorphic Cichlid Fish (51587)

C. Darrin Hulsey, Francisco J. García De León, Kate Bell, Chris Nice.

University of Konstanz ; Centro de Investigaciones Biológicas del Noroeste (CIBNOR); Texas State; Texas State.

Trophically polymorphic species could represent lineages that are rapidly diverging along an ecological axis or could phenotypically mark the collapse of species through introgressive hybridization. We investigated patterns of introgression between the trophically polymorphic

cichlid fish *Herichthys minckleyi* and its relative *H. cyanoguttatus* using a combination of population genomics and species tree analyses. Using rad-tag sequencing, we also investigated whether hybridization could explain the variation in the jaws of this phenotypically variable cichlid.

Poster session A - MAX 412

Meiotic drive and inter-population incompatibilities (51680)

Rudi Verspoor, Tom Price, Gregory Hurst.

University of Liverpool.

Intragenomic conflict is a major contender for driving speciation. X chromosomes that enhance their transmission by killing Y-bearing sperm are particularly likely to drive differentiation. As males carrying X chromosome drive produce few or no sons, the costs are very high for the rest of the genome, potentially causing the evolution of genes that suppress the sperm killing mechanism. This counter-adaptation could create cycles of rapid co-evolution between the driving X and the suppressors. This population specific evolution could create interpopulation differences in reproduction genes, and generate hybrid incompatibilities. However, meiotic drivers themselves could also reduce differences between populations, because a driver that enters a naive population might spread rapidly through it (if the naive population carries no suppressors), potentially homogenising the two populations, at least for the driving chromosome. So does meiotic drive homogenise populations, or create barriers to hybridisation?

We investigate this using an X-chromosome meiotic driver in *Drosophila subobscura*. We show that suppression has evolved in the native population, but not in a nearby naive population. However, meiotic drive carrying males suffer severe fertility costs in crosses with the naive population, suggesting that in this system meiotic drive is causing hybrid incompatibilities and population differentiation.

Poster session A - MAX 412

Adaptation and selection processes at the invasion front of a globally expanding vertebrate (51682)

Irene Kalchauer, Jost Borchertding, Patricia Holm.

University of Basel; University of Cologne.

Ponto-Caspian gobies are invasive fish that have spread through much of Europe and North America during the last decades. Translocation over large distances is attributed to ship traffic.

Ponto-Caspian gobies present a wonderful case of an evolutionary field experiment. These fish are continually exposed to novel environments at the invasion front. Populations in

harbors, which are invasion hotspots, continually receive genetic input from various source populations. Importantly, Ponto-Caspian gobies perform remarkably well in diverse environments and display plasticity in morphology and life history traits.

As a starting point towards using Ponto-Caspian gobies as a model of evolution and adaptation, we analyzed the connectivity of the invasion edge of bighead goby populations in the Rhine.

We genotyped over 500 bighead goby from North-Rhine Westphalia (NRW) and two populations in Basel, Switzerland for 16 microsatellite loci. We find that the Basel harbor populations is genetically closer to the NRW population than to the Basel river population. Mitochondrial D-loop haplotypes, in contrast, reflect the geographic distribution. Ship movement patterns may explain the highly differentiated genetic structure of the Basel population. Tank ships from the Northern Rhine anchor close to the river population, while cargo ships from the Rhine-Main-Danube channel anchor close to the harbor population.

Poster session A - MAX 412

Variability in the incidence of hybrid seed failure within and among wild tomato species (52074)

Morgane Roth, Thomas Städler.

Institute of Integrative Biology, ETH Zurich, Universitätstrasse 16, CH-8092 Zurich, Switzerland.

The tomato clade (*Solanum* section *Lycopersicon*) is emerging as a model system in evolutionary biology and speciation research. Wild tomato species diverged recently and are notable for their dissimilar levels of postzygotic isolation. After performing reciprocal cross-pollinations, we characterized postzygotic barriers within and between three self-incompatible taxa, namely *S. peruvianum*, *S. chilense* and *S. arcanum* var. *marañón*. Based on the proportions of viable and inviable (aborted) seeds and subsequent germination tests, we explored the overall strength and variability of postzygotic isolation. Reciprocal interspecific crosses involving *S. peruvianum* yielded almost no viable seeds whereas crosses between *S. chilense* and *S. arcanum* var. *marañón* produced an intermediate proportion of viable seeds. Moreover, and unlike the “strong” postzygotic barrier between *S. peruvianum* and the two other taxa, the proportion of viable seeds was frequently asymmetric in reciprocal hybrid crosses involving *S. chilense* and *S. arcanum* var. *marañón*. Intraspecific crossings have revealed a considerable proportion of inviable seeds in *S. chilense*, highlighting the possibility of rapid build-up of postzygotic isolation in this group. Our phenotypic data will be augmented by surveys of endosperm transcriptomes from developing seeds, as endosperm is the seed component that is most likely causally involved in hybrid seed failure.

Poster session A - MAX 412

Genomics of speciation and species cohesion in the adaptive radiation of tillandsioids in Neotropical mountains (51754)

de La Harpe Marylaure, Paris Margot, Loiseau Oriane, Olivares Ingrid, Weigand Anna, Till Walter, Kessler Michael, Salamin Nicolas, Lexer Christian.

University of Fribourg; University of Lausanne; University of Zurich; University of Vienna.

The adaptive radiation of bromeliads is one of the most diverse and enigmatic of the Neotropics. The Tillandsioideae subfamily represents a pertinent system for studying the genomic and molecular footprints of divergent ecological selection during adaptive radiation. Our main research aim is to unravel drivers and limits of diversification at different time scales. Tillandsioid taxa were sampled along elevation gradients of various Central and South American mountain regions. Common species (geographic replicates) and local endemics were defined based on their natural distribution ranges and ecological preferences. Geographic replicates were chosen preferentially to disentangle evolutionary mechanisms responsible for speciation and species cohesion. A genomic approach, including RNA-sequencing and restriction site Associated DNA sequencing (RAD-seq), will generate data for both neutral and non-neutral genomic regions. It will be employed to characterize gene flow and allelic diversity within and among populations and species occurring along elevation gradients and across a range of geographic scales. Great emphasis will be given on analyses of population divergence to circumscribe genetic mechanisms responsible for species cohesion and persistence, including genomic scans for allelic diversity, differentiation, gene flow within and between species. Current results and key points from this research will be presented, including proof-of-concept data from RAD-seq, and available sampling designs.

Poster session A - MAX 412

Identifying the genetic basis of ecologically important traits in *Nicotiana attenuata* using advanced-inter crossing recombinant inbred lines (AI-RIL) (51775)

Xu Shuqing, Wenwu Zhou, Pia Backmann, Anke Kügler, Celia Diezel, Ian Baldwin.

Max Planck Institute for Chemical Ecology.

Identifying the genetic basis of ecologically important traits and estimating their fitness effects are essential for understanding how adaptation proceeds. We established the first advanced intercross-recombinant inbred lines (AI-RIL) in *Nicotiana attenuata*, a diploid annual tobacco plant, to investigate the genetic basis of leave and floral traits that are relevant to plant fitness. The two parental lines used to establish the AI-RILs varied in many different traits, such as concentration of phenolics, green leaf volatiles, floral display and volatiles, which are important for plant-herbivore and plant-pollinator interactions, thus allowing us to investigate how insect herbivore and pollinator-imposed selections drive phenotypic divergence in plants. The high density genetic markers for the established AI-RIL population were obtained using genotyping by sequencing. With the combined approaches of genetic mapping and reverse genetics, such as virus induced gene silencing, we aim to identify the causal genetic variations that are involved in plant-herbivore and plant-pollinator interactions. Furthermore, the quantitative fitness effects contributed by each trait and its underlying genetic architecture will be measured in the native environment of *N. attenuata* in the spring

of 2015. Our results will shed light on how plant-herbivore and plant-pollinator interactions drive the evolution of phenotypic traits in plants.

Poster session A - MAX 412

From whole-genome scans for divergence to the discovery of speciation genes in oaks (51801)

Thibault Leroy, Jean-Marc Aury, Catherine Bodénès, Laure Villate, Grégoire Le Provost, Jérôme Salse, Joëlle Amselem, Antoine Kremer, Christophe Plomion.

BioGeCo, INRA/Université de Bordeaux, FR; CEA, Genoscope, FR; GDEC, INRA Clermont-Ferrand, FR; URGI, INRA Versailles, FR.

Understanding the nature, the number and the strength of barriers to gene flow is a major goal in speciation genomics. Yet, few speciation genes have been reported to date in plants. Considering the costs of NGS are still coming down, it becomes possible to identify such speciation genes at the pan-genomic level even for non-model species. This presentation will review our latest advances regarding this research topic within the European white oak complex.

We first established a reference genome for oak (1.5Gb/2C) organized into pseudo-chromosomes and used a deep pool sequencing approach to characterize 4 sympatric and interfertile species (*Quercus petraea*, *Q. robur*, *Q. pyrenaica*, *Q. pubescens*). Even if these species exhibit different ecological requirements (e.g. soil pH or moisture), they are still connected by substantial levels of 'interspecific' gene flow ($F_{ST} < 0.2$). As a consequence, loci related to intrinsic selection against hybrids are expected to be revealed together with the gene driving ecological divergence. A whole-genome scan for divergence was performed using up to 250x genome coverage per species. Here, we report evidences for genomic islands of differentiation and identified some candidate speciation genes for both endogenous and exogenous barriers including some genes involved in flowering or drought tolerance.

Poster session A - MAX 412

Coupling genomics with experiments to study divergence-with-gene-flow in trees (51820)

Luisa Bresadola, Kai N. Stoelting, Céline Caseys, Dorothea Lindtke, Christian Lexer.

University of Fribourg; University of British Columbia; University of Sheffield.

Rapid recent progress in ecological and evolutionary genomics is imparting fresh perspectives to the study of speciation. A particularly active field of research at the current time is the study of “divergence-with-gene-flow”, that is, divergence that involves episodes of sym- or parapatry and thus genetic contact during some stage of the process, before reproductive isolation is complete. In this project, we address key questions regarding the ecological and evolutionary genomics of “divergence-with-gene-flow” in *Populus alba* and *P. tremula*, two

widespread Eurasian tree species related to *Populus trichocarpa*, the first completely sequenced forest tree. In particular, defined key questions and hypotheses concerning the following topics are addressed: (1) roles of early vs. late-acting reproductive barriers in the maintenance of species boundaries, (2) genomic architecture and selective value of species differences maintained in the face of gene flow, (3) role of genetic incompatibilities as early postmating barriers in species isolation. We address these topics with the help of high-throughput "genotyping-by-sequencing" approaches in natural and experimental populations, and by coupling genomics with evolutionary ecology experiments. The results are expected to advance our understanding of the origin and maintenance of reproductive barriers in hybridizing tree species representing keystone or foundation species in terrestrial habitats.

Poster session A - MAX 412

Differential gene expression according to race and host plant in the pea aphid (51835)

Isobel Eyres, Julie Jaquierey, Akiko Sugio, Ludovic Duvaux, Karim Gharbi, Jean-Christophe Simon, Carole Smadja, Roger Butlin, Julia Ferrari.

University of Sheffield; INRA Rennes; University of Edinburgh; University of Montpellier; University of York.

The pea aphid, *Acyrtosiphon pisum*, provides a powerful system for examining the genetics of host-plant adaptation and speciation, as it comprises multiple host-associated races which form a continuum of genetic divergence. Because pea aphids live and reproduce year-round on their chosen host plant, host acceptance differences between races are responsible for multiple components of reproductive isolation, and understanding the genetics of the aphid-host interaction is likely to go a long way towards understanding speciation in this system.

By conducting comparative gene expression studies, it is possible to identify biological functions involved in the adaptation of organisms to their surrounding environments. An ecological understanding of the plant-aphid interaction gives us hypotheses to test by molecular genetic methods. Using aphid clones collected from six host races in England, we examine gene expression both on their collection host and on a 'universal' host using an RNA-seq approach. This enables the identification of genes involved in direct host-plant response as well as genes that differ between aphid races. Recent studies have indicated a role for chemosensory genes in the process of host-race formation, so in addition to analysing overall patterns of expression, we specifically examine the involvement of salivary protein and chemosensory genes.

Poster session A - MAX 412

Comparative and evolutionary studies of lysosomal glycosidases in the liver/hepatopancreas of different aquatic organisms. (51916)

Elizaveta Vdovichenko, Rimma Vysotskaya.

Lysosomal glycosidases are enzymes involved in the metabolism of carbohydrates and glycoconjugates performing a variety of functions in organisms: energy, structural, biological recognition et al. Their role in adaptive responses of aquatic organisms are still under study. So, the aim of the present study was to investigate and compare the activity of 3 lysosomal glycosidases in the liver/hepatopancreas of blue mussels and fish species - pike, white-fish, roach, perch. The activity of β -glucosidase and β -galactosidase was several times higher in the hepatopancreas of mussels in comparison with fish liver. The activity of β -glucuronidase was significantly lower. The main strategy of adaptation for bivalves to get isolated from the environment is to close shell valves and minimize the metabolism. The transition to anaerobic energy supply and regulation of metabolic reconstructions require a high glucosidase and galactosidase activity. Fishes use other mechanisms of biochemical adaptation and β -glucuronidase plays a more important role in their metabolism.

The research was carried out using the facilities of the Equipment Sharing Centre of the Institute of Biology, KarRC of RAS and supported by Grant of the Russian Federation President "Leading scientific school of Russia" 1410.2014.4; COOPENOR: "Combined effects of Petroleum and the Environment in bivalves from the Norwegian-Russian Arctic".

Poster session A - MAX 412

The Effects of Pollination and Range Shifts on the Diversification of the Tribe Antirrhineae (51933)

Ezgi Ogutcen, Jolan Theriault, Daniel B. King, Jana C. Vamosi.

University of Calgary.

Range shifts are considered an important precursor to evolutionary divergence because they place populations in different environments that favour different characters. Long-distance dispersal promotes an expansion in niche breadth in terms of pollination syndromes in angiosperms, potentially explaining a wide variety of pollination syndromes. Antirrhineae, a tribe under Plantaginaceae, is a useful group for studying the interplay between dispersal and pollination in macroevolution because it has members in the Old World and the New World, and exhibits numerous transitions in major pollinating groups.

By integrating predictive modeling and range reconstructions with phylogenetic analysis, We aim to: i) reconstruct where major range shifts have occurred within Antirrhineae; ii) determine whether range overlap increases or decreases with time since divergence within the tribe; and iii) examine whether shifts in geographic distribution and pollination syndromes are associated with differences in speciation rates in Antirrhineae.

We find that distribution or pollination alone does not affect speciation rates, but the interaction of these two characters have a significant effect on speciation rates in Antirrhineae. Our age-range correlation analysis also suggest that sympatric speciation is predominant in the tribe, with a trend towards young nodes having more range overlap than older nodes in the phylogeny.

A colourful genomic landscape: patterns of gene flow in an Australian colour polymorphic finch (51935)

Peri Bolton, Adam Cadelini, Lee Rollins, James Brazill-Boast, Sarah Pryke, Sarah Legge, Kimberley Maute, Simon Griffith.

Macquarie University; Deakin University; Deakin University; Macquarie University; Australian National University; Australian Wildlife Conservancy; University of Wollongong.

Colour polymorphic species are good models for investigating genetic mechanisms of sympatric speciation. Colour can facilitate pre-zygotic isolation through habitat specialisation and sexual signalling, and colour is often correlated with behavioural and physiological traits. The Australian endemic Gouldian finch (*Erythrura gouldiae*) has a simple sex-linked head-colour polymorphism. Previous work has identified the region responsible for head-colour on the avian Z-chromosome. Head-colour is associated with different strategies, and captive birds have been demonstrated to exhibit strong pre- and post-zygotic isolation between morphs. However, microsatellite markers indicate that there is extensive gene-flow between head-colour morphs in the wild, so how are these different morph strategies maintained? Using Genotyping-by-Sequencing, we use a genome-wide approach to clarify population structure across the range and between morphs. We discuss our results in the context of the biogeographic origin of the head-colour polymorphism, and models of speciation with gene flow.

Selection on floral volatiles in sister species of Alpine orchids (*Gymnadenia*) (52009)

Kelsey JRP Byers, Roman T Kellenberger, Philipp M Schlüter.

Institute of Systematic Botany, University of Zürich.

Pollinator-mediated reproductive isolation is a major factor in driving the diversification of flowering plants. Studies of floral traits involved in reproductive isolation have focused nearly exclusively on visual signals, such as flower color. The role of less obvious signals, such as floral scent, has been studied in detail only recently. The genetics of floral volatiles involved in mediating reproductive isolation remains largely unknown, particularly in systems with more generalist pollinators. The sister species *Gymnadenia densiflora* and *G. rhellicani* (Orchidaceae) demonstrate minimal post-zygotic reproductive isolation, and their stable coexistence in sympatry appears to be largely due to floral isolation. Multiple floral traits are divergent in this system, including color, inflorescence size and shape, nectar spur length, and floral scent. Both species emit a complex blend of volatiles, with limited overlap. Previous work has shown multiple floral volatiles found in these species to be important in pollinator neural response and behavior. Genes responsible for three of these volatiles are known, but their evolutionary history remains unclear. I will discuss these volatiles, covering three main areas: species differences in coding and expression in their biosynthetic genes, molecular

signatures of selection on volatiles, and the interplay between selection on these volatiles and population structure.

Poster session A - MAX 412

Evolutionary consequences of the hybridization on the genetic architecture in two close species of *Silene* (Caryophyllaceae) (52093)

Fernanda Baena-Diaz, Niklaus Zemp, Alex Widmer.

ETH Zürich; ETH Zürich; ETH Zürich.

Understanding the consequences of hybridization and introgression in plants is very important because these processes can alter the evolutionary trajectories of the involved species, by increasing extinction rates, but also by promoting the origin of new lineages and adaptive evolution through introgression. When two species hybridize, new combinations of traits from the parental species are formed, however, this new combination of traits will depend on the genetic architecture of the parental species, thus affecting the evolutionary outcome of the hybrids. The goal of this project is to determine the genetic architecture of the species differences between *Silene latifolia* and *S. dioica* by mapping morphological traits on F2 hybrids between these species, with special interest in the role of sex chromosomes. We build a male and female genetic linkage map on F2 hybrids between these two species based on SNP's obtained by rad sequencing and measure 13 traits to obtain QTL's. The markers mapped to 12 linkage groups corresponding to the haploid chromosome number of these species. The QTL analysis reveals that traits related to reproductive isolation are clustered in sex chromosomes, thus reducing recombination of these traits and probably maintaining species differences even when introgression occur in natural populations.

Poster session A - MAX 412

Metabolic adaptations to decomposition of plant biomass in fungus-growing termite symbionts (52129)

Rafael da Costa, Michael Poulsen .

University of Copenhagen.

Fungus-growing termites along with *Termitomyces* fungi and gut bacteria play significant roles in the turnover of organic matter through plant biomass decomposition in the Old-World. The termites predigest plant material before inoculation into the fungus comb, where *Termitomyces* decomposes the main plant components. After the fungus comb has passed a second gut passage, the plant substrate is almost perfectly degraded, supporting that *Termitomyces* and gut microbes play complementary roles in plant decomposition. However, because different fungus-growing termites species collect different plant substrates, it is conceivable that co-evolutionary adaptations have occurred over the course of the 30 MYA tripartite association. To investigate this, we are undertaking comparison of the metabolic

capacities of fungal and bacterial symbionts using growth assays, enzyme assays, polysaccharide content analysis of fungus combs, and fungal and bacterial transcriptomics. The use of combinatorial approaches will allow identification of whether different *Termitomyces* lineages and associated gut bacteria are adapted to decompose specific plant substrates. This will allow for a more thorough understanding of evolutionary adaptations and specificity of symbionts associated with fungus-growing termite species, and more broadly shed light on the understanding of complementary roles played by diverse symbionts in complex mutualisms.

Poster session A - MAX 412

Alternative splicing in candidate genes involved in diapause and cold acclimation in northern *Drosophila montana* (53718)

Maaria Kankare, Ville Hoikkala, Kalevi Trontti.

University of Jyväskylä.

Alternative splicing (AS) structural variation in the messenger RNA and is known to entail adaptive potential of the organisms. However, splice variation is widely unexplored in many important phenomenon connected to adaptation. Several insect species inhabiting high latitudes have evolved different ways to survive the harsh winter conditions with long lasting subzero temperatures. Here we investigate AS under diapause and cold acclimation in a northern malt fly species, *Drosophila montana*. This species is adapted to seasonally varying environments at high latitudes, is relatively cold tolerant and shows robust photoperiodic reproductive diapause. First, we compiled RNA-sequence data to a denovo assembly using Trinity and analyzed differential expression of the contigs from diapausing and cold acclimated females. The 29 M reads used in the assembly were curated for high quality and confirmed to be species specific in order to avoid producing false variation and any non-species contigs. Finally, to identify candidate genes the list of differentially expressed (DE) genes was parsed for contigs having AS variation. Our current results indicate several genes with AS isoforms that are DE under investigated processes. The genes were annotated e.g. to metabolic and structural genes as well as to genes with a putative immune function.

Poster session A - MAX 412

The evolution and development of petal spots in the Angiosperms (52211)

Gregory Mellers, Allan Ellis, Beverley Glover.

University of Cambridge; University of Stellenbosch.

Angiosperms are the most diverse division of extant land plants, occurring in almost every environment on Earth. A key element in the formation of such a speciose group is their intimate co-evolution with pollinator species. Typically such pollination syndromes are gross features such as corolla colouration or floral scent. However, it is becoming increasingly

apparent that finer scale features may also attract pollinator species. One such characteristic is the appearance of petal spots on the corolla which have previously been shown to increase reproductive success.

Our work investigates how petal spots develop in the species *Gorteria diffusa*. Previous work has found there to be multiple “morphotypes” of the species which represent natural mutations fixed within discrete populations. These allow for comparative analyses to be undertaken with the intention of elucidating the molecular regulation of spot generation. Some evidence suggests a role for MYB genes in the formation process hence comparative expression analyses and heterologous expression studies are being undertaken. Furthermore, restriction-site associated DNA (RAD) sequencing is being used to acquire high SNP coverage in an attempt to understand the relationship between these morphotypes. It is hoped that through these techniques a hypothetical model for spot formation may be found and subsequently perturbed for validation.

Poster session A - MAX 412

Genetics of Cold Acclimation in *Drosophila montana* (52250)

Felipe Vigoder, Darren Parker, Nicola Cook, Maaria Kankare, Michael Ritchie.

UFRJ; University of St-Andrews; University of Jyväskylä.

The ability to cold acclimate has important implication to organisms fitness because it allow individuals to remain active for longer when the temperature starts to drop over winter and also allows them recover faster from a cold shock. In insect, despite many physiological studies on the subject little is known about the genetic basis of this phenotype. Recently, transcriptome analyses in *Drosophila virilis* and *Drosophila montana* suggested the involvement of 3 candidate genes involved in cold acclimation; *santa-maria* (*stm*), *period* (*per*) and *Inos*. We aim to test the actual role of these 3 genes candidates genes on cold acclimation in *D. montana* using a RNAi approach. *D. montana* has a circumpolar distribution being adapted to live within a large seasonal temperature variation. Our preliminary results confirm the involvement of both *stm* and *Inos* but not *per* on cold acclimation in *D. montana*. To our knowledge this is the first time any candidate gene from a transcriptome analysis is confirmed as being involved in a phenotype. Further details will be discussed at the presentation.

Poster session A - MAX 412

Whole transcriptome analysis on three Cuban *Anolis* lizard species adapting to different thermal microhabitats (52254)

Hiroshi D Akashi, Antonio Cádiz Díaz, Shuji Shigenobu, Takashi Makino, Masakado Kawata.

Tohoku University; Havana University; National Institute for Basic Biology.

Environmental temperature is a primary factor limiting performance and survival of ectotherms. The physiological mechanisms and its underlying molecular basis with which ectotherms respond to environmental temperature have received considerable recent interest in light of man made climate warming. In Cuba, three *Anolis* lizards, *A. sagrei*, *A. homolechis* and *A. allogus*, coexist in the same forest but occupy different thermal niches. Here, we performed RNA-seq to examine the transcriptional responses among these three species to different thermal environments. We exposed the animals for 5 days to 26 °C and 33 °C prior to transcriptional analysis. The experimental temperatures were chosen as they reflect the selected body temperatures of *A. allogus* and *A. sagrei* in the field, respectively. We found that out of approximately 15,000 transcripts obtained for each species, 75 % were expressed under both temperatures in all species. Most interestingly, transcripts with temperature-dependent differential expressions within species were not shared across species, except for a single gene (*CYP2J2*). Our study indicates that the molecular basis underlying thermal physiology may be strikingly diverse among closely related species with different thermal preferences. We discuss more about other differentially expressed genes detected to show the evolution of thermal physiology.

Poster session A - MAX 412

Specialization to the host plant in Lepidoptera pests: pattern and process (52259)

Marion Orsucci, Réjane Streiff, Emmanuelle d'Alençon, Philippe Audiot, Syvie Gimenez, Nicolas Nègre.

UM2,INRA-DGIMI,INRA-CBGP; INRA-CBGP; UM2,INRA-DGIMI; INRA-CBGP; UM2,INRA-DGIMI; UM2.

Specialization to host plant can be a driver of the high diversification of phytophagous insects. Indeed, in this process, host shifts can lead to the evolution of new specialist races or species. In this context, we study variants of moth species that are genetically differentiated and specialized to different hosts, as shown by their larval performances and preference for oviposition sites. These differently specialized moth variants live in sympatry, which makes them pertinent candidates to study ecological speciation by host plant specialization. We first determined the pattern of specialization of the different variants with a reciprocal transplant experiment on larvae. In this experiment, we measured various life history traits (survival, weight, developmental time) in response to native and alternative host plants. Then, we conducted an RNA-seq analysis to study the molecular processes involved in the larval performance. We collected RNA pools of larval tissues sampled from different experimental modalities (moth strains/host plants). Differential gene expression between modalities is then interpreted in light of the phenotypic variations we measured. This combined approach aims to identify the gene families and biological functions putatively involved in host specialization of moth larvae.

Poster session A - MAX 412

Post-mating pre-zygotic barriers and Haldane's rule (52298)

Joanna Bundus, Asher Cutter.

University of Toronto.

Haldane's rule is one of the most general observations in speciation research, but the influence of post-mating pre-zygotic barriers on Haldane's rule has been relatively underappreciated. For gametic barriers to affect Haldane's rule, gametes bearing different sex chromosomes must differ in fertilization success in interspecific crosses. Outbreeding *Caenorhabditis briggsae* initially produce hermaphrodite offspring (XX), with more male offspring (X0) produced later, due to a competitive advantage of X-bearing sperm over nullo-X sperm. Crosses between *C. briggsae* and its sister species *C. nigoni* exhibit Haldane's rule, producing more females than males. These crosses also stop producing offspring soon after mating, because sperm are rapidly lost from the reproductive tract. We hypothesized that the combination of an X-bearing sperm competitive advantage and rapid sperm loss contributes to Haldane's rule, because many nullo-X sperm are lost before fertilizing any eggs. We compared the sex ratio of hybrids laid on the first day after mating to those laid on the second day after mating. Consistent with our hypothesis, the proportion of hybrid males was lower among early progeny than late progeny, indicating that X-bearing sperm have a fertilization advantage in the interspecific cross, contributing to Haldane's rule.

Poster session A - MAX 412

Feeling the pressure: extremophilic adaptation of hsp90 and hsp70 heat-shock proteins in deep-sea amphipod species (52300)

Heather Ritchie, Alan Jamieson, Stuart Piertney.

Zoology, University of Aberdeen; Oceanlab, University of Aberdeen.

The enormous hydrostatic pressure ranges (60-110 MPa) of the oceanic hadal zone (>6000 m depth) pose great challenges to hadal organisms, affecting growth, viability and distribution. Nevertheless, the hadal zone hosts extremely taxonomically diverse floral and faunal communities, highlighting a capacity for local evolutionary adaptation.

One key mechanism facilitating extremophilic adaptation may be the evolution of heat-shock proteins (HSPs). These are molecular chaperones that assist protein folding, regulation and degradation in response to various environmental stressors such as fluctuations in hydrostatic pressure. Examining the patterns of inter- and intra-specific variation of HSPs can elucidate a species' ability to inhabit extreme environments, such as the hadal zone.

Here we examine the role of HSP evolution in ubiquitous Lysianassoidea amphipod species, whose distributions exceed a kilometre in depth equating to pressure changes exceeding 10 MPa. A total of 28 species across seven Pacific trenches and four Atlantic sites, representing pelagic, abyssal and hadal depths, were characterised at hsp70 and hsp90 genes. Genetic patterns among and within species are combined with environmental data (i.e. hydrostatic

pressure, temperature etc) using phylogenetic and seascape genomics approaches to infer the extent to which HSP evolution is driven by adaptation to the extreme deep sea environment.

Poster session A - MAX 412

Bacterial microbiota associated with *Cottus* (Pisces) across a secondary contact zone (52363)

Sunna Ellendt, Arne W. Nolte.

Max Planck Institute for Evolutionary Biology.

Natural hybrid zones often emerge at habitat clines where distinct populations meet, mate and hybridize. The possible factors that govern the dynamics of a hybrid zone are insufficiently explored. For example symbiotic bacteria can induce selection pressure by influencing the host's immune system, nutrition, development and behavior. These interactions are in turn influenced by environmental factors. We use a contact zone where *Cottus rhenanus* and invasive *Cottus* hybridize at a habitat ecotone to study the association of symbiotic microbiota, habitat and host genotype to infer whether host-bacterial interaction may act as evolutionary force. We extracted genomic DNA from fin samples of wild caught fish and assessed bacteria through pyrosequencing of 16S rRNA markers. The host genetic makeup was inferred based on 80 nuclear SNP markers that permit to classify all fish into parental forms and recent hybrids. Phylogenetic and statistical analyses revealed significant differences in bacterial diversity and abundance in the distinct habitats whereas we did not detect any differences between distinct host genotypes. However, the analysis of hybrids suggests, that the microbial community is altered from both parents which possibly decreases the fitness of hybrids.

Poster session A - MAX 412

Developmental plasticity of a key evolutionary trait in East African cichlids – insights in evolutionary mechanisms that shaped these cichlids' adaptive radiations (52480)

Ralf F. Schneider, Helen M. Gunter, Immanuel Karner, Christian Sturmbauer, Axel Meyer.

University of Konstanz; University of Edinburgh; University of Graz.

The 'modern haplochromine' cichlid fishes are a famous example of repeated rapid adaptive radiations - one in each of the three East African Great Lakes. *Astatoreochromis alluaudi* is a riverine species that is basal to these adaptive radiations, putatively resembling the common ancestor of this group. A mechanically-stimulating diet induces pronounced plasticity in *A. alluaudi*'s pharyngeal jaw apparatus, a structure considered to be a key evolutionary trait in cichlids. We compared the morphological and transcriptional effects of experimentally induced plasticity in this trait in *A. alluaudi*, to three representatives of the adaptive radiations and one out-group. Our results indicate that the adaptive plasticity is most pronounced in non-

radiating species, followed by the recently radiating species and is lowest in the oldest adaptive radiation. Next, we investigated the expression of plasticity-related genes for species that showed a plastic response. Through comparing co-expression between species, we observed that similar sets of functionally related genes were co-expressed in both basal and more derived species, suggesting conserved transcriptional ‘modules’. We conclude that the ancestral cichlid lineage was probably phenotypically plastic and that module-like transcriptional alterations in developmental trajectories putatively shaped the parallel evolution of highly diverse trophic phenotypes among these adaptively radiating cichlid lineages.

Poster session A - MAX 412

Genomic analyses of two differentially migrating bird subspecies (52553)

Max Lundberg, Susanne Åkesson, Staffan Bensch.

Department of Biology, Lund University.

Migration requires adaptations in behavioural, morphological and physiological traits. These traits have been shown to have a strong genetic basis, but very little is known about the underlying genes. Here we use whole-genome resequencing and a customized snp array to detect genetic differences between two differentially migrating subspecies of the willow warbler *Phylloscopus trochilus*. We find that the genomes are extremely similar, with differences clustered in three divergent chromosome regions that potentially represent inversion polymorphisms. One of the regions does not contain alleles that are strictly associated with each of the subspecies, but instead appears to be associated with adaptation to high altitude and latitude. The other two chromosome regions contain alleles specific to either subspecies and may contain differences related to the different migratory phenotypes of the subspecies.

Poster session A - MAX 412

Comparative population genomics in three species of Chorthippus grasshoppers (52560)

Emma Berdan, Camila Mazzoni, **Frieder Mayer**.

Museum für Naturkunde Berlin; Berlin Center for Genomics in Biodiversity Research.

Emerging genomic tools can reveal the genetics of speciation in non-model groups with no previous genetic resources. Grasshoppers of the *Chorthippus biguttulus* species group differ strongly in calling song (and corresponding female preferences) but are almost identical morphologically, suggesting that sexual selection has been the main force driving premating hybridization barriers in this group. Here we performed a population genomic scan by sequencing individuals’ transcriptomes to search for outlier loci. We sequenced 20 individuals of each of the three *Chorthippus biguttulus*, *C. mollis*, and *C. brunneus*. We called SNPs for

all three possible species pairings and used FST based approaches to identify outliers. We found approximately 1% of SNPs in each comparison to be outliers. Between 37 and 40 percent of these outliers were non-synonymous SNPs (as opposed to a global level of 17%) indicating that we recovered loci under selection. Among the outliers were several genes involved in song production and hearing as well as a plethora of genes involved in other traits such as metabolism. This indicates that ecological processes besides sexual selection on acoustic signals contributed to the divergence of these three species.

Poster session A - MAX 412

The role of visual adaptation in cichlid fish speciation (52571)

D. Shane Wright, Ole Seehausen, Ton G.G. Groothuis, Martine E. Maan.

University of Groningen; University of Bern, EAWAG.

In less than 15,000 years, Lake Victoria cichlid fishes have radiated into as many as 500 different species. Ecological and sexual selection are thought to contribute to this ongoing speciation process, but genetic differentiation remains low. However, recent work in visual pigment genes, opsins, has shown more diversity.

Unlike neighboring Lakes Malawi and Tanganyika, Lake Victoria is highly turbid, resulting in a long wavelength shift in the light spectrum with increasing depth, providing an environmental gradient for exploring divergent coevolution in sensory systems and colour signals via sensory drive.

Pundamilia pundamilia and *Pundamilia nyererei* are two sympatric species found at rocky islands across southern portions of Lake Victoria, differing in male colouration and the depth they reside. Previous work has shown species differentiation in colour discrimination, corresponding to divergent female preferences for conspecific male colouration. A mechanistic link between colour vision and preference would provide a rapid route to reproductive isolation between divergently adapting populations. This link is tested by experimental manipulation of colour vision - raising both species and their hybrids under light conditions mimicking shallow and deep habitats. We quantify the expression of retinal opsins and test behaviours important for speciation: mate choice, habitat preference, and foraging performance.

Poster session A - MAX 412

Genomic heterogeneity of species diversification in an avian superspecies complex (52731)

Jelmer Poelstra, Christen Bossu, Nagarjun Vijay, Matthias Weissensteiner, Jochen Wolf.

Uppsala University.

As species diverge, accumulating genetic changes tend to be clustered in few regions of the genome. Yet, our understanding of the underlying evolutionary forces generating

heterogeneous landscapes of genome diversification remains limited. There is a need to disentangle the relative importance of processes such as local differences in recombination rates, gene flow, and positive selection. One way forward is to compare patterns of genome differentiation along the speciation continuum, that is across several levels of overall genomic divergence and gene flow. Here, we re-sequenced 128 genomes of crows from a superspecies complex with striking parallel divergence in plumage colouration, sampling across two independent hybrid zones between all black carrion and black-and-grey hooded crows, as well as from the black-and-white collared crow. While several differentiation peaks were strongly correlated with overall divergence levels, others were unique to specific population comparisons or in accordance with plumage features. We conclude that while most genomic differentiation was best explained as a result of processes independent of speciation, several genomic regions harbour evidence for divergent selection partly in relation to phenotypic divergence.

Poster session A - MAX 412

Association between genotype and plumage pigmentation in the Tytonidae: candidate gene approach (52744)

Vera Uva, Luca Fumagalli, Alexandre Roulin.

University of Lausanne.

The evolution and maintenance of phenotypic variation is a central question in evolutionary biology, and the diversity of plumage colouration in birds has long attracted the interest of scientists. Colour patterns play a relevant role in speciation and adaptation, and the Melanocortin System is known to be involved in the control of melanin pigment synthesis, and to pleiotropically regulate a number of physiological and behavioural traits in vertebrates. It comprises the POMC gene, encoding the MSH and ACTH peptides, the melanocortin receptors (MC1-5Rs and antagonists, agouti proteins (ASIP and AGRP)). Barn owls (*Tyto alba*) vary continuously across continental gradients in ventral plumage colouration from white to dark-reddish, and number and size of black spots located on feather tips. A key MC1R non-synonymous substitution was found in Europe, where the I allele individuals are redder, and homozygous VV individuals are whiter. In the POMC gene, serine repeats were found, which can potentially be associated with pigmentation patterns. Due to their cosmopolitan distribution and striking variation in colouration across continental gradients, the Tytonidae family provides a unique opportunity for a worldwide study on the evolution and maintenance of melanin-based pigmentation, using a candidate gene approach focusing for now on the MC1R and POMC genes.

Poster session A - MAX 412

Gain and loss of GDF6 expression and the evolution of skeletal traits (52798)

Vahan Indjeian, Felicity Jones, David Kingsley.

MRC Clinical Sciences Centre - Imperial College London; Friedrich Miescher Laboratory of the Max Planck Society; HHMI and Stanford University School of Medicine.

Dramatic skeletal changes have evolved within most vertebrate groups. High-resolution mapping experiments with natural populations of sticklebacks identify two distinct, but very closely linked loci that regulate different aspects of armour plate size. The Growth/differentiation factor 6 (GDF6), a secreted bone morphogenetic protein, is the only gene in both intervals. Freshwater fish with reduced armour plates show elevated levels of GDF6 expression and transgenic overexpression of GDF6 in large-plated marine fish results in smaller or missing plates. Gdf6 null mice have skeletal phenotypes, and in humans there is a unique loss of conserved non-coding element in the GDF6 gene. The chimpanzee allele of the enhancer missing in humans drives expression in the hindlimbs but not forelimbs, in anatomic domains that have been specifically modified during the human transition to bipedalism. These results suggest that both upregulation and downregulation of GDF6 contribute to natural variation in skeletal morphology in fish and primates.

Poster session A - MAX 412

Ecological adaptation of a desert-specialist, on the edge of life (52824)

Nina Serén, José C. Brito, Phillip C. Watts, Rui Faria, Tapio Mappes, Zbyszek Boratyński.

CIBIO/InBIO, Research Center in Biodiversity and Genetic Resources, University of Porto; Institute of Integrative Biology, Biosciences Building, Crown Street, University of Liverpool; Department of Biology, University of Oulu; IBE, Institute of Evolutionary Biology (UPF-CSIC), Universitat Pompeu Fabra; Dep. Biological and Environmental Science, University of Jyväskylä.

How climate change impacts biodiversity is one of the hottest topics in evolutionary biology. Among different mechanisms that species hold to resist severe environmental changes, the microevolutionary response is particularly challenging, as adaptation can occur at a slower pace than current climate changes.

One way to circumvent this limitation is to learn from past events where species currently experiencing extremely arid conditions had to cope with environmental changes. We have chosen the Lesser Egyptian Jerboa (*Jaculus jaculus*) to study the genetic mechanisms of adaptation to divergent habitats in the Sahara desert, region exposed to extreme environmental conditions which experienced profound climatic oscillations. Two previously described jerboas ecotypes that differ in fur colour are being analysed for genomic regions involved in adaptation to different habitats. Preliminary results from digital photo RGB code and spectrophotometer light reflectance measurements (phenotypic characterization), and from sequencing mitochondrial and candidate nuclear genes of a mix of museum and contemporary samples, will be presented. Ongoing genomic analyses will permit to identify the genomic regions and genetic mechanisms underlying adaptation.

Poster session A - MAX 412

Effects of genetic divergence between two *Arabidopsis lyrata* populations on germination traits (52833)

Tuomas Hämälä, Päivi H. Leinonen, Outi Savolainen.

University of Oulu, Finland; Duke University, Durham, NC, USA.

Timing of seed germination, one of the most important life-history traits in plants, is known to be significantly differentiated between plant populations. However, the genetic basis of germination differences and their potential roles in postzygotic isolation has not been well studied. We investigated the consequences of genetic divergence on germination traits between two highly diverged *Arabidopsis lyrata* populations from Karelia, Russia and North-Carolina, USA. Comparisons of germination percentages between reciprocal F1 and F2 hybrids and their parents showed evidence of Bateson-Dobzhansky-Muller type incompatibilities, as hybrids germinated worse than both parental populations and F2 seeds worse than F1 seeds. Additionally, reproductive isolation showed asymmetry in the first hybrid generation but not in the second, suggesting a more complex background than simple cytonuclear interactions. By using genetic mapping based on a RAD sequencing modification we hope to clarify the genetic architecture of seed dormancy differences. Are they dominated by few large effect QTLs or by several small ones? And do we find a signal of DOG1 – a locus found to be major effector of seed dormancy in *Arabidopsis thaliana*.

Poster session A - MAX 412

Evolution of antifreeze glycoprotein (AFGP) in Antarctic icefish (notothenioids) (52849)

Marisa Zubler.

Zoological Institute, University of Basel.

Notothenioidei, Antarctic icefish, are a marine species flock that underwent adaptive radiation thanks to the evolution of antifreeze glycoprotein in an ancestral lineage. This protein enables icefish to survive in the ice-cold, thermally isolated and therefore island-like environment of the Antarctic Ocean. Existing phylogenies based on various nuclear and mitochondrial genes show that notothenioids have evolved from a common ancestor. It would be of importance to sequence notothenioid AFGP since this gene is thought to be a evolutionary key innovation. AFGP gene has so far only fully been sequenced in one species (*Dissostichus mawsoni*) since obtaining sequence data is being complicated by highly repetitive sequences and multiple copy variants. Regardless, it would be interesting to shed light on whether or not a phylogeny based on AFGP mirrors existing phylogenies. Furthermore, we will include sequences from a notothenioid species in which AFGP gene seems to have lost its function due to relaxed selection pressure in warmer regions.

To approach this we have amplified AFGP gene of 20 notothenioid species using a High-Fidelity DNA Polymerase and will subsequently use next-generation sequencing to obtain results.

We expect that the phylogeny based on AFGP will be in accordance with existing phylogenies.

Intraspecific diversity and incipient speciation in a planktonic unicellular eukaryote (52857)

Mickael Le Gac, Christophe Destombe, Laure Guillou, Raffaele Siano, Myriam Valero, Annie Chapelle.

Ifremer; UPMC Sorbonne Universités; CNRS; Ifremer; CNRS; Ifremer.

Adaptation, ecological divergence and ultimately speciation are processes that are especially hard to understand when considering phytoplanktonic species. Such organisms are non sessile, their dispersion and distribution almost entirely depend on hydrodynamism, and very often, they live in a highly dispersive and unstable environment. In such system, at what point adaptation may drive evolution and the the kind of selective pressure involved remain virtually unknown. Empirically speaking, studying adaptation and speciation in the pelagic environment is complicated by the dynamic nature of the environment, by the microscopic nature of the organisms, and by the absence of closely related model organisms. In the present study, we investigated intraspecific diversity as well as incipient speciation in the toxic bloom forming dinoflagellate *Alexandrium minutum* using two approaches: 1. performing growth assays under various in vitro conditions using 18 strains isolated from several blooms and 2. analyzing the mRNA sequences (RNAseq) of the same strains. We focused on both the phenotypic and genetic patterns of divergence as well as on the functional implications of this divergence.

Speciation, introgression and molecular evolution in the carnivorous pitcher plant *Nepenthes* (52876)

Mathias Scharmann, Alex Widmer.

ETH Zürich.

The spatial coexistence of species with realised gene flow implies strong selection against certain admixed genotypes, since parental lineages would otherwise have merged. These scenarios hold the promise of being able to distinguish those genetic and phenotypic traits that were and are relevant in (selection-based) speciation processes from mere neutral divergence. On the other hand, novel genotypes created by gene flow might be adaptive, and thus promote divergence. We study these questions in the carnivorous pitcher plant *Nepenthes*. The dioecious genus has radiated across the Malay Archipelago (150+ species); their modified leaves catch and digest insects, canopy litter, or even mammal faeces with a variety of mechanisms and mutualistic interactions. In sympatric communities of up to seven species in Borneo and Singapore, we detect recent hybrids and older signatures of introgression using RAD-seq. Introgression is increased in habitats with human disturbance, indicating that species barriers have an ecological component in *Nepenthes*. Consequently, we compare the

molecular evolution of genes with a function in plant carnivory (shotgun proteomics and RNA-seq) across species pairings with contrasting trapping mechanisms and ages. We hypothesise that carnivory genes should be outliers against the transcriptome background, if this trait is disproportionally contributing to speciation and divergence.

Poster session A - MAX 412

Anthropogenic pressure and introgression in malaria vectors (52880)

Chris Clarkson.

Liverpool School of Tropical Medicine.

Though common in plants, introgression between animal species is rarely reported. However, in malaria vector mosquitoes it may actually be a common occurrence. The intense selective pressure that vector control insecticide regimes impose upon the insects, in concert with high levels of sympatry and the fact that even quite distantly related species naturally hybridise (e.g. *Anopheles gambiae* x *An. Coluzzii* separated by ~1.85 Ma), allows regions of the genome with advantageous insecticide resistance properties to introgress. Using whole genome sequence data from *An. gambiae*, *coluzzii* and *arabiensis* we investigate regions of the genome that have been transferred through introgression and show that this is an important mechanism in the evolution of these insects.

Poster session A - MAX 412

Function and evolutionary consequences of Diplostigmaty (52897)

Jonathan Kissling.

University of Neuchâtel.

Differentiation of female sexual organs in flowering plants is rare, and contrasts with the wide range of male reproductive strategies. An unusual example involves diplostigmaty, the possession of spatially and temporally distinct stigmas in insect-pollinated species of the Cape of South Africa. Here, the single pistil within a flower has an apical stigma, as in most flowering plants, but also a secondary stigma that occurs mid-way down the style. Floral manipulations and measurements of fertility and mating patterns of *Sebaea aurea* provide evidence that this system serves as a mechanism of reproductive assurance in population with low plant density. Furthermore, diplostigmaty is evolutionarily stable and associated with higher diversification rates than related monostigmatic lineages, suggesting long-term ecological advantages to this flexible mixed mating strategy resulting from the possession of dimorphic stigma function.

Poster session A - MAX 412

Divergent selection and reduced dispersal drive phenotypic diversification at a very small spatial scale in an island bird (52954)

Borja Milá, Yann Bourgeois, Joris Bertrand, Josselin Cornuault, Boris Delahaie, Christophe Thébaud.

National Museum of Natural Sciences, Madrid, Spain; University of Basel, Switzerland; National Taiwan University, Taiwan; University of Toulouse, France.

The Reunion grey white-eye, *Zosterops borbonicus*, a passerine bird endemic to Reunion Island in the Mascarene archipelago, represents an extreme case of microgeographical plumage colour variation in birds, with four distinct colour forms occupying different parts of this small island (2512km²). To understand whether natural selection could explain such variability, we compared patterns of variation in morphological and plumage colour traits within and among populations, and found that variation among the different forms was greater than would be expected if genetic drift alone was responsible for phenotypic divergence. Analyses of structure and gene flow using microsatellite and RADseq data also revealed very low levels of historical and contemporary gene flow among populations. Genome-wide divergence and the existence of narrow contact zones across narrow geographic barriers suggest the evolution of incipient reproductive isolation among parapatric forms. We conclude that divergent natural selection and reduced dispersal appears to be the dominant mechanisms explaining phenotypic divergence in morphological and plumage colour traits at an exceptionally small spatial scale in *Z. borbonicus*.

Poster session A - MAX 413

Differentiation in the tomato red spider mite: a novel method to study the genetics of hybrid lethality by genotyping viable and inviable hybrids (52281)

Bram Knegt, Tomos Potter, Martijn Egas.

University of Amsterdam.

When hybrids have reduced fitness, they typically suffer from sterility or lethality. Studying hybrid lethality is notoriously hard, because individuals with lethal genotypes do not develop and thus cannot be sampled. Therefore, most studies in hybridization genetics have traditionally focused on sterility rather than lethality, and when lethality was considered, lethal genotypes could only indirectly be inferred from their absence in viable individuals. However, using molecular tools it is in principle possible to genotype inviable individuals. Here, we present a model system demonstrating this novel method of studying the genetics of hybrid lethality.

The spider mite *Tetranychus evansi* (Acari: Tetranychidae) is a haplodiploid herbivore for which two genetically distinct types have been described. Gene flow between these types occurs, but in the F₂ generation only ~5% of the eggs hatch, demonstrating strong hybrid incompatibility. We collected genetic material from both hatched individuals and unhatched eggs, and could thus genotype viable and inviable hybrids using 8 microsatellite markers fixed for different alleles in the two types. We found that recombination between these

markers frequently leads to inviability, providing direct evidence for Bateson-Dobzhansky-Muller incompatibilities. Our methodology opens up new possibilities for studying the genomics of speciation.

Poster session A - MAX 413

Cryptic species, ecomorphs and GFP/GFP-like profiles in the cnidarian *Anemonia viridis* (52290)

Cédric Mallien, Caroline Olivier, Thamilla Zamoum, Didier Forcioli, Paola Furla.

UMR 7138 EPS UPMC CNRS.

Cryptic species have recently been identified in many cnidarians despite a lack of morphological variation. Only the use of molecular markers allowed the detection of these taxonomic entities. Contrastingly, 5 clearly different morphs have been described in the sea anemone *Anemonia viridis*, based on the expression profiles of GFP-like proteins. However, no clear genetic differences had been found so far among these morphs, even if they were thought to display different reproductive strategies (clonal vs. sexual reproduction). In this study, we tested if these morphs belong to the same species or to independent gene pools, using a set of 10 genes whose expression patterns are modified by environmental factors. For each of these genes, an EPIC marker has been developed (by comparison with published cnidarian genomes) and will be sequenced on individuals of the three most common morphs from population of the Mediterranean Sea and English Channel. Our sampling scheme will allow us to test whether the geographic origin or the GFP morph is the structuring factor for the genetic diversity in *A. viridis*. Moreover, putative adaptive genes, a priori more divergent than neutral markers, should be more efficient to detect independent gene pools within a species.

Poster session A - MAX 413

Genome-wide divergence among population pairs of parasitic and non-parasitic lampreys (52413)

Quentin Rougemont, Sophie Launey, Arnaud Gaigher, Gilles Lassalle, Jerome Goudet, Guillaume Evanno.

INRA; INRA; UNIL; INRA; UNIL; INRA.

The mechanisms underlying speciation with gene flow remain largely unknown and encompass those related to models of sympatric speciation and secondary contact. Lampreys are ancient vertebrates that often exist as pairs of closely related species with distinct life histories representing putative cases of speciation with gene flow. In Europe, such a pair is represented by *Lampetra fluviatilis* that is parasitic and anadromous and *Lampetra planeri* that is non-parasitic and resident in freshwater. Using microsatellite markers we previously showed various levels of gene flow between ten population pairs suggesting different levels of reproductive isolation along the speciation continuum. Here we used a RAD sequencing approach of sympatric, parapatric and allopatric population pairs together with diffusion-approximation analyses incorporating heterogeneous effective migration among loci to i) understand the patterns of genome-wide divergence at different stages along the speciation continuum ii) identify loci putatively involved in the adaptive divergence of the two forms and iii) reconstruct the most probable demographic scenario of divergence between these lampreys. Results will allow investigating the respective effects of neutral processes and divergent selection on the genomic basis of speciation with gene flow.

Poster session A - MAX 413

Mosaic hybridization in two species of the *Jaera albifrons* complex (52535)

Ambre Ribardi re, Thomas Broquet.

Station Biologique de Roscoff, France.

Mosaic hybrid zones allow us to compare the action of isolating mechanisms in mixed populations with and without hybridization. Here we test whether such a mosaic hybridization scenario happens with two marine isopods from the *Jaera albifrons* complex. Morphological descriptions suggested that hybridization exceptionally happens in some populations (Solignac, 1978).

To test this hypothesis, we described the distribution of genetic variance between species *Jaera albifrons* and *Jaera praehirsuta* using nuclear and mitochondrial markers in several sites where hybridization is or isn't suspected (in Normandy and Brittany, respectively). In Normandy, the nuclear genome appeared much more homogeneous, pointing to a reduction of isolating barriers (environmental, behavioral, and genetic) in this region. Yet the two parental species morphs are largely conserved, suggesting that the permeability to interspecific gene flow might be variable across the genome. This hypothesis is further supported by our observation of an outlier microsatellite marker showing a stronger level of differentiation in this population where hybridization occurs compared to other populations where the two species do not hybridize. These populations thus provide an interesting situation for a comparative analysis of the genomic architecture of reproductive isolation, currently under way using genomic analyzes.

Speciation genomics in European columbines (*Aquilegia*) (52562)

Gokce Akoz, Magnus Nordborg.

Vienna Graduate School of Population Genetics & Gregor Mendel Institute of Molecular Plant Biology; Gregor Mendel Institute of Molecular Plant Biology.

The formation of new species has been a major challenge in evolutionary biology. This is partly because of the fact that by the time "species" are recognized, many isolating barriers have accumulated and it has become impossible to identify the initial barrier(s) leading to divergence between populations. The columbine genus *Aquilegia* (Ranunculaceae) could be an important model to reveal genomic scale changes that result from speciation since several findings imply a recent and rapid radiation event in this group. To get a glimpse of the patterns of genetic variation in the poorly studied European taxa, we initially whole-genome sequenced seven individuals of *A. vulgaris*, which as the most widespread species of the genus is found from southern Scandinavia throughout Europe, and one individual of *A. pyrenaica* native to the Pyrenees. Principal Component Analysis on genotypes indicate that *A. pyrenaica* is separated from all *A. vulgaris* individuals, and also that *A. vulgaris* individuals are separated by geography, following a pattern of Isolation by Distance. We aim to sequence a few other *Aquilegia* species to extend our understanding of genetic variation, which will, in turn, be decisive for further sampling required to delve more deeply into within population dynamics.

The fragmented distribution of the Apollo butterflies in Sierra Nevada (Spain): How isolated are they? (52606)

Oscar Mira, Juan G. Martínez, Alberto Tinaut, Cristina Sánchez-Prieto, Deborah A. Dawson, Terry Burke.

Universidad de Granada; University of Sheffield.

Small and isolated populations have high inbreeding levels that may endanger their long-term survival. The Apollo butterfly (*Parnassius apollo*) is represented by small and local populations. In Spain, the mountain ranges isolate different subspecies: *P. apollo nevadensis* inhabits the Sierra Nevada mountain range between 1,950 and 2,700 metres.

18 microsatellite markers specifically developed were used to genotype 400 individuals to estimate inbreeding coefficients, other population statistics and gene flow among populations. The results show limited but significant genetic structure ($F_{st} = 0.01$; $p = 0.0001$) and that the genetic distances among locations are partially explained by geographical distance ($R^2 = 0.216$; $p < 0.0001$). Although the discontinuous nature of the habitat, Bayesian clustering methods (Structure, BAPS, TESS) group all locations into one panmictic population; however, Geneland was able to identify four different populations. Estimated gene flow (BayesAss) was low in most cases, but sufficient to maintain the observed connectivity among locations.

This indicates that no locations are genetically isolated, but the fact that there is genetic structure suggests the operation of metapopulation dynamics. Gene flow appears to be weaker between the more distant locations, but also between locations separated by natural obstacles (mountain peaks and valleys) and human-induced barriers, such as roads or the skiing station.

Poster session A - MAX 413

The Footprint of Adaptive Introgression After Secondary Contact (52621)

Derek Setter, Joachim Hermisson, Jeffrey Jensen.

University of Vienna; Ecole Polytechnique Federale de Lausanne.

The sources of genetic variation and their relative contributions to adaptation is a central topic in the study of evolution, and mounting evidence points to an important role for genetic variation introduced through interspecific gene flow. Introgressive adaptive alleles must overcome the barriers to gene flow generated by locally maladapted alleles and genetic incompatibilities. Using a multi-locus Moran model, we study the influence of such deleterious variants on the process of adaptive introgression. Strongly deleterious alleles may greatly reduce the probability of adaptation from introgressive variation, and this effect increases with tighter linkage. Weakly deleterious alleles reduce the introgression probability only when tightly linked. In this case, they may alter the fixation process of the adaptive allele to generate a genomic signature of selection that is unique to introgressive adaptive variation. We calculate the expected change in the frequency of neutral alleles linked to an introgressive adaptive allele and compare this to adaptive alleles that either appear as new mutations or exist as standing genetic variation. Under a range of biologically-relevant scenarios, adaptive introgression generates patterns in polymorphism data that are distinguishable from those of de-novo mutations and standing genetic variation.

Poster session A - MAX 413

Genomic evolution at the tip of the cichlid phylogenetic bush (52666)

Hugo Gante, Martin Malmstrøm, Michael Matschiner, Emiliano Trucchi, Sissel Jentoft, Walter Salzburger.

University of Basel; University of Oslo; University of Vienna.

Recent efforts in genome sequencing revealed major patterns of genome evolution in a phylogenetic backbone of African cichlids from different lakes and rivers. We use de novo genome sequencing of additional Neolamprologus species with divergent phenotypes to gain insight into processes acting as new species diverge. In these analyses, focused on the tip of the phylogenetic bush, we look at the landscape of genome divergence and patterns of incomplete lineage sorting to gain an understanding of genomic features and mechanisms underlying phenotypic divergence. We complement this search of divergence islands with

genome scans using RADtags. Overall we find relatively few regions involved in adaptive divergence between species.

Poster session A - MAX 413

Population Genomics of Two Teleogryllus Cricket Species that Provide a Rare Exception to Haldane's Rule (52820)

Peter Moran, Mike Ritchie, Nathan Bailey.

University of St Andrews.

Determining the mechanisms and processes underlying the development and maintenance of reproductive barriers is important for understanding speciation and species coexistence. In this talk I report on a broad scale transect of phenotypic and population genomic data, combined with results from lab hybridization experiments on *Teleogryllus commodus* and *T. oceanicus*. These two closely related field cricket species are a classic study system for sexual selection and speciation. Both species overlap across an extensive area and hybrids are easily produced in the laboratory. However, chemical and acoustic signals appear to act as strong premating barriers to gene flow. Here I describe RAD-seq results that test patterns of genomic divergence within and between species and how this relates to variation in acoustic and chemical signals. Additionally lab hybridization experiments reveal that these species provide a remarkably rare exception to Haldane's rule, as both reciprocal F1 hybrid females are sterile, while males are fertile. X linked incompatibilities may contribute disproportionately to reproductive isolation. Integration of these findings with population genomic analysis of sex linked markers raises new insights into the role of sex chromosomes in maintaining species boundaries.

Poster session A - MAX 413

Is selection on habitat gradients correlated with phenotypic and genomic differentiation in cichlid fish populations? (52827)

Jacco C. van Rijssel, Florian N. Moser, Catherine E. Wagner, Ole Seehausen.

Fish Ecology and Evolution, EAWAG, Kastanienbaum, Switzerland; Institute of Ecology and Evolution, University of Bern, Bern, Switzerland.

Textbook examples of adaptive radiation in lakes provide insight into how the origin of species is facilitated. Disruptive selection between habitats and differential resource utilization are thought to play important roles in speciation. However in the majority of cases, speciation does not occur despite the existence of suitable selective environments. The absence of speciation might be due to populations 1) not encountering rugged adaptive landscapes 2) failing to respond to disruptive selection or 3) adapting through mechanisms that do not require speciation. To test these alternatives, we compared individual fitness proxies and genome-wide signatures of selection between sympatric cichlid populations

coexisting along environmental gradients. We chose paired populations, in each case contrasting species which show clear morphological divergence or incipient speciation along environmental gradients to species lacking morphological divergence. Using growth rate as a fitness proxy, we inferred fitness landscapes for phenotypic traits and multivariate phenotypes in these populations. We then used genome-wide SNP data to examine patterns of genomic divergence along environmental gradients. By using morphological, genomic and fitness proxy data, we seek to link selection to morphology and to genomic patterns of divergence, and thus provide a unique window onto the basis of genomic divergence during cichlid speciation.

Poster session A - MAX 413

An insight into Lacertid speciation through the comparative genomics of *L. viridis* and *L. bilineata* (52879)

Rohit Kolora, Anne Weigert, Christoph Bleidorn, Peter Stadler, Klaus Henle, Rui Faria, Katja Nowick, Martin Schlegel.

German Center for Integrative Biodiversity Research - iDiv; Molecular Evolution and Animal Systematics, Institute of Biology, University of Leipzig; Institut für Informatik, Universität Leipzig; IZBI/Bioinformatik, Universität Leipzig; Department of Conservation Biology, Helmholtz Centre for Environmental Research - UFZ; CIBIO, Centro de Investigação em Biodiversidade e Recursos Genéticos, InBio, Universidade do Porto; IBE, Institute of Evolutionary Biology (UPF-CSIC), Universitat Pompeu Fabra, PRBB.

Suppressed recombination models (SRM) suggest that chromosomal rearrangements (CRs), which act as barriers to gene flow, can play an important role in speciation by potentially leading to the accumulation of genetic incompatibilities between parental species that will often manifest in their hybrids in terms of misexpression, inviability and/or loss of the reproductive function. Another important feature of CRs, is that they can directly contribute to gene expression differences between species by disrupting genes or by altering the gene regulatory regions. To test the role of CRs in speciation, we are studying the genomes and transcriptomes of two closely-related species – *Lacerta viridis* and *L. bilineata* that are widely distributed in Europe and are able to form hybrids. We sequenced the genomes of both species using Illumina with libraries of different insert sizes, which allowed us to produce a high-quality contig assembly. We compared the genome assemblies against each other and identified CRs through changes in synteny. We also investigated the relationship between genomic and gene expression changes in our species based on gene annotations and regulatory regions. Finally, we are characterizing genome-wide divergence between these Lacertid species to identify signatures of selection.

Poster session A - MAX 413

The genomic landscape of speciation in a classic “Great Speciator”: the *Myzomela* honeyeaters (52896)

Jason M. Sardell, J. Albert C. Uy.

University of Miami.

Islands systems have played prominent roles in our understanding of the origins of biodiversity, but few studies of speciation genomics have examined divergence within island radiations. In this study, we examine genomic divergence within one of Mayr & Diamond's classic examples of "great speciators", the *Myzomela* honeyeaters of the Indo-Pacific. Specifically, populations of *M. tristrami* and *M. cardinalis* on Makira in the Solomon Islands represent a rare example of recent secondary contact between island species, with sympatry dating to the turn of the 20th-century. These species fill similar ecological niches, but differ significantly in plumage, a presumed sexual signal. Previously, we determined that hybridization is ongoing between these taxa, but asymmetric, with all successful hybridization events involving the matriline of the colonizing species, *M. cardinalis*. Furthermore, sequencing of 6 nuclear introns suggests that alleles associated with melanism in *M. tristrami* are introgressing into the genomic background of *M. cardinalis*, which possesses red carotenoid-based plumage. We used RAD-seq to generate genome-wide data sets for 72 individuals from this complex, representing allopatric and sympatric populations of each species as well as phenotypic intermediates. The resulting insights into the genomic landscape of speciation in this system will be discussed in this presentation.

Poster session A - MAX 413

Is massive introgression limited to the mitogenome? Lessons from whole-genome sequencing in hares. (52907)

Fernando Seixas, Liliana Farelo, Paulo Célio Alves, Pierre Boursot, José Melo-Ferreira.

CIBIO-INBIO, Centro de Investigação em Biodiversidade e Recursos Genéticos, Universidade do Porto; Université Montpellier 2, CNRS UMR 5554, Institut des Sciences de l'Évolution, Montpellier, France; Wildlife Biology Program, College of Forestry and Conservation, University of Montana, Missoula, USA; Departamento Biologia, Faculdade de Ciências da Universidade do Porto, Porto, Portugal.

Introgressive gene flow after speciation is commonly observed and sometimes massive. The evolutionary causes and consequences of this spectacular phenomenon are yet poorly understood but can be valuably addressed by exploring its genome-wide patterns, in relation to variations of structural, functional and transmission characteristics across the genome. The mitogenome of a boreal species, *Lepus timidus*, thrives massively in northern populations of three hare species occurring in Iberia. Massive introgression also occurred species-wide in one case at an X-linked locus, in contrast with the general pattern of limited nuclear gene flow inferred using 20 random other nuclear loci. Such patterns of introgression may result from demographic processes (allele surfing) during species replacements accompanying deglaciation but may have also been driven by selective processes. By analyzing whole-genome sequencing data we will detect genomic regions massively introgressed from *L. timidus* into two species in Iberia, *L. europaeus* and *L. granatensis*. Particular attention will be given to co-introgression of nuclear-encoded mitochondrial genes which may uncover adaptive mito-nuclear co-introgression and/or co-evolution. Comparisons across genomic

regions with various characteristics and functions should allow us to balance the relative roles of historical contingencies and selective processes (adaptive or not) in determining patterns of reticulation and massive introgression.

Poster session A - MAX 413

Iberian Pied flycatchers: differentiation history and local adaptation (52937)

Vera Warmuth, Hans Ellegren.

Evolutionary Biology Center.

The pied flycatcher (*Ficedula hypoleuca*) is part of a relatively young (1.5-2 my) species complex that also includes the collared flycatcher (*F. albicollis*), the Atlas flycatcher (*F. speculigera*) and the semicollared flycatcher (*F. semitorquata*). *Ficedula* flycatchers have emerged as an important study system for speciation research; however, most studies to date have focused on comparisons between pied and collared flycatchers, a taxonomic pair that has evolved strong reproductive barriers and may therefore be considered at one extreme of the speciation continuum. The processes driving or maintaining differences between populations in the latter stages of speciation are not necessarily the same as those in the early stages. Here we present the results of model-based studies of demography and selection in pied flycatchers. Previous work has shown that pied flycatchers from the Iberian Peninsula are significantly differentiated from all other pied flycatcher populations at both neutral and adaptive loci. This makes them an ideal system to study the evolutionary processes driving differentiation at this early stage of divergence. Knowledge of the processes shaping the genetic variation within pied flycatchers will further our understanding of its divergence from other flycatcher species.

Poster session A - MAX 413

Identification of hybrid male-sterility genes in sibling species of *Drosophila* (52971)

Marjorie Liénard, Luciana Araripe, Dan Hartl.

Department of Organismic and Evolutionary Biology, Harvard University, Cambridge, MA 02138, USA; Institute of Biology, Department of Genetics, University of Rio de Janeiro, Brazil.

Hybrid male sterility (HMS) is a common postzygotic reproductive barrier caused by intrinsic incompatibilities between genes that have undergone functional divergence in isolated subpopulations. To understand how genomic incompatibilities relate to postzygotic isolation as well as the molecular nature and epistatic effects of genes driving HMS, we have studied two recently diverged fruitfly species, the cosmopolitan *Drosophila simulans* and the island-endemic *D. mauritiana*, for which interspecific matings conform to the Haldane's rule in producing sterile F1 hybrid males. To complement introgression genetic mapping, we

analyzed fertility in transgenic organisms to identify the genetic factors responsible for male sterility in a small 20-kb autosomal region in chromosome 3R denoted region HMS1. Whereas hybrid SimB fruitfly males homozygous for *D. mauritiana* at HMS1 are typically sterile, we find that, on average, 58% males in all agt-sim-transformed and 45% males in all TAF1-sim-transformed hybrid lines have fertility in the normal range. Our results emphasize the highly polygenic nature of postzygotic reproductive isolation. The findings also indicate that the evolutionary basis of HMS1 likely results from the passive accumulation of functional divergence in the agtmau and TAF1mau alleles leading to negative epistatic incompatibilities affecting male sterility in the hybrid background.

Poster session A - MAX 413

Past episodes of local gene flow in F1 dominated hybrid zones (51827)

Camille Christe, Kai Stölting, Daniel Wegmann, Luisa Bresadola, Christian Lexer.

University of Fribourg, Unit of Ecology & Evolution, CH-1700 Fribourg; University of Fribourg, Unit of Biochemistry, CH-1700 Fribourg.

Hybrid zones are frequently used as tools for understanding the genomics of adaptation, reproductive isolation, and speciation, but very little information is available about patterns of local ancestry along hybrid chromosomes. Our study focuses on two ecologically divergent species of poplar and aspen (*Populus alba* and *P. tremula*) known to hybridize in Eurasia. We use Restriction site Associated DNA (RAD) sequencing and a Hidden Markov approach to study the history of recombination in three large natural ‘mosaic’ hybrid zones at the genome level.

Patterns of local ancestry along hybrid chromosomes indicate that the studied hybrid zones are composed primarily of first generation hybrids (F1) and few backcrosses. The paucity of recombinant hybrids among adult trees from *P. alba* x *P. tremula* hybrid zones and their increased juvenile mortality in a common garden trial point to strong post-zygotic barriers acting during early life stages. Despite strong selection against recombinants, genome scans between the parental species indicate candidate regions for introgression pointing to more ancient episodes of gene flow. Our study raises questions regarding the mechanisms that allow the occasional breakdown of very strong reproductive barriers, resulting in the genetic exchange of defined genome regions between genomically cohesive species.

Poster session A - MAX 413

Secondary contact, reproductive barriers, and introgression: habitat alterations influencing the evolutionary history of two subterranean rodent species (Rodentia: Ctenomyidae) (51841)

Carla Martins Lopes, Simone Souza Freitas Ximenes, Thales Renato Ochotorena de Freitas.

Universidade Estadual Paulista "Júlio de Mesquita Filho"; Universidade Federal do Rio Grande do Sul.

Hybridization events provide insights into central questions in evolutionary biology regarding mechanisms of reproductive isolation and speciation. We investigated in the present study how extrinsic (e.g., geographical barriers, human impacts) and intrinsic (e.g., chromosomal polymorphisms, reproductive barriers, dispersal ability) factors can influence the evolutionary history of two highly karyotype-polymorphic sister species of burrowing rodents (*Ctenomys minutus* and *Ctenomys lami*) from the southern Brazilian coastal plain, which have a narrow contact zone resulted from habitat alterations. We analyzed mitochondrial DNA sequences and 14 microsatellite loci, together with cytogenetic data, for both species and hybrids sampled over their entire distributional ranges. Results suggest that *C. minutus* and *C. lami* were not sufficiently isolated in time and space, resulting in a pattern of incomplete lineage sorting. A pattern of cyto-nuclear genome discordance was observed in the hybrid zone as consequence of pre- and/or post-zygotic isolation mechanisms, combined with sex-biased dispersal, and differential inheritance of cytoplasmic and nuclear genomes. A substantial clinal introgression of microsatellite alleles of *C. lami* into *C. minutus* was observed near to the region of contact. Although *C. minutus* and *C. lami* are incipient species, conservation efforts should focus mainly on preserving the integrity of pure populations of each species.

Poster session A - MAX 413

New insights into European white oaks evolution of reproductive isolation from heterogeneous divergence levels across genomic regions. (51844)

Pauline GARNIER-GERE, Pierre ABADIE, Tiange Lang.

INRA, UMR 1202 Biodiversity Genes & Communities, France; INRA, UMR 1202 Biodiversity Genes & Communities, France; CAS, Xishuangbanna Tropical Botanical Garden, China.

In the European white oaks *Quercus robur* and *Q. petraea*, research spanning more than 20 years has focused on estimating hybridization rates and their significance in terms introgression dynamics, despite acknowledged ecological divergence among species. These studies have led to a paradigm of “weak” reproductive barriers compatible with low molecular divergence at anonymous and low coverage markers, recent publications emphasizing “high rates of interspecific gene flow” or “recurrent” or “ongoing gene flow” between those two species. However, older results and very recent quantitative estimates of the strength and genotypic variation of post-mating reproductive barriers suggest a different story and the existence of significant intrinsic incompatibilities. Using a population genomics approach based on more than 500 gene regions, a few thousands haplotype blocks and ~10000 SNPs, we argue that previous observations are compatible with strong reproductive barriers, and that these barriers probably involve various mechanisms determined by a large number of genes. We then test and compare possible scenarios of divergence among species using coalescent-based and Approximate Bayesian Computation methods and show how they bring new insights into the European white oak species evolutionary history and maintenance of reproductive barriers across their range, despite hybridization events.

Poster session A - MAX 413

Anthropogenic secondary-contact of cryptic penguin species (51926)

Stefanie Grosser, Christopher P. Burridge, Amanda J. Peucker, Nicolas J. Rawlence, R. Paul Scofield, Ian Smith, Jonathan M. Waters.

Department of Zoology, University of Otago; School of Biological Sciences, University of Tasmania; School of Life and Environmental Sciences, Deakin University; Canterbury Museum; Department of Anthropology and Archaeology, University of Otago.

The use of genetic and genomic tools has facilitated the discovery of new species that were previously indistinguishable using traditional approaches due to morphological similarities. These cryptic species complexes have even been found within some conspicuous and well-studied vertebrate taxa and it has been suggested that many well-known and widespread species could harbour substantial unrecognised species diversity. Here we present genetic evidence for two cryptic, reproductively isolated species within the world's smallest penguin. We used mitochondrial, microsatellite and intron markers to reveal two highly divergent *Eudyptula* lineages, one Australian and one New Zealand lineage, which co-occur in southern New Zealand, with minimal hybridisation. This finding exemplifies that even within an iconic group such as penguins the full level of species diversity remains to be uncovered. Coalescent modelling indicates that the Australian lineage likely expanded into southern New Zealand within recent centuries, supporting the hypothesis of an anthropogenic extinction-replacement event. We use ancient DNA analysis and carbon dating of fossil and archaeological *Eudyptula* remains to further assess this hypothesis.

Poster session A - MAX 413

Mitochondrial and nuclear discordance in a widespread passerine: genomic signatures of natural selection and local adaptation (51927)

Hernán Morales, Alexandra Pavlova, Leo Joseph, Richard Major, Paul Sunnucks.

Monash University; Australian National Wildlife Collection, CSIRO; Australian Museum.

Directional selection imposed by environmental variation can reduce intraspecific gene flow and promote population divergence. This is especially true if selection acts on traits with large fitness effect, for example metabolic pathways. The Eastern Yellow Robin (*Eopsaltria australis*) has eastern and western mitochondrial haplogroups (6.6% on ND2) distributed across most of the species' extensive range in eastern Australia; nuclear genetic structure is minimal and perpendicular relative to mtDNA. Interestingly, mitochondrial groups are strongly correlated with maximum temperatures of the warmest month, even after accounting for spatial location. This mitonuclear discordance cannot be explained by selectively neutral mechanisms (e.g. incomplete lineage sorting, sex-biased asymmetries, secondary contact). Instead, it is inferred to be the result of natural selection mainly in females affecting either mitochondrial genes, W-chromosome genes, autosomal genes, or interactions among these. As a first step to test whether the observed mitonuclear discordance is the result of local adaptation, we comprehensively assessed the species' genetic variation using complete mitochondrial genomes and genome-wide reduced-representation scans. We identified outlier

loci and genetic signatures of natural selection and discuss potential drivers of selection, concentrating on environmental factors

Poster session A - MAX 413

Genome Wide Association Studies on a sexually selected trait in two closely related passerines (52090)

Eryn McFarlane, Anna Qvarnström.

Uppsala University.

Sexually selected traits are expected to be polygenic and to evolve quickly, possibly because of high additive genetic variance. Here, we compare the genetics of two *Ficedula* flycatcher species that have been diverged for approximately one million years and that express the same sexually selected display trait, a white forehead patch. Pied flycatchers (PF) have a wider distribution but a smaller effective population size than collared flycatchers (CF), which may lead to local adaption and/or relaxed selection on this trait due to bottlenecks. Using a 50K SNPchip and a wild, sympatric population, we find similar genomic heritabilities between both species, and 6 suggestive SNPs for pied patch size, while collared patch size appears more polygenic. While the effect sizes we have estimated are certainly inflated, I discuss simulations used to address these concerns. Genetic variation in condition may be more strongly coupled to patch expression in collared flycatchers, making it harder to find suggestive SNPs in CF. Future research will investigate whether there is evidence for local adaption of these SNPs associated with patch size in different European populations of PF and whether selection has acted on these SNPs since the recent secondary contact of CF and PF in Sweden.

Poster session A - MAX 413

Using genome-wide data to study the demographic history of two parapatric field cricket species: Approximate Bayesian Computation and analysis of the allele frequency spectrum (52100)

Thomas Blankers, Emma Berdan, Frieder Mayer.

Humboldt University Berlin; Museum für Naturkunde Berlin, Leibniz Institute for Evolution and Biodiversity Science.

Development in sequencing technologies and bioinformatics has enabled demographic inferences in non-model organisms using genome-wide data. Field crickets are an interesting system for these inferences, because many species diverged in close geographic proximity and little intrinsic isolation has developed between the species. The Texas field cricket (*G. texensis*) and its daughter species, the southeastern field cricket (*Gryllus rubens*), co-occur in most of their ranges. The species are mainly separated by behavioral isolation via the calling song (males) and song preference (females). Here, we tested for interspecific genomic

differentiation and investigated the demographic history. Twenty individuals of each species were collected from two populations and we used RNA-Seq to identify polymorphisms in the transcriptome. We uncovered high genetic divergence between species with over 10% of 40,254 polymorphic SNPs fixed and found no intraspecific population substructure. Using approximate Bayesian computation and analysis of the allele frequency spectrum, we tested different demographic models against the data. Population expansion for *G. rubens* and gene flow between *G. rubens* and *G. texensis* were included in the best supported model in both approaches. Despite evidence for recent divergence with gene flow and sparse phenotypic diversification, the species are strongly genetically differentiated with many fixed SNPs.

Poster session A - MAX 413

Genomic atolls of differentiation in coral reef fishes (*Hypoplectrus* spp, Serranidae) (52145)

Oscar Puebla, Eldredge Bermingham, Owen McMillan.

GEOMAR Helmholtz Centre for Ocean Research Kiel, Germany; Patricia and Phillip Frost Museum of Science, Miami; Smithsonian Tropical Research Institute, Panama.

Since the vast majority of species are well-diverged, relatively little is known about the genomic architecture of speciation during the early stages of divergence. Here, we leverage the shallow radiation in the hamlets (*Hypoplectrus* spp, brightly coloured reef fishes from the tropical western Atlantic) to characterize genomic divergence during the early stages of speciation. A survey of approximately 100,000 restriction-site associated SNPs in 126 samples from three sympatric species across three replicate populations reveals extremely slight genome-wide divergence among species ($F_{st}=0.0038$), indicating that ecomorphological differences and reproductive isolation are maintained in sympatry in a backdrop of extraordinary genomic similarity. A very small proportion of SNPs (0.05% on average) are identified as F_{st} outliers among sympatric species, and remarkably a single SNP is identified as an outlier in repeated populations for the same species pair. A mini-contig assembled de novo around this SNP falls into the genomic region containing the *HoxCa10* and *HoxCa11* genes in 10 teleost species, suggesting an important role for Hox gene evolution in this radiation. Behavioural observations made in the same species and populations sampled for genetic analysis and complemented with individual-based simulations suggest a key role for natural and sexual selection in driving the genomic patterns.

Poster session A - MAX 413

Speciation reversal in ravens: genomic evidence of the collapse of cryptic lineages in North America (52170)

Anna Kearns, Arild Johnsen, Silje Hogner, Marco Restani, Ildiko Szabo, Hayley Richardson, Jin Ah Kim, Robert Fleischer, Kevin Omland.

Natural History Museum, University of Oslo; St. Cloud State University; Beaty Biodiversity Museum; University of Maryland Baltimore County; National Zoological Park & National Museum of Natural History, Smithsonian Institution.

There is increasing evidence that gene flow between phenotypically distinct species is a common and important evolutionary process. Introgressive hybridization can result in at least three different outcomes: simple introgression, hybrid speciation or speciation reversal (i.e., collapse of distinct lineages). However, only speciation reversal results in a decrease in species diversity, and only speciation reversal requires the complete breakdown of reproductive isolation. More and more cases have been documented in several animal lineages, especially in fishes. However, most of these cases involve recent divergences (e.g., ~12,000 ybp) and are human caused. In contrast, several cases in birds seem to be much older and show no role for human disturbance. Common Ravens have two deeply diverged mitochondrial clades that are widely sympatric over the western US. We found no evidence of phenotypic differences between the clades and no evidence of assortative mating or reproductive isolation. Data from nuclear introns and RAD SNPs provides strong support for two formerly distinct lineages that now hybridize across most of western North America. We are now using a range of next generation and multilocus coalescent approaches to test the hypothesis that speciation reversal is occurring in ravens against alternative hypotheses.

Poster session A - MAX 413

Fuzzy species limits in the *Eunicella* gorgonians : interaction with adaptation and symbiosis (52238)

Didier Aurelle, Isabelle Dabat-Pivotto, Marine Malfant, Nur Eda Topçu, Anne Haguenauer, Camille Roux, Didier Forcioli.

Aix Marseille Université IMBE; Istanbul University; Université de Lausanne; Université de Nice.

The genetic study of speciation allows a deeper understanding of processes generating or eroding species limits. Thanks to a higher number of molecular markers and to the use of appropriate statistical tools, we can now test and understand a wider range of evolutionary scenarios leading to the observed inter-specific differentiation. The *Eunicella* spp. octocorals provide a good model to study speciation in interaction with adaptation. Three closely related species can be observed in sympatry in the Mediterranean sea : *E. cavolini*, *E. singularis*, and *E. verrucosa*. They present different ecological patterns and *E. singularis* is the only Mediterranean octocoral harbouring photosynthetic symbionts (*Symbiodinium*). We sequenced two introns on a wide range of *Eunicella* individuals to study the phylogeography and species limits of this group : our result demonstrate a lack of clear genetic limits between them with putative hybridization events. The study of transcriptome polymorphism of eight *E. cavolini* and two *E. singularis* allowed to estimate the heterogeneity in differentiation levels. Different scenarios are proposed and tested with approximate bayesian computation to explain these results.

Reproductive isolation and sexual dimorphism driven by natural and sexual selection on a polygenic communication system (51648)

Rüdiger Riesch, Bernard J Crespi, Gerhard Gries, Regine Gries, Rebcca Safran, Patrik Nosil.

Royal Holloway, University of London, UK; Simon Fraser University, BC, Canada; University of Colorado, CO, USA; University of Sheffield, UK.

How exactly natural and sexual selection interact in evolution and species formation remains debated. Cuticular hydrocarbons (CHCs) are waxy chemicals expressed on the skin of all insects that could be subject to natural selection because they control desiccation resistance and sexual selection because they affect mate choice. Here we show how selection on CHCs, genomic variation, and the environment combine to drive ecological speciation in *Timema* stick insects. Perfuming experiments demonstrate a causal role for CHCs in mate choice and sexual isolation. Thus, males choose females as mates based on CHC profiles, which are especially divergent between the sexes. As predicted by natural selection, CHCs vary among populations according to climatic conditions, but this effect is stronger in males. Consistent with sexual selection on female CHCs, induced environmental influences on CHCs are strongest in females. Nonetheless, genome wide association mapping shows that CHC variation in both sexes is affected by a modest to large number of widely distributed genomic regions that often have pleiotropic effects on multiple CHC compounds; however, the genomic basis for CHC variation is sex-specific. The results demonstrate how selection on communication systems can drive biological diversification via combined effects of phenotypic plasticity and polygenic divergence.

Joint effects of history and genetics in maintaining genetic variation under sexual selection (51768)

Aditya Ponkshe, John Endler.

Centre for Integrative Ecology, Deakin University.

The maintenance of genetic variation for sexually selected traits is something of a puzzle (Pomiankowski & Møller 1995). Lande (1981) and Kirkpatrick (1982) were the first to model the dynamics of sexual selection, but these and subsequent models were more concerned with equilibrium than what conditions maintain genetic variation for sexually selected traits. We use an extension of Kirkpatrick's (1982) model and calculate the equilibrium amount of genetic variation in sexual traits for different initial conditions under various scenarios. Initial conditions that favour the maintenance of sexual trait genetic variation form a band or polymorphic zone with distinct boundaries in genotype frequency space. Populations starting with genotype frequencies of males and females anywhere inside the polymorphic zone maintain genetic variation in sexual traits while populations initially outside the zone lose genetic variation. Populations starting on different sides of the zone boundaries have very different evolutionary outcomes even if all other conditions are identical; both history and

genetically determined mating parameters determine the genetic variation in sexual traits and evolutionary outcomes. Populations can differ radically with respect to genetic variation and genotype frequencies even if environmental conditions are identical and populations are too large to diverge due to genetic drift.

Poster session A - MAX 413

A genetic correlate of red ketocarotenoid coloration in ploceids (52216)

Hanlu Twyman, Staffan Andersson, M. Prager, N.I. Mundy.

University of Cambridge; University of Gothenburg.

Red carotenoid-based colours are classic sexual or social signals in animals, particularly in birds where signal selection and evolution are extensively studied. However, the crucial mechanism behind most brilliant red colours in birds, namely metabolic conversion (oxygenation) of dietary yellow carotenoids to red ketocarotenoids, is unknown at the genetic level. Here we explore a candidate ketolase, encoded by a cytochrome P450 gene cluster (CYP2J2), in the African weaverbirds (Ploceidae), where ketocarotenoids are documented or indicated in many genera, especially the iconic widowbirds and bishops (*Euplectes* spp). We find a strong association between red ketocarotenoid pigmentation and expression of a CYP2J2 locus in the liver, the suspected site of conversion, whereas no CYP2J2 expression was detected in the livers of taxa lacking ketocarotenoids. This suggests that the CYP2J2 gene cluster holds one of the key genetic mechanisms underlying the evolution of red carotenoid coloration in birds, with important implications for both adaptive and non-adaptive hypotheses of sexual selection and colour diversification.

Poster session A - MAX 413

Opsin expression reveals sexual dimorphism in the visual system of New World warblers (Birds, Parulidae) (52255)

Natasha Bloch, Trevor Price.

University of Chicago ; University College London.

Asymmetries in reproductive investment between the sexes lead to the expectation that males should be under stronger sexual selection, and that females should be the choosier sex. Accordingly, spectacular examples of sexual dimorphism in plumage have evolved in passerine birds. How these colors are perceived, and thus female visual perception, is predicted to play a critical role in the evolution of such dimorphic plumage colors. We studied the evolution of Sws2 opsins, one of the visual pigments that mediate vision, in 16 species of New World warblers (Parulidae). We found Sws2 expression varies extensively across species and between sexes. Most notably, female, but not male Sws2 expression is associated with the degree of plumage dichromatism across warblers. This fits predictions of classic sexual selection models in which the sensory system changes in females, presumably

impacting female preference, and co-evolves with male plumage. Exactly how opsin expression impacts color perception is unclear, but we suggest possible mechanisms. Spectral tuning for this opsin however, is completely conserved across warblers. We argue that regulation of Sws2 opsin expression allows for fast adaptive evolution of the visual system and could be the target of sex-specific selection pressures leading to divergence in mating preferences.

Poster session A - MAX 413

Costs of reproduction explain a gradual change from a male-biased to a female-biased sex difference in human lifespan (52272)

Elisabeth Bolund, Virpi Lummaa, Ken R. Smith, Alexei A. Maklakov.

Uppsala University; University of Sheffield; University of Utah.

Sex differences in lifespan are common across taxa. In humans, women commonly outlive men. However, this sex difference is generally less pronounced in pre-industrial societies. Using the Utah population database, we show that the population changed from a significant male biased lifespan before (1800-1880) the demographic transition to low mortality and fertility rates to a significant female biased lifespan during (1880-1920) the transition. A rapid and pronounced reduction in female fertility may have precipitated this change in longevity patterns, because we found a cost of reproduction in terms of shortened lifespan at high parities in women but not in men. Because female adult lifespan increased as fertility decreased, while male adult lifespan remained stable over the demographic transition, the differential cost of reproduction in the two sexes may partly explain shifting patterns of sex differences in lifespan across human populations. Further, such rapid phenotypic changes in fertility and lifespan may be reflected in changes in the genetic basis of these traits. We will show how the genetic variances and covariances between family size and lifespan in the two sexes have been affected by the demographic transition and discuss how this might influence the population response to future environmental changes.

Poster session A - MAX 413

Is the expression of specific mitochondrial ORFs involved in sex determination and mitochondrial inheritance in *Mytilus*? (52391)

Artur Burzynski, Sophie Breton, Beata Śmietanka, Tomasz Sańko, Marek Lubośny, Aleksandra Przyłucka.

Institute of Oceanology PAN; University of Montreal.

Unlike the system of strict maternal inheritance described in other animal species, *Mytilus* species instead possess a system of doubly uniparental inheritance (DUI) of mitochondrial DNA (mtDNA). Specifically, DUI is a "mother-to-daughter" and "father-to-son" mtDNA inheritance system where females transmit their mt genomes (F mtDNA) to both sons and

daughters, and males transmit their mt genomes (M mtDNA) to their sons. Recently, the presence of a novel F genome-specific ORF of significant length that most likely has functional significance in *Mytilus* bivalves was demonstrated. The "formerly reported as missing" *atp8* gene has been identified in *Mytilus* mtDNA but it hasn't been shown to actually produce a protein in vivo. There are also controversies regarding the length of some other mitochondrial ORFs associated with the supposedly "non-coding" fragments which differ in length between the *Mytilus* lineages, a situation similar to the one described and positively verified in freshwater Unionoid bivalves. Here we report the results of our investigations into the functional properties of these ORFs. Their existence suggests that animal mitochondrial genomes have a considerably larger functional repertoire than previously believed. In our opinion, novel mitochondrial ORFs with key biological functions await discovery in other animal species, including humans.

Poster session A - MAX 413

The evolution of sex-biased gene expression in *Mercurialis* (52458)

Melissa Touns, Guillaume Cossard, John Pannell.

University of Lausanne.

Several animal species with sex chromosomes present a nonrandom distribution of sex-biased genes. The pattern appears to evolve quickly with the suppression of recombination. For example, sex-biased genes have become enriched in the neo-X chromosome of the Japan Sea stickleback, which formed ~1 MYA. We are still far from knowing how general this phenomenon is, and very little is known about patterns of sex-biased gene expression particularly in dioecious plants. Here, we present analyses of transcriptome sequence data from a large experiment to reveal the patterns of gene expression based on RNAseq for multiple species within the annual clade of the plant genus *Mercurialis*. By including data from both dioecious and related hermaphroditic species of *Mercurialis*, as from populations with different ploidy levels grown under identical conditions, we are able to tease apart the effects of changes in sexual system on sex-biased gene expression from those of polyploidization, which is also currently attracting much interest. Because separate sexes have evolved independently more than once in *Mercurialis* we could test the hypothesis that the same genes, in the same genomic regions, have evolved similar patterns of sex-biased expression after a transition from hermaphroditism.

Poster session A - MAX 413

Purging of mutations via sexual selection is dependent upon which sex chooses a mate (52538)

Brian Mautz, Alexei Maklakov.

Uppsala University.

Spontaneous mutations introduce new alleles in natural populations. The large majority are deleterious and result in relative fitness differences between individuals. Sexual selection is predicted to eliminate these mutations as those with lower mutation loads are chosen as mates. It has been assumed that sexual selection acts most strongly on males, but can also act on females via male mate choice. Thus, male mate choice might also act to increase population fitness. However, sexual selection via mate choice can differentially affect fitness of sons and daughters and potentially eliminate deleterious mutations in a sex-specific manner. We divided replicate homozygous ($f \approx 0.99$) lines of an outcrossing nematode (*Caenorhabditis remanei*) into three mutation accumulation (MA) regimes: MA (control), MA + female mate choice, MA + male mate choice for 20 generations. Female fitness showed the strongest response to sexual selection, but in opposite directions depending on which sex was allowed to choose mates. Male fitness responded in a similar direction within lines, but effects were weak. These results show that sexual selection can have counter intuitive effects on fitness via sex-specific expression of mating preferences resulting in both the purging and accumulation of deleterious mutations.

Poster session A - MAX 413

Mutation, Condition, and the Evolution of Longevity (52551)

Christopher M Kimber, Adam K Chippindale.

Linköping University; Queen's University.

The evolutionary theory of aging predicts that longevity will decline via drift or age-specific tradeoffs when selection favors early life fitness. Many *Drosophila melanogaster* populations continually terminated at young adult ages retain surprisingly long postselection lifespans. We compiled three decades of longevity data from the Ives population, demonstrating that postselective longevity was both substantial (30 days) and temporally stable over this period. Recently, alleles with positive pleiotropic effects between adjacent ages, particularly those affecting overall condition, have been integrated into the theory and may explain the extended longevity observed. We experimentally tested this hypothesis by isolating hemiclones from Ives and allowing spontaneous mutations to accumulate (MA). Fitness and longevity were positively genetically correlated in control females, and both traits declined due to MA. Crucially, MA induced a strong positive genetic correlation between the traits in both sexes, implying that mutations with early-life impacts also reduce late-life survival. Our results suggest that extended postreproductive longevity is actively maintained by selection for early-life fitness, possibly mediated by the positive pleiotropy of alleles affecting overall organismal condition. Thus mutation-selection balance for early fitness may govern variance in longevity in this system: a balance struck remarkably long after selection for continued survival ceases.

Poster session A - MAX 413

Sex differentiation in the ant *Cardiocondyla obscurior* (52701)

Antonia Klein, Eva Schultner, Jan Oettler.

University of Regensburg; University of Helsinki.

Primary signals for sex determination vary among insects. However, common to all systems is the transduction of primary signals into differential transcription of terminal sex differentiation genes. New genomic resources allow the study of sex differentiation in non-model organisms. We use the ant *Cardiocondyla obscurior* to elucidate the transcription of the terminal regulator gene *doublesex* (*dsx*). In addition to two female castes (queens, workers), *C. obscurior* exhibits two male forms (wingless, winged). With RACE-PCR we identified male- and female-specific splice forms of *dsx*. Contrary to the male full-length transcript, the female transcript contains an early stop codon that produces a shortened transcript. Subsequently we measured expression levels of sex-specific splice forms in young female and male larvae (prior to caste determination) and in adult females and males of all castes. To investigate how expression varies across development stages we additionally analysed *dsx* expression using RNAseq data generated from individual late-stage larvae of known sex and caste. In a final step, we will analyse *dsx* expression in gynandromorph individuals who share characteristics of both sexes. The results of this study will shed first light on sex differentiation in ants, and help elucidate the mechanisms that regulate sex-specific phenotypic variation in insects.

Poster session A - MAX 413

Molecular evolution of mammalian testes under polyandry and monandry (52730)

Mehmet Somel, Ekin Saglican, Rori Rohlf, Ezgi Ozkurt, Haiyang Hu, Babur Erdem, Philipp Khaitovich.

Middle East Technical University; University of California, Berkeley; CAS-MPG Partner Institute for Computational Biology.

Female promiscuity, or polyandry, can strongly shape male behavior and anatomy. In polyandrous mammalian species, males have larger testicles and produce faster sperm, compared to monandrous species where females mate with a single male - an example of convergent evolution. Here we asked whether testis transcriptomes also evolve convergently under polyandry or monandry. Combining multiple datasets and performing a phylogenetic test for convergent evolution by mating type, we found an excess of genes with convergent testis expression in polyandrous species, such as chimpanzees and mice, as opposed to monandrous species, such as humans and marmosets. Likewise, polyandrous species' testes were found to contain more spermatocytes/spermatids than non-meiotic or pre-meiotic cell types. We next compared adult testis transcriptomes with testis developmental series. Testis profiles of monandrous species appeared paedomorphic compared to those of polyandrous species, suggesting that heterochrony in testis development could underlie convergent evolution. Finally, we compared nucleotide diversity patterns in testis-specific and testis development-related genes in humans and in chimpanzees, to find evidence for significant shifts in selection pressure since the last common ancestor of the two species. Our results

underscore how evolving mating systems can rapidly change genes, developmental processes, transcriptomes, and anatomy.

Poster session A - MAX 413

Nature via nurture of carotenoid colour evolution: the metabolic conversion of yellow to red pigments is controlled by a cytochrome P450 in widowbirds and bishops (*Euplectes*) (52947)

Staffan Andersson, Maria Prager, Hanlu Twyman, Nicholas I. Mundy.

Dept of Biological & Environmental Sciences; Dept of Zoology, Cambridge University.

The colourful breeding plumages of male widowbirds and bishops (*Euplectes* spp.), with slightly to extremely elongated tails and striking red or yellow carotenoid displays, are iconic and spectacular examples of sexual selection and sexual dimorphism, but the diversity in signal design and expression resist adaptive explanations given the similarities in ecology and behaviour. Also non-adaptive radiation due to drift or Fisherian runaway processes seems unlikely since both the epigamic tails and the agonistic colour signals have evolved in a directional and convergent manner. The increasingly supported scenario is instead one of generalized female and male receiver biases, and diversification due to historical contingencies such as genetic constraints. Here we report on a long predicted but now revealed key innovation behind the evolution of red carotenoid coloration in birds; the ability to convert (oxygenate) dietary yellow carotenoids to red ketocarotenoids. In *Euplectes* and other weaverbirds (Ploceidae), the central (liver) expression of this gene (CYP2J2B) is associated with ketocarotenoid pigmentation, but not found in the equally red species among 'true' widowbirds, a mechanism as yet unknown. We reconstruct the evolutionary history of CYP2J2B in weaverbirds and discuss the implications for sexual selection, costs and honesty, and colour diversification.

Poster session A - MAX 413

Comparison of genetic background of flowering time variation among *Lotus japonicus* in Japan based on whole-genome sequence (52064)

Tomomi Wakabayashi, Stig Andersen, Shusei Sato, Yoshihiro Handa, Masayoshi Kawaguchi, Hiroaki Setoguchi.

Kyoto University; Aarhus University; Tohoku University; National Institute for Basic Biology.

The purpose of this study is to reveal the genetic factors for variant flowering time in *Lotus japonicus* in Japan. Flowering time is critical for plants as the different timing can cause reproductive isolation hence intraspecific differentiation. *L. japonicus*, a legume model plant, distributes throughout the Japanese archipelago and has variant flowering time according to their geographical regions.

131 wild accessions from Japan, which are maintained by National Bio Resource Project, were grown in a same condition to measure the flowering time. They flowered in a different timing correlated with the latitude of their origin. Subsequently whole-genome sequencing of additional five lines to the already sequenced 131 lines by Kazusa DNA Research Institute and Aarhus University and whole-genome comparison between extremely early and late lines among them were conducted. Three SNPs were identified which possibly affected the flowering time. One of the SNPs was on the orthologous to Embryonic flower, one of the famous flowering genes. Prediction of the protein structures suggested that the two of three SNPs could affect the structures of the functional domain of the protein. In addition, there were significant differences of the days between germination and first flowering in 122 wild lines between the genotypes.

Poster session A - MAX 413

(Epi)genetics and ecology of floral colour polymorphisms in the alpine orchid *Gymnadenia* (=Nigritella) *rhellicani* (52094)

Roman T Kellenberger, Kelsey JRP Byers, Florian P Schiestl, Philipp M Schlüter.

University of Zurich.

Selection of novel, adaptive (epi)mutations is the main process behind the incredible diversity of organisms on this planet. In entomophilous plants, adaptation to specific pollinating insect taxa led to the evolution of flowers of an enormous variety of shape and colour. Understanding the evolution of floral traits therefore requires both knowledge about molecular mechanisms behind (epi)mutations and adaptive values of the induced phenotypic alterations. We are investigating the evolution of floral colour polymorphisms in the alpine orchid species *Gymnadenia* (=Nigritella) *rhellicani*. While flowers of *G. rhellicani* are usually dark red, some populations are highly polymorphic with 1-40% light red to entirely white inflorescences. Our work focuses on molecular and ecological experiments to highlight mechanisms and consequences of this phenomenon. Preliminary data suggest an (epi)genetic cause of colour variation and a potential linkage to differences in the floral scent bouquet. We aim to characterize the underlying molecular mechanisms in a forward genetics approach. Phenotypic traits such as levels of different anthocyanins are quantified for the different morphs. A comparison with RNA-seq data should later identify candidate genes for targeted (bisulphite) sequencing. Selection pressure on different morphs will be assessed with pollinator behavioural studies and manipulation experiments under artificial and natural conditions.

Poster session A - MAX 413

Integrating phylogenetics, ecology and evo-devo to understand a key innovation: floral nectar spurs in *Linaria* and related genera (52327)

Mario Fernández-Mazuecos, **Beverley Glover**.

Department of Plant Sciences, University of Cambridge.

Floral nectar spurs are considered a key innovation promoting diversification in angiosperms. Spurs are tubular outgrowths of floral organs containing a nectar reward for pollinators. It is hypothesized that they mediate reproductive isolation by promoting pollinator specialization. Here we apply a multidisciplinary (phylogenetics, pollination ecology, evolutionary developmental biology) and multi-scale (genera, species, populations) approach to understand the evolution of nectar spurs and their role in speciation in the tribe Antirrhineae (Plantaginaceae; c. 330 species). Phylogenetic comparative methods are used to estimate the correlation between nectar spur evolution and speciation rates of Antirrhineae. Ancestral state reconstructions indicate three to four acquisitions of nectar spurs in the course of Antirrhineae evolution, including that in the most successful genus *Linaria* (c. 160 species). In particular, we are investigating mechanisms of speciation and spur evolution in a recently-diversified clade formed by eight species of *Linaria* that display wide variation in spur length. Phylogenetic relationships are resolved using next-generation sequencing techniques (RAD-Seq). The relative roles of pollinators and other isolating factors (including ecological and post-pollination barriers) are quantified, and the ontogenetic and genetic basis of spur length variation and evolution is investigated using an evo-devo approach.

Poster session A - MAX 413

Experimental tests of the effect of flower architecture, fragrance and visual stimuli on the pollination of a dimorphic plant (52845)

Juan Arroyo, César A. Abarca, Rocío Santos-Gally, Rocío Pérez-Barrales, Florian Schiestl.

University of Seville, Spain; Universidad Autónoma Metropolitana, México; Instituto de Ecología, UNAM, México ; School of Biological Sciences, University of Portsmouth, UK; Institute of Systematic Botany, University of Zürich, Switzerland.

Style length polymorphisms are flower traits thought to be related to the specialized activity of pollinators, which promote disassortative mating by transferring pollen between morphs. We investigated whether other flower traits putatively related to olfactory and visual signals play a role in the attraction of them in the daffodil *Narcissus papyraceus*. By means of experimental manipulation of the flower corona, the reputed scent producing organ, and setting on experimental populations, we tested if legitimate long-tongued pollinators (mainly moths) involved in the maintenance of style polymorphism are attracted by corona fragrance. We also tested the effect of the distance between plants on their reproductive success through a possible limitation by compatible pollen. We repeated the experiments in a region where the short-styled morph is absent and pollination is performed mainly by short-tongued insects (hoverflies), to explore if they are differently attracted by the corona. Additionally, we considered the possibility that the flower corona represents a visual stimulus for flower visiting insects, by means of an analysis of reflectance patterns of flower parts. These results show that the maintenance of style polymorphism is more related with flower handling by insects and morphological filters than with different attraction systems of flower parts.

The effect of sex on the repeatability of evolution (51580)

Josianne Lachapelle, Nick Colegrave.

The University of Edinburgh.

If evolution is repeatable, the evolutionary trajectories taken by different lineages and the final outcomes of evolution in given conditions will be the same. The mode of reproduction, either asexual or sexual, can affect repeatability by altering the relative contribution of selection, chance and history to evolutionary change. We tested this idea by propagating experimental populations of the unicellular alga *Chlamydomonas reinhardtii* in a novel environment. The populations differed by their mode of reproduction, and their initial genetic composition. We carried the experiment in four different novel environments. Preliminary results suggest that the amount of divergence among sexual populations can be higher or lower than that among asexual populations, depending on the novel environment. Fitness assays to be carried in the next months will reveal how the contribution of selection, chance, and history varies over time in sexual and asexual populations. By examining how sex contributes to the rise and fall of diversity during evolution, we can better understand the factors that maintain sex in populations. The generality of our findings across all four environments tested will inform us about the role of ecology on the repeatability of evolution in sexual populations.

Genomic evidence for ameiotic evolution and adaptation without sex in an animal lineage, the bdelloid rotifer *Adineta vaga* (51714)

Karine Van Doninck, Olivier Jaillon, Nicolas Debortoli, Boris Hespeels, Jean-François Flot.

University of Namur; Genoscope; University of Namur; University of Namur; University College London.

Loss of sex is an evolutionary dead end for metazoans, but bdelloid rotifers challenge this view having persisted asexually for millions of years. We found that the genome structure of the bdelloid *Adineta vaga* is indeed incompatible with conventional meiosis. At gene scale, the genome is tetraploid and comprises anciently duplicated segments and less divergent allelic regions. In contrast to sexuals, the allelic regions are rearranged and sometimes found on the same chromosome. Such genome structure does not allow meiotic pairing. Instead, we find abundant evidence of gene conversion, limiting the accumulation of mutations in the absence of meiosis. Gene conversion may occur during mitotic recombination repair of broken DNA following cycles of desiccation and rehydration experienced by bdelloids in their temporary habitats. Indeed during desiccation the genome of *A. vaga* is broken in hundreds of DNA fragments that get repaired once rehydrated.

In the genome of *A. vaga* 8% of the genes are likely of non-metazoan origin and probably acquired horizontally. These genes appear to be functional and many of those involved in resistance to desiccation have been acquired through HGT. Whether genetic exchange via

HGT is a key innovative mechanism in those eukaryotes allowing adaptation in the absence of sex is an important question we are investigating.

Poster session A - MAX 414

Inventory of meiotic genes in New Zealand stick insect *Clitarchus hookeri* (Phasmatodea) and their expression in sexual and asexual females (51767)

CHEN WU, RICHARD NEWCOMB, HOWARD ROSS, THOMAS BUCKLEY.

Landcare research; The University of Auckland; Allan Wilson Centre; The New Zealand Institute for Plant & Food Research Ltd.

Meiosis is the process specific to all sexual eukaryotes and genes with well-characterised roles in meiosis promote and regulate this process. Studying meiotic genes in organisms reproducing both sexually and asexually might shed light on the molecular requirements for sexual reproduction and transition between the two reproductive modes. *Clitarchus hookeri* is geographical parthenogen, widely-distributed in New Zealand. They reproduce bisexually in northern New Zealand, generating offspring with relatively equal number of sexes; in comparison, they form parthenogenetic populations in southern New Zealand. The *Clitarchus hookeri* asexual lineage was separated from the sexual lineages approximately 0.43 mya and appears to be isolated from those sexual populations. This primary reproductive isolation was supported by results from a crossover experiment where females from most of the parthenogenetic populations still produce only females after they were mated with sexual males. To investigate whether molecular change within meiosis might be involved in this isolation, we firstly sequenced and annotated the genome of *C. hookeri*, then conducted comparative transcriptomic analysis on the reproductive organs from both bisexual and parthenogenetic females, in which, we specifically focus on meiotic genes. Identification of the *C. hookeri* meiotic genes might also provide insights into stick insect reproductive flexibility.

Poster session A - MAX 414

Fitness consequences of sexual and parthenogenetic reproduction in the Australian spiny leaf insect, *Extatosoma tiaratum* (51878)

Yasaman Alavi, Thérèse Melanie Jones, Mark Adrian Elgar.

University of Melbourne.

Empirical studies investigating the costs and benefits of sexual reproduction have typically been unable to remove confounding effects present in comparisons between sexual and asexual species or populations. Species in which individuals are capable of switching between reproductive modes provide promising model systems to resolve this issue, but many alter their reproductive mode according to their condition or environmental factors and thus comparisons remain confounded. Females of the facultatively parthenogenetic Australian

spiny leaf insect, *Extatosoma tiaratum*, can reproduce sexually or asexually, depending only upon the availability of males/sperm. Virgin females produce parthenogenetic daughters, while mated females produce both sons and daughters through sexual reproduction. In this study, we examine the fitness outcomes of sexual and asexual reproduction of females derived from known modes of reproduction. We compare survival and reproduction in the daughters of virgin, once mated and twice mated mothers. Our results will provide unambiguous and novel insights into the costs and benefits of sexual reproduction.

Poster session A - MAX 414

Genetic diversity and population structure in thrips with different reproductive modes (52086)

Amaranta Fontcuberta, **Zoé Dumas**, Tanja Schwander.

Department of Ecology and Evolution, Uni Lausanne.

Understanding how genetic diversity is generated and maintained in asexual lineages can provide insights into the maintenance of sexual reproduction in natural populations. Here we quantified genetic diversity and population structure in different sexual and asexual populations of the grasshrips *Aptinothrips rufus*. This species is native to Europe, but has been introduced throughout the Holarctic region, whereby all known introduced populations consist of asexual females only. We found extremely high levels of clonal diversity in both native and introduced asexual populations and much greater genetic diversity than in sexual populations. Individual asexual lineages were found on different continents with little or no isolation by distance, indicating extensive mixing and continuous exchange of asexual individuals between geographically distant populations. In contrast to the asexuals, sexual *A. rufus* population were strongly isolated genetically, with little or no gene flow even at short geographic distances. Asexuality in *A. rufus*, induced by an endosymbiont, appears to have entailed population dynamic changes that strongly affect the distribution of genetic variation within and between populations in an unexpected way. Current sexual populations may be transient and disappear upon colonization by genetically diverse clonal assemblages.

Poster session A - MAX 414

Changes in sexual reproduction in response to human-induced eutrophication in a cladoceran community (52120)

Anu Vehmaa, Miia Mannerla, Laura Sartamo, Ulrika Candolin.

Tvärminne Zoological Station, University of Helsinki; University of Helsinki, Department of Biosciences; University of Helsinki, Department of Environmental Sciences.

Continuous records that aquatic organisms leave in the sediments offer an intriguing possibility for time travel. Most cladocerans (zooplankton) are cyclic parthenogens, i.e. the

yearly cycle includes parthenogenic and sexual reproduction. Generations of parthenogenic females are followed by sexual females and males, which produce fertilized resting eggs when environmental conditions deteriorate. Resting eggs hatch after a latent period, however some may be buried in the sediment, where they can survive for decades or even longer. Besides resting eggs, some cladocerans leave also traces of their exoskeleton in the sediments. By comparing the proportion of resting eggs vs. other subfossils of the same species, it is possible to estimate the contribution of sexual reproduction. We took sediment core samples from two coastal sites of the Baltic Sea, which has suffered from severe human-induced eutrophication during the past decades. We dated the cores, and identified and counted the cladoceran resting eggs as well as other subfossils in sliced 1-cm subsamples. The presented results will reveal potential long-term changes in the cladoceran reproductive strategies, and show if periods of high sexual reproduction coincide with rapid changes in the environment, such as the introduction of a new cladoceran predator or intensive algal blooms.

Poster session A - MAX 414

A breakdown of doubly uniparental inheritance (DUI) system in hybridisation area of European *Mytilus edulis* and *Mytilus trossulus* (52204)

Beata Śmietanka, Artur Burzyński, Aleksandra Przyłucka, Marek Lubośny.

Institute of Oceanology of Polish Academy of Sciences.

The doubly uniparental mode of mitochondrial inheritance (DUI) is best known in blue mussel *Mytilus*. Under this system two types of mitochondrial DNA (mtDNA) exist. The female (F) transmitted from females to offspring of both genders and the male (M) transmitted exclusively from males to sons. The genomes are highly divergent but a replacement of typical M genome by the F genome resulting in reduction of sequence divergence has occasionally been observed. Here we present a case of DUI breakdown in *Mytilus* population from the North Sea (Norway). Our comparative analysis is based on the part of coding region sequence (ND2-COIII) of mtDNA of 55 *Mytilus* specimens classified as *M. trossulus* or *M. trossulus*/*M. edulis* hybrids by diagnostic nuclear markers. We have found typical M haplotypes in 6 individuals only, two of them were females. All these M haplotypes were derived from *M. edulis*. We have also found two classes of F haplotypes: one derived from *M. edulis* and the second from *M. trossulus*. The F haplotypes did not show any sex bias either, but heteroplasmy seemed to be positively biased towards males. This apparent breakdown of DUI system seems to be related to the hybridisation between two *Mytilus* species

Poster session A - MAX 414

The tastier sex? Herbivore preference varies among the habitats of *Mercurialis perennis* (52212)

Luka Rubinjoni, Vukica Vujić, Sara Selaković, Dragana Cvetković.

Faculty of Biology, University of Belgrade.

The role of herbivorous insects in plant mating system evolution is a topic of growing interest. This interaction has been studied in the context of plant resistance/tolerance, constitutive versus induced defenses, resistance/reproduction trade-offs, and herbivore affinity to a specific sex. One potential benefit of dioecy is herbivore-related risk distribution between male and female plants. A premise to this is the presence of sex-specific herbivory in natural conditions. The object of our study is *Mercurialis perennis*, a widely distributed dioecious perennial. We collected plants from a range of habitats in Serbia, and estimated the herbivore load by scoring leaf damage on an ordinal scale. The initial analysis, based on transformed herbivory indices representing average leaf damage per plant, did not confirm a significant bias in the observed loads. We further investigated the data using R package ordinal. In a comparison of generalized linear mixed models, plant sex did not emerge as the key factor for describing variation in leaf damage scores in the complete dataset. However, the most informative model showed a significant effect of sex within the sites. We conclude that sex-specific herbivory is present, but the preference varies among the habitats.

Poster session A - MAX 414

MALE REPRODUCTIVE SUCCESS AND INDIRECT GENETIC BENEFITS IN THE ITALIAN TREEFROG (*Hyla intermedia*) (52296)

VALENTINA BOTTO, SERGIO CASTELLANO.

Università degli Studi di Torino; Università degli Studi di Torino.

The present work aims at testing the ‘good genes’ hypothesis in a small population of Italian treefrogs (*Hyla intermedia*). For two years, we recorded the calls and behavior of all males attending the lek, and, in both years, we found that male reproductive success was positively affected by male mating effort (i.e. number of nights spent at the lek and number of recording sessions).

A subset of males was used in a North Carolina II Breeding Design to estimate maternal and paternal effects on two traits known to affect froglets’ fitness, Snout-Vent Length (SVL) and age at metamorphosis. For each half-sib and full-sib family, 30 tadpoles were reared to metamorphosis in two replicates.

We found a statistically significant maternal effect on SVL and age at metamorphosis and a significant paternal effect only on age at metamorphosis. Although we found no evidence for a positive association between male mating success and offspring SVL, we did observe a positive association between offspring age at metamorphosis and paternal mating effort.

Our results confirm the ‘good-genes’ assumption that males’ genes can affect offspring fitness and provide some evidence for a positive association between paternal mating effort and offspring fitness.

Is there an opportunity for sexual selection to aid adaptation and does it increase in novel environments? (52415)

Ivain Martinossi-Alilibert, Göran Arnqvist, David Berger.

Evolutionary Biology Center, Dept of Animal Ecology.

Sexual reproduction imposes a cost on population productivity, but can also create genetic variation and remove deleterious mutations. Males are generally expected to experience stronger sexual selection than females. This selection on males can purge the mutation load on population health and benefit both sexes, at a low demographic cost as population productivity mostly relies on female fecundity. Fisher's geometric model predicts that the strength of selection will increase whenever a population is pushed off its fitness peak. Due to sexual selection, males experience stronger stabilizing selection than females and may fall off their fitness peak faster. Males would consequently exhibit a stronger increase in the intensity of selection, improving the potential for sexual selection to purge the mutation load.

We tested this prediction by measuring the sex-specific variance in fitness of seed beetles (*Callosobruchus maculatus*) from fourteen genetic lines across five environments of varying quality. Total phenotypic variance in fitness increases with stress for both sexes, and increases faster in males. However the genetic component was hard to estimate, and seemed to decrease with increasing environmental stress. Thus, while the strength of selection increases faster in males under stress, the response to selection may be counteracted by declining heritabilities.

Genomic consequences of long-term parthenogenesis in oribatid mites (52455)

Alexander Brandt.

Georg-August-University Göttingen, Dept. of animal ecology.

Oribatid mites are important model organisms for studying the evolutionary consequences of parthenogenetic reproduction. Sex was lost in several lineages of oribatid mites independently – in some of them tens of millions of years ago. We analysed the genome and transcriptome of two sexual and two parthenogenetic oribatid mite lineages for consequences of the absence of sex. In order to check for an accumulation of mildly deleterious mutations, we compared dN/dS ratios between sexual and parthenogenetic lineages. Further, we compared GC-content and codon usage bias of mitochondrial genomes. We found no accumulation of mildly deleterious mutations in protein-coding genes of parthenogenetic oribatid mites. However, we found a marked difference in mitochondrial GC-content, possibly due to selection as revealed by comparisons of the GC-content at third codon positions and the effective number of codons. We argue that the differences in GC-content might be suited to serve as a marker for long-term parthenogenesis in oribatid mites. Accordingly, the absence of the accumulation of mildly deleterious mutations in protein-coding genes of parthenogenetic oribatid mites might be explained by the evolution of mechanisms to counteract the accumulation of deleterious mutations, rather than by cryptic sex.

Hybridisation patterns between sexual and asexual species (52601)

Susana Freitas, Marine Arakelyan, James Harris, Miguel Carretero, Roger Butlin.

Cibio - University of Porto; University of Sheffield; Yerevan State University.

Unisexual species have been found to keep asexuality for millions of years, which disrupts the notion that without sex species would get extinct. However, it is not clear whether asexuals can maintain gene flow with their closest sexual relatives.

The model used is a genus of rock lizards (*Darevskia*) that show both sexual and asexual species. Of its 29 species, seven are parthenogenetic lineages originated from hybridisation between two sexual species.

In the rare cases where parthenogenetic lineages are found in sympatry with their paternal species, hybrids are found.

We studied one sympatric locality with the sexual *D.valentini* and the parthenogens *D.unisexualis* and *D.armeniaca*. Here, the parthenogens are known to backcross with *D.valentini* males originating polyploid hybrids.

PCoA based studies show a clear structure, three groups each corresponding to one of the species present. Even though the hybrid origin, hybrid individuals match the original parthenogenetic parent species, and not the sexual. Polyploid levels are biased for *D.valentini* x *D.unisexualis*.

Here we aim to understand if these parthenogenetic species maintain their genetic identity, or if new parthenogenetic lineages may arise through time. Given the young age of these lineages is it possible that they are being replaced by new parthenogenetic individuals arising from this population?

Female genitalia evolves slower than male genitalia in a coevolutionary scenario in a clade of Neotropical stink bugs (52714)

Bruno Genevcius, Daniel Caetano, Cristiano Schwertner.

University of São Paulo; University of Idaho; Federal University of São Paulo.

Two hypotheses may explain how female genitalia evolve: i) female traits may respond to modifications on its male counterparts in a coevolutionary dynamics; ii) female traits may evolve independently from male modifications under neutral process or stabilizing selection. Although theory predicts that sexually selected genital traits evolve fast, rates of evolution of male and female genitalia have only been assessed separately. We tested between the two hypotheses using a clade of Neotropical stink bugs, a good model for genital evolution because males and females have externally well-developed genitalia. We employed a partial least square approach to test for a coevolutionary scenario, and geometric morphometrics to capture genital variation. We also tested for differences in rates of evolution of the genitalia

using a Brownian motion rate parameter for multidimensional data, and compared them with two non-genital traits. The shape of the genitalia showed positive significant correlation ($r=0.8$; $p=0.02$). Both genitalia evolve faster than the non-genital traits ($p<0.01$), and the male genitalia evolves two times faster than the female genitalia ($p<0.01$). We show for the first time that both genitalia may evolve at quite distinct rates in a coevolutionary scenario, which is consistent with a delayed response of the female genitalia.

Poster session A - MAX 414

Sex related transcriptome differences of the protogynous hermaphrodite red porgy, *Pagrus pagrus* (52746)

Alexandros Tsakogiannis, Tereza Manousaki, Nikos Papandroulakis, Constantinos C. Mylonas, Costas S. Tsigenopoulos.

Hellenic Centre for Marine Research (H.C.M.R.) Crete ; Department of Biology, University of Crete, Greece.

Teleost fish show an extraordinary diversity in terms of reproductive styles. Specifically in the Sparidae family, the full spectrum of sexual reproduction modes is observed. This exceptional variety of sexual mechanisms and the presence of hermaphroditism or gonochorism even in closely related species turn Sparidae into an ideal system for understanding the processes leading to sex differentiation. In red porgy, *Pagrus pagrus*, a protogynous hermaphrodite and economically important member of the family, we performed whole transcriptome sequencing of gonad and brain tissues to identify the gene toolkit and explore the properties of genes exhibiting sex-related expression profiles. The wealth of information coming through RNA sequencing in fish of different sex sheds light into the molecular mechanisms shaping the sex differentiation process. These genes were compared to known sex-related candidates from other teleosts and sparids like the rudimentary hermaphrodite *Diplodus puntazzo*.

Poster session A - MAX 414

Evolving reproduction: from sexual genomic recombination to asexual genome stability. (52823)

Margarida Sofia Nobre, Anja Herrmann, Bernhard Schmid, Ueli Grossniklaus.

Institute of Plant Biology, University of Zürich; Institute of Evolutionary Biology and Environmental Studies, University of Zürich.

The natural genetic variation that makes evolution possible can be attributed to the recombination events during gametogenesis and fusion of maternal and paternal genomes after fertilization. Through sexual reproduction, the allelic combination of an offspring that is better suited to its particular environment is the basis of agricultural selection, the production of superior hybrids that result in crops of higher fitness and yield.

But sexual reproduction of hybrids introduces new recombinations and variation, and ultimately dispersal of the hybrid phenotypical traits. Apomixis, the asexual reproduction through the formation of clonal seeds, circumvents recombination and forms an embryo without fertilization.

In *Arabidopsis thaliana*, mutants have been identified that show unreduced embryo sacs, derived either from a developmentally altered megaspore mother cell or from an adjacent cell, which is the first step towards the production of clonal offspring. We aim to compare the sequence, expression patterns and levels of these genes with *Arabidopsis*' closest apomictic relative, *Boechera*. Evolutionary analysis of the differences in these genes between *Arabidopsis* and *Boechera* species will tell us whether they are indeed involved in the deregulation of the sexual pathway that leads to naturally occurring apomixis; and whether they can be manipulated to induce apomictic development in agriculturally relevant crops, thus preserving hybrid vigour through generations.

Poster session A - MAX 414

Ecological differentiation and the maintenance of sex (52900)

Stephanie Meirmans.

University of Bergen.

There is evidence for ecological differentiation between many related sexual and asexual organisms. Well known is the broad pattern of geographical parthenogenesis, where asexuals occur in relatively more marginal and resource-poor habitats than their sexual relatives. Less known is the much more varied and detailed evidence that has been found on a species-specific level. In principle, such ecological differentiation could reduce competition between the two reproductive types and thus help to maintain sex within those species. So far, however, it is not yet clear whether and to which degree this really is the case. Here, I will review existing theoretical models (including older, half-forgotten ones) together with the existing empirical evidence from nature and lab in order to better assess the importance of ecological differentiation to maintain sex. I will also suggest some rigorous ways in which one could further test this issue.

Poster session A - MAX 414

Sex, salamanders and dimorphism (52923)

Alexander Kupfer, Sandra Renner, Sandy Reinhard.

State Museum of Natural History Stuttgart, Germany ; Institute of Systematic Zoology and Evolutionary Biology, University of Jena, Germany.

The salamanders of the family Salamandridae (Amphibia: Caudata) are highly suitable for studying inter- and intraspecific patterns of sexual size dimorphism (SSD) because they exhibit an extraordinary diversity of reproductive modes including oviparity and viviparity

combined with variable morphologies and body shapes. A diverse array of species representing different mating systems and life histories have been analysed morphometrically. We have also studied the ontogeny of sexual dimorphic traits by including age data and finally we have integrated the most recent phylogenetic hypothesis to follow the evolution of particular morphological traits. Our comparative multidimensional analysis will help to understand the scenario behind the evolution of sexual dimorphism in a phylogenetically ancient vertebrate group.

Poster session A - MAX 414

Evolutionary genomics of sex determination in the common frog *Rana temporaria* (51673)

Wen-Juan Ma, Nicolas Perrin.

University of Lausanne.

Despite sex determination being a fundamental process in all sexually reproducing organisms, the underlying mechanisms are surprisingly labile across taxa. Contrasting with the classic view that recombination between X and Y chromosomes is entirely suppressed and the Y highly degenerated, sex chromosomes in amphibians are generally undifferentiated, due to high sex chromosome turnover rate and/or occasional X-Y recombination. This makes amphibians ideal to investigate the evolution of sex determination.

Previous studies of the common frog (*Rana temporaria*) have provided evidence for both genetic and epigenetic components to sex determination, showing that the two mechanisms can coexist both between and within populations (Rodrigues et al. 2013, 2014). In this project, we aim to investigate the genomic basis of sex determination in *R. temporaria*, by combining approaches of candidate gene and temporal dynamics of genome-wide gene expression in a range of developmental stages. We show that allelic polymorphism of the candidate gene *Dmrt1* is strongly associated with phenotypic gender in a population with genetic sex determination, but not in a population with epigenetic sex determination. The ongoing project on temporal dynamics of genome-wide gene expression and methylation pattern will provide further insights in understating the genetic and epigenetic basis of sex determination in the common frog.

Poster session A - MAX 414

Faster-Z evolution of gene expression in birds (51687)

Rebecca Dean, Peter Harrison, Alison Wright, Fabian Zimmer, Stephen Montgomery, Judith Mank.

University College London.

The elevated rate of evolution of sex chromosomes (Fast-X or Fast-Z Evolution) can result from positive selection in the heterogametic sex or from non-adaptive consequences of

reduced effective population size. Recent work in birds suggests that Fast-Z of coding sequence is due to relaxed purifying selection, however gene sequence and expression are often subject to distinct evolutionary pressures. We tested for Fast-Z in gene expression using next-generation RNA-sequencing data from multiple avian species. Similar to studies of Fast-Z in coding sequence, we also recover clear signatures of Fast-Z in gene expression, however our data indicate that Fast-Z in expression is due to positive selection acting primarily in females. In the soma, where gene expression is highly correlated between the sexes, we detected Fast-Z in both sexes. In the gonad, where inter-sexual correlations are much lower, we detected Fast-Z for gene expression in females, but crucially not in males. Taken together, our results indicate that Fast-Z is the product of positive selection acting on recessive beneficial alleles in the heterogametic sex. These results indicate that the adaptive potential of Z chromosome expression may be much greater than that of coding sequence.

Poster session A - MAX 414

Testing hypothesis of sex-chromosome degeneration using bryophytes as a model system (51777)

Linley Jesson, Cody Parker, Stuart McDaniel, Stefan Rensing.

University of Marburg; University of New Brunswick; University of Florida.

Degeneration of one sex-chromosome has independently happened in mammals, birds, insects, and flowering plants. What causes this? In organisms with diploid determination of sex expression two key features influence degeneration: sheltering of non-functional genes on the heterogametic sex chromosome by the other sex chromosome, and a lack of recombination in the sex determining regions. However in other organisms, such as bryophytes, sex is expressed at the haploid phase, allowing us to separate the effects of sheltering vs. recombination. To examine this, we are using sex-linked markers in a polyploid series of the bryophyte *Atrichum*, where haploid females are determined by a single U chromosome and haploid males by a V. Deleterious mutations in genes expressed in the haploid phase do not have an homologous chromosome to shelter the expression of mutations, but can be masked in the diploid phase. Furthermore, in polyploid *Atrichum* bivalent pairing of homologous sex chromosomes should result in the potential of masking of deleterious alleles by genes on a homeologous chromosome. However, polyploids can be hermaphroditic or strictly dioecious suggesting changes in potential for recombination. These contrasts allow a broader understanding of the factors influencing the evolution of sex chromosomes.

Poster session A - MAX 414

Sex-chromosome differentiation and ‘sexual races’ in the common frog (*Rana temporaria*) (51825)

Nicolas Rodrigues, Yvan Vuille, Jon Loman, Nicolas Perrin.

University of Lausanne; Rana Konsult, Sweden.

Sex-chromosome differentiation was recently shown to vary among common-frog populations in Fennoscandia, suggesting a trend of increased differentiation with latitude. By rearing families from two contrasted populations (respectively from northern and southern Sweden), we show this disparity to stem from differences in sex-determination mechanisms rather than in XY-recombination patterns. Offspring from the northern population display equal sex ratios at metamorphosis, with phenotypic sexes that correlate strongly with paternal LG2 haplotypes (the sex chromosome); accordingly, Y haplotypes are markedly differentiated, with male-specific alleles and depressed diversity testifying to their smaller effective population size. In the southern population, by contrast, a majority of juveniles present ovaries at metamorphosis; only later in development do sex ratios return to equilibrium. Even at these later stages, phenotypic sexes correlate only mildly with paternal LG2 haplotypes; accordingly, there are no recognizable Y haplotypes. These distinct patterns of gonadal development fit the concept of 'sexual races' proposed in the 1930's, with our two populations assigned to the 'differentiated' and 'semi-differentiated' races respectively. Our results support the suggestion that 'sexual races' differ in the genetic versus epigenetic components of sex determination. Analyzing populations from the 'undifferentiated race' with high-density genetic maps should help to further test this hypothesis.

Poster session A - MAX 414

Suppression of X chromosomal gene expression in the male germline of *Drosophila melanogaster* (51880)

Eliza Argyridou, John Parsch.

Ludwig-Maximilians-Universität München.

When sex chromosomes determine sex, their ploidy differs between males and females. In the XY system, males are hemizygous for the X chromosome. This exposes the X chromosome to unique selective forces that cause it to evolve differently from the autosomes. Previous studies of *D. melanogaster* have shown that the expression of testis-specific genes residing on the X chromosome is suppressed in the male germline. However, it is not clear whether this phenomenon is restricted to the male germline or if it occurs in other tissues. To examine the extent of the suppression, we compared the expression of X-linked and autosomal reporter genes expressed specifically in various tissues, including male accessory gland, ovary, and Malpighian tubule. The reporter genes were integrated randomly into the genome, resulting in multiple, independent lines with the insertion on either the X chromosome or an autosome. Our preliminary results provide no evidence for suppression of X-linked gene expression in the female germline or in somatic tissues, suggesting that the mechanism is specific to the male germline.

Poster session A - MAX 414

Extreme X-chromosomal enrichment of genes with male-biased expression in the *Drosophila melanogaster* brain (51892)

Ann Kathrin Huylmans, John Parsch.

Ludwig-Maximilians Universität München.

Genes expressed differently between males and females (sex-biased genes) often show a non-random distribution in the genome, particularly with respect to the sex chromosomes. Previous studies of *Drosophila melanogaster* found a general paucity of male-biased genes on the X chromosome in comparisons of whole flies or body segments containing reproductive organs. To better understand the chromosomal distribution of sex-biased genes in various tissues, we used a common framework to analyze high-throughput data comparing male and female gene expression in individual tissues, composite structures, and whole flies. In the brain, we find a strong, highly significant enrichment of male-biased genes on the X chromosome. Weaker enrichment of X-linked male-biased genes is seen in the head, suggesting that most of this signal comes from the brain. In all other tissues, there is either no departure from the random expectation or a significant paucity of male-biased genes on the X chromosome. The brain and head also differ from other tissues in that their male-biased genes are significantly closer to binding sites of the dosage compensation complex. We propose that the interplay of dosage compensation and sex-specific regulation can explain the observed differences between tissues and reconcile disparate results reported in previous studies.

Poster session A - MAX 414

Sex determination in *Silene*: male and female heterogamety (51972)

Bohuslav Janousek, Veronika Slancarova, Jitka Zluvova, Roman Gogela, Jana Zdanska, Bengt Oxelman, Alex Widmer, Boris Vyskot.

Institute of Biophysics, Brno, Czech Republic; University Gothenburg, Gothenburg, Sweden; ETH Zürich, Zürich, Switzerland.

The plant genus *Silene* (namely section *Melandrium*) has become a model for evolutionary studies of sex chromosomes and sex-determining mechanisms in plants. In spite of this, the subsection *Otites*, that includes even more dioecious species than section *Melandrium*, remained neglected for a long time. Studies in *S. colpophylla* and *Silene otites* show that dioecy and the sex chromosomes in these species (subsection *Otites*) evolved independently from those in *S. latifolia* (section *Melandrium*) and we have further found that the sex-determining system in *S. otites*, a species closely related to *S. colpophylla*, is based on female heterogamety, a sex determination system that is unique among the *Silene* species studied to date. Our phylogenetic data suggest that a switch from XX/XY sex determination to a ZZ/ZW system (or vice versa) probably must have occurred in the subsection *Otites*. This is the first report of two different types of heterogamety within one plant genus of this mostly non-dioecious plant family. Current availability of high throughput sequencing technologies enables us to study evolution of these sex determining systems in detail and to compare the results obtained in the subsection *Otites* with the results obtained in the section *Melandrium*.

Poster session A - MAX 414

Transition in sexual system and sex chromosome evolution in the tadpole shrimp *Triops cancriformis* (51998)

Africa Gomez, Thomas C. Mathers, Robert L. Hammond, Ronald Jenner, Jennifer Atkins.

University of Hull; University of Leicester; Natural History Museum.

Transitions in sexual system and reproductive mode may affect the course of sex chromosome evolution, for instance by altering the strength of sexually antagonistic selection. However, there have been few studies of sex chromosomes in systems where such transitions have been documented. The European tadpole shrimp, *Triops cancriformis*, has undergone a transition from dioecy to androdioecy (a sexual system where hermaphrodites and males coexist), offering an excellent opportunity to test the impact of this transition on the evolution of sex chromosomes. To identify sex-linked markers, to understand mechanisms of sex determination and to investigate differences between sexual systems, we carried out a genome-wide association study using Restriction-site Associated DNA sequencing (RADseq) of 47 males, females and hermaphrodites from a dioecious and an androdioecious population. We analyzed 22.9 Gb of paired-end sequences and identified and scored >3,000 high coverage genomic RAD markers. Marker presence/absence, SNP association, and read depth identified 52 candidate sex-linked markers. We show that sex is genetically determined in *T. cancriformis*, with a ZW system conserved across dioecious and androdioecious populations and hermaphrodites likely having evolved from females. Results indicate that the structure of the sex chromosomes differs strikingly, with a larger sex-linked region in the dioecious population.

Poster session A - MAX 414

Unique evolutionary features of the pseudoautosomal region of the *Ectocarpus* UV sex chromosomes (52079)

Agnieszka Lipinska, Remy Luthringer, Alexandre Cormier, Akira Peters, Denis Roze, Mark Cock, Susana Coelho.

Sorbonne Universités, UPMC Univ Paris 06, Station Biologique de Roscoff, Roscoff, France; Bezhin Rosko, 29250 Santec, France.

While the processes shaping the evolution of sex chromosomes are increasingly well understood in diploid organisms, haploid sex determination systems (U/V) have been understudied. We have recently sequenced and analysed the sex determining region of the model brown alga *Ectocarpus* (Ahmed et al. 2014). In *Ectocarpus*, sex is expressed in the gametophyte generation, during the haploid phase of the life cycle, and both the female (U) and the male (V) sex chromosomes contain non-recombining regions. Using experimental and theoretical approaches, we have investigated here the extensive pseudoautosomal regions (PARs) that border the SDR on the *Ectocarpus* sex chromosome. We show that recombination events are unevenly distributed along the PARs, and reveal the distinct evolutionary features of this region, that include accumulation and accelerated evolution of not only sex-biased genes but, remarkably, of genes differentially expressed during the gametophyte versus sporophyte generation of the life cycle (generation-biased genes). In agreement with our

experimental data, theoretical models predict that the evolution of the PAR in haploid sex determining systems may be shaped by generation-antagonism, provided that different selection pressures act on males and females.

Poster session A - MAX 414

Partial inactivation of the chicken Z chromosome is a response to selection for dosage compensation (52104)

Fabian Zimmer.

University College London.

The loss of gene content on the non-recombining Y or W chromosome results in a reduction in gene dose for the heterogametic sex. For dosage sensitive genes, reduced gene dose leads to selection in the heterogametic sex for dosage compensation. However up-regulation in the heterogametic sex to balance gene dose effects can lead to hyper-transcription in the homogametic sex. We recently investigated the status, mechanism and consequences of dosage compensation in chicken using RNA-Seq data from multiple somatic and gonadal tissues. Our results reveal the conflict between the heterogametic and homogametic sexes over dosage compensation. We show that a subset of highly expressed genes on the Z chromosome are dosage compensated in females (the heterogametic sex). These same genes show allele-specific expression in males, indicating that they are partially activated in the homogametic sex. This results in a system of Z inactivation analogous to X inactivation in mammals, although the system has not spread to the entire Z chromosome. Our findings indicate that the combination of partial Z inactivation and gene-by-gene dosage compensation results effective dosage compensation for dosage sensitive genes in chicken, and that sex chromosome inactivation in the homogametic sex may be a common consequence of dosage compensation.

Poster session A - MAX 414

Characterization of Northern pike (*Esox lucius*, Esociformes, Teleosts) master sex determining gene and evolution of sex determination in Esociformes (52161)

Qiaowei Pan, Ayaka Yano, Jennifer Anderson, Julien Bobe, Laurent Journot, John Postlethwait, Manfred Scharl, Amaury Herpin, Yann Guiguen.

INRA, Laboratoire de Physiologie et Génomique des Poissons; MGX (Montpellier Genomix); University of Oregon; University of Wuerzburg.

The understanding of the evolution of sex determination (SD) in vertebrates is limited by the scarcity of known SD genes. Although in mammals SRY is highly conserved as the master SD gene, the recent discovery of new SD genes in fish reveals an important diversity of genetic sex determination systems. Following the identification in Salmoniformes of sdY, as a

novel SD gene in vertebrates, we expanded our studies into its sister group Esociformes. Using a transcriptomic approach we identified in *Esox lucius* a duplicated copy of an autosomal gene that could act as a strong candidate master SD gene. This gene was found to be expressed only in the testis and is unique to the male genome which is in agreement with the known XX/XY SD system of *E. lucius*. Subsequent functional targeted inactivation of this gene resulted in male to female sex reversal, providing a first and strong functional proof of its role as a master SD gene. We are currently examining whether this sex determining gene is conserved in closely related species within this family and exploring the potential diversity of SD systems and their evolution in more distant species of Esociformes.

Poster session A - MAX 414

Modeling the evolution of recombination in sex chromosomes (52188)

Elisa Cavoto, Nicolas Perrin, Jérôme Goudet, Samuel Neuenschwander.

University of Lausanne.

One of the key factors involved in the evolution of sex chromosomes is the interaction between the evolution of a sex antagonistic trait and the accumulation of deleterious mutations. These two processes affect recombination in opposite directions. A sex antagonistic variant arising on a sex chromosome favors the arrest of recombination; as a consequence, deleterious mutations accumulate, generating an opposite selective force favoring recombination. Using individual based simulations, we explore the interaction of these two processes in a finite sexual population. We vary the strength of selection on a sex antagonistic trait and the genetic load due to deleterious mutations, and track the evolution of recombination. We find that when the sex antagonistic effect is strong, recombination is heavily repressed in males, independently of the genetic load, while in the absence of the sex antagonistic trait, sex chromosomes recombine freely. Surprisingly, the transition between these two opposite states is not gradual, and always occurs for a specific strength of sex antagonistic selection, largely independent of how many and how deleterious the mutations are. These results will be discussed in the light of existing theories for sex chromosome evolution.

Poster session A - MAX 414

Evolution of the guppy sex chromosomes (52217)

Alison Wright, Felix Breden, Niclas Kolm, Judith Mank.

University College London; Simon Fraser University; Uppsala University.

Early coloration genetics research in the guppy revealed that many colouration genes are Y-linked, and these findings formed the basis of Fisher's theory of sex chromosome evolution nearly a century ago. In order to characterize the degree of differentiation and population variation in sex chromosome evolution, we sequenced the genomes of male and female P.

reticulata and *P. parae*, two closely related species. Our de novo genome assembly has a total length of 685,443 kbp and consists of 135,564 scaffolds with an N50 and N90 of 14,019 and 2,403 respectively.

Poster session A - MAX 414

Does female meiotic drive affect the evolution of multiple sex chromosomes in amniote vertebrates? (52486)

Martina Johnson Pokorna, Marie Altmanova, Lukas Kratochvil.

Faculty of Science; Charles University in Prague; Institute of Animal Physiology and Genetics, The Academy of Sciences of the Czech Republic.

The difference in the involvement of sex-specific sex chromosomes in female meiosis subjected to the female meiotic drive under male versus female heterogamety is theoretically well known. Essentially, the male-specific Y chromosome is not involved in female meiosis and is therefore sheltered against the effects of the female meiotic drive affecting the X chromosome and autosomes. Conversely, the Z and W sex chromosomes are both present in female meiosis. Non-random segregation of these sex chromosomes may be a consequence of their rearrangements leading to the emergence of multiple sex chromosomes. We hypothesize that under female heterogamety, where both sex chromosomes are involved in female meiotic drive, this would result in a biased sex ratio, which should be penalized by selection. Therefore, the emergence of multiple sex chromosomes should be less constrained in the lineages with male rather than female heterogamety. Our broader phylogenetic comparison across amniotes fully supports this prediction. We suggest that our results are consistent with the widespread occurrence of female meiotic drive in amniotes.

Poster session A - MAX 414

Comparisons of introgression at sex-linked vs. autosomal markers in secondary hybrid zones of two anuran systems with XY-sex determination (52527)

Christophe Dufresnes*, Jörn Frederik Gerchen*, Tomasz Majtyka, Stuart J.E. Baird, Maria Ogielska, Nicolas Perrin, **Matthias Stöck**.

University of Lausanne, Dep. Ecology and Evolution, Lausanne, Switzerland; Leibniz-Institute of Freshwater Ecology & Inland Fisheries (IGB), Müggelseedamm 301, D-12587 Berlin; Dep. Evol. Biology & Conserv. of Vertebrates, Wroclaw University, Poland; Research Facility Studenec, Inst. of Vertebrate Biology, Acad. Sciences of the Czech Republic, Brno.

Dominance hypothesis, faster X (Z), faster male and faster-heterogametic-sex theory may explain or contribute to Haldane's rule, stating that in interspecies crosses, the heterogametic sex (XY-males, ZW-females) suffers greater fitness depressions than the homogametic (XX, ZZ). For XY-systems under secondary contact (allopatric speciation), introgression at

autosomes should be greater than X-chromosomal and both should surpass Y-linked introgression. However, in animals (including amphibians) with homomorphic, occasionally recombining sex chromosomes, this rule remains poorly studied. Using classical and transcriptome-based microsatellite markers, we study sex-linked vs. autosomal introgression. Genome-wide versus linkage group-specific hybrid index estimates (HI) in a secondary contact of tree frogs (*Hyla arborea*/*H. orientalis*) across Poland revealed stronger introgression at randomly chosen autosomal vs. sex-linked markers. We currently test whether differential introgression can also be observed in hybrid zones of Palearctic green toads (*B. sibilatrix*/*B. balearicus*/*B. viridis*) in Italy. We compare both systems and discuss alternative hypotheses like sex-biased dispersal and hybrid zone movement. (*equal contribution).
Ackn.: C. Betto-Colliard, L. Bonato, A. Borzée, A. Brelsford, C. Dieterich, B. Janic, A. Ogrodowczyk, W. Kloas, N. Novarini, S. Tamschick, M. Rybacki, J. Röhr, A. Sicilia, G. Turrisi, P. Zielinski.

Poster session A - MAX 414

The genomics and genetics of male ornaments and sex determination supergene in the Trinidadian guppy *Poecilia reticulata* (52567)

Axel Künstner, Margarete Hoffmann, Paloma Medina, Verena A Kottler, Detlef Weigel, **Frank Chan**, Christine Dreyer.

Max Planck Institute for Developmental Biology, Tübingen, Germany; Max Planck Institute for Evolutionary Biology, Plön, Germany; Lübeck Institute of Experimental Dermatology, University of Lübeck; Friedrich Miescher Laboratory of the Max Planck Society, Tübingen, Germany.

Attracting mates, to a male Trinidadian guppy, is of utmost evolutionary significance. Under strong selection for male ornaments, theory predicts and genetic evidence supports that tight linkage may evolve between genetic sex determination and male ornament loci to form a “supergene”. The guppy *Poecilia reticulata* has long been an outstanding ecological model organism for studying sexual selection. Here we will present our work towards establishing the guppy as a genomic evolutionary model organism. To discover parts of the genome specific to the male, we have separately constructed male and female high-quality genome assemblies from inbred Guanapo guppy siblings (approximately 760Mb; N50: female 5.38Mb; male 2.82Mb). We extend our previous genetic results showing that the guppy linkage group 12 is the sex chromosome and we highlight its evolutionary turnover from rearrangements and transposable element insertions. Combining transcriptomics, population genetic and comparative genomics, we will discuss features of the male-specific genome and potential candidates for the guppy sex determination locus. The genomic resources allow us to consolidate past and current genetic mapping work on male pigment patterns, showing strong yet incomplete linkage with sex determination. Our results herald an exciting new chapter for this classical ecological model organism.

Poster session A - MAX 414

Chameleons out of disguise: evolution of karyotypes and sex chromosomes (52611)

Michail Rovatsos, Martina Johnson Pokorná, Marie Altmanova, Lukáš Kratochvíl.

Department of Ecology, Faculty of Science, Charles University in Prague, Prague, Czech Republic; Institute of Animal Physiology and Genetics, ASCR, Liběchov, Czech Republic.

Chameleons are well-known, highly distinctive lizards characterized by their unique morphological and physiological traits. Despite the popularity of chameleons, their karyotypes and sex determination system have remained largely unstudied. We prepared metaphase chromosome spreads in both sexes from 13 species of chameleons. The karyotype of all individuals was studied by classical (conventional stain, C-banding) and molecular (comparative genomic hybridization, in situ hybridization with rDNA and telomeric sequences) cytogenetic approaches. Subsequently, we carried out phylogenetic analyses combining our results and previously published data. In contrast to most sauropsid clades, our results show an extensive chromosomal variability, even between closely related species of chameleons. Furthermore, we identified for the first time a ZZ/ZW sex determination system in the genus *Furcifer*, resolving the long-standing question of whether or not environmental sex determination exists in this group of chameleons. Together with recent findings in other reptile lineages, our work demonstrates that female heterogamety is widespread among amniotes, adding another important piece to the mosaic of knowledge on sex determination in amniotes needed to understand the evolution of this important trait.

Poster session A - MAX 414

Sex-chromosome homomorphy in Palearctic tree frogs proceeds from both turnovers and X-Y recombination (52631)

Christophe Dufresnes, Amaël Borzée, Agnès Horn, Matthias Stöck, Massimo Ostini, Roberto Sermier, Jérôme Wassef, Alan Brelsford, Nicolas Perrin.

Department of Ecology & Evolution, University of Lausanne; Laboratory of Behavioral and Population Ecology, Seoul National University; Leibniz-Institute of Freshwater Ecology and Inland Fisheries.

Contrasting with birds and mammals, poikilothermic vertebrates often have homomorphic sex chromosomes, possibly resulting from high rates of sex-chromosome turnovers and/or occasional X-Y recombination. Strong support for the latter mechanism was provided by four species of European tree frogs, which inherited from a common ancestor (~ 5 Mya) the same pair of homomorphic sex chromosomes (linkage group 1, LG1), harboring the candidate sex-determining gene *Dmrt1*. We tested sex linkage of LG1 across six additional species of the Eurasian *Hyla* radiation with divergence times ranging from 6 to 40 Mya. LG1 turns out to be sex linked in six out of nine resolved cases. Mapping the patterns of sex linkage to the *Hyla* phylogeny reveals several transitions in sex-determination systems, including one switch in heterogamety. Phylogenetic trees of DNA sequences along LG1 are consistent with occasional X-Y recombination in all species where LG1 is sex linked. Sibship analyses show that LG1 recombination is strongly reduced in males from most species investigated,

including some in which it is autosomal. This intrinsically low male recombination, together with the presence of important genes from the sex-determination cascade, might predispose LG1 to become a sex chromosome.

Poster session A - MAX 414

Sequence and structural evolution of the feminizing X chromosome of African pygmy mice (*Mus minutoides*). (52865)

Pierre Boursot, Paul Saunders, Vladimir Bajic, Khalid Belkhir, Frederic Veyrunes.

Institut des Sciences de l'Evolution.

Sexual reproduction and dimorphism imply the evolutionary challenges of producing different phenotypes from a single genome, and dealing with the resulting genetic conflicts. The ways by which the differentiation of chromosomes with sex-linked transmission addresses this challenge is the object of intense theoretical and empirical research. Cases of recent modification of chromosomal sex-determination system are of particular interest in this framework. Two types of X chromosomes segregate in natural populations of the African pygmy mouse (*Mus minutoides*), one of which (designated X*) is feminizing. This switch to female-limited transmission must have had consequences on the evolution of the genetic information content of the non-recombining part of X* (the extent of which is yet unknown), with phenotypic effects attested by the observation of significant life-history trait differences (fertility and behavior) between XX, XX* and X*Y females. This system also induces bi-sexual transmission of the Y and must enhance male transmission of the X-specific genomic portion, given the observed high frequencies of X*. We present here a preliminary exploration of the correlates of these spectacular changes on the evolution of the structure and sequence of sex-chromosomes by comparing whole-genome shot-gun sequencing of the XX and X*Y genotypes.

Poster session A - MAX 414

Developing sex markers for studying birds, sex ratios and chromosome rearrangements (52988)

Deborah Dawson, Gavin Horsburgh, Natalie dos Remedios, Terry Burke.

University of Sheffield.

In most bird species the sexes are morphologically indistinguishable. No sex-typing markers exist that can be used universally for all birds, and few of those applicable to a wider range of species can be multiplexed. Blood samples are often used for sex-typing birds; however, taking blood can cause stress and discomfort and requires training and appropriate permits. Therefore, less invasive sampling techniques are preferred, especially when studying endangered species – for example, using shed feathers, museum specimens and mouth swabs.

Furthermore, studies of fertility and sex ratio require the ability to sex-type degraded tissue (e.g. unhatched eggs). However, allelic dropout is common when attempting to PCR-amplify large products from degraded samples and dropout causes errors in sex typing. We therefore used the recently released data from multiple sequenced avian genomes to develop new primer sets, including some that amplify small PCR products (<150 bp) on both the W and Z chromosomes to enable sex typing of degraded samples. These markers are of utility for sex-typing a wide range of species and a combination of the ZW and Z markers developed can be used to identify rearrangements on the Z chromosome.

Poster session B - POL 300

Habitat segregation in an allopolyploid and its parent species in Cardamine (51686)

Reiko Akiyama, Masaomi Hatakeyama, Rie Shimizu-Inatsugi, Xiangchao Gan, Miltos Tsiantis, Jun Sese, Kentaro K. Shimizu.

Institute of Evolutionary Biology and Environmental Studies, University of Zurich; Functional Genomic Center Zurich; Department of Comparative Development and Genetics, Max Planck Institute for Plant Breeding Research; Computational Biology Research Center (CBRC), AIST, Japan.

Whole genome duplication (polyploidy) is pervasive in plants. Polyploids are generally expected to have intermediate and broader environmental distributions than diploids. However, empirical data on environment of polyploids and its diploid parents in field are limited. We quantified habitat environment of diploids *C. hirsuta* and *C. amara* and the allopolyploid *C. flexuosa* originated from *C. hirsuta* and *C. amara* in their native area in Switzerland in order to examine whether habitat environment differs among species. The diploids *C. hirsuta* and *C. amara* segregated in that *C. hirsuta* occurred in dry, bright, and nutrient-rich habitat in contrast to *C. amara*, while the allopolyploid *C. flexuosa* occurred in intermediate and fluctuating environment. These findings provided evidence that the parent species occurred in extreme environments, while the allopolyploid occurs in intermediate environment. They also suggest that the *C. amara*, *C. hirsuta*, and *C. flexuosa* serve as a useful system to study the molecular basis of adaptive significance of allopolyploidy in wild plants.

Poster session B - POL 300

Is hybridization impacting the diversification rates of land plant polyploids ? (51697)

Nils Arrigo, Michael S. Barker.

Unil; University of Arizona.

We assess the evolutionary significance of hybridization by comparing the extinction and speciation rates of species with a hybrid ancestry to those of non-hybrids. We focus on land

plants, and more particularly on polyploids because their high prevalence allows the comparison of allopolyploids (i.e. stabilized hybrids) to autopolyploids (i.e. non-hybrids). The study is based on 38 comprehensive genus-level phylogenies (built from publicly available DNA sequences), and on over 3,500 species for which we reviewed the polyploidy origin based on the current literature. Using this survey, we first show that allo- and autopolyploids are equally abundant in the majority of the inspected genera. State-specific diversification rates (i.e. the polyploidization, speciation and extinction rates of diploids, allo- and autopolyploids) are then estimated using the Multiple State Speciation and Extinction model (FitzJohn et al., 2009). We show that the extinction rates of allopolyploids are significantly lower than those of the autopolyploids. No differences are however observed in speciation rates, resulting in a significantly increased net diversification rate for the allopolyploids. These results are discussed in light of the classic hypotheses about the importance of hybridization in evolution.

Poster session B - POL 300

Mesopolyploid evolution in the Australian and New Zealand crucifers (51887)

Terezie Mandáková, Milan Pouch, Klára Harmanová, Martin A. Lysak.

CEITEC - Central European Institute of Technology, Masaryk University.

We showed previously that three endemic Australian crucifer species (Brassicaceae) have undergone a whole-genome duplication (AUS-WGD) followed by lineage-specific diploidization, generating some of the lowest chromosome numbers known for crucifers (Mandáková et al. 2010, *Plant Cell*). The New Zealand genus *Pachycladon* has undergone either the AUS-WGD or an independent WGD followed by less extensive fractionation towards $n = 10$ genomes (Mandáková et al. 2010, *BMC Plant Biol.*).

To further elucidate the origin and fate of Australian/New Zealand mesopolyploid genomes, we analyzed 12 species (9 genera) with variable chromosome numbers ($n = 4, 5, 6, 7$) by comparative chromosome painting (CCP) and gene sequencing. We concluded that:

- (i) all Australian members of the Microlepidieae tribe share the AUS-WGD, which most likely spurred the diversification of the group on the Australian continent,
 - (ii) cytogenetic signatures and multi-gene phylogenies suggest that the allopolyploid ancestral genome ($n = 15$) was formed through an inter-tribal hybridization (Crucihimalayae x Smelowskieae/Descurainieae) and a long-distance dispersal from Asia,
 - (iii) the AUS-WGD was followed by independent and massive genome diploidizations towards the extant diversity of quasi-diploid genomes ($n = 4 - 7$),
 - (iv) the New Zealand *Pachycladon* was formed by an independent and younger WGD event.
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Poster session B - POL 300

Multiple patterns of genome evolution in the polyploid-rich genus *Cardamine* (51944)

Terezie Mandakova, Aleš Kovařík, Judita Zozomová-Lihová, Rie Shimizu-Inatsugi, Kentaro K. Shimizu, Klaus Mummenhoff, Karol Marhold, Martin A. Lysak.

CEITEC, Masaryk University; Institute of Biophysics, AS CR, Brno, Czech Republic; Institute of Botany, SAS, Bratislava, Slovakia; Institute of Evolutionary Biology and Environmental Studies, University of Zurich, Switzerland; University Osnabrück, Germany.

Cardamine (bittercress) is one of the largest Brassicaceae genera (200 spp.). Most *Cardamine* species are polyploids with chromosome numbers up to $n = 128$. Due to the feasibility of chromosome painting, we documented both recurrent and deviating patterns of genome evolution in *Cardamine* polyploids of contrasting age:

- (i) some tetraploid ($2n = 32$) populations of *C. pratensis* are on the way to decrease their chromosome number by „chromosome fusions“ ($2n = 30, 28$).
- (ii) hybridization and polyploidization is ongoing – we reconstruct the origin of the triploid hybrid *C. x insueta* ($2n = 24$, RRA) through hybridization between *C. amara* (AA) and *C. rivularis* (RR) ca. 100 years ago. Hybridization involving *C. x insueta* and hypotetraploid *C. pratensis* ($2n = 30$, PPPP) resulted in the origin of the hypoheptaploid *C. x schulzii* ($2n = 46$, PPPPRA). This shows how a semifertile triploid hybrid can promote the origin of trigeneric allopolyploids.
- (iii) we elucidate the origin of several European and Asian tetra- to octoploid species through hybridization events involving three diploid species.
- (iv) some taxa are high polyploids - we demonstrate that *C. bulbifera* ($2n = 96$) is a largely sterile dodecaploid.
- (v) several species, including watercress and horseradish, are shown to be autopolyploids.

Poster session B - POL 300

Multiplex amplicon sequencing for genotyping and phylogenetic inference in polyploid wild wheats (51996)

Stella Huynh, François Felber, Christian Parisod.

University of Neuchâtel; Musée et jardins botaniques cantonaux de Lausanne.

Inferring the evolutionary history of polyploid species remains a major challenge. Recent theoretical advances have dramatically improved inference of reticulation and incomplete lineage sorting from genome-wide data (e.g. using Bayesian statistical modeling such as BEAST and PADRE). Obtaining good quality data from complex polyploid genome however currently remains a bottleneck. Capturing polymorphisms within and among homeologous genes is indeed crucial for such phylogenetic work. Here, we report on a multilocus dataset of

50 low-copy loci in hundreds of individuals from four diploid and four polyploid wild wheat species (*Aegilops* spp.). Loci of 400bp, encompassing polymorphic introns, are PCR amplified and individually tagged for multiplexed paired-end sequencing with Illumina MiSeq in one step. This work thus contributes to progress of methodologies offering high quality data to decipher the evolutionary history of polyploid species.

Poster session B - POL 300

Does genome duplication results in reproductive isolation in tetraploid-octoploid complexes? The case study of *Gladiolus communis* (52038)

Mariana Castro, João Loureiro, Brian Husband, Sílvia Castro.

CFE, Centre for Functional Ecology; Department of Integrative Biology, University of Guelph.

Polyplodization is an important mechanism of sympatric speciation in flowering plants. Under random mating, the establishment of new polyploids is restrict bystrong positive frequency-dependent selection. Consequently, the establishment and spread of cytotypes will only occur when assortative mating is promoted. Our main objective was to assess breeding barriers operating between tetraploids and octoploids of *Gladiolus communis* at a contact zone in Western Iberian Peninsula. Spatial segregation, phenological isolation and crossing ability were investigated in 108 natural populations and common garden experiments. We observed that *G. communis* has a complex contact zone. There were two dominant cytotypes occurring in pure-ploidy populations (4x and 8x, 43.5% and 38.9%, respectively); mixed-ploidy (13.0%) and hexaploid populations (4.6%) were also detected, suggesting that both cytotypes can co-occur and produce viable hexaploid populations. Within mixed-ploidy populations each cytotype appeared to show different micro-habitat distributions . Also, overlap in flowering phenology was observed suggesting that pollen can be freely exchanged between cytotypes. Controlled pollination experiments revealed that, despite fitness being lower in inter-cytotype crosses than within-cytotypes, both produced viable offspring. Overall, our results indicate low reproductive isolation between cytotypes which could constrain polyploid speciation and promote a complex and dynamic contact zone.

Poster session B - POL 300

Fertility restoration during polyploid speciation in *Mimulus* (52173)

Sofie Meeus, Mario Vallejo-Marín.

University of Stirling.

Interspecific hybridisation between evolutionary divergent parental genomes produces hybrids which often are sterile due to genic incompatibilities, erroneous meiotic pairing and/or odd chromosome number establishing a reproductive barrier among diverged species. However, when accompanied by polyploidisation (“allopolyploidy”), sterile hybrids may give

rise to an entirely new euploid species which is reproductively isolated from its parental species. However, even though polyploidisation leads to even chromosome numbers which is essential for chromosomal pairing during meiosis, and thus fertility, new polyploids have to face the challenges of chromosome segregation brought about the additional set(s) of homologous chromosomes that lead to multivalent formation. Current research indicates that genome restructuring occurs rapidly during the earliest generations of polyploid speciation. However, much remains unknown about both the mechanisms responsible for and the rate at which fertility is restored after polyploidisation. To investigate the rate and mechanisms of fertility restoration during polyploid speciation, three subsequent generations of a newly discovered allopolyploid from the UK, *Mimulus peregrinus*, are experimentally generated from different synthetic sterile triploid hybrid lines using colchicine. Fertility measured as pollen viability is linked to early-generation chromosomal rearrangements using FISH to assess the rate of fertility restoration in new allopolyploids.

Poster session B - POL 300

Reference-guided de novo assembly: improved genome of a non-model plant species (52224)

Heidi Lischer, Damianos Melidis, Masaomi Hatakeyama, Kentaro Shimizu.

URPP Evolution in Action, University of Zurich; Institute of Evolutionary Biology and Environmental Studies, University of Zurich; Swiss Institute of Bioinformatics, Lausanne; Functional Genomics Center Zurich.

The development of next-generation sequencing has made it possible to sequence whole genomes at a relatively low cost. However, de novo assembly of genomes still remains challenging due to short read length, repetitive regions, missing data, polymorphisms and sequencing errors. We implement a reference-guided assembly approach, which uses an available reference sequence from a close relative in order to improve the genome assembly outcome. The main idea is to first map reads against a reference genome to reduce the complexity of de novo assembly within continuous covered regions. In a further step, reads with no similarity to the reference are integrated. We apply this approach in the assembly of the *A. halleri* genome and simulated reads. The genus *Arabidopsis* is an important model to study environmental adaptation and polyploid speciation. With our reference-guided de novo assembly strategy the number of scaffolds is reduced and the N50 highly increased compared to a de novo assembly approach. The improved genome will facilitate the study of polyploidy speciation at the genetic level, as this requires high quality genomes of the parental species. We show that the de novo assembly of a genome can be improved by integrating information of a related genome.

Poster session B - POL 300

Polyploidy, morphology, and systemic fungal endophyte frequencies of *Festuca rubra* L. in a broad scale geographic distribution (52316)

Serdar Dirihan, Marjo Helander, Irma Saloniemi, Henry Väre, Pedro E. Gundel, Kari Saikkonen.

Section of Ecology, Department of Biology, University of Turku, 20014 Turku, Finland; Natural Resources Institute Finland (LUKE) Itäinen Pitkäkatu 3 20520 Turku, Finland; Division of Genetics and Physiology, Department of Biology, University of Turku, 20014 Turku, Finland; Botanical Museum, Finnish Museum of Natural History, University of Helsinki, 00014, Finland; IFEVA - CONICET – Faculty of Agronomy, Buenos Aires University (UBA), Buenos Aires, Argentina.

We conducted studies of ploidy levels and presence of systemic fungal endophyte infection in the grass *Festuca rubra* L. across latitudes from Spain to northernmost Finland and Greenland. First we implemented a time- and cost-efficient flow cytometry procedure which is based on to use a plate-based analysis with a fully automated software tools. Using this procedure we analyzed 29 *F. rubra* populations. Most of the plants were hexaploids ($2n=42$; 83%), but also tetraploid ($2n=28$; 10%) and octoploid ($2n=56$; 7 %) plants were detected. While ploidy levels seemed to be positively correlated with latitude, we could not detect explicit geographic gradients. The endophyte infection frequencies of plants varied from 0% to 81%. Our results suggest that variation in infection frequencies and ploidy levels might partly reflect *Festuca* distribution after the glaciation period, and be partly the consequences of local selective forces. We also analyzed morphological characters of 17 *F. rubra* populations from a broad latitudinal gradient across Europe. We found correlations among some morphological measurements and ploidy; e.g. the correlation between basal leaf width and plant height was strong for tetraploids and octoploids, but not for hexaploids. Our results suggest that selection favored similar morphology in each study site in spite of different ploidy levels.

Poster session B - POL 300

Temporal and spatial context of phylogeographic structure in the hexaploid KwaZulu-Natal Yellowfish (*Labeobarbus natalensis*) (52414)

Connor Stobie, Kerry Reid, Carel Oosthuizen, Paulette Bloomer.

University of Pretoria.

Labeobarbus natalensis (the KwaZulu-Natal Yellowfish) has a narrow distribution and limited dispersal capabilities, making it an ideal model species for phylogeographic analysis. However, the genus has undergone historical genome duplication events and is hexaploid. This complicates many traditional genetic analyses based on nuclear DNA. A previous study by our group revealed the pattern of mitochondrial DNA (mtDNA) diversity across the species' distribution, with several genetically divergent lineages restricted to different rivers. In the present study we explore the use of several different nuclear molecular markers in this polyploid species – microsatellites, exons, introns and a Next-Generation Sequencing (NGS) technology, Restriction-site Associated DNA sequencing (RAD-seq). Analyses of these nuclear DNA regions will also enable testing as to whether *L. natalensis* is functionally a hexaploid or a diploid despite its physical karyotype. Here we present some of the successful markers from each of the four categories and explore their relevance in identifying the patterns and processes affecting *L. natalensis* diversity. We focus primarily on the results

obtained from RAD-seq, which has been completed for 23 individuals. Future directions include exploring transcriptomics in *L. natalensis* as a potentially superior method for analysis in polyploid species.

Poster session B - POL 300

Interploid reproductive isolation variation within the *Campanula rotundifolia* polyploid complex (52509)

Brittany Sutherland, Laura Galloway.

University of Virginia.

Whole genome duplication often confers reproductive isolation (RI) between polyploids and their diploid progenitors. Strong or complete RI is documented in numerous diploid-tetraploid systems. Similar RI levels are often assumed in complexes comprising higher-order polyploids. However, evidence for strong RI among higher-order polyploids is sparse, and sometimes does not demonstrate high RI. We investigate the pattern and strength of interploid RI in *Campanula rotundifolia* s.l., a polyploid complex comprising diploids, tetraploids, and hexaploids. Tetraploid populations from throughout the geographic range were reciprocally crossed with diploid and hexaploid test populations. Maternal and F1 characters were then evaluated and compared to intraploid crosses to assess RI. RI was considerably lower among tetraploid-hexaploid crosses. However RI occurred at different life history stages for diploid and hexaploid hybrids. Diploid-tetraploid hybrids had extremely low germination while germination of tetraploid-hexaploid hybrids was indistinguishable from intraploid controls. Tetraploid-hexaploid hybrids experienced lower fertility while surviving diploid-tetraploid hybrids often had high fertility. Interestingly, these fertile diploid-tetraploid offspring were often even-ploidy instead of the expected triploid, suggesting that meiotic irregularity may be a mechanism for successful interploid reproduction. This study suggests RI estimates based on diploid-tetraploid systems may not apply to higher-order polyploid complexes.

Poster session B - POL 300

Sweet vernal grass in Europe: The origin of polyploid genomes in one genus (52511)

Zuzana Chumová, Pavel Trávníček, Eliška Záveská, Terezie Mandáková.

Department of Botany, Faculty of Sciences, Charles University in Prague, 128 01, Czech Republic; Institute of Botany, Academy of Sciences of the Czech Republic, Průhonice, 252 43, Czech Republic; CEITEC - Central European Institute of Technology, Masaryk University, Brno, 601 77, Czech Republic.

The genus *Anthoxanthum* (sweet vernal grass, Poaceae) represents a taxonomically intricate polyploid complex with large phenotypic variation and still poorly resolved evolutionary relationships. Our study was aimed at elucidating i) phylogenetic relationships among all

European taxa belonging to *Anthoxanthum odoratum* complex and ii) the evolutionary history of polyploids.

In order to get insight into the geographic distribution of ploidy levels and assess the taxonomic value of genome size data, flow cytometry was used. To answer the phylogenetic and evolutionary questions, single-copy nuclear loci (GBSSI), ITS and cpDNA sequencing was used together with FISH and GISH analyses.

Eight taxonomic groups that partly corresponded to traditionally recognized species (*A. odoratum* 2x and 4x, *A. alpinum* 2x and 4x, *A. aristatum*, *A. ovatum*, *A. gracile*, *A. amarum*) were delimited on the basis of genome size values and phenotypic variation. While our data supported the merger of *A. aristatum* and *A. ovatum*, eastern Mediterranean populations traditionally referred to as diploid *A. odoratum* were shown to be cytologically distinct and may represent a new taxon. Autopolyploid origin was suggested for 4x *A. alpinum*, on the contrary, 4x *A. odoratum* is an allopolyploid based on the molecular and GISH analyses.

Poster session B - POL 300

Whole genome duplication does not show consistent response in fish and plant lineages fate. (52552)

Sacha Laurent, Nicolas Salamin, Marc Robinson-Rechavi.

Departement of Ecology and Evolution, University of Lausanne; Swiss Institute of Bioinformatics.

Impact of whole genome duplications upon species fate has been debated since the discovery of their pervasiveness in the tree of life. Stemming from this and the apparent increase in species number in clades emerging from paleopolyploidy, many hypothesis have been proposed to explain those patterns. Neutral patterns such as reciprocal gene loss could theoretically lead to such observation, although this mode of action has been recently discussed and cast down. Adaptive processes, such as neofunctionalization of one of the duplicate genes, could also favor the apparition of new species. Data in favor of or against an increase in diversity following paleopolyploidy have been alternatively presented in the past few years. Using recent methods for estimating diversification of lineages, we analyse already published but also new phylogenies of species belonging to various plants and fishes group. Overall we do not find a consistent signal, indicating diverging responses in lineages fate after whole genome duplication.

Poster session B - POL 300

The role of ploidy in host resistance: an experimental test of triploid and tetraploid snails (52615)

Christina Jenkins, Mark Dybdahl, Scott Nuismer.

Washington State University; Washington State University; University of Idaho.

The evolution of sexual reproduction is widely believed to be driven by host-parasite coevolution. Meanwhile, elevated ploidy is expected to alter host-parasite coevolution through increased heterozygosity and dosage from the expression of duplicated genes. Interestingly, many asexual populations exhibit higher ploidy compared to their sexual ancestors. Yet, there are gaps in our understanding of the confounding effects of ploidy variation on the maintenance of sex. If resistance to parasites is based on self recognition, then the increased heterozygosity associated with polyploidy could decrease host resistance. However, if resistance is based on a quantitative model of infection, then higher host ploidy should lead to an increase in immune molecules that neutralize parasites. Here, we experimentally inoculated triploid and tetraploid asexual hosts to explicitly address if an increase in ploidy changes an individual's resistance. We used the snail, *Potamopyrgus antipodarum*, and its coevolved parasite, *Microphallus*. We tested hosts from five different populations with parasites from three different sources. We found that there was no significant difference in infection rate in triploids and tetraploids across all populations suggesting that host resistance is not driven by the quantitative model of infection.

Poster session B - POL 300

Terra incognita of contemporary plant biosystematics: untangling the sources of complexity in *Ranunculus* subg. *Batrachium* (52638)

Jan Práněl, Zdeněk Kaplan, Petr Koutecký, Pavel Trávníček.

Institution of Botany of the CAS; Department of Botany, Faculty of Science, University of South Bohemia.

Water crowfoots (*Ranunculus* subg. *Batrachium*) can be considered as a perfect model group for the study of polyploidy and hybridization in aquatic environment, comprising of several polyploid lineages of different origin, showing frequent intraspecific ploidy variation, frequently hybridizing across ploidy levels, and also possessing specific morphological adaptations reflecting the evolution (e.g. heterophyly). On the other hand, they belong between the most intricate European angiosperms. We applied flow cytometry on the extensive dataset (ca. 2700 *Batrachium* individuals from >600 populations) from the Czech Republic (for the detailed point of view), 23 other European and 3 non-European countries (for the broad point of view). Flow cytometry was proved to be an efficient method for determination of *Batrachium* species and also revealed numerous cases of recent hybridization, including introgression. Preliminary results of direct sequencing (ITS, cpDNA) has already revealed a number of remarkable findings, such as parallel evolution of traits in unrelated taxa and intraspecific cryptic variation. A gene flow between large-flowered and small-flowered species is probably unequal; we detected „chloroplast capture“ phenomenon. The situation is particularly complex in running waters, where even sterile hybrids are fixed via clonal propagation.

Poster session B - POL 300

Deep genetic splits in a diploid-polyploid *Arabidopsis arenosa* species complex (52642)

Filip Kolar, Eliska Zaveska, Gabriela Fuxova, Lucie Hyklova, Magdalena Lucanova, Atsushi J. Nagano, Hiroshi Kudoh, Stanislav Spaniel, Karol Marhold.

Natural History Museum, University of Oslo; Institute of Botany, University of Innsbruck; Department of Botany, Faculty of Science, Charles University in Prague; Institute of Botany, Academy of Sciences of the Czech Republic, Průhonice; Center for Ecological Research, Kyoto University; Institute of Botany, Slovak Academy of Sciences, Bratislava.

Knowledge on eco-geographical distribution of genetic variation within and across ploidy levels is a necessary prerequisite for any experimental or molecular study of plant systems that underwent genome duplication. The *Arabidopsis arenosa* group, an intricate diploid-autotetraploid complex, still remains largely neglected with respect to the evolutionary history and distribution of genetic variation across its range (spanning through most of the Europe). We conducted a large population-level sampling across its whole range and evaluated patterns of cytotype and genetic diversity of approx. 140 populations of *A. arenosa* using flow cytometry, RAD sequencing and nuclear microsatellites. We detected a largely parapatric distribution of the diploid (SE Europe) and tetraploid cytotype (NW Europe) that form two contact zones – narrow one in Slovenia and a wide mosaic-like one in South-Eastern and Western Carpathians. The diploid populations split into five genetically very distinct groups that are geographically segregated but do not reflect the most obvious morphological differentiation between lowland vs. alpine areas. The presence of marked ploidy-level, morphological, ecological and hitherto largely neglected genetic variation highlights *A. arenosa* as very promising model for addressing various evolutionary questions on origins and consequences of plant genome duplication.

Poster session B - POL 300

A haploid fungus that appears like a polyploid. (52697)

Pawel Rosikiewicz, Tania Wyss, Frederic Masclaux, Ian Sanders.

University of Lausanne.

Rhizophagus irregularis is an arbuscular mycorrhizal fungus (AMF) used commercially to increase yields of crop plants, such as rice and wheat. Despite its potential to increase food production, AMF genetics and genomics has not been well studied. This is partially due to their unusual genetic structure. Each individual AMF carries multiple genetically different haploid nuclei. Therefore, we have to consider AMF as similar to polyploids. Different nuclei are transferred to the offspring in multinucleate spores. Moreover, different AMF can fuse, giving rise to progeny that are genetically and phenotypically distinct from the parents. I will present how I produced new crossed offspring of genetically different parental AMF. These crossed lines were genotyped with next generation sequencing (NGS). Then, NGS data were analyzed with the combination of methods typical for analysis of genetic data from polyploid organisms and cancer cell lines. My results showed that a process of nuclear exchange in AMF was not random and one genome was always dominant. The non-random

nature of AMF genetic exchange presents an opportunity to predict future genotypes of AMF crosses and produce novel AMF with known benefits to plant hosts.

Poster session B - POL 300

Growth differences between diploid and tetraploid cytotypes in a mixed ploidy population of the Patagonian steppe plant *Hypochaeris incana* (Asteraceae) (52711)

Karin Tremetsberger, Estrella Urtubey, Katharina Lapin, Christiane König.

Institute of Botany, BOKU, Vienna, Austria; Instituto de Botánica Darwinion, San Isidro, Argentina; Division of Systematic and Evolutionary Botany, University of Vienna, Austria.

Hypochaeris incana grows in the Patagonian steppe of southern South America. It is a self-incompatible, perennial herb with leaves in rosettes. A phylogeographic study suggests that *H. incana* reacted to Pleistocene climate changes through in-situ persistence. Today, tetraploid northern populations are thriving in isolation from each other, whereas diploid southern populations have recently expanded. Moreover, the data suggest that diploids have repeatedly been replaced by tetraploids in the northern Patagonian region. Here, we evaluate vegetative and reproductive growth parameters of diploids and tetraploids in a mixed ploidy population in northern Patagonia. For competitive exclusion to occur, we expect that - in the absence of habitat segregation - tetraploids are vegetatively and/or reproductively more vigorous than diploids. Whereas diploids do better with respect to growth (number of rosettes) and reproduction (number of ovules/head, fruit set), tetraploids have the ability to form large clones via underground stolons, with genets up to 90 m distant, a feature not encountered in diploids. Moreover, tetraploids might have better ability to withstand drought and show delayed phenological development in comparison to diploids. Thus, altered growth parameters of tetraploids compared to their diploid progenitors could ultimately lead to the replacement of diploids in local populations.

Poster session B - POL 300

Phylogenetic and biogeographical patterns of allopolyploid speciation in an intertidal furoid seaweed assemblage (52902)

Joao Neiva, Licinia Gouveia, Cristina Paulino, Nelson Coelho, Gareth Pearson, Ester Serrao.

Algarve University.

The development and application of new molecular tools has contributed to a renewed interest on the roles of hybridization and polyploidy in evolution. These processes are associated in allopolyploid speciation, best known from plants and a few vertebrate lineages. New models beyond traditional plant systems may provide new insights underlying the factors contributing to allopolyploid establishment and evolutionary success. We investigated the evolutionary history of the intertidal seaweed *Hesperophycus*/*Pelvetiopsis* complex by screening a diverse

panel of populations of *Hesperophycus californicus* and *Pelvetiopsis limitata* sensu lato for a range of different nuclear/organelle sequencing/typing markers. Four well defined species were recovered, including the taxonomically dubious *P. arborescens* and a new undescribed species. Gene paraphyly, cyto-nuclear conflict, fixed heterozygosity and allele states supported the allopolyploid nature of two of these entities and the male contribution of *P. arborescens* for both. This latter species exhibited an extremely reduced geographical distribution that did not overlap with the most recent (and possibly still expanding) allopolyploid taxa. Conversely, the older allopolyploid is presently the most widespread taxa, and its maternal ancestor is presumed extinct. Our results provide evidence for ecological divergence allowing allopolyploids to locally co-exist with diploid parental species, and show that in the long-term they can even outperform them.

Poster session B - POL 300

The evolution of the ability to learn (52092)

Machteld Verzijden, Jessica Abbott, Volker Loeschke.

Aarhus University; Lund University.

The ability to learn is important because it allows animals to cope with unpredictable environments. Animals can learn from experience to guide their future actions, and do so in many contexts, such as food finding, nesting and choosing a mate. Species differ in their ability to learn, which indicates that this trait can evolve. However, we have a very limited understanding of how learning can evolve, and lack knowledge in particular, for learning in the context of mate choice. I will present data from an on-going study addressing how the ability to learn to choose a mate can evolve, by using laboratory populations of a fruit fly species as a model to mimic evolution experimentally. In particular, in this study males are selected on their ability to learn to associate female virginity with an arbitrary trait.

Poster session B - POL 300

The regulation of evolvability through Hsp90 expression (52097)

Robert Peuss, Hendrik Eggert, Sophie A.O. Armitage, **Joachim Kurtz**.

University of Münster, Institute for Evolution and Biodiversity.

The balance between robustness and evolvability is a long-standing question in evolution. It has been suggested that heat shock protein 90 (Hsp90), a chaperone, serves as a capacitor for evolution, since reduced availability of Hsp90 releases cryptic genetic variation. Hsp90 down-regulation might moreover serve to increase novel genetic variation, since it also is involved in transposon silencing in the germline. We addressed the question of whether Hsp90 expression, and thus evolvability, might be regulated upon demand. Specifically, we tested whether Hsp90 shows reduced transcription under stressful environmental conditions where increased variation, leading to increased evolvability, might have fitness advantages. We

simulated such a situation by placing untreated (focal) *Tribolium castaneum* flour beetles together with wounded conspecifics. This treatment exposed the focal beetles to an environmental condition that indicates a stressful environment without directly stressing the focal individuals themselves, which might have unwanted direct effects on their stress response. Using RT-qPCR, we found a consistent reduction in the Hsp90 expression of focal beetles. Our study for the first time finds indirect down-regulation of a key gene involved in evolvability, and poses the exciting question of whether evolvability might be regulated through the use of information derived from the social environment.

Poster session B - POL 300

The effect of worker mediated environmental stress on colony fitness in common black ant *Formica fusca* (52125)

Siiri Fuchs, Liselotte Sundström, Dalial Freitak.

University of Helsinki, Finland; Tvärminne Zoological Station, University of Helsinki, Finland; Centre of Excellence in Biological Interactions, University of Jyväskylä, Finland.

Organisms need to adapt to environmental changes, such as variation in pathogen pressure, in order to survive. Adaptation can occur by developmental plasticity during the life of an individual or via inherited traits across generations. Adaptation entails alterations in life-history strategies and, hence, trade-offs between essential functions such as growth, disease resistance, and reproduction. Social insects, such as ants, form colonies with high population density, which favours the spread of pathogens. To fend off epidemics social insects have developed behaviours that protect them collectively, among others the spread of immune factors by a mechanism similar to vaccination. We investigated how the common black ant *Formica fusca* workers deal with environmental stress (bacterium and oxidative stress) and how this affects the brood they help to raise. Our study shows that workers mediate stress, which can be seen as changes in brood development, survival and size. We also see differences in gene expression depending on diet, caste and age. This study shows how organisms respond to varying environmental conditions and use different strategies to adapt and gain fitness.

Poster session B - POL 300

Effects of nest microclimate on maternal effects in a small passerine bird (52264)

Josefa Bleu, Claudy Haussy, Clotilde Biard.

Institute of Ecology and Environmental Sciences - Paris.

Maternal effects are a source of phenotypic plasticity. They can have extremely large effects, affecting the morphology, physiology and/or behaviour of the offspring. In particular, they allow a plasticity that may play an important role in shaping responses to rapid environmental

changes, such as those generated by climate change. Yet, maternal effects are seldom studied in the context of the adaptation to climate change. Previous studies have shown the sensitivity of small passerine birds to climate change in Europe. These effects may be driven by changes in pre-natal maternal investment, as it is crucial for offspring development and success. The aim of this study is to test this hypothesis by investigating how pre-natal maternal effects change in response to nest micro-temperature during egg laying. More precisely, we will compare reproductive investment between control and experimentally heated nests in a great tit population. In particular, clutch size, hatching and fledging success and egg characteristics such as egg mass, lysozyme and carotenoid content will be compared. These results will allow a better understanding of the mechanisms involved in the response to global change which is primordial to better predict responses of natural populations.

Poster session B - POL 300

Inconsistency of whole genome transcription responses to diet in *Drosophila* (52292)

Jelle Zandveld, Joost van den Heuvel, Erik van den Akker, Bas Zwaan.

Wageningen University; Newcastle University; Leiden University Medical Centre; Technische Universiteit Delft.

In *Drosophila*, the response of whole genome transcription to diet is extremely plastic. On dietary restriction, a reduced food intake without malnutrition that extends lifespan and reduces fecundity, many whole genome transcription studies are performed. We performed a meta-analysis between studies using a highly similar protocol to test the consistency of the transcriptome responses to dietary restriction. Striking inconsistent patterns between studies were found for the up/down regulation on the gene level, the associated GO-terms and gene expression top-hits. The addition of another dataset that includes egg laying data suggests that differential egg laying responses with age may account for these inconsistencies. We recommend that availability of phenotypic data is essential for the right interpretation of an organism's whole genome transcription pattern to diet in particular, but potentially to many environmental interventions in general.

Poster session B - POL 300

Trans-generational effects of Diuron herbicide on the methylome of the Pacific Oyster *Crassostrea gigas* (52314)

Rodolfo Rondon, Evelyne Bachère, Farida Akcha, Guillaume Mitta, Caroline Montagnani, Céline Cosseau, Christoph Grunau.

Laboratoire d'Interaction Hôte Pathogènes Environnement (IHPE), CNRS, UMR5244; Centre Atlantique, Laboratoire Ecotoxicologie.

Environmentally induced epigenetic transgenerational effects involve the transmission of phenotypic changes to the offspring. It is well established that various environmental stressors including chemical pollutants can modulate the epigenome of individuals. The Pacific Oyster *Crassostrea gigas* is the main oyster species exploited worldwide. It currently suffers from devastating summer mortality outbreaks. It is well established that these mass mortalities are the result of a complex pathosystem including both biotic and abiotic factors among which toxic chemicals are major actors. It has been previously demonstrated that the parental exposure of *C. gigas* to Diuron has consequences on the phenotypes of the offspring. Altogether, these data suggest that Diuron could act on the epigenome of the parental germ cells and subsequently impact the transcriptional profile and phenotype of the subsequent generation. To examine these questions, we established the transcriptional profile and the methylome of *C. gigas* offspring of diuron-exposed genitors. We provide evidence that differences exist between spat produced from exposed or non-exposed parents both in the transcriptome and methylome. These differences occur in specific loci and we will discuss the molecular mechanisms that link methylome modifications to changes in life history traits of *C. gigas*.

Poster session B - POL 300

Parasite-induced changes in host phenotype and gene expression after infection (52319)

Barbara Feldmeyer, Johanna Mazur, Hannes Lerp, Harald Binder, Susanne Foitzik.

Mainz University; University Medical Center Mainz.

Parasite infections, next to their detrimental consequence for host fitness, can influence host organisms on several levels from physiology, morphology, and life history to behavior. Parasite-induced changes in the host can either be attributed to host defenses, they can be by-products of infection, or the result of parasite manipulation. In social insects, not only the infected individual itself, but the whole colony is affected by the parasites' presence and has to suffer the consequences as a community. In the ant *Temnothorax nylander*, individuals parasitized by a cestode, show a suite of phenotypic changes, including smaller body size, decreased activity and increased survival. Moreover, parasitized colonies show lower aggression levels than healthy colonies. To understand the proximate mechanisms of parasite-induced behavioral changes, we compared brain gene expression patterns between workers from infected and healthy colonies. We report on candidate genes and associated functional categories involved in the parasite-induced phenotypic alterations. The most striking finding is a large-scale down-regulation of muscle-related genes in infected workers, fitting well to their inactive phenotype and increased survival. These altered host phenotypes may in turn benefit the parasite through an increased transmission probability to its final host.

Poster session B - POL 300

Maternally-derived thyroid hormones in avian eggs: variation and function (52362)

Suvi Ruuskanen, Ton G.G. Groothuis, Veerle M. Darras, Sonja Schaper, Marcel E. Visser.

University of Turku; University of Groningen; KU Leuven; Netherlands Institute of Ecology.

Maternal effects via eggs are a powerful way to influence offspring phenotype and fitness, thus strong selection is expected. For example, avian maternal steroid hormone levels in egg yolk vary systematically with environmental factors, are heritable and affect offspring fitness-related traits. However although data from mammals and fish suggests a prominent role for maternal thyroid hormones (TH) on offspring growth and survival, sources of avian egg TH variation and effects on offspring have so far been largely neglected in ecological studies. We studied variation in yolk TH concentrations (thyroxine, T4 and triiodothyronine, T3) in wild great tits (*Parus major*) and estimated heritability using siblings in captivity. We further experimentally elevated yolk TH in a wild population to study effects on fitness-related traits. Yolk T4 concentration correlated negatively with ambient temperature and positively with laydate. There was significant variation in yolk TH among females. Yolk T4 increased with layorder within clutches. However, experimental yolk TH elevation had no effect on skeletal or body mass growth, metabolic rate or hatching or fledging success. To understand more of the potential function of maternally-derived TH, an experimental yolk TH reduction should be conducted and effects of yolk TH on pre-hatching development should be studied.

Poster session B - POL 300

Adaptive Integrative Shape Variations in Phenotypic Plasticity (52431)

Kinya Nishimura.

Graduate School of Fisheries Sciences, Hokka.

Stability and plasticity are antithesis essential ability of organism to cope with the environments. "Phenotypic plasticity" is an important conceptual issue in evolutionary biology. Generally, even though morphogenesis makes a stabilized constitutive morphology, some organisms were gifted morphological plasticity with cell proliferation and tissue restructuring in various environmental circumstances.

The Hokkaido salamander (*Hynobius retardatus*) is in the list of organisms having ability of phenotypic plasticity. Larvae of *H. retardatus* change morphology to deal with predators and prey. The emerging morphologies can be classified into some distinctive morph categories establishing the polyphenism. We can perceive differences among typical individuals belonging in each category. However, discrimination by perception is dubious, and application of a conventional criterion is also unreliable. Previous studies of the morphological plasticity cannot touch on various important biological issues such as individual variation within each morph category, integrative shape variations and the natural selection acting on the variations.

I adopted the geometric morphometric analysis to the larvae of *H. retardatus* that changed morphological development in experimentally manipulated trophic interaction environmental settings. I clarified adaptive integrative shape variations among individuals within each morph category that suggests developmental shape module integration evolved by natural selection.

Negative public information in mate-choice copying helps the spread of a novel trait (52462)

Susana Varela, Mauro Santos, Margarida Matos.

CE3C - Faculdade de Ciências, Universidade de Lisboa; GBE - Universitat Autònoma de Barcelona, Spain.

Numerous field and laboratory experiments have shown that many species have the capacity for social learning, including mate-choice decisions that can be influenced by witnessing the mating decisions of others. This phenomenon, known as mate-choice copying, is a type of non-genetic information that can increase the behavioural plasticity of the copying individuals, and cause genetic changes across generations in the genotype of the copied individuals. Here we develop a numerical model of mate-choice copying that follows the population genetics tradition, consisting in tracking allele frequencies in a population over time under scenarios with and without copying. In contrast to previous evolutionary models, we consider both positive and negative social information because many mating systems are driven by males in pursuit of a mate, and female refusal of copulation may provide negative social information. The inclusion of negative social information to mate-choice copying helps the spread of a novel trait, even if female innate mate-choice preference is biased towards the common male-type. We argue that the presence or absence of copying might simply mirror the associated cost-benefit relationship of the mating system of a given species, and suggest how to test this prediction.

Memory and learning in gene-regulation networks (52464)

Kostas Kouvaris, Jeff Clune, Loizos Kounios, Markus Brede, Richard Watson.

University of Southampton; University of Wyoming.

The ability of a single genotype to control the development of multiple distinct phenotypes, e.g. differentiation of cell types or multicellular dimorphism, is important for understanding the environmental sensitivity of development, epigenetic inheritance of phenotype states, phenotypic variability under mutation and the evolution of evolvability. Recent work (Pavlicev et al. 2010, Watson et al. 2014) shows that the constraints and biases of development, e.g. as controlled by the structure and organisation of gene regulation networks, can be shaped by natural selection to 'record' the pattern of functional dependencies imposed by past selection, as per Rupert Reidl's suggestion (1978). This enables a single gene-network (given random perturbations to embryonic expression levels) to (re)produce multiple distinct phenotypes that have been selected for in past environments. Moreover, we show that principles of memory, learning and generalisation, well understood in the context of connectionist (neural network) models of memory and learning, can be used to characterise the capabilities and limitations of such 'developmental memory' in gene networks. We also demonstrate how conditions that avoid 'over-fitting' in machine learning, such as the

application of a connection cost that reduces model complexity, can be used to predict conditions that enhance phenotypic flexibility in evolved gene networks.

Poster session B - POL 300

The role of nucleic acid methylating enzymes in the red flour beetle *Tribolium castaneum* (52484)

Nora Stolte, Hendrik Eggert, Julia Ebeling, Maike Diddens-de Buhr, Frank Lyko, Joachim Kurtz.

Institute of Evolution and Biodiversity, Westfälische Wilhelms-Universität Münster; German Cancer Research Centre, Heidelberg.

Epigenetic regulation enables rapid phenotypic adaptation of organisms to environmental changes. Cytosine methylation of DNA and certain RNAs is an important epigenetic mechanism, which is generated by an evolutionarily conserved family of enzymes, so called DNA methyltransferases (DNMTs). The ancestral DNMT toolkit consists of three enzymes DNMT1, 2 and 3, however, the evolution of cytosine methylation systems has generated great variation in the sets of Dnmt genes between species. For example, while *Drosophila* lacks a functional DNA methylation system, honeybees possess all three DNMTs, and DNA methylation is crucial for caste determination.

We investigated the status of a functional DNA methylation system in the Red Flour Beetle *Tribolium castaneum*, which possesses Dnmt1 and Dnmt2 but lacks Dnmt3. In the present study, we show that DNMT1 is essential for early embryonic development, although we were not able to detect functional levels of DNA methylation via whole genome bisulfite sequencing. Parental RNAi knock-down of Dnmt1 in the mothers caused a developmental arrest in the offspring embryos.

This, to our knowledge, first evidence of a functional role of DNMT1 during embryogenesis in *T. castaneum*, calls for further studies investigating additional functions of this enzyme and its role beyond DNA methylation.

Poster session B - POL 300

Ephemeral vs persistent triploids: two epigenetic modus operandi (52522)

France Beauregard, Christelle Leung, Bernard Angers.

Université de Montréal.

Phenotypic variation is generally a prerequisite to occupy different niches. Clones can only rely on epigenetic processes to regulate the expression of their genes and produce different phenotypes. Consequently, allopolyploids are benefited by a wider range of alleles they can express for a given gene. Multiple clonal lineages with different ploidy levels are found in gynogenetic hybrid complexes *Ambystoma* spp. and *Chrosomus eos-neogaeus*, both widespread in North America. In *Chrosomus* fish, only diploid reproduce clonally while

triploids are constantly formed de novo. In contrast, triploids not only perpetuate clonally in *Ambystoma* salamanders, but represent the most common biotype. The objective of this project is to compare the effects of additional haplome on the epigenetic variation in these hybrid complexes. When genetic and environmental effects are taken into account, the third genome has little effect on the epigenetic profiles in fish *Chrosomus eos-neogaeus* while it is more important than the environmental effect for salamanders *Ambystoma*. These results suggest that the additional genome may provide a niche diversification from a unique diploid hybrid in the *Ambystoma* complex.

Poster session B - POL 300

Life history consequences of dietary mismatches in *Drosophila melanogaster* (52550)

Elizabeth Duxbury, Tracey Chapman.

University of East Anglia.

Changes in nutritional environment can lead to evolved and plastic responses in life history traits such as lifespan and reproductive rate. Using *Drosophila melanogaster*, we first investigated the effect on life history traits of changes in the quality (high or low protein content) of developmental (larval) diet versus adult diets within a single generation. We compared the fitness of individuals maintained on mismatched diets (i.e. low quality larval followed by high quality adult diet, or vice versa) with those on constant diets (low or high quality larval and adult diets throughout). We measured larval traits, age-specific survival and age-specific reproductive output. The results showed that, contrary to predictions from 'Thrifty Phenotype' theory, individuals maintained on mismatched diets did not suffer fitness costs in comparison to those maintained on constant diets. We next investigated evolutionary responses of life histories to diet manipulations, using replicated populations experimentally evolved on different dietary regimes. The evolutionary treatments were populations that had an evolutionary history of food supplied at either regular or unpredictable intervals (the latter creating periods of feast and famine). I discuss the results in the context of the evolution of lifespan, of responses to dietary restriction and of life history trade-offs.

Poster session B - POL 300

Plasticity and evolutionary divergence in ovariole number in *Drosophila* (52563)

Cláudia Mendes, Élio Sucena, Christen Mirth.

Instituto Gulbenkian de Ciência, Oeiras, Portugal; Universidade de Lisboa, Faculdade de Ciências, Departamento de Biologia Animal, Lisboa, Portugal.

Developmental plasticity, the ability of an organism to adjust its developmental trajectory in response to environmental variation, may facilitate success in novel environments and

promote evolutionary diversification. Here, we sought to understand the contribution of developmental plasticity to the evolution of morphological diversity by comparing the underlying developmental mechanisms of the plastic response and of the evolutionary divergence in ovariole number, an important reproductive trait in *Drosophila*. Our analysis in *Drosophila melanogaster* revealed that ovariole number is severely reduced when early third instar larvae are malnourished. This reduction in ovariole number is a result of a slower rate of ovary growth and a delayed onset of terminal filament (TF) differentiation, the first step in ovariole morphogenesis. Interestingly, we found that similar developmental mechanisms are likely responsible for the considerable differences in ovariole number between two geographical races of *Drosophila mojavensis*. These desert-adapted populations utilize distinct cacti for all stages of their life cycles. Thus, our results suggest that environmental and genetic variation can affect ovariole number through similar developmental mechanisms, supporting the view that developmental plasticity may play an important role in the evolution of morphological diversity.

Poster session B - POL 300

Phenotypic plasticity and adaptive potential for climate change in mountain birch – analysis of mature siblings in tree-line common gardens (52573)

Irma Saloniemi, Marjo Helander, Kari Saikkonen.

University of Turku; University of Turku; The Natural Resources Institute Finland.

Simultaneous studies of genetic variation and plasticity are demanding in natural populations, especially in long-lived organisms like trees. Mountain birch (*B. pubescens* spp. *czerepanovii*) is a tree-line species that occurs above the Arctic Circle in Northern Scandinavia, but previous studies suggest that it has high level of phenotypic and genotypic variation in fitness and morphology related traits. Our aim is to estimate the adaptive potential for the species as temperatures increase in high latitudes. We base our study on 25-40 years old siblings that grow in 4 common gardens in natural, but locally variable northern environments, and one garden in southern Finland. Each of the twenty sib-families originates from seeds of a single tree of northern origin. Each family is divided between the 3-5 gardens, and the gardens are divided in 3-6 blocks with 16 progeny per family in each of the blocks. Performance of these tree families was intensively monitored during the first decade of their growth, and we continue the measurements on the adult trees. Phenotypic plasticity may explain high variation, but it may hinder adaptation by increased phenotypic variation. On the other hand, it may also restrict too fast responses, or even accelerate adaptation

Poster session B - POL 300

Reproductive tactics and sperm competition related to oxidative stress in the Seba's short tailed bat, *Carollia perspicillata*. (52758)

Nicolas Fasel, Charlotte Wesseling, Fabrice Helfenstein, Heinz Richner.

Institute of Ecology and Evolution, University of Bern; Institute of Biology, University of Neuchâtel.

Securing privileged access to mates is costly, and hence may lead to the evolution of alternative reproductive tactics (ARTs), such as sneaking copulations with lower pre-copulatory costs but higher sperm competition. It predicts a stronger investment by sneakers in sperm traits that increase fertilization efficiency. In order to investigate the role of oxidative stress as a potential mediator of different reproductive physiologies associated with ARTs, we assessed ejaculate and blood redox profile of male Seba's short tailed bat (*Carollia perspicillata*). We found a significant increase in oxidative solicitation (proportion of oxidized glutathione) in the blood of harem males, indicating a cost, without however leading to more damage (lipid peroxidation). Sperm quality (velocity and longevity) was significantly higher in bachelor males, but did not correlate with the ejaculate redox profile. The important ingestion of dietary antioxidant may efficiently protect both somatic and reproductive functions in this frugivorous bat species, since an important endogenous antioxidant (superoxide dismutase) did not correlate with social status or sperm competition level. It suggests that a privileged access to mates implies costs for harem holders, and intense sperm competition for bachelors leads to adaptations in sperm traits.

Poster session B - POL 300

Context-dependent plastic response to the presence of predator cues in a widespread newt species (52844)

Zoltán Tóth.

Lendület Evolutionary Ecology Research Group, Plant Protection Institute, HAS.

Previous research on phenotypic plasticity mostly focused on developmental plasticity (i.e. different developmental trajectories triggered by environmental cues) in amphibian model systems, so we have limited information about how anticipatory parental behaviours and maternal effects interact and jointly contribute to individuals' reproductive success. In this study I examined behavioural and maternal responses of gravid female smooth newts, *Lissotriton vulgaris*, to the presence of chemical cues originating from invertebrate predators. I found no indication for substantial oviposition preference among individuals, as many of them deposited eggs both into the 'predator-cue' and the 'clear-water' environment. However, these latter females were also found to adjust the size of the laid eggs to the perceived environment: egg size decreased with time during the reproductive season in the absence of predator cues, but not when such cues were present. Besides, females differed in the extent of egg-wrapping between ponds of origin, but individuals did not adjust their wrapping behaviour to the perceived environment. According to these results, female smooth newts have the potential to exhibit activational plasticity in the form of a maternal effect when chemical cues from predators are present, with which individuals may improve their offspring's fitness in risky natal environments.

Poster session B - POL 300

Environment modifies equilibrium proportions of alternative reproductive strategies in the bulb mite. (52850)

Anna Maria Skrzynicka, Jacek Radwan.

Jagiellonian University, Institute of Environmental Sciences; Adam Mickiewicz University, Institute of Environmental Biology(Poznan,PL).

The bulb mite (*Rhizoglyphus robini*) expresses alternative reproductive phenotypes (ARPs). Aggressive fighters, possessing modified pair of legs used as a weapon, may coexist in populations with unarmed, benign scramblers. Male morph in this species is heritable, but given no evidence of frequency-dependence in earlier work on this system, it is not clear what maintains genetic variance underlying ARPs. If the polymorphism is balanced, proportion of fighters should come back to equilibrium value after being disturbed. We used artificial selection to alter fighters' proportions to 50% or 94%, and then for 14 generations we traced how the proportion changes in 5 replicate populations. To investigate if equilibrium point is affected by environmental conditions, we ran this protocols under two temperatures: 24 and 18°C. We found that under both temperatures, proportions evolved to stable values regardless of initial proportion of morphs, indicating that the polymorphism is balanced. However, the equilibrium proportion differed significantly between the temperatures (76% at 24°C, and 98% at 18°C), indicating that morph success can be affected by environment. Finally, we found that fighters' proportion was also affected by maternal effects. Overall, the proportion of morphs seems to be shaped by interaction between historical and current environmental state.

Poster session B - POL 300

Epigenetic modifications in moth sexual communication signals (52903)

Rik Lievers, Peter Kuperus, Dennis van Veldhuizen, Astrid T. Groot.

IBED.

The evolutionary diversification of moth sexual communication signals is puzzling as it is believed to be under stabilizing selection, which limits evolutionary change. Yet, several moth species show significant intraspecific variation in the pheromone composition. The observed variation can in large part be explained by genetic variation, however, the sexual communication signal has also been shown to be plastic¹. Moth sexual signals can be modulated depending on the prevailing olfactory cues present in the environment. This suggests that behavioral differentiation may precede genetic differentiation in the sexual signals of moths. The molecular mechanism behind this phenotypic plasticity is poorly understood. Epigenetic modifications, such as DNA methylation, are an important candidate. We investigate whether DNA methylation is involved in regulating heritable and plastic variation in the sexual communication signals of noctuid moths. Our first results show that females indeed vary in their methylation patterns, that these methylation patterns seem heritable, and that DNA methylation could potentially contribute to plasticity in sex pheromone composition.

1 Groot et al. 2010. Phenotypic plasticity in sexual communication signal of a noctuid moth. J. Evol. Biol. 23: 2731-2738.

Poster session B - POL 300

Seasonality maintains alternative life history phenotypes (51633)

Sami Kivelä, Panu Välimäki, Karl Gotthard.

Stockholm University; University of Oulu.

Many organisms express discrete alternative phenotypes (polyphenisms) in relation to predictable environmental variation across generations, seasonal polyphenisms in insect morphology being well-known examples of this. However, the evolution of alternative life-history phenotypes, which are also common, remains poorly understood. We analyse the evolution of alternative life histories in seasonal environments by using temperate insects as a model system. Temperate insects provide an excellent system to study alternative life history phenotypes as they typically express alternative developmental pathways of diapause and direct development that have life-history correlates. We develop a methodologically novel and holistic simulation model and optimize development time, growth rate, body size, reproductive effort, and adult life span simultaneously in both developmental pathways. The model predicts that direct development should be associated with shorter development time (duration of growth) and adult life span, higher growth rate and reproductive effort, smaller body size as well as lower fecundity compared to the diapause pathway, because the two generations divide the available time unequally. These predictions are consistent with many empirical data. In conclusion, the analysis shows that seasonality alone can explain the evolution of alternative life histories.

Poster session B - POL 300

Live fast, die young? – Trans-generational effects of parental food stress in a butterfly (51665)

Luisa Woestmann, Marjo Saastamoinen.

Metapopulation Research Group, University of Helsinki.

Environmental conditions experienced by parents are potentially important factors that shape the offspring's phenotype and are known as trans-generational effects. Poor environmental conditions often have negative effects on offspring via low provision of resources to the eggs, resulting in poor quality offspring with reduced fitness. Maternal effects are well-studied in many organisms, whereas paternal effects have received less attention. There are, however, important effects driven also by the father. Male butterflies, for example, transfer spermatophores during mating that comprise sperm and accessory gland secretions, which contain nutrients that are contributed to the female and can increase her fecundity and life span. In this study, we investigated the effect of food deprivation of males and females during

the reproductive stage in the Glanville fritillary butterfly (*Melitaea cinxia*) on life-history traits including fecundity as well as possible trans-generational effects by both parents. Food deprivation of mothers resulted in a direct effect on female reproduction leading to reduced lifetime reproductive success, whereas stressed fathers sired more offspring, possibly due to higher investment into their spermatophores.

Poster session B - POL 300

Grandparental immune priming in the sex-role reversed pipefish *Syngnathus typhle* (51849)

Anne Beemelmans, Olivia Roth.

Helmholtz Centre for Ocean Research Kiel (GEOMAR).

Trans-generational immune priming (TGIP), the transfer of non-genetic information about parental pathogenic experience to the progeny boosts the offspring immune response and permits a more efficient reaction against parasite genotypes. While TGIP was discussed as a short-term effect, selection could favor TGIP that goes across generations in case the parasite assemblage is stable and costs are limited.

We experimentally assessed the evolution of grandparental-TGIP in the sex-role reversed pipefish *Syngnathus typhle* on life history and gene-expression of F2-offspring.

We found strong grandparental effects with additive, sex-specific contribution to different pathways of the immune system and clear involvement of epigenetic effects. While genes of the adaptive immune system and complement component system were affected by grandmaternal effects, genes of the innate immune system revealed grandpaternal effects.

DNA-methylation and especially histone-acetylation genes were influenced by the grandfathers demonstrating that epigenetic regulation mechanisms are essential for transferring non-genetic information over more than one generation down the paternal line. While adaptive if similar parasitic assemblage is met, grandparental-TGIP involves costs displayed as reduced growth of F2-offspring.

We conclude that the transfer of phenotypic experiences does not cease after one generation: additive grandparental effects may seriously affect the phenotype of their grandchildren.

Poster session B - POL 300

An evolutionary analysis of dizygotic twinning in humans (51914)

Richard Smock, Wade Hazel, Joseph Tomkins.

DePauw University; DePauw University; University of Western Australia.

Dizygotic twinning results from double ovulation and is a heritable trait that occurs in all human populations at low, but variable rates. Females producing twins typically are older, taller, have larger body mass indices and higher lifetime reproductive success, relative to females that do not produce twins. We develop an analytical model that compares the fitness

of four reproductive strategies: (1) never producing twins, (2) producing twins at a low but constant rate, (3) producing twins conditionally at a rate dependent on age and quality, and (4) double ovulating conditionally, but carrying only a single offspring to term. When we parameterized the model using estimates of demographic variables from a natural population, we found that when either egg quality declines with female age, or females vary in their optimal interbirth interval, the strategy with the greatest fitness is conditional double ovulation, but carrying only a single offspring to term. These results suggest that dizygotic twinning is a byproduct of adaptive phenotypic plasticity in ovulation rate.

Poster session B - POL 300

Genotype and phenotype changes over generations on a multinucleated fungus (52016)

Ivan Mateus, Fred Masclaux, Tania Wyss, Ian Sanders.

University of Lausanne.

Arbuscular mycorrhizal fungi (AMF) are one of the most important endo-symbionts of plants. They provide mineral nutrients to the plant in exchange of photosynthesized carbon. These fungi have been considered as ancient asexual organisms that reproduce clonally by producing multinucleate spores. Recently whole-genome sequencing of in-vitro cultures of the model AMF species *Rhizophagus irregularis* revealed little genetic polymorphism among coexisting nuclei. However, single-spore cultures segregated from parental cultures differentially alter rice growth, suggesting significant polymorphism between the single-spore cultures.

In addition *R. irregularis* present hyphae without divisions. This feature has as consequence that nuclei coexist within the same hyphae. From an evolutionary point of view, this feature challenges the definition of an individual. Therefore, we studied how the genetic variation is partitioned among different spores over different generations and its consequences on the phenotype of the descendants. The results of this study 1) give more insights about how an asexual organism could exist for million of years without a sexual cycle and 2) help to understand at what level selection acts on *R. irregularis*.

Poster session B - POL 300

Predator-induced plasticity of tadpoles: a search for developmental windows (52040)

Günter Gollmann, Barbara Fischer, Christine Mayer, Philipp Mitteroecker.

University of Vienna, Department of Theoretical Biology; University of Oslo, Department of Biosciences.

Many organisms vary in their plasticity over their lifetime and the induction of plastic traits is sometimes limited to certain developmental windows of an organism's lifetime. In a mesocosm experiment with tadpoles of the agile frog, *Rana dalmatina*, we varied the timing of introduction of caged dragonfly larvae. The tadpoles were photographed in lateral view at weekly intervals, to study growth as well as shape variation assessed by geometric morphometrics. In the presence of predators, tadpoles reduced growth and developed higher tail fins. These effects on growth rates and body shape were stronger in tadpoles first confronted with predators in the second week, than in those exposed to caged predators from the onset of the experiment (a few days after hatching). Our results indicate that there exist windows of predator-induced plasticity in *Rana dalmatina* tadpoles.

Poster session B - POL 300

Evolutionary medicine and intrinsically vulnerable facultative adaptations (52044)

Randolph Nesse.

Arizona State University.

A major focus for evolutionary medicine has been how natural selection shapes mechanisms that regulate facultative responses, especially defensive responses such as vomiting or the fight-flight response. A signal detection analysis reveals that optimal systems give rise to many false alarms, a phenomenon described as the Smoke Detector Principle. However, some systems enter runaway positive feedback loops, such as in panic disorder. This presentation offers mathematical models describing the characteristics of systems that are intrinsically vulnerable because their thresholds adjust adaptively to increased sensitivity on repeated arousal. This phenomenon is likely to provide explanations for vulnerability to anxiety disorders and chronic pain. The tradeoffs involved are likely to constrain selection for mechanisms that adjust thresholds or response intensity as a function of experience in a particular environment.

Poster session B - POL 300

Annual and seasonal variability in leaf traits of *Iris variegata* genotypes growing in contrasting light conditions (52088)

Uros Zivkovic, Stevan Avramov, Natasa Barisic Klisaric, Danijela Miljkovic, Ljiljana Tubic, Danijela Misic, Branislav Siler, Aleksej Tarasjev.

Institute for Biological Research "Sinisa Stankovic".

During their evolution plants developed a set of mechanisms to adapt to the varying environmental conditions, resulting in diversified phenotypes. We were interested in the response of plants towards changing environmental parameters, to light in particular. For this study we selected genotypes of *Iris variegata* that experienced different light

conditions in their habitats: a) genotypes situated along the top and slope of a dune, where it coexisted with annual and perennial herbs and low shrubs; b) genotypes inhabited the woodland understories.

We grew *I. variegata* genotypes in two experimental light treatments (high and low) and tested differences between spring, summer and autumn as well as between two successive years. The plants responses were analysed at different levels of biological information and it was revealed that dissimilar light conditions markedly affected all aspects of plant anatomy and physiology. Repeated measures model ANOVA detected a significant effect of year, habitat and genotype in most analysed traits. Models of changes during growing seasons were treatment- and year-specific.

We also present results from an on-going study which aims to assess occurrence patterns of phenotypic plasticity based on system-level analysis of the same samples that includes metabolic profiling approach combined with robust statistical analysis.

Poster session B - POL 300

Evolutionary and ecological patterns of global DNA cytosine methylation in angiosperm plants (51693)

Monica Medrano, Conchita Alonso, Ricardo Pérez, Azucena Canto, Víctor Parra-Tabla, Carlos M. Herrera.

Estación Biológica de Doñana, CSIC, Sevilla, Spain; Instituto de Investigaciones Químicas, CIC-Cartuja, CSIC-US, Sevilla, Spain; Centro de Investigación Científica de Yucatán, A.C., CONACYT, Mérida, México; Departamento de Ecología Tropical, Universidad Autónoma de Yucatán, Mérida, México.

DNA cytosine methylation is an ubiquitous epigenetic mechanism involved in many important functions, including regulation of gene expression and maintenance of genomic integrity. In plants, intraspecific variation in cytosine methylation has been related to genetic and ecological factors. Genome-wide cytosine methylation is also known to vary substantially between the few species that have been thoroughly studied, but little is known on interspecific patterns, or the degree to which differences between species in methylation levels are related to evolutionary history, ecological settings and/or biogeography. DNA methylation has been implicated in plant macroevolution through effects on speciation and appearance of evolutionary novelty, although these suggestions still lack compelling empirical support. We will contribute to fill this gap by analyzing global DNA cytosine methylation levels obtained by HPLC in a large sample of phylogenetically diverse angiosperms (ca. 100 families) from a broad range of habitat types on two continents. The following three questions will be addressed: (i) is interspecific variation in DNA methylation levels phylogenetically structured?; (ii) are there discernible regional or ecological patterns in genome methylation levels?; and (iii) what are the relative importances of phylogeny, ecology and biogeography in determining plant community-wide levels of cytosine methylation?

Poster session B - POL 300

Fine-scale population epigenetic structure in relation to gastrointestinal parasite load in red grouse (*Lagopus lagopus scotica*) (51779)

Marius Wenzel, Stuart Pierniey.

University of Aberdeen; University of Aberdeen.

Cytosine methylation patterns may be altered by environmental stresses and consequentially affect phenotypic plasticity and adaptation. Parasites are potent stressors, but there is little understanding of the epigenetic consequences of long-term parasite insult. Here, we estimate epigenetic diversity and differentiation among 21 red grouse (*Lagopus lagopus scotica*) populations in north-east Scotland and test for association of gastrointestinal parasite load (caecal nematode *Trichostrongylus tenuis*) with hepatic genome-wide and locus-specific methylation states assayed through methylation-sensitive AFLP. The populations differed significantly in genome-wide methylation levels and were also significantly epigenetically (FSC = 0.0227; $P < 0.001$) and genetically (FSC = 0.0058; $P < 0.001$) differentiated. However, parasite load was not associated with either genome-wide methylation levels or epigenetic differentiation. Instead, eight ep locus-specific methylation states were disproportionately differentiated and 35 ep locus-specific methylation states were significantly positively and negatively associated with parasite load. Following Sanger sequencing, genome mapping and GENEONTOLOGY (GO) annotation, some of these ep loci were linked to genes involved in regulation of cell cycle, signalling, metabolism, immune system and notably rRNA methylation, histone acetylation and small RNAs. These findings demonstrate a locus-specific epigenetic signature of parasite load in populations of a wild bird and suggest intriguing physiological effects of parasite-associated cytosine methylation.

Poster session B - POL 300

Epigenetic signatures of parental effects in soil mites (51911)

Stuart Pierniey, Marianne Mugabo, Tim Benton.

University of Aberdeen; University of Leeds.

Variation among individuals in their life-history phenotype is influenced by past environmental conditions communicated across generations via parental effects. The extent to which such parental effects influences epigenetic variation remains underexplored, despite offering a mechanism through which phenotypic plasticity can be generated.

Here we describe a study that examines interrelationships between parental effects and cytosine methylation in the soil mite *Sancassania berlesei*. Multiple microcosm populations of soil mite were established from a single natural population that differ in their parental environment by manipulating the age, quality and sex ratio of the adults that comprise the different breeding populations. The age and size at maturity, fecundity, egg size, egg protein content and survival of offspring was followed for the subsequent four generations. The patterns of genome-wide DNA methylation were assayed using a modified version of RAD-genotyping that involves parallel restrictions with methylation sensitive and insensitive

isoschizomers. Comparison of the levels of DNA methylation between different parental backgrounds provides estimates of the extent to which environment affects epigenetic signatures and how it is correlated with phenotype. Comparison between parental backgrounds highlights whether epigenetic variation is heritable. In both cases epialleles are examined using gene ontology and pathway analyses to highlight any functional linkages with phenotype.

Poster session B - POL 300

Contribution of epigenetic mechanisms to phenotypic plasticity in *Neurospora crassa* (52183)

Ilkka Kronholm, Jouni Laakso, Tarmo Ketola.

University of Jyväskylä; University of Helsinki.

Organisms respond to environmental changes by altering their development to produce a different phenotype and by maintaining physiological homeostasis on the face of fluctuating environments, a phenomenon called phenotypic plasticity. Plasticity can be achieved by regulation of gene expression. These gene expression patterns can also be directed and maintained by epigenetic mechanisms, chemical modifications of DNA or associated proteins.

Altering epigenetic patterns can have effects on phenotypic plasticity but few examples exist so far. Thus, the generality of this phenomenon remains unknown. We investigated to what extent epigenetic mechanisms contribute to phenotypic plasticity in the filamentous fungus *Neurospora crassa*. We used knockout mutants for different epigenetic mechanisms, such as DNA methylation, histone modifications, histone deacetylation, and RNA interference. To quantify phenotypic plasticity we measured reaction norms for the different mutants in different environments, such as NaCl stress, oxidative stress, pH and sugar concentration.

We show to what extent and which epigenetic mechanisms contribute to phenotypic plasticity in different environments in *Neurospora*. These results can resolve if epigenetic mechanisms are responsible for phenotypic plasticity and the ability to cope with adverse environmental conditions. Furthermore, they will help us to understand if and how epigenetics interacts with evolutionary adaptation via phenotypic plasticity.

Poster session B - POL 300

DNA methylation patterns, CpG o/e ratio and Non-Gaussian distributions : a pan-species study (52309)

Benoit Aliaga, Jan Bulla, David Duval, Christoph Grunau.

*Laboratoire Interactions Hôtes-Pathogènes-Environnements (IHPE) UMR5244
CNRS/University of Perpignan; University of Bergen.*

Epigenetic mechanisms contribute to generate phenotypic variability and could therefore be involved in evolution. The most studied of these mechanisms is DNA methylation i.e. the addition of a methyl group to cytosines leading to 5-methyl-cytosine (5mC). Methylation is predominantly (but not exclusively) located in CpG dinucleotides. Whereas in vertebrates and plants, DNA methylation is known to be involved in control of gene expression, its role in invertebrates is far less understood. Being one of the most analysed epigenetic information carriers does not mean that DNA methylation was exhaustively studied in many species. Its analysis remains expensive and needs expertise. Since 5mC is spontaneously deaminated to thymine, CpG underrepresentation can be used as a proxy to estimate 5mC levels and distribution patterns. Our work has consisted in predicting the methylation status in transcriptomes for 365 species from CpG observed to expected ratios (CpG o/e). We developed new statistical methods based on different Gaussian and non Gaussian distributions. Best results were obtained with a non Gaussian distribution for more than 80% of the studied species. We will present this new method that allows prediction of DNA methylation using mRNA data alone.

Poster session B - POL 300

Impact of coastal pollution on epigenetics and reproductive fitness of marine snail *Hexaplex trunculus* (52365)

Maja Šrut, Anamaria Štambuk, Anita Erdelez, Dorotea Polović, Martina Furdek, Melita Peharda, Goran Klobučar.

Department of Biology, Faculty of Science, University of Zagreb, Croatia; Institute of Oceanography and Fisheries, Croatia; Division for Marine and Environmental Research, Ruđer Bošković Institute, Croatia.

Hexaplex trunculus is a marine gastropod whose reproductive fitness can be severely affected by very low concentration of antifouling compound tributyl-tin (TBT). TBT has strong xenoandrogen impact in snails, causing development of imposex, e.g. superimposition of male sexual characteristic in females, thereby affecting the fitness of entire populations. TBT is also known as a DNA demethylating agent. The aim of this study was to unravel the interactions between TBT bioaccumulation, reproductive fitness, epigenetic and genetic endpoints in murex snail *H. trunculus*. Four populations inhabiting polluted sites with intense marine traffic and boat maintenance activity and three inhabiting sites with low anthropogenic impact were sampled in the coastal eastern Adriatic. Higher incidence of imposex was observed in snails inhabiting polluted than the reference sites. Analysis of methylation sensitive amplification polymorphism (MSAP) revealed existence of epigenetic differentiation among populations and lack of genetic population structure. Level of DNA methylation significantly correlated with the imposex level, suggesting epigenetic background of imposex development.

Poster session B - POL 300

Epigenetic variation and selection by aphids in *Arabidopsis thaliana* (52372)

Klara Kropivšek, Christian Heichinger, Tobias Züst, Lindsay Turnbull, Bernhard Schmid, Ueli Grossniklaus.

Institute of Plant Biology & Zurich-Basel Plant Science Center, University of Zurich; Institute of Evolutionary Biology and Environmental Studies, University of Zurich; Department of Ecology and Evolutionary Biology, Cornell University; Department of Plant Sciences, University of Oxford.

Aphids, plant parasites, exert strong selective pressure that leads to stronger defense responses in plants, such as higher trichome densities (Levin, 1973). Different aphid species led to selection of distinct phenotypes in experimentally evolved populations of *Arabidopsis* (Züst et al., 2012). Preliminary experiments indicate that this can occur within a given genotype, which suggests a role for epigenetic variation in this adaptive response (Hirsch et al., 2012). We measured trichome densities in 2 accessions of *Arabidopsis* that were exposed to different aphid species over 5 generations (Züst et al., 2012), and grown in absence of aphids for 2 generations. Both accessions responded with higher trichome densities in one aphid species treatment compared to the other. This finding is in concordance with other data on epigenetic inheritance (Scoville et al., 2011), yet the causal relationship between epigenetic changes and observed phenotypes needs to be elucidated at the molecular and genetic level. We will analyse the genome-wide distribution of DNA-methylation to identify differentially methylated regions and to identify candidate genes involved in this defense response. We will investigate the function of selected genes by altering their DNA-methylation status using RNA-directed DNA-methylation to establish a causal link between adaptive phenotypic changes and the underlying epigenetic variation.

Poster session B - POL 300

Heritable methylation patterns in widespread apomictic dandelions (52806)

Veronica Preite.

NIOO.

Evidence has been found for stress-induced methylation changes in different plant species, but it is unclear how stable these methylation changes are over multiple generations. We studied heritable methylation patterns triggered by environmental stress in apomictic dandelions, using methylation-sensitive (MS) AFLPs.

We exposed apomictic clone members to control, drought and salicylic acid stress and evaluated the offspring under control conditions for two subsequent generations. We found spontaneous methylation changes that occurred in the control as well as the stressed groups which showed a heritable fraction that was stable across three generations. Additionally, clone members that originated from different geographic sampling locations showed distinctive methylation patterns derived possibly from accumulating methylation changes. In contrast to our expectations, we found no evident stress-induced methylation changes. We also studied natural variation across dandelion populations which revealed a modest fraction of heritable methylation variation that could not be explained by genetic variation. Thus autonomous epigenetic variation potentially adds to the adaptive capacity of apomictic dandelions.

These results suggest that spontaneous rather than stress-induced methylation changes may play a role in building up heritable epigenetic variation that adds to adaptive differences within clonal lineages and across populations.

Poster session B - POL 300

DNA Methylation, Epigenetics, and Evolution in Vertebrates (52390)

Annalisa Varriale.

Università degli Studi di Napoli Federico II.

DNA methylation is a key epigenetic modification in the vertebrate genomes known to be involved in biological processes such as regulation of gene expression, DNA structure and control of transposable elements. Despite increasing knowledge about DNA methylation, we still lack a complete understanding of its specific functions and correlation with environment and gene expression in diverse organisms. To understand how global DNA methylation levels changed under environmental influence during vertebrate evolution, we analyzed its distribution pattern along the whole genome in mammals, reptiles and fishes showing that it is correlated with temperature, independently on phylogenetic inheritance. Other studies in mammals and plants have evidenced that environmental stimuli can promote epigenetic changes that, in turn, might generate localized changes in DNA sequence resulting in phenotypic effects. All these observations suggest that environment can affect the epigenome of vertebrates by generating hugely different methylation patterns that could, possibly, reflect in phenotypic differences. We are at the first steps towards the understanding of mechanisms that underlie the role of environment in molding the entire genome over evolutionary times. The next challenge will be to map similarities and differences of DNA methylation in vertebrates and to associate them with environmental adaptation and evolution.

Poster session B - POL 300

Social and dietary stress and its implications on the life-history traits in wild rodents (bank vole – *Myodes glareolus*) through epigenetic changes. (52873)

Joannes van Cann, Esa Koskela, Mappes Tapio, Sims Angela, Watts Phill.

University of Jyväskylä; University of Oulu.

Cyclic mammals can experience different forms of stress such as low food availability and high population densities. Especially for prenatal or early life stress, individuals may incur profound effects on life-history traits. It is theorized that the environment of the mother can lead to predictive adaptive changes in the offspring which can persevere over multiple generations, and that this is regulated by epigenetic mechanisms. In this study pregnant bank voles were exposed to either one or both stressors consisting of a low-protein diet, which mimics an environment with low food availability, and repeated close contact between

pregnant females, which mimics a high population density. Life-history traits of the offspring were measured after which they were placed in semi-natural enclosures with high or low population densities, where they were allowed to breed. Preliminary results show that social stress has a negative effect on the litter size, while food stress has a negative effect on birth weight. However, exposure to both stressors does not result in a lower birth weight, indicating a role for terminal investment as an adaptation to stress. These life-history modifications may indicate persisting epigenetic changes, in turn leading to differential breeding success and survival in natural rodent populations.

Poster session B - POL 300

Epigenetics in forest trees - Do methylation patterns in conifers change with environmental conditions? (52912)

Katrin Heer, Kristian Ullrich, Stefan Rensing, Lars Opgenoorth.

Conservation Biology, University of Marburg; Department of Ecology, University Marburg; Plant Cell Biology, University of Marburg.

Forest trees are particularly challenged by climate change due to their sessile lifestyle and long generation times. While adaptation based on genetic changes might be too slow to permit a reaction to rapid environmental changes in long-lived species, epigenetic mechanisms might enable a faster response to a changing environment. In a proof-of-concept study, we compare genome-wide methylation patterns in clone pairs of Norway spruce (*Picea abies*) of which the ortet and ramet grow under different environmental conditions since 1990. By using SeqCap Epi Kit (NimbleGen) we combine exome capture and bisulfite sequencing and target ~80 Gb in genes that were identified and annotated in the Norway spruce genome project. If we find consistent changes in methylation patterns across clone pairs this would strongly indicate that methylation patterns are involved in the reaction to changing environmental conditions within the lifetime of the trees. First results of this proof-of-concept study and a critical review of the feasibility of this approach will be presented during the conference.

Poster session B - POL 300

Plasticity and epigenetics between native and invasive *Phragmites* lineages, between genotypes, and within genotypes (53023)

Vladimir Douhovnikoff, Amy Spens.

Biology Department, Bowdoin College.

We hypothesize that epigenetic control, a form of plasticity that is transferable across cell divisions as well as sexual generations, confers dynamic and stable responses to environmental heterogeneity, characteristics that may be critical for successful plant invasions. *Phragmites* provides an exceptional opportunity for the comparison of invasive and

non-invasive lineages within the same species, across a range of environmental conditions. *Phragmites* is also a facultatively clonal plant making possible the study of replicated identical genotypes. In an environmentally variable field based study in three marshes in Maine, USA we have measured epigenetic variation between clonal ramets, between genotypes, and between conspecific native and invasive lineages. Epigenetic variation was quantified using methylation sensitive amplified fragment length polymorphisms (MS-AFLPs). Results found large and significant differences ($p < 0.001$) in epigenome between lineages (native vs. invasive) and within genotypes (clonal ramets) but smaller difference between genotypes within lineages (genetically distinct genotypes). This suggests that the native and invasive lineages have distinct epigenomes, most epigenetic variation within a lineage is independent of genetic variation, and clonal ramets have distinct epigenomes in response to local site variation. In our working model, these results would indicate high levels of epigenetic plasticity within genotypes.

Poster session B - POL 300

Adaptations in the brains of Neotropical butterflies (51638)

Stephen Montgomery, Richard Merrill, Swidbert Ott.

University College London; University of Cambridge; University of Leicester .

Interspecific comparisons of brain structure can inform our functional understanding of brain regions, identify adaptations to species-specific ecologies, and explore what constrains adaptive changes in brain structure and shapes co-evolution between functionally-related structures. The value of such comparisons is enhanced when the species considered have known ecological differences. Lepidoptera have long been a favoured model in evolutionary biology, but to date descriptions of brain anatomy have largely focused on a few commonly used neurobiological model species. Through a combination of inter-specific and intra-specific comparative analyses my research explores how ecological selection pressures shape brain structure across different phylogenetic timescales in mimetic, Neotropical butterflies. Results to date have identified adaptive divergence in sensory neuropil, reflecting diel pattern and habitat preference, and the first description of sexual dimorphism in the antennal lobes of a diurnal butterfly, which is hypothesised to be linked to heightened reliance on pheromone communication in ithomiines. Further analyses concern the evolution and developmental plasticity of the mushroom bodies in Heliconiini. These structures, which are linked to memory and learning, are notably expanded in *Heliconius*. I am using comparative and experimental analyses to test the hypothesis that this expansion is related to a derived diet and foraging behaviour.

Poster session B - POL 300

Large brains enhance female, but not male survival in the guppy (51994)

Alexander Kotrschal, Séverine Buechel, Sarah Zala, Alberto Corral, Dustin Penn, Niclas Kolm.

Stockholm University; Veterinary University Vienna.

Brain size is remarkably variable in vertebrates. To fully understand how brain size may evolve in natural populations, data on the fitness effects of brain size is required. However, to date such evidence is lacking. Using guppies (*Poecilia reticulata*) that were artificially selected for large and small relative brain size, we investigated how brain size affects survival. We cohoused mixed groups of 4800 marked small- and large-brained individuals equally distributed in six large semi-natural streams with their natural predator, *Crenicichla alta*, and monitored survival in weekly censuses until a predefined criterion of 50 % survival was met. Five months later, large-brained females had 13 % higher survival compared to small-brained females while brain size had no discernible effect on male survival. We suggest that large-brained females have a cognitive advantage that allow them to better evade predation, whereas large-brained males are more colorful, which may counteract any potentially beneficial effects of brain size. Our study provides the first experimental evidence that a larger brain size may confer survival benefits under naturalistic conditions and shows that the advantages can be sex-specific. We conclude that such fitness benefits provide an important selective force in the evolution of brain size.

Poster session B - POL 300

A mathematical model for brain development (52118)

Mauricio González-Forero, Timm Faulwasser, Laurent Lehmann.

University of Lausanne; École Polytechnique Fédérale de Lausanne (EPFL).

Growing and maintaining a large brain entails energetic costs. A large brain can evolve if these costs are compensated by benefits from correspondingly high cognitive abilities. Benefits are thought to arise from ecological and social pressures, and mostly verbal theories have yielded predictions that have received some support. Here we develop a mathematical model for energy allocation into brain growth. We consider a body composed of brain cells, reproductive cells, and aneural, non-reproductive cells. Brain cells give the body skills to solve problems. Problem solving allows the body to obtain energy from the environment. The energy obtained can be allocated into maintaining and producing one or more of the three cell types. Under standard life-history assumptions, energy allocation maximizes lifetime number of offspring. Performing this maximization, we obtain ontogenetic curves for brain size. The model depends on measurable metabolic parameters, and is thus testable. The model can be extended to include social environmental pressures by letting problem solving depend on social partner's skill. Such an extension may yield discerning predictions among hypotheses for the evolution of brain size.

Poster session B - POL 300

Genetic mechanisms of caste differentiation in response to stress imposed by dominant female breeders of naked mole rats. (52303)

Bitao Qiu, Qiye Li, Pei Zhang, Zongji Wang, Lijun Jin, Yang Zhou, Vadim N. Gladyshev, Jacobus J Boomsma, Guojie Zhang.

Centre for Social Evolution, University of Copenhagen; China National GeneBank, BGI-Shenzhen; Centre for GeoGenetics, Natural History Museum of Denmark, University of Copenhagen; School of Bioscience & Bioengineering, South China University of Technology; Division of Genetics, Department of Medicine, Brigham and Women's Hospital, Harvard Medical School.

Naked mole rats evolved eusocial division of labor by behavioral suppression, but the regulatory mechanisms and evolutionary underpinning of behavioral caste differentiation in mammals are largely unknown. We sequenced transcriptomes and DNA-methylomes of brains and gonads of male and female breeders and subordinates, and mapped these data on the genome. Only 4-5% of the brain genes were differentially expressed between castes, and a significant fraction of them interacted in gene networks with similar functional modules for both sexes. Gonadotropin-releasing hormone (GNRH1) was central in one of these modules, and linked with differentially expressed stress-response-genes, particularly neuropeptide-Y (NPY) and corticotrophin-releasing hormone (CRH). However, ovaries showed large expression differences between female castes with the estrogen synthesis pathway being blocked in subordinate females. Testes showed only modest gene expression differences with sperm-related genes being down-regulated in subordinates. Spermatogenesis in naked mole rats appeared to be degenerated, consistent with lack of sperm competition and complete mate-choice control by the breeding female. Caste differences in brain DNA methylation were also modest, but some of them were likewise associated with a stress response module. Our study strongly reinforces that reproductive suppression of both males and females is maintained by stress imposed by the bullying dominant female.

Poster session B - POL 300

Vomeroneasal receptor families in the deer mouse *Peromyscus maniculatus*: Towards an evolutionary analysis (52867)

Jean-Marc Lassance, Yoh Isogai, Catherine Dulac, Hopi Hoekstra.

Harvard University; Howard Hughes Medical Institute.

Chemoreceptors are the first element in a complex pathway that can ultimately affect behavior -- changes in their biochemical properties or expression pattern have the potential to modulate specific behavioral responses. In particular, the activation of sensory neurons in the VNO is directly associated with changes in behavior, such as aggression, avoidance or mating. To understand the diversity and evolution of pheromone systems in wild populations, we are studying deer mice (genus *Peromyscus*), which diverged from *Mus* approximately 25 MYA. Here, we report on the characterization of VNO receptors from the most common and widespread species in North America, *P. maniculatus*. In total, we identified 150 and 90 putative V1R and V2R genes, respectively, in the *Peromyscus* genome, fewer than in *M. musculus* (239 and 120, respectively). While clades previously identified in *Mus* have representatives in *Peromyscus*, our phylogenetic reconstructions indicate that most gene duplications took place after the split between the two lineages; several clades show sign of

lineage-specific expansion or contraction. These differences in the chemosensory receptor repertoires likely reflect the unique habitats as well as social and mating behavior of deer mice.

Poster session B - POL 300

Bloodmeal size defines ejaculate production and impacts on male mating behaviour in bedbugs (51677)

Oliver Otti, Bettina Kaldun.

Animal Population Ecology, Animal Ecology I, University of Bayreuth.

Reproductive costs have been investigated mainly in females, even though males certainly also pay costs. As nutrition provides the basis for the production of biomass and reproductive tissues, variation in food availability might cause variation in sperm and seminal fluid production. We assume that meal size is directly associated with ejaculate size. Here we analysed the production of sperm and seminal fluid within three different feeding regimes with the result that large meals produced significantly more sperm and seminal fluid than smaller meals. While the number of offspring produced after a single mating was not influenced by feeding-status, copulation duration and ejaculate expenditure were shorter respectively smaller under food restriction. Food restricted males maintained mating for a shorter time than fully fed males, suggesting in a multiple mating context males pay a cost of reproduction and a direct effect of feeding on ejaculate production and male mating behaviour. Therefore, environmental variation, e.g. food availability, has a direct effect on variation in male reproductive traits, indicating that natural selection and sexual selection interactively define selection pressure on reproductive traits. As males often modulate their ejaculate size depending on the mating situation, future studies are needed to elucidate whether the amount of ejaculate available might interfere with different mating strategies.

Poster session B - POL 300

Parental roles, offspring fitness and gene expression under flexible parenting strategies (51699)

Darren J. Parker, Christopher B. Cunningham, Craig A. Walling, Clare E. Stamper, Megan L. Head, Eileen M. Roy-Zokan, Elizabeth C. McKinney, Michael G. Ritchie, Allen J. Moore.

University of St. Andrews; University of Georgia; University of Exeter; University of Edinburgh; The Australian National University.

Parenting in the burying beetle *Nicrophorus vespilloides* includes direct feeding of offspring and flexibility in both which and how many parents provide care. This flexibility is unusual and raises questions of why both sexes should care. We first examine the consequences of flexibility, and find that offspring do equally well regardless of the sex or number of parents. We used RNA-seq to examine differential gene expression associated with parenting and

found a largely overlapping set of expressed genes in both uniparental and biparental females and in uniparental males. These include genes such as vitellogenin, more commonly associated with reproduction in females, and takeout, associated with sex-specific behaviour. Biparental males did not differentially express many genes associated with parenting. Instead, gene expression was similar to non-caring states. Thus, by combining our behavioural and genetic analyses, our study shows that biparental care involves reduced male care rather than parental specialisation.

Poster session B - POL 300

Evolution of communication in socially polymorphic halictid bees (51720)

Bernadette Wittwer, Mark A. Elgar, Naomi E. Pierce, Sarah D. Kocher.

School of BioSciences, University of Melbourne; Department of Organismic and Evolutionary Biology, Museum of Comparative Zoology, Harvard University.

Communication is a key component for the maintenance and evolution of social behaviour. Studies into the evolution of communication in social insects focus primarily on chemical signals, with remarkably few investigating the functional importance of the receiving apparatus: the antennae. Here, we examine antennal diversity in halictid bees. Within the Halictidae, eusociality has been gained and lost a number of times, making the group ideal for investigating how communication systems are modified as social structure changes. We focus primarily on a socially polymorphic halictid bee, *Lasioglossum albipes*, where different populations produce either solitary or eusocial nests. An initial screen for genetic differences between behavioural morphs indicated there could be genotypic differences in genes associated with olfaction. Our research combines this behavioural and genomic data with morphological assays of antennal structures to provide insights into the role of communication in the evolution of eusociality.

Poster session B - POL 300

Predicting individual behaviour of wild crickets from lab measures of personality? (51873)

David Fisher, Adèle James, Rolando Rodríguez-Muñoz, Tom Tregenza.

University of Exeter, Cornwall, UK; Université François, Tours, Rabelais, France.

Examining the relevance of “animal personality” involves identifying the eco-evolutionary processes that lead to consistent among-individual behavioural variation. Typically, personality is assayed in captivity and related to important traits such as lifespan or fitness in the wild. However, behaviour is characteristically context specific and personalities in the laboratory may not represent personalities displayed in the wild. We compared laboratory and field measurements of the behaviour of wild field crickets (*Gryllus campestris*), by repeatedly measuring individual behaviour in the wild and repeatedly capturing the same individuals and

measuring their behaviour in captivity. We focused on three traits: boldness, activity and exploration. For all traits, behaviour in the laboratory did not predict behaviour in the wild. Boldness and activity were repeatable in the laboratory, but in the wild only activity was repeatable, despite measuring over 170 individuals 900+ times for boldness and 4000+ times for activity and exploration. Traits measured in the wild were predominantly influenced by external factors. We explored links between personality measures in both contexts and life-history traits and mating success in the wild. We discuss our results in the context of the Pace of Life Syndrome hypothesis as an explanation for the ubiquity of animal personalities

Poster session B - POL 300

Associations between personality and life-history traits differ across blue tit populations (51923)

Gabrielle Dubuc Messier, Anne Charmantier, Denis Réale.

Université du Québec à Montréal; Centre d'écologie fonctionnelle et évolutive, CNRS.

The pace-of-life syndrome hypothesis predicts that populations experiencing contrasted conditions will differ in a suite of behavioural, physiological and life history traits because these traits have coevolved under habitat-specific selective pressures. Such differences in coevolution among traits should thus be reflected by different P (co)variance matrices depending on the population and on the habitat. We compared mean phenotype and P matrices for personality (exploration patterns and handling aggression) and life-history traits (laying date and clutch size) across three blue tit (*Cyanistes caeruleus*) populations leaving in contrasted habitats. At the metapopulation level, we found a covariance between some behavioural and life history traits that is consistent with the pace-of-life hypothesis. Mean phenotypes and the covariance between traits varied substantially among populations, although habitat did not explain this variation as expected initially. Overall, our results support the pace-of-life hypothesis but they also reveal that we need considerable knowledge on the biology of a species and on the populations' ecological contexts before we can predict the relationships between personality and life history traits.

Poster session B - POL 300

Brain size affects the predator response of female guppies (*Poecilia reticulata*) (52000)

Wouter van der Bijl, Malin Thyselius, Alexander Kotrschal, Niclas Kolm.

Stockholm University.

There exists large variation in both absolute and relative brain size throughout the vertebrate lineages. While there has been a large effort to identify ecological drivers of this variation using comparative analysis, there exists little experimental work. Artificial selection in guppies (*Poecilia reticulata*) has produced small and large brained individuals. Recent work

on these selection lines has shown that large brained females had better survival when exposed to prolonged predation pressure under semi-natural conditions.

To elucidate the proximate mechanism behind this result we examined the behavioral response of these artificially selected guppies towards a model predator. Large brained females, but not males, spent less time performing predator inspections, an inherently risky behavior. Video tracking revealed that large brained females were further away from the predator while the response to a novel object control (a coffee mug) revealed no brain size differences.

These results suggest that large brained female guppies take less risk when confronted with a predator. They might be able to assess risk from a larger distance due to a superior visual system, or need less sensory information to reach an accurate conclusion. In natural situations, the threat of predation may thus result in selection for large brains.

Poster session B - POL 300

Allelic variation at TrpA1 and trpl regulates thermal-mediated behavior in the lab and field in *Drosophila* (52026)

Subhash Rajpurohit, Justin Walsh, Alan Bergland, Dmitri Petrov, Paul Schmidt.

University of Pennsylvania; Stanford University.

In genomic screens for SNPs that vary predictably over spatial and temporal gradients in natural populations of *D. melanogaster*, we identified seasonal/clinal polymorphism in two transient receptor potential ion channel (TRP) genes, TrpA1 and trpl. These ion channels are associated with Ca²⁺ influx, are light sensitive, and regulate aspects of sensory behavior related to temperature. Temperature varies predictably with season/latitude in eastern North America, generates context-dependency to multiple fitness parameters, and may underlie a series of adaptive life history tradeoffs. We hypothesized that these candidate cation channel polymorphisms were of functional significance and affected organismal response to temperature in the wild. To test this hypothesis, we constructed a replicated series of population cages to evaluate the focal SNPs of interest in a randomized genetic background. After ten generations of recombination, we evaluated the behavior of TrpA1 and trpl alleles using three distinct methodologies in the laboratory and field. The data demonstrate that, for both genes, the allele associated with northern locales and winter season exhibits a pronounced preference for cooler temperatures whereas the allele associated with southern/summer habitats prefers warmer temperatures. These data suggest that naturally occurring, cis-regulatory variation at these genes affects thermal behavior and contributes to climatic adaptation.

Poster session B - POL 300

Variation of absorption spectrum and gene expression pattern of red opsins under different light environments and its effect on behavioral spectral sensitivity in guppies, *Poecilia reticulata* (52171)

Yusuke Sakai, Satoshi Kasagi, Shoji Kawamura, Hajime Ohtsuki, Masakado Kawata.

Department of Ecology and Evolutionary Biology, Graduate School of Life Sciences, Tohoku University; Graduate School of Frontier Sciences, The University of Tokyo.

Color vision can facilitate finding food, avoiding predators and selecting mates. Color vision is enabled by utility of different spectral types of cone visual pigments which comprise an opsin and a chromophore. The guppy exhibits variation of spectral sensitivity among its four subtypes of long-wavelength sensitive opsin genes (LWS-1, LWS-2, LWS-3 and LWS-4). Additionally, allelic spectral variation is known for LWS-1 (A180 and S180). However, not know is if gene expression level differs among the loci and the alleles and if the spectral and expression variation is associated with variation of behavioral response to varying light spectra. In this study we examined the effect of different LWS-1 genotypes (A180/A180 and S180/S180) and opsin gene expression levels on behavioral response to different light regimes by optomotor response. The A180/A180 fish showed higher sensitivity to lights (546nm) than S180/S180 fish. Furthermore, juveniles reared in different light environments showed variation of gene expression in LWS-1. Individuals reared under orange light showed increased expression levels of LWS-1 and were more sensitive to orange than other lights. These results depict plasticity of opsin gene expression under different lightings and its interaction with opsin absorption spectra and behavioral response under varying light environment.

Poster session B - POL 300

Image analysis of weaverbird nests reveals signature weave patterns (52308)

Ida E Bailey, André Backes, Patrick T Walsh, Kate V Morgan, Simone L Meddle, Susan D Healy, **Eira Ihalainen**.

University of St Andrews; Universidade Federal de Uberlândia, Faculdade de Computação, Brazil; School of Biological Sciences, University of Edinburgh, Ashworth, King's Buildings, Mayfield Road, ; Roslin Institute, Royal School of Veterinary Studies, University of Edinburgh, Easter Bush, EH25 9RG.

In nature, many animals build structures. Individuality in construction behaviour within species may allow for more flexible use of building sites and materials, a potentially advantageous trait in stochastic environments. While measuring structures at the scale of their gross morphology (e.g. length, volume, weight) is relatively easy this level of detail may be insufficient for detecting individuality in construction patterns. Capturing individuality in animal-built structures, such as can be done with the structures designed and built by human architects or artists, is therefore more challenging. Here we tested whether computer-aided image texture classification approaches can be used to describe textural variation in the nests of weaverbirds (*Ploceus* species) in order to attribute nests to the individual weaverbird that built them. We found that such an approach does allow the assignment of a signature to weaverbirds' nests. We suggest that this approach is a useful tool with which to examine individual variation across a range of animal constructions and not just for nests.

Effects of colony genotype composition on a single brain methylome (52375)

Oksana Riba-Grognuz, DeWayne Shoemaker, Laurent Keller.

University of Lausanne; Swiss Institute of Bioinformatics; USDA-ARS Center for Medical, Agricultural, and Veterinary Entomology.

Epigenetic mechanisms regulate behavioral plasticity by translating environmental cues into stable transcriptional responses. In eusocial insects the morphological and behavioral phenotypes can be influenced by the genotypic composition of a colony. The red fire ant *Solenopsis invicta* provides a unique opportunity to study the role of genotypic composition, because they exist in two social forms determined by two variants (SB and Sb) of a social chromosome. Monogyne colonies contain a single queen with SB/SB genotype and exclusively SB/SB workers. By contrast, polygyne colonies contain multiple queens with an SB/Sb genotype and a mixture of SB/SB and SB/Sb workers. Experiments showed that SB/SB workers change their behavior and accept several SB/Sb queens if their colony contains more than 10% SB/Sb workers. To investigate how the genotypic composition of a colony affects patterns of brain DNA methylation and worker behavior we performed RNA-seq and BS-seq on single brains of SB/SB and SB/Sb workers introduced in host colonies of both social forms. Our results reveal the effect of DNA methylation on transcriptional response of single brains and the resulting behavioral response mediated by changes in social environment.

I am too old for this: ageing great tits (*Parus major*) innovate less and persist less at a problem-solving task (52382)

Maria Poujai.

University of Lausanne.

Ageing is known to reduce animals' fitness over time, but few studies have examined its effect on their behavioural traits. Innovative problem-solving is a cognitive trait of particular interest as it is increasingly viewed as a manifestation of animals' ability to adjust to changing environments. Solving a novel problem requires several qualities, including low neophobia, high persistence, and learning. We chose adult wild great tits (*Parus major*) to investigate age differences in problem-solving performance, neophobia, and persistence. Using 5 years of cross-sectional data, we isolated within-individual behavioural changes by taking into account between-individual differences and demographic effects. Our results revealed that great tits experience a consistent within-individual decline in problem-solving ability. We also witnessed a within-individual decrease in persistence, but not in neophobia. These findings suggest that great tits undergo cognitive ageing over time, a process which appears to be induced by a reduction in persistence. However, persistence did not explain all age-dependent variations in cognitive ability. A number of other factors could underpin this decline, including a lack of motivation, stress management, learning difficulties, and limited motor

diversity. Behavioural consequences of ageing may be disadvantageous for older individuals and thus be a proximate mechanism of reproductive senescence.

Poster session B - POL 300

Genetic underpinning of a major evolutionary trait: eusociality in the facultative eusocial sweat bee *Halictus rubicundus* (52417)

Antonella SORO, Ioana LEMNIAN, Markus BÖNN, Ivo GROSSE, Margarita URIBE-LOPEZ, Sophie CARDINAL, Bryan N. DANFORTH, Robert J. PAXTON.

University Halle-Wittenberg, Halle (Saale), Germany; Cornell University, New York, USA; German Centre for Integrative Biodiversity Research (iDiv), Halle-Jena-Leipzig, Germany.

Eusociality is a major evolutionary innovation that has independently arisen multiple times in insects and has led to the ecological dominance of social species, but candidate genes that underpin this trait have not yet been identified. The application of advanced sequencing technologies to facultative eusocial species, in which some individuals are solitary and others are eusocial, is a powerful approach for the identification of such genes. Here, we perform a comparative transcriptome analysis of the facultative eusocial sweat bee *Halictus rubicundus*, chosen because of phylogeographic evidence for genetic differences between social phenotypes (solitary versus eusocial populations) in North America. Specifically, we analyze the transcriptomes of one solitary population and two eusocial populations of *H. rubicundus* using 454 and Illumina RNA-seq data, assemble a draft transcriptome of *H. rubicundus* comprising approximately 48,000 unigenes, and use it to map SNPs between the two eusocial populations and the one solitary population. We find marked genetic differentiation between the two social phenotypes of *H. rubicundus*, suggesting different demographic histories of the two forms, and point to putative candidate genes underpinning the 'eusocial transition' in this species.

Poster session B - POL 300

Social effects on parental care in the cooperatively breeding Seychelles warbler (52427)

Hannah Dugdale, Lotte van Boheemen, Martijn Hammers, Sjouke Kingma, David Richardson, Jan Komdeur, Terry Burke.

University of Sheffield; Monash University; Wageningen University; University of Groningen; University of East Anglia.

How and why social behaviours evolve is a central question in evolutionary biology. The expression of social behaviours may be affected by the behaviour of the interacting individuals, which can have both a genetic and environmental component. For example, in cooperatively breeding species, both dominants and subordinates can raise the offspring of the dominants. The additional care provided by helpers may allow dominants to reduce their

parental care, providing indirect fitness benefits through increased dominant survival. Dominants may also modify their behaviour dependent on the identity of their social partner, which may have a genetic component. We tested the load-lightening hypothesis in the Seychelles warbler, and investigated social (indirect) genetic effects on parental care. We detected load-lightening, with dominants reducing their provisioning rates when they have more helpers, and discuss the fitness benefits. There was little between-individual variance in the amount of provisioning by dominants, but the variance in dominant provisioning was influenced by the identity of their social mate. The social environment therefore plays a strong role in parental care levels in the Seychelles warbler. We discuss the genetic component of these social mate effects, and their role in the evolution of social behaviour in wild systems.

Poster session B - POL 300

Are dispersing and non-dispersing individuals on different life paths? Looking at telomere lengths in the Collared flycatcher. (52470)

Charlotte Recapet, Blandine Doligez*, Pierre Bize*, *These authors share seniorship.

Département Ecologie et Evolution, Université de Lausanne, Switzerland; Laboratoire Biométrie et Biologie Evolutive UMR CNRS 5558, Université Claude Bernard, Lyon, France; School of Biological Sciences, University of Aberdeen, UK.

In natural populations, trade-offs set the range of possible life histories. Nevertheless, variation in individual strategies is frequently observed within populations. Our previous results in a patchy population of a small passerine, the Collared flycatcher, suggest dispersing and non-dispersing individuals manage differently the trade-off between reproduction and maintenance in the short-term. However the longer-term consequences of such variation need to be examined to test whether dispersing and non-dispersing individuals reach the same lifetime fitness outcome. Because assessing survival and future reproduction prospects in a spatially limited study site can be biased with respect to dispersal, an alternative is to use cumulative, long-term markers of fitness-related traits. As telomere dynamics depend on physiological condition and often predict survival, we first investigate whether telomere length is a good marker of survival and reproduction prospects in our study population. We then test whether dispersing and non-dispersing individuals differ in telomere length and whether such difference depends on reproductive constraints. Based on our previous results, we hypothesise that dispersing birds will invest more in maintenance and exhibit longer telomeres, especially under constrained conditions, than non-dispersing ones. Such differences would be consistent with the integration of dispersal behaviour into a pace-of-life syndrome.

Poster session B - POL 300

The role of the aggression neuropeptide tachykinin in caste differentiation of ants (52500)

Jack Howe, Morten Schiøtt, Jacobus J. Boomsma.

Centre of Social Evolution, Department of Biology, University of Copenhagen.

Tachykinin is a neuropeptide known to control aggression in a wide range of animals, and appears to control the position of the stimulus response threshold for aggressive behaviour in *Drosophila* (Asahina et al., 2014).

We investigated whether the conserved gene Tachykinin has been coopted in ants that evolved physically differentiated female castes. We used the leaf-cutting ant *Acromyrmex echinator* as a model because it has a reference genome, facilitating gene expression comparisons between: 1. founding queens (aggressive) and virgin queens (non-aggressive), and 2. large, aggressive foraging workers, and small nursing workers that are generally less aggressive.

We found that relative expression levels of tachykinin and its receptor agreed with hypothesised motivation states of the worker castes and their roles in colony defence, but expression appeared to disagree with aggression shown by founding queens, although this conclusion changed when adjusting for brain-mass differences between castes.

Tachykinin expression may therefore be important for explaining the extent of aggression by workers for different aspects colony defence, but it remains possible that aggression of founding queens is regulated by alternative genes involved in ancestral nest foundation and defence that predate the evolution of eusociality in the Hymenoptera.

Poster session B - POL 300

Inbreeding impacts reproductive success but not sperm performance in wild male song sparrows (52572)

Sylvain Losdat, Lukas F. Keller, Pirmin Nietlisbach, Peter Arcese, Ryan R. Germain, Jane M. Reid.

University of Aberdeen; University of Zürich; University of Zürich; University of British Columbia; University of British Columbia; University of Aberdeen.

Reproductive success is an extremely variable fitness component resulting from numerous behavioural and physiological processes, yet the genetic and environmental determinants of male reproductive success remain to be elucidated. We used long-term genetic pedigree data from wild song sparrows to demonstrate strong inbreeding depression in major components of male reproductive success. However, understanding the evolution of reproductive strategies and fitness in nature requires that the key life-history and physiological constraints underlying such inbreeding depression is understood. Sperm performance is a major determinant of male reproductive success in species with intense sperm competition. However the prediction that inbreeding depression in sperm performance could underlie inbreeding depression in male reproductive success has not been tested in nature. We therefore quantified inbreeding depression in sperm performance in the focal song sparrow population across three years. Contrary to prediction, sperm swimming velocity, motility, and longevity, which are key components of sperm performance, did not show significant inbreeding depression. These data imply that the severe inbreeding depression observed in male reproductive success may

not stem primarily from reduced sperm performance in inbred males, but instead may stem from inbreeding depression in other fitness-related traits such as sexually-selected behavioural traits.

Poster session B - POL 300

Plasticity of aggression: the effects of current and past predation risk, social environment and sex (52579)

Gábor Herczeg, Nurul Izza Ab Ghani, Juha Merilä.

Behavioural Ecology Group, Department of Systematic Zoology and Ecology, Eötvös Loránd University; Department of Biology, Faculty of Science, University of Putra Malaysia; Ecological Genetics Research Unit, Department of Biosciences, University of Helsinki.

Behaviours are plastic traits allowing fast changes and fine-tuning in trait expression in response to situational demands. Aggression is a behaviour where the right behavioural decisions can have immediate fitness consequences. Using a factorial common garden experiment we tested how past and present perceived predation risk, the social environment and sex affected two components of aggression (viz. hesitation to attack and attack intensity) in a social fish species, the three-spined stickleback (*Gasterosteus aculeatus*). Significant individual differences in both hesitation and aggression suggest that these traits represent animal personality. The social environment influenced expression of aggression: fish kept in pairs attacked quicker than fish reared either alone or in large groups. Treatment influences on attack intensity were more complex. While males were on average more aggressive than females, males reared alone in the absence of past exposure to predator cues and alone-reared females in the absence of current predatory cues were more aggressive than the rest of the groups. The results demonstrate complex underpinnings to plasticity-driven behavioural variation, and draw attention to the fact that the interpretation of the presence/absence of an expected behavioural response may be difficult if it is influenced by both past and present environmental conditions.

Poster session B - POL 300

The effect of brain size on mate choice and mating competition in guppies artificially selected for relative brain size (52713)

Alberto Corral-Lopez, Alexander Kotrschal, Niclas Kolm.

Zoology, Stockholm University.

Variation in aspects of brain morphology has been suggested as a plausible mechanism underlying variation in sexual behavior. However, our knowledge of this potential association is based almost exclusively on comparative analyses. In this study, we used guppies that had been artificially selected for large or small relative brain size to experimentally test this association and bridge the gap between micro- and macroevolutionary studies concerning the

link between brain morphology and sexual behavior. A previous study in these artificially selected lines demonstrated that relative brain size is unlikely to affect variation in male sexual behavior in the guppy when individuals interacted in pairs. Therefore, in this study we extended the scope and investigated the effect of relative brain size on female sexual behavior by means of a dichotomous choice test where females with different brain size were allowed to choose between males which also differed in brain size. In addition, we investigated male and female sexual behavior in a situation that permitted social interactions between multiple individuals, allowing for direct and indirect competition. We discuss our findings in light of existing theory on the effect of brain size and cognitive ability on mate choice and complex social interactions during mating.

Poster session B - POL 300

The evolution of “good parent” signals in birds: a meta-analysis (52727)

Gergely Hegyi, Dóra Kötél, Miklós Laczi.

Eötvös Loránd University.

Mate choice is generally costly for the choosy sex, so fitness benefits are necessary for the maintenance of choosiness. Genetic benefits are widely examined and have received overall support from the published literature. On the other hand, direct benefits such as the signaling of parental quality are broadly assumed to be important but their testing is rare and their status in the literature is poorly known. Furthermore, in the case of parental quality signals, there is always a possibility that the observed pattern is modified by the preferential investment of the partner. In a phylogenetically corrected meta-analysis, we collated correlative results from birds concerning parental plumage coloration and the feeding rates of the ornamented parent and its partner. Overall evidence for both parental quality indication and preferential partner investment was weak and this was hardly influenced by the sex of the signaler. However, the correlations of feeding rates and ornamentation in both the ornamented sex and the partner showed a robust phylogenetic effect. Feeding correlations of the partner also differed among plumage color types. Finally, there were characteristic patterns in the relative investment of the two parents, indicating that partner investment cannot be neglected when assessing signals of parental quality.

Poster session B - POL 300

Spider aggression reflects within-group conflict, not group adaptation (52747)

Jay Biernaskie, Kevin Foster.

University of Oxford.

Why do populations and groups vary in individual aggressiveness? In some group-living spiders, individuals can be classified as ‘docile’ or ‘aggressive’, and this has become a key example of animal personality. However, it is unclear why groups vary in their composition

of docile and aggressive types. A recent study of spider groups claims that the docile to aggressive ratio is a collective trait that is finely adapted for the good of the group. In contrast, we use simple models of adaptive social behaviour to show that aggressive types are most common in contexts that promote within-group conflict. We conclude that variation in spider aggression is best explained by a careful consideration of between- and within-group selection.

Poster session B - POL 300

Personality-related survival and sampling bias in wild cricket nymphs (52751)

Petri Niemela, Niels Dingemanse.

LMU-München; Max Planck Institute for Ornithology.

Studies of adaptive individual behavior ask whether individuals differ in behavior(s) and whether individual-level behavior is under selection. Evidence for adaptive personality is biased towards species where behavioral and life-history information can readily be collected in the wild, e.g. ungulates and birds. Here, we report repeatability for behaviors expressed by a wild insect (the field cricket; *Gryllus campestris*). We used mark-recapture models to simultaneously estimate personality-related survival and sampling bias, focusing on a life-history phase where all individuals can readily be sampled (nymphal stage). We assayed home range, flight initiation distance (FID) and emergence time after human-induced disturbance; all behaviors were repeatable. FID alone predicted both encounter and daily survival probability: bolder individuals were observed more often but lived less long. Individuals were also somewhat repeatable in the temperature under which they were assayed. Such environment repeatability can bias repeatability in behavior upwards though this was not the case. Our findings therefore demonstrate that personality variation exists in wild insects, and that it is associated with components of fitness (cf. survival). The opposite effects of FID on survival versus encounter probability illustrates the importance of applying specific study designs that control for sampling bias in the estimation of personality-related fitness components.

Poster session B - POL 300

Peas in a pod: nestling activity is influenced by social interactions and state but not social hierarchy (52782)

Isabel Winney, Mirre JP Simons, Yu-Hsun Hsu, Julia Schroeder, Shinichi Nakagawa, Terry Burke.

University of Sheffield; University of Otago; Max Planck Institute for Ornithology.

To understand why individuals differ and how this variance is maintained is an important aim of evolutionary biology. These interests have propelled the study of animal personality (individual behavioural consistency). The two main mechanisms proposed for generating

between-individual differences in personality are social interactions (imposing frequency-dependent selection) and state (stable physical traits). State dependent models are split as to whether state and behaviour should be positively or negatively correlated. These mechanisms have been tested a few times in adults but rarely in offspring, yet early life-history can have long-lasting consequences for an individual's later life-history and phenotype. Therefore, we pull apart social and state effects on a heritable personality trait in nestling house sparrows on Lundy Island, UK. We used cross-fostering to separate social from natal brood and maternal effects, and represented social structure with the within-brood competitive hierarchy. Overall, nestling activity was unaffected by social hierarchy, but between-individual differences in behaviour were based on mass (larger nestlings moved more) and general social interactions (activity was more similar within a social brood). Similarity within broods could be driven by shared genes, environment, or social interactions. These findings support state-dependent models that stipulate positive feedback between state and behaviour.

Poster session B - POL 300

Parent-offspring co-adaptation: generating between-family variation in behavioural reaction norms for parental provisioning and offspring begging? (52812)

Peter Korsten, Jan Komdeur.

Department of Animal Behaviour, Bielefeld University; Behavioural Ecology and Self-organization Group, University of Groningen.

Recent quantitative genetics theory predicts that coadaptation of the supply of parental care and offspring demand for care can generate between-family variation in parental provisioning and offspring solicitation. Hence, family-level parent-offspring coadaptation may be an important evolutionary source of individual behavioural variation. Key predictions are: (1) there is individual variation in the behavioural reaction norms (BRNs) for parental provisioning and offspring solicitation; (2) these BRNs are correlated between parents and their offspring; (3) cross-fostering creates mismatches between co-adjusted parental and offspring behaviours, leading to fitness costs to parents/offspring. To test these predictions, we carried out a large-scale experiment in a free-living population of blue tits (*Cyanistes caeruleus*). In two years, we cross-fostered 2/3 of the population's broods, while 1/3 served as controls. We estimated BRNs of individual parents by measuring provisioning rates as a function of short-term (6h) brood size manipulations, which created experimental variation in total offspring demand. We estimated BRNs of individual offspring by measuring begging intensity as a function of experimental variation in food deprivation. Our analyses reveal individual variation in the BRNs for parental provisioning and offspring begging, while we find limited evidence for parent-offspring coadaptation on a family level.

Poster session B - POL 300

Colony composition, division of labor and fitness in clonal ant societies (52837)

Yuko Ulrich, Jonathan Saragosti, Daniel Kronauer.

The Rockefeller University; The Rockefeller University; The Rockefeller University.

Testing hypotheses on division of labor requires the ability to manipulate colony composition. In particular, the distribution of individual age and genotype across members of a social group, as well as the size of the group, are expected to affect division of labor and colony performance. However, how each of these factors affects individual and group level behavior is still poorly understood. We present results from a series of experiments manipulating these factors independently from one another in *Cerapachys biroi*, a queenless, parthenogenetic ant. The unconventional biology of *C. biroi* affords precise experimental control over 1) individual age and group demography, because of cyclic reproduction leading to discrete age cohorts, 2) individual genotype and the genetic composition of groups, because of clonal reproduction and 3) group size, because colonies of any size can be set up from totipotent workers. We set up replicate colonies of known composition and use automated tracking of individual ants in 100+ experimental colonies in parallel over a month to quantify how colony composition affects division of labor and group fitness. We show, for example, a positive effect of group size on fitness, and link this to differences in individual and group-level behavior.

Poster session B - POL 300

Evolution of behaviors in response to chronic malnutrition in *Drosophila melanogaster* (52872)

Roshan Kumar Vijendravarma, Sunitha Narasimha, Tadeusz Kawecki.

UNIL.

Adaptations to changing ecological factors impinge on changes in several life-history traits. However, in comparison to the physiological and morphological traits very little is known about how behaviors evolve and mediate such adaptations. We experimentally evolved replicate *Drosophila melanogaster* populations for over ~170 generations for increased tolerance to chronic larval malnutrition by rearing them on poor larval diet. In comparison, to the control populations reared on standard food the malnutrition tolerant populations evolved several behaviors that mediate adaptation to poor nutrition. The behavioral changes in these evolved populations included: firstly, a 'sitter'-like larval foraging behavior; secondly, an increased propensity for larval predatory cannibalism and finally a reduction in their prepupal tunnel building behavior. In conclusion, these behavioral adaptations evolved in response to nutritional stress, serve two key functions: increased nutritional acquisition and reduction in energy expenditure.

Poster session B - POL 300

Genetic basis for seasonal and circadian adaptation in *Nasonia vitripennis* (52875)

Elena Dalla Benetta, Leo Beukeboom, Louis Van de Zande.

University of Groningen.

Light and temperature are important environmental factors that show daily and seasonal oscillations. In most organisms, physiological rhythms are regulated by an internal clock. Timing of migration, hibernation and reproduction need to be adapted to annual changes in the environment to maximize survival and offspring production. *Nasonia vitripennis* overcomes the unfavourable season by maternal induction of larval diapause, in the offspring. Populations of *N. vitripennis* collected along a latitudinal gradient in Europe show a cline in diapause induction, most likely caused by the seasonal fluctuations of day length. Interestingly, allelic variation of the clock gene period follows a similar cline. Clock genes Period (*per*), Cryptochrome2 (*cry2*) and Cycle (*cyc*) are part of a feedback loop, leading to circadian oscillations of mRNA and proteins of these genes. Changes in their cyclical expression pattern might indicate how the circadian clock of *N. vitripennis* processes seasonal changes. The expression levels of *per*, *cry2* and *cyc* in two populations from the extremes of the cline were examined using quantitative PCR. We found that expression in the heads of wasps from northern and southern regions is dependent on the applied photoperiod and on latitude of origin. This suggest that clock genes are involved in photoperiodic response and their adaptive evolution.

Poster session B - POL 300

Breeding a hybrid line to overcome selection limits for voluntary wheel running in mice (52877)

Layla Hiramatsu, Theodore Garland, Jr..

University of California, Riverside (UCR).

An ongoing selection experiment for increased voluntary wheel running (a highly repeatable and widely varying behavior in mice) resulted in four high runner (HR) lines that run ~3-fold more revolutions per day than control lines.

One study showed that HR lines differed in amount and rate of response to uniform selection and in number of generations to reach selection limits (Careau et al. 2013). In another study, a cross between two HR lines showed sex-specific heterosis for wheel running (Hannon et al. 2011), suggesting different genetic factors underlying wheel running for the two sexes and in replicate lines, i.e., multiple solutions.

A study on thermoregulatory behavior in mice showed that selection limits in replicate lines for nest building could be overcome with continued selection on hybrid lines (Bult and Lynch 2000). Therefore, we crossed two HR lines and continued selection on this hybrid line concurrent with the parental lines.

Results: Both sexes showed heterosis in F1. However, continued selection resulted in sex-specific responses. Male hybrids show potential to break the selection limit, while female

hybrids run intermediate to parental lines. We will examine wheel-running component traits (mean revolutions/minute and minutes/day) and estimate heritability using an animal model.

Poster session B - POL 300

Genetic basis of variation in circadian rhythms in moth sexual communication (52905)

Sabine Haenniger, David Heckel, Astrid Groot.

Max Planck Institute for Chemical Ecology; Max Planck Institute for Chemical Ecology; University of Amsterdam, IBED.

Many moth species show specific daily activity rhythms in their sexual activities, which seems to have arisen to minimize communication interference between closely related species: co-occurring species with overlapping sex pheromone blends show temporal differentiation in their daily sexual activities. However, the genetic differentiation of this allochronic separation has barely been examined in any species so far. We investigate differential timing of sexual communication in the noctuid moth *Spodoptera frugiperda* that consists of two strains significantly differing in their timing of sexual activity^{1,2}. We conducted QTL analysis on the variation in timing in the two strains and found that one chromosome explains most of the variance³. Interestingly, this chromosome harbours the clock gene *vrille*, making this our main candidate gene. Even more interestingly, this same chromosome is also the QTL for the pheromone variation between the two strains³, suggesting a possible genetic interaction or hitchhiking between the two traits.

¹Pashley et al. 1992. *Ann. Entomol. Soc. Am.* 85: 400-405.

²Schöfl et al. 2009. *J. Evol. Biol.* 22: 1447-1459.

³Haenniger et al. 2015. Submitted.

Poster session B - POL 300

The evolution of technical innovation in primates (52941)

Ana Navarrete, Andrew Whalen, Sally Street, Simon Reader, Kevin Laland.

University of St Andrews; University of Hull; McGill University.

Previous studies on behavior evolution in birds reported that measures of both technical innovation (e.g. tool using) and non-technical innovation (e.g. novel food discovery) correlate with brain size. In primates, a correlation between general innovation and brain size has been corroborated, but no analyses on the differences between technical and non-technical innovation had been reported before. Using a new dataset on brain measures and behavioral data from the literature, we found that diverse measures of brain size correlate strongly with technical, but not non-technical, innovation. Additionally, using causal graph analysis, we found that direct relationships between technical innovation and brain size, social

transmission and social group size. Diet breadth shares an indirect relationship with innovation and brain size. We interpret this result as consistent with Wilson's behavioral drive hypothesis, in which innovation and social learning drive brain evolution, with the additional roles of social group size and diet breadth.

Poster session B - POL 300

ANALYSIS OF PREZYGOTIC ISOLATION BETWEEN ROBERTSONIAN AND STANDARD HOUSE MOUSE (*Mus musculus domesticus*) IN TUNISIA (53543)

Said Lamia, Ould Brahim Ikhyarhoum, Chatti Nouredine, Said Khaled.

University of Monastir, Tunisia; University of Monastir, Tunisia; University of Monastir, Tunisia; University of Monastir, Tunisia.

In Tunisia, the Robertsonian mice ($2n=22$) occupy the towns and are exclusively commensal whereas standard ones ($2n=40$) in these locations are pushed to rural constructions. The scarcity of hybrids of several generations and the lack of large hybrid zone can be explained by postzygotic isolating mechanisms. However, the absence of F1 ($2n=31$) hybrids between the two races could not be related to such mechanisms and behavioural prezygotic isolating mechanisms are suggested. A caging mice of both chromosomal races was performed to evaluate the spatial distribution of mice according to their karyotypes and their geographical origins and to estimate the nature of real crossbreedings by analyzing the karyotypes of the offsprings. Our results showed a significant grouping of mice of the same chromosomal karyotype whatever their origin is, a preference for intra-racial couplings in both chromosomal races and a well dominance of Robertsonian mice. Therefore, these prezygotic isolating mechanisms could account for the rarity of F1 hybrids and could strengthen, with postzygotic mating, the chromosomal speciation model in house mouse.

Poster session B - POL 300

Large variations in HIV-1 viral load explained by shifting-mosaic metapopulation dynamics (51614)

Katrina Lythgoe, Francois Blanquart, Lornenzo Pellis, Christophe Fraser.

Imperial College London; University of Warwick.

An important question in HIV research is why, without therapy, the time it takes to progress to AIDS varies so dramatically among individuals. Although set-point viral load (SPVL) is the most robust predictor of disease progression, standard well-mixed mathematical models of viral dynamics struggle to capture the orders of magnitude variation in SPVL. Here, we develop a biologically plausible model that captures the metapopulation dynamics of HIV within individuals and show that, under a broad range of parameters, a 'shifting-mosaic'

equilibrium is reached where the whole body's viral population is stable over time, but results from an underlying process of local infection and clearance within T-cell centers. Notably, this model can explain the large differences in SPVL observed among patients, and why evolution does not proceed as predicted from well-mixed models. Ultimately, our model demonstrates that taking into account levels of selection in HIV (sites of replication versus the whole host individual) gives a plausible explanation for how viral genotype/phenotype (infectivity) influences host phenotype (viral load).

Poster session B - POL 300

Antiviral drug resistance as an adaptive process: a survey (51751)

Kristen Irwin, Jeffrey D. Jensen.

EPFL.

Antiviral drug resistance is a matter of grave clinical importance that, historically, has been investigated mostly from a virological perspective. While the proximate mechanisms of resistance can be readily uncovered using these methods, larger evolutionary trends often remain elusive. Recent interest by population geneticists in studies of antiviral resistance has spurred new metrics for evaluating the demographic history of infection, mutation rate, and selective pressures incurred during viral adaptation to antiviral drug treatment. We review recent advances in the field, with a focus on outstanding questions of clinical significance for a range of drug and viral types. We find that the demographic and selective histories revealed by population genomic inference are integral to assessing the evolution of resistance as it pertains to human health.

Poster session B - POL 300

A novel classification for genetic elements in prokaryotic vehicles: inter-cellular mobility, symbiotic relationships, cell-level phenotypes and the levels of selection (51785)

Matti Jalasvuori.

University of Jyväskylä.

Prokaryotes harbor a variety of genetic replicators including plasmids, viruses and chromosomes, each having differing effects on the phenotype of the hosting cell. It is possible to classify the replicators of Bacteria and Archaea based on their horizontal transfer potential and the type of relationships, mutualistic, commensal or parasitic, that they have with the host cell vehicle. Horizontal movement of replicators can be either active or passive, reflecting whether or not the replicator encodes means to mediate its own transfer from one cell to another. From the perspective of the cell vehicle, the different types of replicators form a continuum from genuinely mutualistic to completely parasitic replicators. This classification

provides a general framework for dissecting prokaryotic systems into components that induce cell-level phenotypes that may be selected for on various levels.

Poster session B - POL 300

Are the effects of coevolution with a host equal for each parasite in a clonal population? (52068)

Michaela Klösener, Vera Kühlkamp, Rebecca Schulte, Joy Bose.

Universität Osnabrück, Behavioural Biology, Barbarastr. 11, 49076 Osnabrück.

The reciprocal evolutionary effects pathogens and their hosts have on one another are one of the most powerful selective forces in evolution, leading to adaptive genetic changes in two or more species. Especially microparasites are thought to adapt fast. However, these selective forces may have different consequences for individuals within a clonal population and lead to phenotypic or genetic diversification. To get insight into these individual changes we performed a laboratory-based evolution experiment by using different clonal strains of *Bacillus thuringiensis* as a bacterial microparasite and its nematode host organism *Caenorhabditis elegans*. This system allows us to observe consequences of adaptation in single as well as in mixed infections. After 10 host generations we tested changes in virulence in whole evolved parasite populations as well as in single clones isolated out of these populations. Our results revealed significant differences between the clones of one population in single as well as in multiple infections of the host. This indicates that during evolution, populations can diversify and population based analyses might neglect new, rare clones although these may be key elements for parasite adaptation.

Poster session B - POL 300

Evolutionary conflicts between *Staphylococcus aureus* during transmission and infection (52302)

Bernadette Young, Jessie Wu, Derrick Crook, **Daniel Wilson**.

University of Oxford.

Staphylococcus aureus presents a paradox, because despite its notoriety as a dangerous hospital-associated pathogen, it is a common constituent of the body's natural flora, carried harmlessly in the noses of one in three adults. From the perspective of the pathogen, invasive disease occurs rarely compared to asymptomatic carriage. One explanation is that the body's natural flora could be capable of evolving over time to become more virulent, but that virulent strains are less fit for onward transmission. In previous work, we investigated the evolutionary dynamics of nasal carriage in 16 people, and discovered that in one persistently carried nasal population, an excess of protein-truncating substitutions was associated with the transition to a life-threatening invasive blood stream infection. Here, I exploit a new systematic study of 1000 bacteria from 100 patients with invasive *Staphylococcus aureus* infections to ask

whether selection pressures during infection conflict with successful transmission, and whether this could play an important role in the progression of invasive staphylococcal disease within the body. Our results reveal the evolutionary pathways differentially associated with life-threatening infections versus onward transmission, and the repeatability of bacterial evolution during infection.

Poster session B - POL 300

Choose your partner carefully: variation in aphid phenotypes when multiple bacterial symbionts coexist. (52306)

Melanie Smee, Sally Raines, Julia Ferrari.

University of York.

Bacterial communities within insects play an integral role in the biology of the host. For aphids, the phenotype is a result of both aphid and bacterial symbiont genotype. Little is known about the interactions between multiple species of facultative symbionts occurring within an individual. Selection will be acting on the individual aphid, but also within the aphid where symbiont species may be competing. In the pea aphid, *Acyrtosiphon pisum*, symbionts have a wide range of ecological effects, from protection from natural enemies to host plant utilisation. It has become clear that different strains of the same facultative symbiont species vary in their effects. Multiple symbiont species that coexist within the same host therefore allow us to study how a community evolves in response to selection on multiple levels. We used *A. pisum* individuals infected both singly and doubly with strains of *Hamiltonella defensa* and the X-type symbiont, to investigate how combinations of two common symbionts affected aphid phenotypes in different ecological situations. We found that the outcome of double infections is strongly dependent on the combination of individual strains of the two symbionts present and on the ecological context, highlighting the importance of genotype x genotype x environment interactions.

Poster session B - POL 300

Embryo genetics affects composition of host-associated bacteria in brown trout (*Salmo trutta*) (52368)

Laetitia Wilkins, Luca Fumagalli, Claus Wedekind.

University of Lausanne.

Fish embryos are associated with microbial communities whose composition can significantly influence embryo development. Recent experiments demonstrated that such microbial effects depend on host factors, i.e., on additive genetic and maternal environmental effects. We tested whether host characteristics can in turn influence the composition of symbiont bacterial communities. Brown trout (*Salmo trutta*) were sampled from a natural population and their gametes were used to produce embryos in vitro in a full-factorial breeding design. Embryos

were raised singly, and different concentrations of nutrient broth were added to create different environments. We applied 16S rRNA MiSeq technology to characterize bacterial communities on the embryos. As expected, adding nutrient broth to stimulate microbial growth increased embryo mortality and changed the composition of bacterial communities. There were significant dam and sire effects explaining the variation in bacterial community composition associated with their offspring. With regard to bacterial diversity we only found evidence for significant sire effects. Due to the full-factorial experimental breeding, such sire effects directly reveal additive genetic variance. We therefore conclude that host genetics influences symbiont microbial communities even before hatching.

Poster session B - POL 300

Population genomics of the symbiotic fungus *Rhizophagus irregularis* suggests intercontinental dispersal. (52717)

Romain Savary, Frédéric Masclaux, Tania Wyss Lozano Hoyos, Ian Sanders.

DEE.

The symbiosis formed by arbuscular mycorrhizal fungi (AMF) and the vast majority of vascular plant is known to be present worldwide. This association is important for ecosystem stability and some evidence suggests its role in the colonization of vascular plants on land. However little is known about how *Rhizophagus irregularis* the model fungus for this clade has colonized most places on earth. Moreover the population genomics tools have not been used to explore such patterns of genetic diversity. This is probably due to the difficulty to isolate and cultivate such obligate symbionts in order to obtain clean DNA. Advances in sequencing technics allow us to study the population of this fungus. We used a novel sequencing technique: Restriction site Associated DNA marker (RAD) to obtain a large number of SNPs markers from 63 isolates of 17 countries. We found that isolates from Europe and North America are genetically very similar, but at the same time, very high local genetic differences can be found. This indicates long distance migration, which is mysterious, as no known dispersal mechanism is known.

Poster session B - POL 300

The role of drug interactions and collateral effects in the evolution of antibiotic resistance in *Pseudomonas aeruginosa* (51662)

Camilo Barbosa, Hinrich Schulenburg, Gunther Jansen.

Department of Evolutionary Ecology and Genetics, CAU Kiel.

The crisis of antibiotic resistance has led to the development of different deployment strategies aiming to limit adaptation to drugs. For instance, combination therapy is hypothesized to have a stronger effect than monotherapies while still limiting resistance evolution. In this context, the interaction between drugs in a combination and the availability

of mutations conferring simultaneous resistance to multiple drugs (collateral resistance) seem to modulate resistance evolution. However, this has not been systematically tested for opportunistic pathogens like *Pseudomonas aeruginosa*, where combination therapy is routine. Here we use experimental evolution to test the long-term effects of the interactive and collateral effects of antibiotic combinations in *P. aeruginosa*. We found that despite influencing the success of a combination in the long-term, the interactive and collateral effects of combinations are not sufficient to predict the outcome of evolution. Instead we observed that antibiotics like ciprofloxacin or carbenicillin have a restrictive potential that dramatically constrain antibiotic resistance evolution in *P. aeruginosa*. Moreover, by properly combining these antibiotics with aminoglycosides or cell-wall inhibitors, the restrictive potential can be strengthened, even to the point of extinction. Our results illustrate how proper identification of antibiotics showing this restrictive potential could aid the selection of drug combinations for the treatment of *P. aeruginosa*.

Poster session B - POL 300

Genomic coevolution of natural phage communities with antibiotic resistant *Pseudomonas* (51692)

Robert Hertel, Lisa Stuckenschneider, Heiko Liesegang, Gunther Jansen.

Genomic and applied microbiology, University of Göttingen; Evolutionary Ecology and Genetics, University of Kiel.

Over 25000 people die yearly in the EU as a result of infections with antibiotic resistant bacteria, a number unlikely to decrease soon. Because the antibiotic arsenal to treat common infections such as *Pseudomonas aeruginosa* is depleting fast, we need novel solutions. An old idea that, at least among evolutionary biologists, is going through a revival is phage therapy. This approach promises to circumvent antibiotic resistance evolution by deploying viruses that infect and kill bacteria, and also (co)evolve with hosts that become resistant to viral attack. Although phage-bacteria coevolution has been well-studied phenotypically, a precise, quantitative understanding of the longer-term impact of coevolution on the genomic makeup of a diverse viral community is less understood. It also remains unclear how diverse viral communities interact with host genomes and potential host-associated prophages. In this study we therefore isolated and genomically characterized natural communities of bacteriophages able to infect the *Pseudomonas aeruginosa*. We coevolved these communities with highly antibiotic resistant *Pseudomonas* and investigated how the dynamics of the evolving interaction shaped the genomic diversity of viral communities. Our research improves the understanding of mechanisms underlying phage-bacteria coevolution, and may aid development of better, genomically informed phage therapies for the treatment of multi-, extensively and panresistant bugs.

Poster session B - POL 300

Killing in a team - Cooperation and virulence evolution in an opportunistic pathogen (51702)

Elisa Granato, Rolf Kümmerli.

University of Zurich, Switzerland.

Virulence in bacterial infections is typically mediated through secreted metabolites that can be cooperatively shared across the bacterial collective within the host. Thus, populations of metabolite producers can potentially be invaded by “cheating” mutants, which no longer contribute but still benefit from the shareable metabolites produced by others. Consequently, conditions favoring cheats should ultimately select for reduced virulence.

Here, we test this hypothesis using the opportunistic pathogen *Pseudomonas aeruginosa* infecting a nematode host. We predict that: (a) cheats should invade, and therefore lower virulence in unstructured habitats, where metabolites and cells mix readily; (b) the spreading of cheats should be hampered and high virulence preserved in structured habitats, where metabolite sharing occurs more locally among cooperators; (c) higher levels of cooperative metabolite production might be maintained in the presence than in the absence of hosts, because hosts provide a structured haven even in an otherwise unstructured environment. To test these predictions, we let *P. aeruginosa* experimentally evolve in the absence or presence of its host in liquid (unstructured) and agarized (structured) medium. Subsequently, we measured the evolved level of virulence and related this measure to the evolved production levels of cooperative virulence factors (toxins, siderophores, rhamnolipids) and cheat frequency.

Poster session B - POL 300

Quantifying transmission fitness cost of MDR Tuberculosis (51708)

Julija Pecerska.

ETH.

Nowadays tuberculosis is mistakenly thought by many to be an easily curable and non-prevalent disease. However, only due to HIV/AIDS it takes second place as the greatest killer worldwide. A more pressing problem is that of multidrug-resistant (MDR) tuberculosis - bacteria that are immune to first line drug treatments.

Drug resistance is always a problem for the infected individual due to the difficulty of treatment. If MDR strains are furthermore transmitted between hosts, we may encounter a future epidemic for which no optimal treatment is available. In order to select most efficient treatment strategies, it is necessary to differentiate between highly transmissible and unsuccessful MDR strains.

Using whole genome sequencing data of tuberculosis strains from different hosts, we aim to quantify transmission fitness for the drug sensitive and various MDR strains using a novel phylogenetic inference tool. We present a simulation study showing that for simulated tuberculosis epidemics, we can infer the transmission fitness for the various strains. This will allow us to analyse empirical sequencing data which is currently collected in Georgia.

Reversibility of phage-induced loss of conjugation among drug-resistant bacteria depends on the type of evolutionarily rescuing mutation (51739)

Ville Ojala, Sari Mattila, Matti Jalasvuori.

University of Jyväskylä.

Horizontal gene transfer via conjugative plasmids is an important contributor to the worrying spread of antibiotic resistance in bacterial communities. However, there is also a natural counter-selective force against bacterial conjugation in so-called plasmid-dependent phages which utilize the conjugation machinery to infect and kill plasmid-harboring bacteria. Here, by combining in vitro selection experiments and sequence analyses, we associated phage-induced changes in bacterial ability to conjugate with genetic and phenotypic characteristics. We found that various types of spontaneous mutations can evolutionarily rescue plasmid-harboring bacteria by providing a linked phenotype of phage resistance and reduced or lost potential for horizontal gene transfer. Promisingly, most of the changes in conjugation were irreversible even under prolonged antibiotic selection for restoring the previous phenotype. Only when the loss of conjugation was due to a dynamic mutation, namely a tandem repeat addition, the plasmid rapidly reverted back to full conjugation ability. However, in these cases the susceptibility to the phage also returned. Our results suggest that plasmid-dependent phages could be used to prevent the conjugative spread of antibiotic resistance, with long-lasting effects.

Interactions between horizontally acquired genes create a fitness cost in *Pseudomonas aeruginosa* (51910)

Alvaro San Millan, Macarena Toll-Riera, Qin Qi, R Craig MacLean.

University of Oxford; University of Zurich.

Horizontal gene transfer (HGT) plays a key role in bacterial evolution, especially with respect to antibiotic resistance. Fitness costs associated with mobile genetic elements (MGEs) are thought to constrain HGT, but our understanding of these costs remains fragmentary, making it difficult to predict HGT. Here we use the interaction between *P. aeruginosa* and a costly plasmid (pNUK73) to investigate the molecular basis of the cost of HGT. Using RNA-Seq, we show that the acquisition of pNUK73 results in a profound alteration of the transcriptional profile of chromosomal genes, including DNA damage response genes. Mutations that inactivate two genes encoded on chromosomally integrated MGEs recover these fitness costs and transcriptional changes by decreasing the expression of the pNUK73 replication gene. Our study demonstrates that interactions between MGEs can compromise bacterial fitness via altered gene expression, and we argue that conflicts between mobile elements impose a general constraint on evolution by HGT.

Relationship between siderophore availability and virulence in *Pseudomonas aeruginosa* (52013)

Michael Weigert, Adin Ross-Gillespie, Sam Brown, Rolf Kümmerli.

University of Zürich; Ludwig Maximilians University Munich; University of Edinburgh .

The ability of bacteria to establish an infection typically relies on the production of virulence factors. While the relationship between pathogenicity and virulence factor secretion is well established, little is known about the optimal level at which a virulence factor should be expressed. If production level scales linearly with pathogenicity then virulence factor overproduction may lead to the premature killing of the host, whereas underproduction may compromise the ability of bacteria to establish an infection. Both effects can lead to reduced bacterial fitness, which should select for intermediate levels of virulence factor production. We tested this hypothesis by experimentally manipulating the availability of pyoverdine – a key virulence factor, produced by *Pseudomonas aeruginosa* – within a model host, the greater waxmoth larvae. We found that pyoverdine availability indeed scaled linearly with host mortality. Furthermore we showed that within-host bacterial fitness peaked at intermediate levels of pyoverdine availability, supporting our hypothesis that both pyoverdine over- and under-availability compromise bacterial fitness. At the mechanistic level, we found that increased pyoverdine availability lowered pathogen fitness not because it altered bacterial gene expression, but rather because it triggered a stronger host immune response.

Within-host evolution decreases virulence in an opportunistic bacterial pathogen (52109)

Lauri Mikonranta, Johanna Mappes, Jouni Laakso, Tarmo Ketola.

University of Jyväskylä; University of Helsinki.

Most pathogens evolve in a close antagonistic relationship with their hosts. The conventional theory proposes that evolution of virulence is highly dependent on the efficiency of direct host-to-host transmission. Opportunistic pathogens, however, are not strictly dependent on the hosts due to their ability to reproduce in free-living environment. Therefore it is likely that conflicting selection pressures for survival and reproduction outside versus within the host, rather than transmission potential, shape the evolution of virulence in opportunists. We tested the role of within-host selection in evolution of virulence by letting a pathogen *Serratia marcescens* sequentially infect *Drosophila melanogaster* hosts and then compared the virulence to strains that evolved only in the outside-host environment. We found that the pathogen adapted to both *Drosophila melanogaster* host and novel outside-host environment, leading to rapid evolutionary changes in the bacterial life-history traits including motility, growth rate, biomass yield and secretion of extracellular proteases. Most significantly, selection within the host led to decreased virulence while the selection lines in the outside-host environment maintained the same level of virulence with ancestral bacteria. This

experimental evidence supports the idea that increased virulence is not an inevitable consequence of within-host adaptation even when the epidemiological restrictions are removed.

Poster session B - POL 300

Antibiotic dose specialization in bacterial experimental evolution (52261)

Noémie Harmand, Romain Gallet, Guillaume Martin, Thomas Lenormand.

Centre d'Ecologie Fonctionnelle et Evolutive-UMR 5175; Institut des Sciences de l'Evolution de Montpellier.

Antibiotic resistance is an adaptive process which poses a worldwide medical challenge. Whereas many complex mechanisms of resistance have been investigated since the 40's, the evolution of resistance has mostly been described in a simplified ecological context: treated versus non-treated environments. Evolutionary ecology studies, however, have often emphasized fitness trades-off between environments along a gradient. Thus, considering only treated and untreated environments highly simplifies an antibiotic dose gradient context. In this context, several adaptive strategies could exist between doses and reveal trades-off along the gradient. This would be crucial to understand the role that low doses play on the evolution of super-resistant mutants and in general the role of dose variation in evolution of resistance. We performed experimental evolution of an *Escherichia coli* strain at five antibiotic doses to investigate whether specialization occurs in resistance evolution. We measured the relative fitness of mutants in each dose as well as without antibiotics, after short and long term evolution. The results have been interpreted in the light of fitness landscape models and provide new insights in the role of dose gradient for the evolution of resistance.

Poster session B - POL 300

The genomic architecture of metabolic evolutionary innovation in *Pseudomonas aeruginosa* (52271)

Macarena Toll Riera, Alvaro San Millan, Wagner Andreas, Craig MacLean.

*Institute of Evolutionary Biology and Environmental Sciences, University of Zurich;
Department of Zoology, University of Oxford.*

Novel phenotypes that emerge in evolution often have obscure genetic origins. Here we elucidate these origins by evolving populations of the bacterium *P. aeruginosa* in 95 different chemical environments distinguished by their carbon substrates. Evolutionary adaptation to some environments requires qualitatively novel traits (innovations), but in other environments mere improvement (optimization) of existing traits suffices. Whole-genome sequencing of evolved clones revealed profound differences in the genetic architecture of these two classes of traits. Innovation was characterized by mutations in regulatory and metabolic genes, and optimization by mutations in sensory and signalling systems. Whereas novel gene duplicates

arose at equal frequency during innovation and optimization, mutations in existing duplicates were much more common during innovation, demonstrating that the divergence of existing gene duplicates is a key driver of evolutionary innovation. Both optimization and innovation were associated with fitness costs, but the cost associated with innovation was almost two-fold greater than the cost of optimization, suggesting that pleiotropic trade-offs constrain metabolic innovation. Pleiotropic trade-offs, however, were reduced in clones carrying mutations in recent duplicates, suggesting a link between duplication, mutational robustness and functional innovation. Our observations suggest that phenotypic innovation and optimization can be caused by different classes of genetic change.

Poster session B - POL 300

Evolution of *S. aureus* during nasal carriage involves cross-lineage transfer of mobile genetic elements (52378)

Tanya Golubchik, Antonina Votintseva, Daniel Wilson, Rosalind Harding, Rory Bowden, Sarah Walker, Derrick Crook.

Nuffield Department of Medicine, University of Oxford, Oxford, UK; NIHR Oxford Biomedical Research Centre, Oxford, UK; Wellcome Trust Centre for Human Genetics, Oxford, UK; Department of Zoology, University of Oxford, Oxford, UK.

Staphylococcus aureus is a major cause of serious soft tissue infections and bacteraemia, yet it is also a successful commensal, readily isolated from the nasal flora of around one-third of healthy adults. This state of asymptomatic carriage, which can persist over many months, provides the ideal opportunity for new *S. aureus* lineages to emerge, particularly where different genotypes can interact and share genetic information. We were interested in investigating how this process occurs in vivo. To maximise the potential for interaction between different lineages, we sequenced 36-72 *S. aureus* isolates from each of 7 persistent long-term carriers of at least 2 distinct genotypes (as determined by spa typing). Despite 10-20 months of prolonged co-colonisation, homologous recombination appeared rare; genotype identity was preserved, and most chromosomal changes appeared to be due to mutation rather than recombination, as expected for a predominantly clonal organism. However, there was overwhelming evidence of mobile genetic element (MGE) activity, including transfer of conjugative plasmids, and gain/loss of bacteriophage and genomic islands. MGE activity occurred both within and between the distinct lineages present within a host. These findings add to the growing body of evidence suggesting that much *S. aureus* evolution is due to intense MGE activity.

Poster session B - POL 300

The genetic basis of phenotypic switching in *Pseudomonas fluorescens* SBW25 (52419)

Gayle Ferguson, Philippe Remigi, Jenna Gallie, Paul Rainey.

Institute of Natural and Mathematical Sciences, Massey University, Auckland, 0745, New Zealand; New Zealand Institute for Advanced Study, Massey University, Auckland, 0745, New Zealand; Department of Environmental Microbiology, Eawag, 8600 Dübendorf, Switzerland; Department of Environmental Systems Science, ETH Zürich, 8092 Zürich, Switzerland; Max-Planck Institute for Evolutionary Biology, 24306 Plön, Germany.

When challenged with repeated selective cycles through two contrasting environments, the bacterium *Pseudomonas fluorescens* SBW25 evolved, de novo, the ability to switch repeatedly between two bistable states – one where cells secrete an extracellular colanic acid-like capsule (Cap+), and an ancestral, uncapsulated state (Cap-). Subsequent characterisation showed the switch to be epigenetic, though underpinned by mutation at the start of the pyrimidine biosynthesis pathway. Taking a genetic approach, we sought to identify the ultimate cause of bistability. Exploration of the genotype-phenotype map reveals a complex network of ‘players’ whose activities modulate Cap-/Cap+ switching. Among these are the Gac/Rsm signalling pathway and the stringent response, specifically, RpoD and the nucleotide alarmone ppGpp, recently shown to underpin another bistable phenotype – that of antibiotic ‘persisters’.

Poster session B - POL 300

Do antibiotic resistance alleles affect adaptation to phages? (52496)

Flor Ines Arias Sanchez.

ETH Zurich.

Bacteria evolve in complex environments with a variety of selection pressures, including antibiotics and parasitic viruses (phages); yet the interactions among these different selection pressures are unclear. We are addressing this question by performing fluctuation assays and looking at differences in mutation rates to phage resistance. We use a panel of eight *E. coli* strains carrying various antibiotic-resistance alleles (including chromosomal mutations and plasmids) against a variety of phages from different taxonomic groups. Our results may have far reaching consequences for the development of antimicrobial strategies. Knowing if AB-resistant pathogens are different in their adaptive response to the presence of viral parasites, not only when compared with AB-susceptible variants but also among other strains with different resistant mechanisms will (a) provide insights into how bacteria adapt to ecologically complex scenarios, and (b) will determine whether the efficacy of phage therapy (using phages to treat bacterial infections) will depend on the evolutionary history of pathogenic bacteria in terms of exposure to antibiotics.

Poster session B - POL 300

Molecular basis of drug resistance-related fitness costs in *Mycobacterium tuberculosis* (52695)

Sebastian Gygli, Olga Schubert, Sonia Borrell, Andrej Trauner, Julia Feldmann, Xueli Guan, Mireia Coscollá, Ruedi Aebersold, Sébastien Gagneux.

Swiss Tropical and Public Health Institute, Basel, Switzerland; University of Basel, Basel, Switzerland; Institute of Molecular Systems Biology of the ETH Zürich, Zürich, Switzerland; Systems Biology Graduate School, Zürich, Switzerland.

The antibiotic rifampicin (RIF) targets the bacterial DNA-dependent RNA polymerase. RIF resistance mutations often carry a fitness cost in *Mycobacterium tuberculosis* (Mtb) in absence of the drug. Recently, secondary, so-called compensatory mutations have been described, which restore the fitness of RIF resistant Mtb mutants. The molecular basis of drug resistance-associated fitness costs and their compensation is poorly understood.

As RIF targets the information pathway (DNA → mRNA → proteins), resistance and compensatory mutations will likely influence the proteome of Mtb. To gain more insight into the molecular basis of drug resistance-related fitness costs, we are analyzing the proteomes of drug resistant and susceptible Mtb strains using a quantitative mass spectrometric approach. First, we will compare the proteome of a susceptible Mtb strain to that of a RIF resistant strain derived from it. Furthermore, we will analyse the effect of a putative compensatory mutation on the proteome of the RIF resistant strain.

We anticipate that the analysis of proteomes of drug resistant Mtb strains will lead to a deeper understanding of how drug resistance and compensatory mutations impact on the fitness, and therefore on the transmission potential of drug-resistant Mtb.

Poster session B - POL 300

Testing Discrepancies in Mutation Rate Estimations (52712)

Huw Richards, Rok Krašovec, Andrew McBain, Christopher Knight.

Faculty of Life Sciences, University of Manchester; Manchester Pharmacy School, University of Manchester.

Mutation rate is a central evolutionary parameter that has been studied intensively for nearly a century. For microbes, a key assay used to estimate mutation rate is the fluctuation test, where phenotypically identified mutant cells, arising in the absence of selection, are counted.

However, published mutation rates estimated by this method vary substantially between studies, even of the same bacterial strains. This can make comparison difficult or impossible.

Here we test the possibility that these issues may not merely reflect limited accuracy or reproducibility in the method but have a biological origin. Specifically, recent findings on mutation rate plasticity (mutation rate variation at a given site in a single genotype) suggest that the density to which bacteria are grown can affect their mutation rate. Final population density may be calculated for the fluctuation tests behind many published mutation rates. We therefore collated a dataset comprising hundreds of mutation rate estimates across tens of studies. With this we assess the dependence of mutation rate on final population density. We find that population density can explain a substantial proportion of variation in mutation rate estimates. This suggests that fluctuation tests may be a better tool for mutation rate estimation than widely assumed.

Evolution of commensal bacteria through experimental transmission (52764)

Anaid Diaz, Olivier Restif.

University of Cambridge.

Intestine microbes are an important component of many organisms. Microbes prevalence among individuals in a population raises questions about what adaptations do microbes have in order to spread and persist. We hypothesise that bacterial transmission, which is often neglected, can change the trajectory of microbial evolution, for instance, by selecting on bacterial colonisation rate inside the host and bacteria attractiveness to the host. We are investigating this hypothesis by using experimental evolution of a lab microcosm: *Caenorhabditis elegans* as a host and *Salmonella enterica* as intestinal bacteria. *C. elegans* can transmit its enteric microbes to conspecifics through faecal-oral route; we recently showed that bacteria can thrive among worms by this process. We are developing this system further by allowing transmission of enteric bacteria among worms over multiple generations. We are assessing the phenotypic and genetic changes of the evolved bacteria compared to two treatments: ancestral population and passages of random bacteria. We will discuss our results and provide new insights about the importance of host-to-host transmission in the evolution of intestinal bacteria.

Population size and Parallel evolution during the evolution of antibiotic resistance (52790)

Tom Vogwill, Robyn Phillips, Danna Gifford, Craig Maclean.

Department of Zoology, University of Oxford.

How repeatable is adaptation? There are many striking examples of parallel molecular evolution from clinical pathogens, particularly for genes involved in antibiotic resistance evolution. This is often interpreted as suggesting there are relatively few routes through which adaptation can proceed, and adaptation is therefore highly repeatable. However, the probability of parallel evolution is predicted to be strongly dependent on population size. We tested the role of population size in parallel evolution by experimentally evolving antibiotic resistance in the bacterium *Pseudomonas fluorescens* at three different population sizes. Following whole-genome sequencing of 93 evolved populations, we find that increasing population size does lead to increased parallelism within several genes. However we also find examples where increasing population size decreased the probability of adaptation. We find that the probability of parallel evolution within a gene is dependent on (i) the definition of parallel evolution; (ii) how strongly beneficial a gene is; (iii) whether the gene is a primary or secondary mechanism of adaptation. Overall, we conclude that in some cases parallel evolution may be due as much to demography as it to a restricted adaptive landscape.

Photonic Crystals Cause Active Colour Change in Chameleons (52909)

Michel Milinkovitch, Jérémie Teyssier, Suzanne Saenko, Dirk van der Marel.

University of Geneva, www.lanevol.org.

Many chameleons, and panther chameleons in particular, have the remarkable ability to exhibit complex and rapid colour changes during social interactions such as male contests or courtship. It is generally interpreted that these changes are due to dispersion/aggregation of pigment-containing organelles within dermal chromatophores. Here, combining microscopy, videography, photometry and photonic band-gap modelling, we show that chameleons shift colour through active tuning of a lattice of guanine nanocrystals within a superficial thick layer of dermal iridophores. In addition, we show that a deeper population of iridophores with larger crystals reflects a substantial proportion of the sunlight power, especially in the near-infrared range. The organisation of iridophores into two superposed layers constitutes an evolutionary novelty for chameleons that allows some species to combine efficient camouflage with spectacular display and passive thermal protection.

How does the ocellated lizard (*Timon lepidus*) develop its color pattern? (51747)

Sophie Montandon, Liana Manukyan, Michel Milinkovitch.

University of Geneva.

Animal color patterns are of wide adaptive value for camouflage and display. Although mutational analyses have shed some light on the mechanisms underlying Turing pattern formation in the zebrafish, virtually nothing is known on how reptiles achieve their tremendous diversity of colors and color patterns. Like fishes, reptiles exhibit three types of color-producing cells: i) melanophores, that produce melanin, ii) xanthophores/erythrophores that synthesize pteridines or store carotenoids and iii) iridophores that contain photonic crystals generating structural colors such as green, blue or white. To study color pattern formation in reptiles, we use the ocellated lizard (*Timon lepidus*), which dorsal scales are white or brown in hatchlings and change to green, blue or black in adults. To understand how color changes occur, we used TEM to identify the skin cells involved in colors production. To follow the color state of each dorsal scale, we reconstructed the high-resolution 3D geometry and color texture of specific individuals at regular time intervals. We identified the color of more than 5000 scales per animal and follow their state from newborn to adulthood. We used this data to statistically analyze how scales are changing colors with time. Finally, we mathematically modeled how color pattern is evolving through the life of an animal.

Not just a colour shift: insect melanism and fecundity (52103)

Panu Välimäki, Sami M. Kivelä, Netta Keret, Markku Orell, Toomas Tammaru.

University of Oulu; University of Stockholm; University of Tartu.

The life history theory is grounded upon trade-offs that hinder trait evolution; an increase in fitness due to a change in one trait is opposed by fitness costs due to a concomitant change in another trait. To study the role of trade-offs in maintaining larval polymorphism in insects, we applied artificial selection and quantitative genetic methods to a geometrid moth with discrete melanic and non-melanic larval morphs. Larval coloration appeared a heritable trait that responded to artificial selection in a predictable way, proving the genetic basis of the phenotypes. Larval development time is a key determinant of survival in temperate insect populations. There was, however, no genetic correlation between larval coloration and development time that would constrain phenotypic evolution. Instead, melanism was genetically linked to a small body size at maturation. The reduced body size was not due to melanisation process itself because non-melanic larvae from the melanic selection lines pupated at a smaller size than melanic larvae from the non-melanic selection lines. We conclude that directional selection on melanism affects an underlying costly trait or function, which is adaptive under certain conditions (e.g. under a risk of desiccation or pathogen/parasitoid attack), but traded-off against body size, and thus fecundity.

Understanding the demography of divergence and the genetics of adaptation in White Sands lizards (52116)

Stefan LAURENT, Susanne PFEIFER, Matthieu FOLL, Matthew SETTLES, Sam HUNTER, Christine PARENT, Evelien Diepeveen, Jeffrey D. Jensen, Erika Bree Rosenblum.

EPFL; University of Vienna; IARC, WHO; University of Idaho; University of California.

The White Sands National Monument in New Mexico (USA) is a large geological formation of white gypsum dunes that accumulated following the end of the last Ice Age. The light soil color presented an evolutionary challenge for terrestrial animals relying on cryptic coloration to escape visually-hunting avian predators. In the lizard species *Aspidoscelis inornata* and *Sceloporus undulatus*, populations living in the white sands environment evolved a lighter dorsal color than populations living on the darker soils of the surrounding Chihuahuan Desert. The genetic basis of light dorsal color has been linked to non-synonymous mutations in the melanocortin-1 receptor (Mclr) gene in both species but with opposite dominance patterns. Here we present new data describing genetic variation at the Mclr locus and a large number of neutral loci across the genome in light and dark populations of both species. We show that patterns of variation are consistent with a strong selective sweep at the Mclr locus in *A. inornata* but not in *S. undulatus*, which indicates that different histories are responsible for a similar adaptive phenotype. Furthermore, we infer the neutral demographic history of white

sands populations using a recently developed maximum likelihood framework and use these results to compare the divergence process between light and dark populations.

Poster session B - POL 300

Differential regulation of melanin-related genes contributes to plumage coloration differences between morphs of the dark-eyed junco: a common-garden experiment (52681)

Etienne Kornobis, Paolo Ribeca, Mark Peterson, Mikus Abolins-Abols, Ellen Ketterson, Borja Milá.

National Museum of Natural Sciences, CSIC, Madrid, SPAIN; The Pirbright Institute, Pirbright, Woking, UK; Dept. of Biology, Indiana University, Bloomington, USA.

The dark-eyed junco (*Junco hyemalis*) represents a case of rapid diversification and is composed of at least six geographically structured, melanic morphotypes distributed across North America. Increased sexual dimorphism in the most recently diverged morphs is consistent with the role of sexual selection in driving fast plumage divergence. To understand the genetic basis of melanic coloration in the junco radiation, we carried out a controlled experiment using individuals from two highly distinct morphs (Oregon and slate-colored juncos) housed under common-garden conditions. We used RNA-seq to generate transcripts from growing feathers in four differently-colored body parts per morph, and examined the relative roles of genetic variants vs. differential regulation for pigmentation-related transcripts. We observed significant differential regulation of 161 transcripts among tissues from different morphs, five of which correspond to genes involved in melanin metabolism and storage (ASIP, TYR, TYRP1, OCA2 and PMEL). Moreover, we found differential regulation in other genes potentially involved in pigmentation, such as solute carrier genes and HOX genes. Overall, we find a relationship between the extent and pattern of eumelanin and pheomelanin deposition and differences in the regulation of a few genes, whereas SNP variants do not appear to be closely associated with color phenotypes.

Poster session B - GEN 2000

Host specificity in ticks (51575)

A Raoul Van Oosten, Erik Matthysen, Dieter JA Heylen, Kurt Jordaens, Thierry Backeljau.

Evolutionary Ecology Group, University of Antwerp; Joint Experimental Molecular Unit, Entomology Section, Royal Museum for Central Africa, Tervuren, BE; Royal Belgian Institute of Natural Sciences—OD Taxonomy and Phylogeny, Brussels, Belgium.

Ticks are a numerous group of hematophagous ectoparasites, and under natural circumstances most species infest one or only very few hosts. It is, however, largely unknown whether this is due to host specialisation or simply because ticks do not come into contact with other hosts. Therefore we investigate population dynamics and host specificity in the endophilic tick

Ixodes arboricola, whose life cycle is limited to tree holes and therefore infests only cavity-nesting birds such as great and blue tits.

Our studies indicated that the life cycle of *I. arboricola* is strongly associated to that of its hosts (Heylen et al, 2014, Parasitology) and that therefore its populations are genetically differentiated even at small spatial scales (Van Oosten et al, 2014, Heredity). In two recent studies, we found no differences in feeding performance of this tick among several cavity-nesting birds but lower feeding performance on an unnatural host, while such differences were absent in the generalist tick *Ixodes ricinus*. This provides evidence that ticks are host-specialised and not just constrained by habitat (Van Oosten et al, 2014, Parasitol Res; Van Oosten et al, in prep).

Poster session B - GEN 2000

Effects of abiotic environment on the impact of a manipulative parasite on his host (51772)

Sophie Labaude, Frank Cézilly, Xavier Tercier, Thierry Rigaud.

University of Burgundy.

Many parasites are known to manipulate the behaviour of their intermediate hosts, supposedly in a way to increase their probability of transmission to their definitive host. This manipulation has been shown to vary in intensity at the intra-specific level. Considering the important effect of trophically-transmitted parasites on the modulation of trophic chains, understanding the variations of manipulation intensity and other infection parameters could lead to a better understanding of the dynamic of an ecosystem as a whole.

I tested the effects of two abiotic parameters, temperature and quality of food, on the success of infestation and the intensity of parasite manipulation. I conducted experimental infestations using the acanthocephalan *Pomphorhynchus leavis* and its intermediate host, the amphipod *Gammarus pulex*. We followed the development of parasites and the survival of hosts, and conducted metabolism and behaviour measures on infected and control hosts.

Despite a positive effect on hosts survival and parasites development, food level did not affect the intensity of manipulation. In addition, temperature was a strong determinant parameter for the speed of development of parasites. Those results suggest that variations in abiotic environment could have several effects on host-parasite interactions, leading to modifications at the scale of the ecosystem.

Poster session B - GEN 2000

Resistance evolution within a spatial framework (51773)

Layla Höckerstedt, Anna-Liisa Laine.

University of Helsinki; University of Helsinki.

There are several examples of plant pathogens adapting to their hosts, but very little evidence of hosts evolving resistance under the pressure of pathogen attack. The diverse resistance structure detected within host populations suggests that natural plant populations have the capacity to evolve in an adaptive manner in response to pathogen attack. One of the key challenges in disease biology is to understand when and where disease resistance evolves, and what the consequences are for epidemiological dynamics

The aim of this study is to determine how the resistance structure is distributed within *Plantago lanceolata* populations in Åland islands. The obligate parasite *Podosphaera plantaginis* infects small proportion of the populations each year. An earlier study has demonstrated that highly connected host populations support higher resistance than isolated host populations, yet the role of pathogen imposed selection on resistance evolution remains unclear. This study consists highly and poorly connected host populations with different disease history. Variability in resistance has been tested in a large inoculation experiment using sympatric and allopatric mildew strains. The obtained results from inoculation experiments linked to epidemiological data will help us to understand how host population evolutionary potential changes with degree of population connectivity and past selection intensity.

Poster session B - GEN 2000

Genomic insights into the evolution of *Borrelia* resistance along altitudinal gradients in the Alps (51774)

Luca Cornetti, Méliissa Lemoine, Barbara Tschirren.

Institute of Evolutionary Biology and Environmental Studies, University of Zurich, Switzerland.

Lyme borreliosis is a prevalent zoonotic disease in Europe, having major debilitating effects in humans. It is caused by the spirochete *Borrelia* sp., which is transmitted by ticks to animal hosts, in particular small rodents. Natural hosts, such as bank voles (*Myodes glareolus*), are commonly infested with ticks throughout their life. However, only about 20-30% of the animals become *Borrelia*-infected, demonstrating that natural hosts have evolved powerful defence mechanisms, which prevent and/or control *Borrelia* infection. To date, this variation in *Borrelia* resistance remains poorly understood.

Recent temperature increases in the Alps allowed the pathogen to colonize altitudes that were previously *Borrelia*-free. This natural experiment provides a unique opportunity to investigate resistance evolution in newly exposed host populations, providing a powerful model to study rapid evolutionary changes in response to emerging pathogens. Using a combination of RADsequencing and candidate gene approaches, we compare genomic variation in rodent populations with a long co-evolutionary history with *Borrelia*, rodent populations that are newly exposed to *Borrelia*, and populations that are still *Borrelia*-free. This combination of top-down and bottom-up approaches allows us to gain novel insights into the role of parasites in shaping immune gene evolution in the wild.

Poster session B - GEN 2000

Genetic consequences of an extraordinary lifestyle (51866)

Anne Andersen, David Richard Nash.

Centre for Social Evolution, University of Copenhagen.

Antagonistic coevolution caused by strong selective pressures has been shown to play an important role in the maintenance of genetic diversity in natural populations. The socially parasitic butterfly *Maculinea arion* experiences strong selective pressures from its host ants. The caterpillars are adopted by ant workers and stay in the ant nest all winter, feeding on the ant larvae. The caterpillars have high, but variable, mortalities before and after their adoption by ants, and only a tiny fraction of eggs will survive to adulthood. The species might thus experience genetic bottlenecks in every generation. All Swedish populations of the species have low effective population sizes and show signs of recent genetic bottlenecks even in large, stable populations. The low effective population sizes are expected to increase genetic drift, causing rapid genetic differentiation and high temporal turnover in allele frequencies within populations. This suggests that the extraordinary phyto-predacious lifestyle of *M. arion* leads to inherently low but rather constant genetic diversity. We tested this hypothesis in a contemporary Swedish population using neutral genetic markers.

Poster session B - GEN 2000

"Mycobacterium ulcerans dynamics and virulence strongly depend on chitin concentration in the environment" (51931)

Daniel Sanhueza.

Institute de recherche et developpement.

M. ulcerans is the causative agent responsible for the devastating skin infection Buruli ulcer, which is prevalent in many tropical countries, notably in western and central Africa. The incidences of the disease are significantly higher on floodplains and where there is an increase of human aquatic activities. Despite this, our understanding of the disease remains limited. With the purpose to elucidate this lack of knowledge, in the laboratory *M. ulcerans* was cultured into different abiotic conditions measured in French Guiana and Cameroun. In our research we are interested to test if these abiotic factors have an effect in the development and genetic expression of *M. ulcerans*. Our results show for the first time that the presence of chitin has a significant effect on the growth and genetic expression of *M. ulcerans*. One of the hypotheses of transmission of this disease proposes aquatic insects as vectors, transmitting the infection to humans by biting. Our results suggest that the chitin presents in the cuticle of these insects helps developing the mycobacterium in nature. Moreover *M. ulcerans* possesses an enzyme chitinase, so it's possible that chitin is not just an environmental support for *M. ulcerans*, but also could be a source of nutriment.

Poster session B - GEN 2000

Priority effect in the competition between the intracellular pathogens *Nosema apis* and *Nosema ceranae* in the midgut of the honey bee (*Apis mellifera*) (51943)

Myrsini Natsopoulou, Dino McMahon, Vincent Doublet, John Bryden, Robert Paxton.

Martin Luther University; Queen's University Belfast; Freie University Berlin; German Centre for Integrative Biodiversity Research (iDiv); Royal Holloway, University of London.

Both humans and animals are exposed to a wide range of parasite species; harbouring more than two species at the same time is quite frequently observed in nature. Yet the epidemiological and ecological processes determining the outcome of mixed infections are poorly understood. We explore multiple parasite interactions within a single species host, focusing on the western honey bee (*Apis mellifera*) and the two Microsporidia species that infect it, one exotic (*Nosema ceranae*) and one coevolved (*Nosema apis*). We evaluated the outcome of mixed infections by comparing pathogen growth in single vs double infections given simultaneously vs sequentially. We demonstrate that parasite growth depends on order of infection, with the exotic species being a better competitor than the native one. To investigate further the implications of this asymmetric interspecific competition on the rapid emergence of *N. ceranae* as a global disease threat to honey bees, we use a mathematical model of disease prevalence. We find that, incorporating the asymmetric competition observed in our lab experiment into the model, we were able to capture the observed patterns of prevalence of these two pathogens in nature. Our findings demonstrate that knowledge of complex multi-species interaction is critical to understand host-parasite community structure.

Poster session B - GEN 2000

Does recombination accelerate adaptation of RNA viruses to a local host? (52072)

Vincent Doublet, Dino P. McMahon, Andreas Gogol-Döring, Myrsini E. Natsopoulou, Silvio Weging, Robert J. Paxton.

German Centre for Integrative Biodiversity Research (iDiv), Halle-Jena-Leipzig, Germany; Institute for Biology, Martin-Luther-Universität Halle-Wittenberg, Halle (Saale), Germany; School of Biological Sciences, Queen's University Belfast, UK; Institute of Biology, Freie Universität, Berlin, Germany; BAM Federal Institute for Materials Research and Testing, Berlin, Germany.

RNA viruses have amongst the highest recombination rates in nature. The role of recombination in adaptation to a host is, however, debatable as recombination can combine mutations into one genome, regardless of whether they are advantageous or deleterious. In the honeybee (*Apis mellifera*), two RNA viruses from the same virus complex, Deformed wing virus (DWV) and Varroa destructor virus (VDV), are known to recombine in nature. To test whether recombination is involved in adaptation to a local host, we first co-inoculated DWV and VDV in naïve experimental honeybees. After deep-sequencing of the ancestral inoculates and the viral population in co-infected honeybees (one week post-infection), we found that recombination was extensive and occurred across the entire length of the viral genome, and

more specifically at regions of high sequence similarity. Infections with both viruses were as virulent as infection by VDV alone, but we did not detect predominance of any particular recombinant sequence. We hypothesize that recombination could enable rapid virus adaptation to novel host environments. We aim to test whether one or more recombinants can be evolved experimentally under controlled conditions, and ask whether these are linked to selectively advantageous differences and may accelerate adaptation to new hosts.

Poster session B - GEN 2000

Immature larvae of the eyefluke *Diplostomum pseudospathaceum* enhance anti-predatory behavior of fish: evidence supporting the “predation suppression” hypothesis. (52137)

Mikhail Gopko, Victor N Mikheev, Jouni Taskinen.

A.N. Severtsov Institute of Ecology and Evolution, Moscow, RAS; University of Jyväskylä, Finland.

Tropically-transmitted parasites need time to reach infectivity, when developing in the intermediate host. A theoretical model (Parker et al., 2009) predicts that before full development, parasite larvae should make their hosts less vulnerable to predators (predation suppression hypothesis) to increase probability of surviving until infectivity. However, there is still little evidence of such manipulations by non-infective parasite stages. We studied experimentally the influence of immature metacercariae of the eyefluke, *Diplostomum pseudospathaceum*, on the anti-predator behaviour of the young-of-the-year rainbow trout and cyprinids (several species), to test the predation suppression hypothesis. Infected fish harbouring on average 7.7 (range 1-26) larvae, which corresponds to naturally occurring parasite numbers in YOY fish, were significantly less vulnerable to simulated predation (both rainbow trout and cyprinids), less active (rainbow trout) and preferred deeper layers of water (cyprinids) when compared with control fish harbouring no larvae. Our findings suggest that immature larvae of *D. pseudospathaceum* induce changes in host behavior that can protect them from predation, supporting predation suppression hypothesis and indicating that manipulations of non-infective parasites may play an important role at modulating predator-prey interactions in the natural habitats.

Poster session B - GEN 2000

Adaptation of a holoparasitic plant to new hosts – genetic differentiation or phenotypic plasticity? (52195)

Bojana Stojanova, Philippe Simier.

LBPV LUNAM Université de Nantes.

Phelipanche ramosa is a holoparasitic plant of the Orobanchaceae family. Contrary to most of the species in this family, its lifecycle follows that of an annual weed, allowing its spread

among a large range of cultivated crops. The genetic diversity of this species has not been extensively studied, though it could help the understanding of evolutionary mechanisms underlying adaptation to novel hosts, such as the one recently observed on rape in western France. We genotyped over 60 populations of *P. ramosa* coming from different geographical regions and three main host plants in France (rape, hemp, tobacco) using 22 SSR markers. AMOVA and PCA analysis show low intrapopulation variation and high and significant inter population genetic variation that seems to be influenced by geographic origins and host plants to different extents. In Western France, populations found on rape, hemp and tobacco are all genetically very distant whereas in eastern France the hemp type from west is found on both hemp and rape. We will further test these genotypes on a range of hosts in a growth chamber to clarify to what extent do genetic differentiation and phenotypic plasticity influence the adaptation of *P. ramosa* to different hosts on different geographic scales.

Poster session B - GEN 2000

A new method to analyze the dynamics of multivariate distribution of fitness traits in large asexual populations: application to the evolution of virulence-transmission trade-off (52244)

Yoann Anciaux.

ISEM.

Modelling the dynamics of pathogen adaptation implies following the evolutionary dynamics of several fitness traits (virulence, transmission etc.) with a typically complex genetic basis (many alleles, epistasis). Furthermore, these dynamics are often coupled with the demographic dynamics and evolution of the host. Such processes often become analytically intractable.

Here, we explore the use of an analytical tool to model the dynamics of the full multivariate distribution of fitness traits in large asexual populations, through their generating function. This allows following the effect of selection among many co-segregating types and of background-dependent mutation effects (epistasis).

We will study the insights obtained from this approach in a model where virulence and transmission are distinct optimizing functions of a set of underlying phenotypes. We will consider adaptation from standing variance alone, and the impact of de novo mutations. Within our framework, the virulence-transmission trade-off is allowed to evolve and the host's demographic feedback explicitly enters the dynamics of parasite evolution.

Poster session B - GEN 2000

Variation of life history traits of nematode parasites in undisturbed habitats of Serbia (52270)

Vladimir M. Jovanović, Ivana Budinski, Borislav Čabrilо, Tanja Adnađević, Olivera Bjelić-Čabrilо, Jelena Blagojević, Mladen Vujošević.

Institute for Biological Research "Sinisa Stankovic", University of Belgrade; Department of Biology and Ecology, Faculty of Sciences, University of Novi Sad.

Varying climatic conditions can impose constraints on life history of both hosts, and parasites. We studied variation of parasite life history traits (sex ratios, extent of the sexual size dimorphism and fecundity) as a result of local adaptations to climatic conditions, host age and genetic background. For the object of research, we chose four parasitic nematodes of a single host species, yellow-necked field mouse (*Apodemus flavicollis*), known for the common presence of B chromosomes in individual genotypes. The B chromosomes were previously shown to influence the interaction of this species with some parasitic nematodes, together with standard genes included in adaptive immune response. We analysed parasites of 136 host individuals from 14 localities in Serbia. Variation in parasite infrapopulation sex ratios was correlated with the habitat temperature factors in two nematode species, despite the life cycle differences between them. For only one parasite species, the range of fecundity could be explained by climatic factors. Host-related factors (age and the presence of B chromosomes) partially explained observed variation in studied life history traits of parasites. Further studies of parasite life history traits in the undisturbed habitats are needed in order to draw more decisive conclusions.

Poster session B - GEN 2000

Fine-tuned, context-specific manipulation of an intermediate crustacean host by its acanthocephalan parasite (52289)

Timo Thünken, Theo C. M. Bakker, Sebastian A. Baldauf.

University of Bonn; University of Bonn; University of Bonn.

Parasites with a complex life cycle are supposed to influence the behaviour of their intermediate host in such a way that the transmission to the final host is enhanced, but reduced to non-hosts. Here, we examined whether the trophically transmitted acanthocephalan bird parasite *Polymorphus minutus* adaptively alters the anti-predator behaviour of its intermediate host, the freshwater amphipod *Gammarus pulex*. Uninfected gammarids showed negative phototaxis, whereas infected ones were photophilic indicating that the parasite manipulates the phototactic responses of its intermediate host thereby increasing the probability of ingestion by final bird hosts. In response to specific non-host predatory cues (fish cues in our study) infected gammarids showed stronger anti-predator behaviour than uninfected ones suggesting that the bird parasite manipulates anti-predator behaviour of its intermediate host to reduce the probability of transmission to dead-end hosts. When phototaxis and fish avoidance were jointly examined, uninfected gammarids showed increased photophobia suggesting that both factors act additively. Interestingly, *P. minutus* infected gammarids showed photophobia in this context as well suggesting fine-tuned context-dependent parasitic manipulation.

Poster session B - GEN 2000

When parasites disagree: Interspecific conflict over host manipulation (52341)

Nina Hafer, Manfred Milinski.

MPI for evolutionary biology.

Host manipulation is a common strategy by which parasites alter host behavior to enhance their own fitness. In nature, hosts are usually infected by multiple parasites with potentially conflicting interests with regards to their host's behavior. This can lead to a conflict over host manipulation. Experimental studies of such a conflict including parasites from different species are lacking. The cestode *Schistocephalus solidus* and the nematode *Camallanus lacustris* both use copepods as their first intermediate host. They need to spend some time inside this host before they are ready to be trophically transmitted to their subsequent fish host. Accordingly, not yet- infective parasites lower host activity to reduce fatal premature predation. Infective ones increase host activity to enhance predation to continue their life cycle. We experimentally infected lab-bred copepods such that they harboured either an infective *S. solidus* and a not yet- infective *C. lacustris* or vice versa. Such an interspecific conflict can, as we found, lead to a compromise between the manipulation effects each parasite would achieve when alone. This result differs from pure *S. solidus* infections in which the infective parasite completely sabotages the manipulation effect by the not yet-infective one. These and further results will be presented.

Poster session B - GEN 2000

Experimental evolution of the spider mite, *Tetranychus urticae*, on tomato plants: which traits matter in adaptation to a novel host? (52421)

Cassandra Marinosci, Ophélie Ronce, Sara Magalhães, Isabelle Olivieri.

Université Montpellier 2, Institut des Sciences de l'Evolution, UMR5554, Place Eugène Bataillon, 340; CBA Centro de Biologia Ambiental, Faculdade de Ciências da Universidade de Lisboa, Edifício C2, 3°.

Plants and herbivores exert strong selection upon each other, resulting in a coevolutionary arms race. In fact, plants evolve wide physical and chemical defences in response to attacks by herbivores. Conversely, herbivores develop mechanisms to cope with these plant defences. This diversifying and recurring antagonistic coevolution is particularly relevant for polyphagous species that experienced a diversity of host plants with a large range of systemic defences. The present study describes adaptation to a new host plant. By using experimental evolution with a spider mite species, *Tetranychus urticae*, we addressed the following questions: are populations evolving previously on tomato plants more adapted to this host plant relative to ancestral populations (evolving on bean plants)? In this case, is this adaptation due to the capacity of these populations to inhibit or resist to plant defences? This work underlines the diversity of responses of pest herbivores to host plant defences and shows that a variety of strategies are used by spider mites to respond to shift in host plant.

Pathogen emergence and evolution in a network of wild living house mice. (52447)

Jonas Ismael Liechti, Martin Mueller, Gabriel Etan Leventhal, Barbara Koenig, Sebastian Bonhoeffer.

ETH Zurich; University of Zurich.

Contact structure heterogeneity has been shown to influence both disease spread[1] and pathogen evolution[2] in simulated epidemics. The relative importance of such contact heterogeneity for the epidemiology of real host-pathogen systems has remained unclear due to the technical challenges of observing real host contact networks in wild populations. Furthermore, these models assume static networks where contacts between individuals exists for the whole duration of an epidemic. Here, we present results on the spread and evolution of a model pathogen in a population whose dynamic contact pattern has been parametrized based on data of wild house mice for which interactions between individuals have been monitored for several years. The resolution of the data is high such that we can construct a detailed temporal contact network of the host population. This allows us to study the spread and evolution of pathogens in a biologically relevant contact network.

[1] J. Lloyd-Smith et al., Nature, 438:355-359 (2005)

[2] G. Leventhal, A. Hill et al., Nature Communications, in press

Multiple infections in the anther smut fungus *Microbotryum* (52485)

Taiadjana Fortuna, Michael E. Hood, Manuela Lopez-Villavicencio, Hélène Badouin, Alodie Snirc, Stéphanie Le Prieur, Christian Raquin, Jacqui Shykoff, Tatiana Giraud.

Université Paris-Sud, CNRS, Dept. Écologie, Systématique et Évolution, Orsay, France; Amherst College, Department of Biology, Amherst, Massachusetts, USA; Muséum National d'Histoire Naturelle, Dept. Systématique et Évolution, Paris, France.

Theory predicts that virulence should be higher when multiple strains of parasites regularly compete within hosts. This is because, under conditions of multiple infections, parasites that rapidly exhaust limiting host resources produce more offspring than those following a prudent strategy. Conversely, virulence can be reduced in hosts with multiple infections if competitors inhibit one another. We study multiple infections in *Microbotryum* phytopathogenic fungi, responsible for the anther smut disease in Caryophyllaceae plants. Previous studies have shown that multiple infections of *M. lychnidis-dioicae* occur frequently in natural populations of *Silene latifolia*. Competitive inhibition and exclusion occur between unrelated strains within the infected plant, i.e. pathogen relatedness impacts virulence. Here, we assessed the frequency of multiple infections of *M. saponariae* infecting the plant *Saponaria officinalis* in natural populations, and we studied the mechanism of competitive exclusion and inhibition. Hyphae of *M. saponariae* can indeed grow in vitro allowing observation of fungal hyphae interactions. New microsatellite markers have been developed to identify fungal genotypes of

M. saponariae. Controlled inoculations have also been carried out in the greenhouse to investigate how parasite fungal genotypes interact within plants and the effects of multiple infections and pathogen relatedness on infection success and virulence.

Poster session B - GEN 2000

Are parasitoids locally adapted to their hosts' endosymbionts? (52507)

Christoph Vorburger, Romain Rouchet, Luis Cayetano.

ETH Zürich & Eawag; Academy of Sciences of the Czech Republic, Brno; UC Berkeley, USA.

Many organisms rely on 'helpers' in the form of microbial endosymbionts for defence against parasites. Aphids enjoy increased resistance to parasitoids when infected with the facultative bacterial symbiont *Hamiltonella defensa*, which reduces parasitism in the field and thus hampers biological control of pest aphids. Parasitoids, on the other hand, have the capacity to adapt to the presence of defensive symbionts in their host, as shown by experimental evolution in the lab. This suggests that parasitoids may be locally adapted to the prevalence of defensive symbionts in their host populations. Across 17 populations of the aphid parasitoid *Lysiphlebus fabarum*, we do indeed see a positive association between their ability to parasitize *Hamiltonella*-protected aphids and the local prevalence of this symbiont, but this correlation is weak and non-significant. An assessment of intraspecific variation in both antagonists provided a possible reason for this apparent lack of local adaptation. Different strains of *Hamiltonella* protect well against some but not against other genotypes of the parasitoid. This genotype-specificity precludes a general adaptation of parasitoids to the defence provided by *Hamiltonella*. The mechanistic basis of this specificity and whether parasitoids are adapted to the symbiont strains they encounter most frequently are the topic of ongoing research.

Poster session B - GEN 2000

Gyrodactylus salaris transcriptome: functional characterization and analysis in relation to adaptations to parasitism. (52629)

Ksenia Zueva, Tiina Sävilämmi, Craig R Primmer.

University of Turku.

Gyrodactylus salaris is a parasitic flatworm that poses a great threat to North Atlantic populations of Atlantic salmon. We studied transcriptome characteristics of *G. salaris*, in order to better understand the mechanisms and evolution of parasitism. We present a de novo assembly of the parasite transcriptome, approximately one third of which could be functionally annotated using the Gene Ontology, protein families and Kyoto Encyclopedia of Genes and Genomes databases. This annotated sequence collection represents an important genomic resource for *G. salaris*, and is discussed in the light of suggested genomic adaptations to obligate parasitism in neodermatan flatworms. Based on the recently published

first draft of *G. salaris* genome such adaptations have been proposed to include reduction or absence of a number of essential genes, among which are genes encoding peroxisomes, heat shock proteins, and proteins in the fatty acid synthesis pathway. Such genes were also absent or reduced in our study. Moreover, the possible reduction of genes in the fatty acid synthesis pathway in *G. salaris* is in line with our earlier observations of signals of parasite-driven selection in Atlantic salmon genomic regions including fatty acid metabolism genes, thus possibly suggesting genomic co-evolution of host and the parasite.

Poster session B - GEN 2000

Local differences in parasitism and competition shape defensive investment in a polymorphic eusocial bee (52723)

Christoph Grüter, Lucas von Zuben, Francisca Segers.

University of Lausanne, Switzerland; University of São Paulo, Brazil.

Adaptive colony demography theory predicts that colonies should flexibly adjust the investment in different worker castes depending on the colony needs in a given environment. For example, colonies should invest more in soldiers in a more dangerous environment. However, evidence for this prediction has been mixed. We examined whether defensive investment is adjusted to local ecology in the only known bee with a morphologically distinct soldier caste, *Tetragonisca angustula*. We studied three populations that differed in the density of food competition and the occurrence of a parasitic robber bee. We found that colonies coexisting with robber bees had on average 45-97% more soldiers defending the nest entrance, while colonies facing stronger foraging competition had c. 7-8% smaller guards. When released from intense competition by colony relocation, body sizes of guards and foragers increased. When we introduced chemical robber bee cues at nest entrances, we found both a short-term and a long-term up-regulation of the number of soldiers defending the colony. Our study supports adaptive colony demography theory and highlights the importance of colony threats and competition as selective forces shaping colony phenotype.

Poster session B - GEN 2000

A cryptic species in a generalist parasitic wasp (Hymenoptera: Braconidae: Aphidiinae): Host range and reproductive isolation (52750)

Yoann NAVASSE, Manuel PLANTEGENEST, Anne LE RALEC.

Université Rennes 1; Agrocampus Ouest; INRA.

In agroecosystems, specialist or generalist character of natural enemies may have implications in the regulation of pest populations. Insects, such as aphids, can cause major damage to cultivated plants. A group of natural enemies of aphids presents a much higher degree of specialization: parasitoids. However, among the four hundred species composing this Aphidiinae, various degrees of specialization are observed: while most species parasitize only

one or two species of aphids, some species have been recorded on more than twenty different host species. But these generalists species are challenged because recent work suggests that they could include specialized biotypes or cryptic species.

Diaeretiella rapae is the most generalist Aphidiinae, host range including more than sixty aphid species. We used *D. rapae* to test the hypothesis of structuration of generalist species in several specialized sub-units, possibly being real species. We compared host range of various strains coming from different aphid species and geographic areas by host switching experiments. Then, we tried to assess their taxonomic status by checking their reproductive compatibility.

Our results showed differences in the parasitic success between strains. Moreover, reproductive isolation was detected. *D. rapae*, known as a generalist species, seems to include more or less specialized entities, some of them being cryptic species.

Poster session B - GEN 2000

Fast spread of a fungal parasite in ant supercolonies (52762)

Simon Tragust, Heike Feldhaar, Xavier Espadaler, Jes S   Pedersen.

University of Bayreuth; Autonomous University of Barcelona; University of Copenhagen.

Many ant species are highly successful invaders and can dominate vast areas by forming dense networks of connected nests in contrast to the smaller and spatially dispersed colonies of most social insects. However, it was recently proposed that such supercolonies are more vulnerable to infection by parasites and diseases as they would serve as large targets with high rates of transmission from nests to nest. Here we studied the invasive garden ant *Lasius neglectus*, a pest species which is currently spreading throughout Europe where several populations are infected with the ectoparasitic fungus *Laboulbenia formicarum*. The fungus is also introduced so a new host-parasite relationship is formed. In two populations (supercolonies) we followed the prevalence and intensity of the infection over four to 10 years, revealing independent epizootic spread of the parasite with a 14% annual increase in prevalence until c. 80% of all ants were infected. In contrast, no other local ant species with normal colonies carried the parasite. These results give the first direct support to the hypothesis that supercolonies potentially face an important challenge from parasites and diseases, implying that such ant species are likely to have evolved efficient ways to cope with their most important co-evolved threats.

Poster session B - GEN 2000

Adaptation of plant pathogens to disease control on heterogeneous landscapes (52793)

Alexey Mikaberidze.

ETH Zurich, Institute of Integrative Biology.

Plant diseases often lead to severe crop losses in agriculture. Depending on the pathogen's dispersal range, disease control strategies should be coordinated over a scale of a single field, several adjacent fields or a regional spatial scale. We investigate population dynamics of host-pathogen interaction and pathogen adaptation to disease control using a spatially-structured population dynamical model coupled with a model describing pathogen adaptation. Favorable patterns of simultaneous application of fungicides and resistant host varieties to control major fungal diseases of wheat are explored over different spatial and temporal scales. An optimal disease control strategy will suppress the disease level in the short term and slow down or prevent pathogen adaptation in the long term.

Poster session B - GEN 2000

Evidence for extrinsic postzygotic isolation between sympatric host races of leaf beetle *Lochmaea capreae* (52832)

Shaghayegh Soudi, Klaus Reinhold, Leif Engqvist.

Evolutionary Biology, Bielefeld University, Germany; Evolutionary Biology, Bielefeld University, Germany; Evolutionary Biology, Bielefeld University, Germany.

Ecological speciation is a classic scenario for speciation in which reproductive isolation evolves between populations exploiting different habitats. We examined predictions of the ecological model regarding the fitness of hybrids between sympatric host races of leaf beetle *Lochmaea capreae* specialized on willow and birch host plants. The Survival of F1 hybrids, willow backcrosses and birch backcrosses, as well as both parent species, was evaluated on both parental host plants. The comparison of backcrosses survival on both host plants estimates an ecologically dependent component of their fitness while controlling for any intrinsic genetic incompatibilities that may exist between each race genomes. Our findings showed a striking pattern of ecological dependence: the switch in relative fitness of the backcrosses on the two parental host plants and the expected rank order of each cross type performance. These findings provide strong evidence that divergent natural selection has played some roles in the evolution of postzygotic isolation between the host races of *L. capreae*. Implications of these results provide a rare but strongly supported evidence of ecologically dependent postmating isolation during ecological speciation in nature.

Poster session B - GEN 2000

Contrasting phylogeographic patterns of a phytophagous insect and its host plants (52884)

Neus Marí-Mena, Carlos López-Vaamonde, **Horacio Naveira**, M. A. Auger-Rozenberg, Marta Vila.

Universidade da Coruña; INRA ; Universidade da Coruña; INRA; Universidade da Coruña.

Gene pools become subdivided because of many different reasons, but it is generally quite difficult to pinpoint the main factors contributing to that process. In each generation, individual phenotypes are confronted with changing environments and their fitness is assessed. If the bet to some variant proves correct, the prize can be a magnificent adaptive radiation; if wrong, extinction is the maximum penalty, because some choices may become irreversible. Systems formed by host plants and phytophagous insects are, a priori, very good candidates for this kind of studies. In this communication we explore the phylogeographic relationships between populations of the Spanish Moon moth *Graellsia isabellae* and those of different *Pinus* spp. hosts. *G. isabellae* is a montane species whose larvae feed either on *P. sylvestris*, *P. nigra* or *P. halepensis*, depending on the population. Attending to morphological characteristics, the species is subdivided into five subspecies, associated to different mountain systems. Our results indicate that the mitochondrial genomes of these subspecies are indeed differentiated, that the time of coalescence of many of the identified mutations precedes the LGM, and that none of the *Pinus* hosts offers a phylogeographic pattern completely concordant with the relationships observed among them.

Poster session B - GEN 2000

A parasite's dilemma: weediness-specialization conflict in *Orobanche*? (52894)

Salman Rahimi, Mohsen Beheshtian Mesgaran, Ali Ghanbari.

Ferdowsi University of Mashhad; The University of Melbourne.

Orobanche spp., (synonymous *Phelipnache*) is the largest genus of obligate non-photosynthetic holoparasitic in *Orobanchaceae* family. Weediness is a human-mediated character that co-evolved in some plants since human started cultivation of useful plants. In *Orobanche*, weediness may come into conflict with parasite specialization that relies on predictable resources such as association with perennial hosts in natural ecosystems. *Orobanche* species differ in the host specificity and host range. Whereas a specific host is a dimension of the n-dimensional hypervolume, host specificity and broad host ranges could be considered as niche dynamics and extension in *Orobanche*. Most *Orobanche* species exhibit high host specificity that is expected to lead to strong parasite specialization. Equilibrium between these narrow host-range species and their hosts introduces a well-adapted relationships on population level based on evolutionary adaptation. Broad host ranges and physiological and ecological diversity of seed properties, e.g. dormancy, conditioning, great longevity, very high seed output, are distinct characters to separate weedy from non-weedy *Orobanche*. In anthropogenically disturbed habitats, *Orobanche* species occur in large numbers on many annual hosts where they can be lethal to their hosts which implies a poorly-adapted relationship. It is therefore hypothesized that the evolution of weediness in *Orobanche* follows a trajectory that may contradict the parasite specialization.

Poster session B - GEN 2000

Genetic basis of biogeographic variation in periodic timing of the parasitoid *Nasonia vitripennis* (52901)

Jelena Prodic, Leo W. Beukeboom, Louis van de Zande.

University of Groningen.

Many organisms have evolved ways to timely anticipate periodic fluctuations in environmental conditions. Such time-keeping mechanisms detect and process biotic or abiotic external cues (such as photoperiod) and govern internal metabolic and physiological processes. One open question is to what extent the regulation of circadian timing is similar to that of seasonal timing. An example of seasonal timing is photoperiodic diapause induction. In Europe, the jewel wasp *Nasonia vitripennis* shows a geographical cline in photoperiodic diapause induction which is correlated with genetic polymorphisms in the clock gene period. In order to determine the role of these polymorphisms, period alleles from field-derived lines of different latitudes were introgressed into a homogeneous laboratory line genetic background to investigate the effect on circadian activity and diapause induction. Subsequently, isofemale lines established from an intermediate latitude were tested for circannual periodicity in diapause induction. In addition, the dependence on temperature relative to photoperiod as cue for seasonal timing was compared between northern and southern lines. The results provide insight in the genetic regulation of an important life-history trait in response to different latitudinal conditions.

Poster session B - GEN 2000

Host-parasite specificity in the Apis – Varroa complex in Asia (52926)

Paul Page, Ninat Buawangpong, Zheguang Lin, Huoqing Zheng, Fu-Liang Hu, Panuwan Chantawannakul, Peter Neumann, Vincent Dietemann.

Agroscope – Swiss Bee Research Centre, Schwarzenburgstrasse 161, Bern, Switzerland; Bee Protection Center, Department of Biology, Faculty of Science, University of Chiang Mai, Thailand; College of Animal Science, Zhejiang University, Hangzhou, People's Republic of China; Institute of Bee Health, University of Bern, Bremgartenstrasse 109, Bern, Switzerland; Social Insect research Group, Dpt of Zoology and Entomology, University of Pretoria, South Africa.

Various haplotypes of ectoparasitic mites of the *Varroa* spp. naturally infest colonies of the Eastern honey bee *Apis cerana* and appear to be specific to their respective host populations. However, strong behavioral (reproductive) and genetic data are often lacking to ascertain the basis of this specificity. We investigated host specificity in the *Apis*-*Varroa* system at a higher resolution by cross-infesting, in vitro, mites from various lineages onto *A. cerana* populations at three locations in Thailand and one in China. We then genotyped mites that reproduced as well as those that did not, to confirm their haplotype. Host specificity was not exclusively explained by an absence of reproduction in putative new hosts. This approach allowed us to better define host specificity and will provide a solid basis to explain which traits, both in the genetically diverse parasite lineages and in the host species, are involved in or constrain novel host adaptation.

Impacts of a hyperparasite on pathogen spread and virulence (52993)

Steven Parratt, Anna-Liisa Laine.

University of Helsinki; University of Helsinki.

The influence of intrinsic biotic and abiotic factors on the dynamics of infectious diseases is well studied. Yet the impact of a pathogen's own natural enemies, such as hyperparasites, on its spread and severity remains comparatively under-researched. Given the ubiquity of parasitism, and by extension hyperparasitism, we may be overlooking a key determinant of pathogen success or failure and thus coevolutionary dynamics. Previous studies have demonstrated that hyperparasites can reduce disease severity in infected host individuals, however the effect of hyperparasites on the population dynamics of pathogens remains enigmatic. Here, we combine laboratory experiments with field studies across a plant-pathogen metapopulation in order to demonstrate the impact of a mycoparasitic fungus (*Ampelomyces* sp) on key life-history traits of a powdery mildew (*Podosphaera plantaginis*). We hypothesized that the hyperparasite will curtail key fitness traits of the pathogen, potentially reducing disease severity at the population level and limiting its spread and persistence. Our results lend insight into the complexity of interactions between multiple species and raise further questions as to the evolutionary relationships within hierarchical chains of parasites.

Phylogenetically estimated HIV diversification rates reveal prevention of HIV-1 by antiretroviral therapy (51816)

Jeffrey Joy, Richard Liang, Rosemary McCloskey, Thuy Nguyen, Chanson Brumme, Robert Hogg, Julio Montaner, P. Richard Harrigan, Art Poon.

British Columbia Centre for Excellence in HIV/AIDS; Department of Medicine, UBC; Faculty of Health Sciences, Simon Fraser University.

Treatment of HIV infection with antiretrovirals decreases transmission risk. Despite epidemiological evidence supporting 'Treatment as Prevention' quantifying this success remains a significant challenge. Phylogenetic analysis of viral sequence data yields crucial insights into epidemic processes, including transmission dynamics. We evaluated the impact of treatment on HIV transmission rates in the British Columbia (BC), Canada epidemic using phylodynamic methods. We recovered 27,296 anonymized HIV sequences from 7,747 HIV patients in BC annotated with: sample collection date, treatment status at collection, date of first antiretroviral treatment, and HIV risk factor. We inferred a distribution of phylogenetic trees under maximum likelihood. We calculated a lineage level phylogenetic branching rate for each HIV lineage in the trees, providing an approximate measure of transmission rates. Comparison of HIV branching rates between treatment-experienced and treatment-naïve lineages across the BC epidemic as a whole, among risk factors, and among different drug classes revealed branching rates were significantly lower among treatment-experienced HIV

lineages relative to treatment-naïve lineages ($p < 0.001$), implying reduced rates of HIV transmission in the former and suggesting these results are not driven by penetrance of health care into particular risk groups or therapeutic regimens. Our results provide independent evidence that HIV treatment has limited onward transmission.

Poster session B - GEN 2000

Determining the heritability and molecular determinants of virulence in HIV in Europe using whole genome sequencing (51819)

François Blanquart, Chris Wymant, Marion Cornelissen, Luuk Gras, Astrid Gall, Paul Kellam, Christophe Fraser.

Imperial College London; University of Amsterdam; HIV monitoring foundation; Sanger Institute.

HIV is highly variable and subject to strong selection, and must therefore adapt rapidly to its host population. The set-point viral load (SPVL) in particular, a strong predictor of clinical outcomes, can be considered as a viral trait under selection. Understanding the evolutionary dynamics of SPVL requires knowledge of its heritability and genetic determinants. Current estimates of heritability vary widely (6% to 59%) and genetic determinants are largely unknown.

We use whole-genome HIV sequence from 802 patients of the UK and The Netherlands sampled between 1985 and 2014, coupled with SPVL and CD4 count for these patients, to investigate the genetic determinants of HIV virulence. Phylogenetics reveals a very good correlation between genetic distance to an outgroup and sampling date ($R^2 = 0.6$) which allows a more precise dating of the origin of the HIV epidemic in Europe. A phylogenetic method estimates heritability of set-point viral load at a medium to high value with much narrower confidence intervals than previous estimates. Last, SPVL is higher when the patient is dually infected, and, intriguingly, also correlates with the nucleotidic composition of the sequence. A whole-genome association study (work in progress) will allow identification of SNPs associated with variation in SPVL.

Poster session B - GEN 2000

Phylogenetic reconstruction of viral quasispecies dynamics (51869)

Veronika Boskova, Tanja Stadler.

Department of Biosystems Science and Engineering, ETH Zurich, Basel, Switzerland; SIB Swiss Institute of Bioinformatics, Basel, Switzerland.

Especially in fast evolving and reproducing populations such as RNA viruses, the population of sequences present in one host at a time is often very rich but also very repetitive. Deep-sequencing approaches allow for quantification of sequences and their diversity.

The amount of sequences from such sequencing efforts represents a computational overload for current phylodynamic and phylogenetic model implementations in full Bayesian framework. Heuristic approaches aimed at reducing the computational burden apply the inference models only to the unique sequences, i.e. ignoring frequencies of the different sequences and instead assuming each one occurs only once, or to only a random subsample of the full dataset.

We set out to investigate these heuristics in terms of how much loss of information on dynamic properties of the process occurs. Based on the identified drawbacks of the heuristics, we propose a new tool for efficient reconstruction of viral epidemiological and evolutionary dynamics from full quasispecies datasets. The framework involves first reconstructing the haplotypes and their frequencies within the quasispecies from the raw reads. Phylogenetic analyses are then performed on the haplotype alignment and the frequency information. Use of such complete datasets should lead to a more complete picture of pathogen dynamics, insight into transmission bottlenecks, and in more reliable parameter estimation.

Poster session B - GEN 2000

Phylodynamics on sexual contact networks (51894)

David Rasmussen, Tanja Stadler.

ETH Zurich.

We present a new modeling framework for understanding how sexual contact networks shape the phylogenetic history of sexually transmitted pathogens like HIV. This framework is built upon a phylodynamic model that statistically describes how host network structure influences the shape of pathogen phylogenies by extending earlier coalescent models for infectious diseases to include local contact network structure. These phylodynamic models allow us to explore how network properties such as clustering, contact heterogeneity and assortative mixing shape tree structure. Moreover, this framework allows for network properties to be directly estimated from phylogenies using likelihood-based inference in a way that takes into account how network structure and epidemiological dynamics interact to shape a pathogen's phylogenetic history. We also demonstrate how these methods can be applied to real world HIV sequence data to test for differences in sexual contact structure among different human populations.

Poster session B - GEN 2000

Metabarcoding bacterial and intestinal nematode communities in free-ranging rufous mouse lemurs (*Microcebus rufus*) (51895)

Tuomas Aivelo, Juha Laakkonen, Jukka Jernvall.

Institute of Biotechnology, University of Helsinki; Department of Biosciences, University of Helsinki; Department of Veterinary Biosciences, University of Helsinki.

There is strong interest in microbiome, but there is a lack of studies connecting intestinal parasites and symbiotic bacteria. Nevertheless, we expect the species co-inhabiting intestine to have interactions which shape their respective communities.

We mark-recaptured mouse lemurs for 3 years during the mating season in Ranomafana National Park, Madagascar and tracked both microbiome and parasitic nematode community. We were able to follow 21 individuals for multiple years.

We identified communities by metabarcoding approach: we used standard 16S gene approach to microbiome, while we developed a method to identify operational taxonomic units of nematodes from feces using 18S gene. We also collected data for other parasites, both intestinal eimeriids and helminths and ectoparasitic lice and ticks.

Within-individual parasite communities in mouse lemurs are shaped by facultative hibernation as parasites seem to go extinct during hibernation and quickly (re)colonize individuals after mouse lemurs' activity starts. While between-individuals community of the parasites was stable over mating season, within-individual communities experienced drastic turnover. In contrast, microbiome composition differed between individuals but microbiome was stable throughout the sampling. There was no clear correlation between parasite community and the bacterial composition. Nevertheless, the initial succession in microbiome and parasite colonization after hibernation was very clear.

Poster session B - GEN 2000

Interacting species - interacting traits (52032)

Krzysztof Bartoszek.

Department of Mathematics, Uppsala University.

The need for multivariate methods is very well established in the phylogenetic comparative methods community. They are predominantly used to analyze co-functioning traits of the same species. However there is no methodological objection for using the same methods to analyze coevolution in a multiple species system e.g. host-pathogen, host-parasite. Apart from understanding how the species interact on the phenotype level such methods, like my mvSLOUCH R package, can aid in identifying the correct phylogeny from a set of competing trees (host species tree, virus tree, consensus tree ...) using trait measurements. I will discuss the mathematics behind modelling multiple traits evolving and speciating. I will then continue to show how one can use model selection of evolutionary models to find support for a species tree and illustrate it with a simple analysis of gene expression levels in different bacterial species.

Poster session B - GEN 2000

Killer bees or bee killers? the recent global spread of multi-host pollinator pathogens (52755)

Lena Wilfert.

University of Exeter.

Pollinating insects form communities that, in our temperate regions, are dominated by honeybees and bumblebees. Here, we show that viral pathogens, originally identified in the heavily studied honeybees, are generally multi-host pathogens that can freely circulate between species rather than being limited to honeybees. However, within these communities, some host species play a dominant role, which depends upon the insect community composition and the particular virus. Deformed Wing Virus is a formerly benign honeybee virus that has become a virulent emerging pollinator disease following the emergence of the varroa mite in European honeybees, which provide a novel horizontal transmission route. Using phylodynamic reconstruction, we show that this virus originated in East Asia but is now being propagated globally through European honeybee populations. This suggests that pathogens, and in particular RNA viruses, may be playing a role in the widespread declines of many pollinator species.

Poster session B - GEN 2000

Ancestral polymorphism or recent gene flow? Insight from comparative genome scans in allopatry and sympatry (51863)

Mark Ravinet, Kohta Yoshida, Jun Kitano.

National Institute of Genetics.

How informative are genome scans for understanding speciation? Peaks and troughs of differentiation metrics have become a central focus in speciation studies yet relatively few attempts have been made to address the difficulties of interpreting these patterns. For example, does low divergence reflect gene flow or shared ancestral polymorphism? One way to deal with this is to investigate systems where it is possible to compare populations in sympatry and allopatry. If low divergence is due to shared ancestral polymorphism, we would expect no difference in differentiation between comparisons. We therefore focused on the recent speciation between two highly divergent three-spined stickleback species in the Japan Sea (*Gasterosteus nipponicus*) and the Pacific Ocean (*Gasterosteus aculeatus*). We constructed a large population genomic dataset of 280 individuals from sympatric and allopatric populations across the distributions of both species. Our spatially distributed sampling design allows us to identify introgression (lower differentiation in sympatry relative to allopatry) as well as candidate loci underlying reproductive isolation during divergence (divergence common to allopatry) and on secondary contact (divergence found only in sympatry). We suggest that careful consideration of study design can improve the interpretation of genome scan approaches.

Poster session B - GEN 2000

Determining and managing adaptive potential in threatened populations – there is hope! (51928)

Anna Santure, Patricia Brekke, John Ewen.

University of Auckland; Institute of Zoology, Zoological Society of London.

For species of conservation concern, one of the most promising applications of genomics is to understand the genetic basis of adaptation in wild populations. For example, knowledge of genetic variants that increase or decrease fitness will be an important tool aiding decisions on which individuals should be translocated to found new populations, thus maximising evolutionary potential of the new population while reducing risk from deleterious variants. In this talk, I will give an overview of our work to date in developing a genomic toolkit to understand adaptive potential in the threatened New Zealand hihi (stitchbird; *Notiomystis cincta*). I will discuss more generally why I think there is hope for managing adaptive potential in threatened populations, with bottlenecks and inbreeding likely to have somewhat “simplified” the typically multi-genic architecture of quantitative trait variation. Borrowing from genomic prediction, I will argue that a thorough understanding of molecular mechanisms may not be necessary in order to accurately identify high value individuals for breeding programs and translocations, thus maximising the evolutionary potential of threatened species. However, as exemplified by excellent work from the Soay sheep group, gene mapping in pedigreed wild populations does offer exciting possibilities for understanding selection and evolution in the wild.

Poster session B - GEN 2000

The never-ending effect of introgression on genome evolution in broadcast spawning marine species (52034)

Christelle Fraïsse, Khalid Belkhir, Camille Roux, Pierre-Alexandre Gagnaire, John J. Welch, Nicolas Bierne.

ISEM; University of Cambridge; UNIL.

Introgressive hybridization often leads to reticulated evolution in which diverging species remain connected by periodic gene-flow of different efficiency across the genome. Although widely accepted, its effect on patterns of divergence remains incompletely understood, mainly because of insufficient geographic and taxonomic sampling. Open questions are still numerous: How long can species boundaries remain permeable? Why are some genome regions more porous than others? How widespread are adaptive introgression, introgression swamping or local reshuffling of genetic barriers? We used reference genome assemblies to investigate introgression in two species complexes of broadcast spawning marine organisms: *Mytilus* mussels and *Ciona* sea squirts. Demographic inferences reveals that both species complexes are characterized by ongoing gene-flow despite strong molecular divergence (up to 0.15 in *Ciona*). Our analysis reveals wide variability in introgression rates along the genomes and across geographical samples. In sea squirts we uncovered hotspots of introgression due to adaptive introgression or genomic deserts of genetic incompatibilities. In mussels we observed a widespread contribution of differential introgression in generating geographic differentiation within species (up to half the intra-specific outliers). Reticulated evolution should be seriously considered when interpreting regions of outlying differentiation in

genome scans, especially when allelic divergence is old and taxonomic sampling has been neglected.

Poster session B - GEN 2000

Using population re-sequencing data to study patterns of genetic variation in butterflies. (52202)

Ramprasad Neethiraj, Emily Hornett, Jason Hill, Christopher Wheat.

Stockholm University; Penn State University.

Does recombination dynamics change across chromosomes? Does genetic variation vary across chromosomes? What is the relationship between recombination dynamics and genetic variation? Questions such as these fascinate our research community but are hard to answer in novel species in an economical and timely fashion without a high quality genome. Although advances in sequencing technologies make it possible to sequence whole genomes in days, effectively assembling and using such data is challenging. We have developed a method called MESPA (Mining Exons for Scaffolding Poor Assemblies) that takes as input a candidate protein gene set along with a low quality genome and returns high quality gene models. Using MESPA in combination with Pool-seq, I report on the patterns of genetic variation and recombination dynamics in a few species of butterflies without having had to invest time and money in a high-quality genome.

Poster session B - GEN 2000

Genetic structure of populations with different B chromosome frequency assessed by two genome scan methods (52286)

Tanja Adnađević, Jelena Blagojević , Vladimir M. Jovanović , Ivana Budinski , Marija Rajičić , Mladen Vujošević .

Institute for biological research " Siniša Stanković".

B chromosomes present a diverse group of extra chromosomes heterogeneous in nature, behaviour, and evolutionary dynamics. B chromosomes in non-model organisms, such as yellow necked mouse, *Apodemus flavicollis*, has been in a focus of a long term research. In order to detect B chromosomes possible contribution to genetic structure of populations, we used samples from different habitat types, and with different frequency of animals with B chromosomes. Since whole genome coverage is required, genome scans employing neutral markers such as dominant amplified fragment length polymorphisms (AFLPs), and co-dominant microsatellites (SSRs) were performed. We obtained 471 AFLP markers and analyzed 8 microsatellite markers from 4 populations in Serbia. Consequently population and landscape genomic analysis was performed. Characterization of the adaptive genetic variation in relation to environmental factors may contribute to the understanding of adaptive differentiation of populations to diverse habitats in species harboring extra

chromosomes. Limitations and advantages of used genome scan methods will be discussed in the light of B chromosome presence. This study will improve our knowledge of B chromosome maintenance and inheritance since 15% of all species possess them.

Poster session B - GEN 2000

Post-bottleneck genetics in wild populations: Do we see what we expect and do patterns differ from neutrality? (52424)

Deborah Leigh, Christine Grossen, Andreas Wagner, Lukas Keller.

IEU, University of Zurich ; Swiss Institute of Bioinformatics, Switzerland; The Santa Fe Institute, USA.

Bottlenecks, periods when a population is at a reduced size, are globally increasing in their frequency. Such declines can elevate extinction risk. Accordingly, an accurate understanding of their long-term consequences is required to optimize conservation management and mitigate the loss of biodiversity. Current understanding on the state of genetic variation and ongoing evolutionary processes after a bottleneck is predominantly from theory, laboratory experiments or neutral markers. In contrast, most bottlenecks occur in the wild. Wild populations are exposed to processes often naturally excluded from previous studies, such as variable environments and selection. These can affect the maintenance of variation and adaptive potential. Therefore, patterns in genetic diversity and evolutionary processes in the wild may deviate from expectations. Here we are examining genome wide SNP variation across several bottlenecked populations of Alpine ibex (*Capra ibex*). Through outlier scans and changes in allele frequencies across populations, we are investigating if marker patterns differ from neutral expectations and if recent selective events vary between populations. Ultimately, we aim to characterize genome wide variation and ongoing evolutionary processes across multiple wild bottlenecked populations.

Poster session B - GEN 2000

Estimating selection from clines across the genome (52441)

Eniko Szep, David Field, Nick Barton.

IST Austria.

In principle, narrow spatial gradients, or clines, indicate strong selection. However, with genome-wide data, it can be difficult to distinguish selected loci when they are embedded in a very large number of neutral loci. We simulate contact between distinct populations that meet in a one-dimensional habitat, following a linear genome that contains a few selected loci. We compare different methods for estimating cline widths and positions from marker frequencies, and show that the power to detect selected loci is limited by the time since contact and by the population density.

APPLICATION OF RESTRICTION-SITE ASSOCIATED DNA-SEQUENCING FOR THE STUDY OF GENOMIC DIVERSITY AND DIVERGENCE IN EASTERN BRAZILIAN MARMOSETS (52525)

Joanna Malukiewicz, Anne Stone.

Federal University of Viçosa; Arizona State University .

Here, we apply RADseq (restriction site associated DNA sequencing) in the characterization of intra- and interspecific genomic variation as well as divergence between two marmoset species, *Callithrix jacchus* and *C. penicillata*. These two species are the youngest members of the *Callithrix* genus, having diverged as sister species less than a million years ago. This study represents the first application of this technique to the *Callithrix* genus, and RADseq holds great potential to address several issues about the *Callithrix* phylogeny, identification of speciation genes, and hybridization. The main focus of this study is to establish the utility of RADseq in performing a *Callithrix* genomic scan, using 6 *C. jacchus* and 7 *C. penicillata*. The overall level of divergence between *C. jacchus* and *C. penicillata* was low at the variant sites recovered by RADseq STACKS analysis, but the former species showed less genetic variability than the latter. However, there are a number of genomic regions that showed high levels of statistically significant divergence, especially on chromosome 12, and these regions group into “islands” throughout the genome. The observed patterns of genomic variation and divergence will provide a foundation for future speciation and genomic studies within the *Callithrix*.

The remarkably limited explanatory power of molecular ecology (52646)

Patrick Meirmans.

University of Amsterdam.

We undoubtedly live in the era of genomics, with a continuous development of increasingly sophisticated molecular genetic tools. Together with those molecular tools, the statistical inferences used to analyse such data are getting increasingly refined. It has now become standard in analyses of population genetic data to estimate migration rates, barriers to gene flow, detect loci under selection, and associations between genetic and ecological variation. However, few users of these methods realise that their explanatory power is in fact highly limited and many of the methods are prone to biases and errors. Using results from my own research, I will explain several of these pitfalls and show when certain types of inferences can lead to erroneous results. I will then provide suggestions for the proper use of these analyses. Above all, I will warn against any overenthusiastic use of methods in cases for which they are not suited, which unfortunately includes the great majority of their applications.

The blueprint of genomic architecture: does adaptation involve genetic trade-offs? (52777)

Stuart Dennis, Anamaria Štambuk, Dorotea Polović, Maja Šrut, Victor Soria-Carrasco, Zachariah Gompert, Vid Baković, Goran Klobučar, Patrik Nosil.

The University of Sheffield; University of Zagreb; Utah State University.

A central tenet of adaptive evolution is the differential fitness of genotypes in different environments. Theory suggests that these fitness differences may arise from genetic variability that is beneficial in some environments but deleterious in others, yet evidence to support this genetic trade-off is scarce. In this study we conducted a field transplant experiment and recorded differences in survival of 900 transplanted *Mytilus galloprovincialis* mussels in different environments. We use these survival data as a proxy for fitness in a genome-wide association scan with ~20,000 GBS variants. Our results show that fitness differs between environments and there is a genotypic signature involving around 60 genetic markers, but that these markers are different between environments. Our results challenge the hypothesis that adaptation involves genetic trade-offs. Implications of these data will be discussed.

Analysing Evolve and Resequencing Experiments (52789)

Srdjan Sarikas, Katarina Bodova, Nick Barton.

IST Austria.

Experimental studies of populations evolving in conditions with artificial selection (evolve and resequencing experiments) are becoming more common due to more affordable sequencing technology. The candidates for selected loci are typically identified by strong increase in allele frequencies. However, determining a single locus as a selected one is virtually impossible since recombination does not break associations between loci on the typically short timescales of these experiments. Instead, selection acts on the whole blocks of linked loci from the original haplotypes, so it is the haplotype frequencies that carry the key information about the underlying evolutionary mechanisms, not the observed allele frequencies. We show how to reconstruct the haplotype frequencies from the pooled allele frequencies, how to bound the errors of the estimate, and how to optimally design the experiments.

Genome-wide population differentiation and local adaptation in Atlantic cod (52952)

Michael Matschiner, Bastiaan Star, Paul R. Berg, Ole K. Tørresen, Alexander J. Nederbragt, Olav S. Kjesbu, Nils Chr. Stenseth, Kjetill S. Jakobsen, Sissel Jentoft.

Centre for Ecological and Evolutionary Synthesis, Department of Bioscience, University of Oslo, Oslo; Institute of Marine Research, Box 1870 Nordnes, N-5817 Bergen, Norway.

Populations of Atlantic cod (*Gadus morhua*) are differentiated in a variety of phenotypic traits, including alternate life history strategy and migration behavior. In contrast to Norwegian local cod populations which reside near the coast all-year round, the North-East Arctic Cod is a highly migratory population, feeding most of the year in the open water of the Barents Sea, but spawning along the Norwegian coast, with the main spawning area at the Lofoten archipelago. Besides long-distance migration between the Barents Sea and the spawning area, the North-East Arctic Cod is further characterized by vertical migration and the use of deeper habitats, as well as the crossing of thermal fronts between warm Atlantic and cold Arctic waters. These differentiated populations of Atlantic cod could therefore represent an example of speciation in progress.

Here, we investigate genetic differentiation and patterns of selection between coastal cod and North-East Arctic Cod, using genome sequences of 48 individuals. We identify over 10 million single nucleotide polymorphisms (SNPs) and find strong support for genetic population separation between the two groups. We further characterize patterns of selection across the Atlantic cod genome and investigate the directionality of gene flow in different genomic regions.

Poster session B - GEN 2000

Parental care buffers against inbreeding depression in burying beetles (51584)

Natalie Pilakouta, Seonaidh Jamieson, Jacob Moorad, Per Smiseth.

University of Edinburgh.

Inbreeding depression is a major evolutionary and ecological force that influences population dynamics and the evolution of mating systems. Inbreeding depression can be exacerbated by various environmental stresses, such as starvation, predation, parasitism, and competition. Parental care may play an important role as a buffer against inbreeding depression in the offspring by alleviating these stresses. We examined this potential role of parental care in a burying beetle with facultative care. We used a 2x2 factorial design with the following factors: (i) the presence or absence of the mother during larval development and (ii) inbred or outbred offspring. We hypothesized that maternal care would improve the performance of inbred offspring more than outbred offspring. Indeed, the mother's presence led to a higher increase in larval survival in inbred than in outbred broods. Receiving care at the larval stage also increased the lifespan of inbred but not outbred adults, suggesting that the buffering effects of care can persist long after the offspring have become independent. Our results show that parental care has the potential to moderate the severity of inbreeding depression, which

may favor inbreeding tolerance. These buffering effects could thus influence the evolution of mating systems and other inbreeding avoidance mechanisms.

Poster session B - GEN 2000

Testing for Punctuated Evolution in New Zealand Marine Snails (Penion) (51588)

Felix Vaux, Simon F.K. Hills, James S. Crampton, Steve A. Trewick, Mary Morgan-Richards.

Massey University; GNS Science; Victoria University of Wellington.

Stasis and rates of evolution have been popular research topics since the beginning of evolutionary theory, but there have been few comprehensive, empirical investigations of the original (and controversial) predictions of 'punctuated equilibria.' We are testing these hypotheses using the supposed ideal dataset of Penion (Buccinidae, Neogastropoda).

The investigation integrates genomic and geometric morphometric analyses under a phylogenetic framework, and it combines living and fossil record data. The study genus exhibits significant extant diversity in New Zealand and Australia, and there is an exceptionally detailed fossil record extending to 27 Ma. Extant genetic lineages have fossil records reaching 5 Ma, this allows for changes in morphology to be directly linked to genetic variation, and for morphology-based taxonomic classification to be tested against population genetics. Individuals are large, morphologically complex, and developmental morphology is also preserved.

Preliminary mtDNA and rDNA phylogenetics indicates that Penion is paraphyletic with the geographically distant clade Kelletia, meaning that the possibility of allopatry and invasion (rather than geologically abrupt morphological change) is present in this supposedly ideal dataset. Based on current data however, the vast majority of extant lineages represent an Australasian-restricted monophyletic group. Ongoing analysis is testing the accuracy of morphology at predicting genetic lineages.

Poster session B - GEN 2000

EVOLUTIONARY AND CONSERVATION GENETICS STUDIES IN Damithrax spinosissimus, the Caribbean king spider crab (51594)

Julio Hurtado, Nestor Campos, Edna Marquez.

Universidad EAFIT, Medellín, Colombia - Universidad Nacional de Colombia Sede Medellín; CECIMAR, Universidad Nacional de Colombia Sede Caribe; Universidad Nacional de Colombia Sede Medellín.

Damithrax spinosissimus is a large Majid crab distributed throughout the sub-tropical Atlantic Ocean in the United States of America, the Bahamas and the West Indies in the Caribbean Sea. There is a lack of information about evolution, conservation genetics and phylogeography aspects of this species. Oceanic and coastal islands from Caribbean Sea have differences in geological origins and environmental conditions and life history traits of *D. spinosissimus* populations (short larval period) could affect their distribution across Caribbean ecosystems. We present important information in evolutionary and conservation genetic aspects in *D. spinosissimus* by using molecular markers and ecological information. By using the 454 pyrosequencing approach, we assembled the nuclear and mitochondrial genomes and designed de novo primers for population genetics and phylogeography analysis in five Colombian populations of *D. spinosissimus*. We tested phylogenomic relationships of *D. spinosissimus* with other 43 crustacean species, and by using microsatellite and mitochondrial regions we found two management units (the first one an oceanic island, the second one four continental populations). This information may be important as a complementary study in molecular evolution of Malacostracan crustaceans, and for future studies in management strategies for marine protected areas and their conservation for food security in developing countries.

Poster session B - GEN 2000

The evolutionary nature of high population density in insular lizards (51652)

Maria Novosolov, Gordon Roda, Anat Feldman, Amy Kadison, Roi Dor, Shai Meiri.

Tel Aviv University; US Geological Survey.

Islands organisms usually have fewer predator and competitors species than mainland ones. This is thought to select for high population densities on islands. We hypothesize that insular lizards have denser populations than mainland species and that density is negatively correlated with competitor and predator richness. We collected population density data for 317 species – 94 small island species, 31 large-islands species, 32 mainland populations of species also found on islands and 160 from mainland ‘endemics’. We controlled for phylogenetic affinities, body mass and study area, which are strongly correlated with population density. Population density was the highest in small-island species and lowest in mainland ‘endemics’. Mainland populations of species also found on islands had higher population density than mainland ‘endemics’. Population density of insular species increases with decreasing lizard richness and NPP. Population density of mainland species increases in areas of low lizard species richness and predation risk. We hypothesize that the tendency to live in high population densities gives a ‘head start’ for species to successfully colonize islands. Interspecific competition has a strong affect in controlling population density thus species on lizard-poor islands can increase their population density even when NPP is low.

Poster session B - GEN 2000

MOLECULAR SYSTEMATICS OF THE ASIAN SPECIES OF THE GENUS METAGONIMUS (51664)

Urusa Thaenkham, Hideto Kino, Yukifumi Nawa, Tomáš Scholz, Jiraporn Ruangsittichai, Naowarat Saralamba.

Department of Helminthology, Faculty of Tropical Medicine, Mahidol University; Department of Infectious Diseases, Hamamatsu University School of Medicine, Hamamatsu, Japan; Research Affairs Office, Faculty of Medicine, Khon Kaen University, Khon Kaen, Thailand; Institute of Parasitology, Academy of Sciences of the Czech Republic. České Budějovice, Czech Republ; Department of Medical Entomology, Faculty of Tropical Medicine, Mahidol University, Thailand; Department of Molecular Tropical Medicine and Genetics, Faculty of Tropical Medicine, Mahidol Univer.

Metagonimus is genus of intestinal parasite in the family Heterophyidae. Metagonimus consists of seven nominal species in the oriental region and one in Europe. Among the oriental Metagonimus species, the relative sizes of oral and ventral suckers have been used as major morphological diagnostic characteristics, and these parasites have been divided into two groups. Group 1 consists of Metagonimus yokogawai, M. takahashii, and M. miyatai – their oral sucker is smaller than the ventral sucker. In contrast, species in Group 2 has an oral sucker larger than the ventral sucker, and consists of M. hakubaensis, M. katuradai, and M. oturui. In this study, these six oriental Metagonimus were collected from fish at different localities in Japan. Phylogenetic relationship was investigated by using three genetic markers, 28S rDNA, ITS 2 region, and cox1 gene. By molecular phylogeny, Metagonimus could also be divided into two clades. Four species were grouped together in clade I, except M. katuradai, and M. oturui which were in clade II. These two species were found to be very closely related genetically, and rather distantly related to M. hakubaensis, which is surprising considering their morphological similarities. It suggested that morphological characteristics alone are not enough for systemizing Metagonimus.

Poster session B - GEN 2000

Male diapause exists in *Drosophila montana*; diapause affects CHC composition and mating behaviour in *D. montana*. (51735)

Outi Ala-Honkola, Thomas Schmitt, Venera Tyukmaeva, Hannele Kauranen, Anneli Hoikkala.

University of Jyväskylä; University of Würzburg; University of St Andrews.

Environmental cues, mainly photoperiod and temperature, control reproductive diapause (arrest of oocyte development) in female insects. Diapause serves two adaptive functions: it improves survival during unfavourable seasons and/or restricts oviposition to the season favourable for the survival of eggs. Male diapause (defined as a reversible inability to inseminate receptive females) is much less studied than the female one, but if males maximise their chances to fertilize females while minimizing energy expenditure (sperm production is costly), we expect males to be in diapause at the same time as females are. We investigated whether male *Drosophila montana* are reproductively inactive when kept in conditions that induce diapause in females and we found that indeed, they are. We also found that males can recognise diapausing females as they do not court them. This is probably due to cuticular hydrocarbon (CHC) profile change in diapausing flies. Diapausing flies have more long-

chained hydrocarbons, which have been shown to increase desiccation tolerance in other *Drosophila* species, in their cuticula than non-diapausing flies. Males may use these as a cue to assess female reproductive state.

Poster session B - GEN 2000

Antibiotic restriction might facilitate the emergence of Multi-Drug Resistance (51776)

Uri Obolski, Lilach Hadany.

Tel Aviv University.

High antibiotic resistance frequencies have become a major public health issue, and cause substantial limitations in treatment options for some bacterial infections. To diminish overall resistance, and especially the occurrence of bacteria that are resistant to all antibiotics, certain drugs are deliberately scarcely used - mainly when other options are exhausted.

We use a mathematical model to explore the efficiency of such antibiotic restrictions. The model is examined for two strategies of antibiotic prescription: cycling and mixing, in which the drugs are periodically switched, or randomly assigned, respectively. Data obtained from Rabin medical center, Israel, is used to estimate realistic antibiotic resistance frequencies in incoming patients.

We find that broad usage of the hitherto restricted drug can reduce the number of incorrectly treated patients, and reduce the spread of bacteria resistant to both common antibiotics. Such double resistant infections are often treated with the restricted drug, and therefore are prone to become resistant to all three antibiotics. Thus, counter intuitively, a broader usage of a formerly restricted drug can sometimes lead to a decrease in the emergence of bacteria resistant to all drugs. We recommend re-examining restriction of specific drugs, when multiple resistance to the relevant alternative drugs already exists.

Poster session B - GEN 2000

Evidence for the emergence of a lethal genetic disease in a wild bird population of conservation concern (51781)

Amanda Trask, Jane Reid, Stuart Piertney, Davy McCracken, Eric Bignal.

University of Aberdeen; Scotland's Rural College; Scottish Chough Study Group.

Populations of conservation concern are often small or inbred. Theory predicts that deleterious recessive mutations that are masked in outbred populations will be expressed, potentially leading to increased expression of genetic diseases. Few studies, however, have demonstrated the emergence of a deleterious recessive genetic disease in a wild population of conservation concern, meaning that the real world importance of such processes has been questioned. Red-billed choughs (*Pyrrhocorax pyrrhocorax*) have suffered an historic decline and currently number less than 60 breeding pairs in Scotland. This population has recently

been affected by a lethal disease characterized by blindness and associated brain abnormalities in nestlings. We used pedigree data to show that the pattern of occurrence of blindness within and among families matched that expected given Mendelian inheritance of a single-locus recessive mutation. Such analysis of observational pedigree data assumes an absence of extra-pair parentage, and indeed extra-pair parentage rates were estimated to be low (4.2-6.6% of offspring). A candidate gene approach, based on known genetic polymorphisms underlying the similar human condition 'Peters' anomaly', did not detect polymorphisms associated with blindness in choughs. Nevertheless, we provide strong evidence of the emergence of a lethal recessive genetic disease in nature.

Poster session B - GEN 2000

Elephants born in the high stress season age faster (51803)

Hannah Mumby, Adam Hayward, Khyne U. Mar, Virpi Lummaa.

University of Sheffield; University of Edinburgh.

Senescent declines in reproduction and survival are found across the tree of life, however little is known of the factors individual variation in these rates, such as early developmental conditions. Only a few studies exist on the effects of early life environment on reproductive ageing and there are no studies beyond those of humans concerning very long-lived species. We use a large dataset (N=1078) of female working Asian elephants (*Elephas maximus*) from Myanmar to test these concepts. We analyse the effects of birth conditions, measured as concentration of stress hormones in reproductive-aged females, to categorise birth season into stressful vs. not-stressful periods. We show that the months in which adult females (potential mothers) have highest glucocorticoid concentrations and most intense workload are June to August; with a mean of 68.1ng/g feces compared to 45.6ng/g feces in the other months. Female elephants born in these months exhibit faster reproductive senescence in adulthood (interaction between age and birth season, $X^2(df=1)=6.07$, $P=0.014$) and have lifetime reproductive success reduced by 15.9% in comparison to their counterparts born at other times of year. These findings have implications for our understanding of senescence theory and conservation strategies in endangered Asian elephants.

Poster session B - GEN 2000

Parallel divergence of landlocked freshwater gobies from an amphidromous ancestor in the Ryukyu Islands of Japan (51861)

Yo Yamasaki, Hirohiko Takeshima, Yuichi Kano, Mutsumi Nishida, Katsutoshi Watanabe.

Kyoto University; Research Institute for Humanity and Nature; Kyushu University; University of the Ryukyus.

The genus *Rhinogobius* is the largest group of freshwater gobies, consisting of ~85 species with several life-history types. *Rhinogobius* sp. YB is a landlocked form occurring in the

Ryukyu Islands of Japan, and previous studies suggested that its populations in respective islands or rivers originated by parallel divergence from the related amphidromous form (*Rhinogobius brunneus*). However, there have been no statistical comparisons between parallel and single origin hypotheses. To confirm the parallel landlocking patterns, we conducted genetic analysis using microsatellite markers. The genetic relationships among specimens supported polyphyletic patterns for landlocked populations, which seem to be derived from the amphidromous populations in the respective islands. Further, we performed statistical comparisons between alternative hypotheses on the origin of landlocked populations using the Approximate Bayesian Computation method. This analysis also supported the idea of independent origins of landlocked populations among islands. Moreover, the results suggested that the periods of their divergence differed among islands. Within islands, on the other hand, no positive support for the idea of independent origins of landlocked populations was obtained. The present study suggests that comparisons among landlocked populations in different islands will be useful to study the mechanisms and processes of parallel adaptation and speciation.

Poster session B - GEN 2000

Fine-scale genetic structure, distant matings and inbreeding depression in natural populations of *Fucus vesiculosus* (51868)

Sara Teixeira, Gareth Pearson, Rui Candeias Candeias, Céline Madeira Madeira, Myriam Valero, Ester Serrão.

CCMAR; CNRS, UPMC Sorbonne Université, PUCCh, UACH, UMI EBEA .

Restricted gene flow can lead to neighbouring individuals having higher genetic similarity among themselves than among distant ones. Here we studied small scale spatial genetic structure and mating patterns in the brown seaweed *Fucus vesiculosus*, a dioecious marine broadcast spawner. Given the mating system and life history traits of this species we expected to find spatial genetic structuring, and widespread heterozygote deficiency resulting from mating between neighbouring related individuals. *F. vesiculosus* occurs in habitats with contrasting exposures and patchiness, therefore we analysed 5 adult populations and recruits from 2 of these populations, in both natural open coast and estuarine ecosystems. Genetic diversity showed a North-South decreasing trend, while highly significant heterozygote deficits were found for most adult populations. The analysis of the recruits and their adult population seems to indicate the occurrence of inbreeding depression. The very fine spatial resolution of this study revealed a lack of spatial genetic structuring for three of the five populations studied, across different habitats. We propose three non-exclusive hypothesis for our findings: 1) unrestricted gene flow 2) inbreeding depression eliminating most inbred individuals resulting from nearby related parents or 3) temporal Wahlund effects, through the genetic pool of a bank of microscopic forms.

Poster session B - GEN 2000

Quantifying clade-specific speciation and extinction rates from phylogenies (51906)

Joelle Barido-Sottani.

ETHZ.

With an increasing number of empirical phylogenies being available, it becomes possible to study the associated phylodynamics, i.e. the processes giving rise to the phylogeny, in great detail. Our work focuses on quantifying the speciation-extinction processes based on a phylogeny. In particular, we present a computational framework to identify clade-specific changes in speciation and extinction rates. We provide speciation and extinction rate estimates for each identified clade, and thus are able to quantify species-level selection patterns. Such analysis can produce useful hypotheses for downstream work on looking for the underlying reasons of rate changes.

We assess the reliability of our tool in a simulation study, and compare it to the existing BAMM (Bayesian Analysis of Macroevolutionary Mixtures) method, which uses a different conceptual setup to achieve the same goal of quantifying speciation and extinction rates. Finally we apply this tool, which will be available as an R package, to empirical phylogenies, demonstrating its performance on real data.

Poster session B - GEN 2000

Strong genetic differentiation of the goby *Rhinogobius duospilus* in Hong Kong streams revealed by a multilocus approach (51948)

Tsz Huen Hu, I-Shiung Chan, **Ka Hou Chu.**

The Chinese University of Hong Kong; National Taiwan Ocean University.

Little is known about how regional landscape affects the genetic differentiation among fish populations on a small spatial scale. We report here the population genetics of *Rhinogobius duospilus*, an indigenous goby in Hong Kong (~1,104 km²). Analyses of mitochondrial genes (cyt b and CR) on >100 individuals from 25 localities recover four genetically distinct lineages with discrete geographical distribution. Two major, widely distributed lineages occur on the western and eastern sides of Hong Kong respectively, while two rare lineages are endemic to Lantau Island and Hong Kong Island respectively. Extensive genetic structuring is also observed within each lineage, even among streams of close proximity. The strong population structure is attributed to the local landscape such as mountain ranges and the poorly connected streams. On the contrary, analyses of nuclear markers (Rag 1 and RR-9) including microsatellites reveals a different population genetic pattern, with some alleles observed across mitochondrial lineages. The discrepancy between the two datasets may be due to factors such as incomplete lineage sorting of nuclear loci and strong genetic drift of mitochondrial genes. Our study suggests that the incorporation of information from analysis of nuclear markers is essential for reconstructing the evolutionary history of a species.

On the importance of uncertainty quantification and modelling in regression covariates (51969)

Stefanie Muff, Lukas F. Keller.

University of Zurich.

Evolutionary Biology has become a very quantitative scientific field, and as such it relies heavily on the use of sound statistical methods. Regression models are probably the most popular tools to obtain inference from data. Important variables are, however, often difficult to measure and thus may contain considerable uncertainty or error. If such uncertainty is ignored, parameter estimates and confidence intervals of regression parameters often suffer from serious biases.

I will briefly discuss and illustrate the effects of measurement error in covariates when included in generalized linear (mixed) regression models. Two examples with inbreeding coefficients as covariates, where the latter were estimated from genetic data, will be presented.

The aim of my talk is to underline the importance of a careful quantification of uncertainties and measurement error in covariates or the outcomes of regression models. Given that the data collection process can be very time consuming and expensive, an extra effort in the analysis is often worth to obtain more precise answers to research questions.

Understanding patterns of trait expression: trade-offs and correlations (51992)

Øistein Haugsten Holen, Thomas Owens Sønningsen.

CEES, University of Oslo.

The set of phenotypes an organism can develop is constrained. Traits that enhance fitness but are subject to a trade-off are usually predicted to correlate negatively. One well-known exception is when the units under study (e.g. individuals, populations) vary so much in state (e.g. resource level, condition) that the underlying trade-off is masked. We present a game-theoretical analysis of trait expression, using an organism with two defence traits as an example. Instead of a traditional two-way trade-off, we consider the more general case where one or both defence traits trade off with a third trait such as fecundity or growth. Both positive and negative correlations between the focal traits are found to be generic outcomes of the model, even in the absence of variation in state. A positive correlation can arise when variation in selection pressure causes variation in relative investment in the two focal traits versus the third trait across the units of study. The shape of the trade-off has a decisive influence on the outcome. We relate our findings to current empirical examples in the literature and discuss some of the pitfalls of using trait correlations as a shortcut for identifying trade-offs.

Understanding the ecology and genetics of adaptive traits in *Drosophila* embryos (51993)

Barbara Horvath, Alex Kalinka.

Institut für Populationsgenetik, Vetmeduni Vienna, Austria.

Determining the genetic basis of fitness-related traits is crucial for understanding how populations adapt to their environments. By assaying phenotypes across different ecological settings, it is possible to uncover genetic variation responsible for adaptation in natural populations. Here we examined a fitness-related trait – the length of embryonic development – on the phenotypic level. By phenotyping 31 DGRP (*Drosophila melanogaster* Genetic reference Panel) strains, we uncovered genetic variation for the length of embryogenesis, measured as the median hatching time. We also characterized the egg-to-adult competitive fitness of these strains, both under low- and high larval densities, and found substantial Genotype x Environment interactions for fitness. By bringing together our phenotype data with information on previously measured phenotypes (zygotic genome activation, adult-to-adult competitive fitness) as well as genomic data, we have confirmed the ecological and evolutionary importance of the rate of embryonic development in *D. melanogaster*.

Joint estimation of sibships and population parameters in the NGS era (52024)

Thomas Ellis.

IST Austria.

Pedigrees are powerful tools for investigating selection and mating patterns in wild populations. The power to infer pedigrees is improved by incorporation of information on phenotypes and sibships, but approaches which integrate both of these are currently lacking. Furthermore current software is not designed to deal with modern SNP data. I have been developing methods to jointly estimate pedigrees and evolutionary parameters which makes use of shared alleles among siblings, and which can deal with SNP data in minutes rather than months. I illustrate this with a half sibling arrays from open pollinated seed capsules from a snapdragon hybrid zone.⁵²⁵

Molecular characterisation of MHC class II in the Australian invasive cane toad reveals multiple splice variants (52060)

Mette Lillie, Richard Shine, Katherine Belov.

Faculty of Veterinary Science, University of Sydney; School of Biological Sciences, University of Sydney.

The cane toad (*Rhinella marina*) has gained notoriety after its introduction and invasion across the Australian landscape, with significant impacts on the native Australian fauna. This invasion has shown rapid adaptation for dispersive traits, but at a cost to the immune system. To investigate their immunogenetics, we characterised the MHC class II in the Australian cane toad and found four class IIA and three class IIB loci. Very low allelic diversity was observed at all loci; the likely result of the complex history of introductions en route to Australia. We also observed two splice isoforms at two class IIA and two class IIB loci. One isoform seen at IIA and IIB loci involved the removal of the domain essential to peptide binding and presentation. The other isoform, observed at a class IIA locus is likely to be a soluble MHC product. This is the first observation of MHC class II splice variants in any anuran species, and similar splice variation has only been observed in caudate amphibians. These results suggest a significant role of MHC class II alternative splicing in the Australian cane toad, and may provide the first indication of it playing a wider functional role within Amphibia.

Poster session B - GEN 2000

A post-copulatory pre-zygotic barrier between collared and pied flycatchers (52083)

Emily Cramer, Murielle Ålund, S Eryn McFarlane, Arild Johnsen, Anna Qvarnström.

University of Oslo Natural History Museum; Uppsala University.

Post-copulatory, pre-zygotic (PCPZ) barriers are poorly studied in internally fertilizing vertebrates, but could play a major role in species that commonly copulate with heterospecifics. Pied (*Ficedula hypoleuca*) and collared (*F. albicollis*) flycatchers are closely-related species that occasionally form heterospecific breeding pairs, which is very costly due to the low reproductive success of hybrids. Extra-pair (EP) copulations with conspecifics, combined with PCPZ barriers, could mitigate the evolutionary cost of pairing with a heterospecific. We test one possible PCPZ barrier using an in vitro, blocked experimental design. Specifically, we examine the swimming speed of sperm from each species in fluid from the reproductive tract of females of each species. Pied flycatcher female fluid slowed down the swimming speed of collared flycatcher sperm, compared to all other female-male combinations. Females of both species have a higher proportion of EP offspring when socially paired to a heterospecific, but ecological factors make pied flycatcher females particularly likely to mal-adaptively pair with heterospecific males. The PCPZ barrier we document here may contribute to the heightened production of EP offspring by pied flycatcher females paired to heterospecifics, and it may be a substrate on which selection can act, strengthening the reproductive barrier between species.

Population genomics on a non model fish species through Genotyping by Sequencing (52113)

Carlos Carreras, Enrique Macpherson, Marta Pascual.

Department of Genetics and IRBio, University of Barcelona, Av.Diagonal 643, E-08028 Barcelona, Spain; Centre d'Estudis Avançats de Blanes (CEAB-CSIC), Car. Acc. Cala St. Francesc 14, Blanes 17300 Girona.

New genomic tools based on high-throughput sequencing enable the design and genotype of thousands of markers thus enhancing the power of classical population genetic analyses and bringing new research opportunities to date reserved to model species. However, their application to ecologically relevant species is not yet fully implemented due to the limitations of working without genome or transcriptome of reference. The East Atlantic peacock wrasse (*Symphodus tinca*) raises several ecological and biological relevant questions including the fine scale detection of oceanographic discontinuities, the assessment of adaptation under the scope of a global warming or the study of the effect of larval dispersion on population structuring. We used genotyping-by-sequencing (GBS) to develop a genome-wide panel of SNPs in 76 individuals from three populations under different environmental conditions in the Black and the Adriatic Seas. We obtained a set of 8,619 SNPs and genotypes suggested low inbreeding and similar variability across populations. We also found high levels of population differentiation, although inter-individual variation was higher than inter-population variation. Finally, the expected population structure was reconstructed and individuals were clearly grouped by populations. Thus, GBS is a very promising approach to develop markers for population genomics and adaptation studies in ecologically relevant species.

MetaPIGA 4.0, maximum likelihood and Bayesian phylogenomics using Genetic-Algorithm and Monte-Carlo samplers (52128)

Djordje Grbic, Michel C. Milinkovitch.

LANE, Dept. of Genetics & Evolution, University of Geneva; SIB Swiss Institute of Bioinformatics, Switzerland; Institute of Genetics and Genomics of Geneva (iGE3), University of Geneva.

The MetaPIGA phylogeny inference software has reached its fourth version with multiple new functionalities. First, the MetaPIGA user-friendly and intuitive graphical interface allows users to partition, visualise, and manipulate data as well as infer ancestral states based on Bayesian statistics. Note that command-line execution on local machines or remote clusters is also possible. Second, the user can choose to run analyses either on multicore CPUs or on GPU Nvidia graphics cards. The latter provides enough speedup for the use of codon models in practical computing time on single computer environments. Third, MetaPIGA 4.0 enables analyses of DNA, Protein, and codon data in the Bayesian and maximum likelihood frameworks with a palette of optimisation algorithms such as Hill climbing, Consensus

Pruning, and MC3.

Access of multiple algorithms in a single software allowed us to estimate their relative computing efficiencies and accuracies through comparisons of final tree likelihood, posterior probabilities, and execution time. Finally, we propose a modification of the Consensus Pruning algorithm that transforms it into a Markov Chain Monte Carlo sampler.

Poster session B - GEN 2000

Disentangling the complex evolutionary history of the Western Palearctic blue tits (*Cyanistes* spp.) – phylogenomic analyses suggest radiation by multiple colonisation events and subsequent isolation (52189)

Martin Stervander, Juan Carlos Illera, Laura Kvist, Pedro Barbosa, Naomi P. Keehnen, Peter Pruisscher, Staffan Bensch, Bengt Hansson.

Molecular Ecology and Evolution Lab, Dept of Biology, Lund University, Lund, Sweden; Research Unit of Biodiversity (UO-CSIC-PA), Oviedo University, Campus of Mieres, Asturias, Spain; Department of Biology, University of Oulu, Oulu, Finland; Present affiliation: Population genetics, Dept of Zoology, Stockholm University, Stockholm, Sweden.

Isolated islands and their often unique biota play key roles for understanding the importance of drift, genetic variation, and adaptation in the process of population differentiation and speciation. One island system that has inspired and intrigued evolutionary biologists is the blue tit complex (*Cyanistes* spp.) in Europe and Africa, in particular the complex evolutionary history of the multiple genetically distinct taxa of the Canary Islands. We combined Sanger sequencing at a population level (20 loci; 12,500 nucleotides) and next generation sequencing of single population representatives (>3,200,000 nucleotides), analysed in coalescence and phylogenetic frameworks. We found that (i) Afrocanarian blue tits are monophyletic and represent four major clades; (ii) the blue tit complex has a continental origin, and that the Canary Islands were colonised three times; (iii) all island populations have low genetic variation, indicating low long-term effective population sizes; (iv) populations on La Palma and in Libya represent relicts of an ancestral North African population; and (v) the Canary Islands, contrary to recent suggestions, hold sink populations, which have not served as source for back colonisation to Africa. Our study demonstrates the importance of complete taxon sampling and an extensive multi-marker study design to obtain robust phylogeographical inferences.

Poster session B - GEN 2000

Phylogeny and biogeography of *Primula* sect. *Armerina* in the Qinghai-Tibetan Plateau (52234)

Guangpeng Ren, Elena Conti, Jianquan Liu, Nicolas Salamin.

DEE; Institute for Systematic Botany, University of Zurich; Lanzhou University ; DEE.

Understanding what shapes geographical and ecological distribution of biodiversity is one of the most challenging questions in evolutionary biology and ecology. This is particularly true for the regions that have experienced rapid habitat changes and harbor high species diversity. In this context, we firstly examined the diversification history of *Primula* section *Armerina* on species level based on five chloroplast DNA fragments and one nuclear gene. Our dating analysis based on chloroplast dataset suggested that this section began to diverge from its relatives around 3.55 million years ago, which largely coincided with the last major uplift of the Qinghai-Tibetan Plateau (QTP). Incongruences between the chloroplast and nuclear trees are mostly present among closely related species, which might be accounted for hybridization and/or introgression. Biogeographical analysis supports the origin of the section in the Himalayas Mountains and the dispersal from Himalayas to Northeast QTP, West QTP and Hengduan Mountains. Secondly, three very interesting species, *P. fasciculata*, *P. tibetica* and *P. nutans*, are chosen as our study materials to further investigate their phylogeography and population genomics using double digest RAD sequencing on population level. The data is collecting, and some of the results will be present in this poster.

Poster session B - GEN 2000

Quantifying Nature's appearance: combining high-resolution, coloured 3D reconstruction and mathematical tools to analyse skin patterns in *Pantherophis guttatus* (52279)

António F. Martins, Michel C. Milinkovitch.

Laboratory of Artificial & Natural Evolution, Dept. of Genetics & Evolution, University of Geneva; SIB Swiss Institute of Bioinformatics, Switzerland.

An expanding number of studies investigate the biophysical mechanisms generating intra- and inter-specific complexity and diversity of morphological traits. However, classification of morphologic characters is often limited to qualitative descriptions or simple quantitative analysis. To address this issue, we have combined state-of-the-art robotics, high-resolution digital cameras and image-based 3D reconstruction algorithms to build a scanning system capturing geometry and colour texture details down to 20 microns. This system is (i) greatly flexible, allowing a scanning range that extends from above the meter to sub-millimeter details; (ii) highly repeatable, making it suitable for a systematic approach; (iii) fast, with scanning times below 5 minutes, a critical feature when animals under anaesthesia are used. These fully-coloured 3D virtual mesh models are accurate representations of the real animal and its external morphological traits. This allows for the systematic and rigorous quantification of features such as colour variations and gradients, repetitive patterns, shapes, areas, or correlation among specific traits. Moreover, they can be used to perform numerical simulations of biophysical processes on realistic geometries. By using the colour patterns of corn snakes (*Pantherophis guttatus*) as an example, we argue that this approach has practical importance for innovative biophysical analyses of phenotypes in 3D.

Poster session B - GEN 2000

Endogenous control of sexual size dimorphism: Gonadal androgens have neither direct nor indirect effect on male growth in a gecko (52326)

Lukas Kubicka, Zuzana Starostova, Lukas Kratochvil.

Charles University in Prague, Faculty of Science, Department of Ecology; Charles University in Prague, Faculty of Science, Department of Zoology.

Changes in the effect of gonadal androgens (GA) on male growth are considered to be the proximate mechanism of evolutionary shifts in sexual size dimorphism (SSD) in reptiles. Positive effect of GA on male growth was found in male-larger species of squamates, while negative in female-larger species. Nevertheless, previously we documented that in geckos, GA do not affect male growth under constant thermal conditions. This discrepancy could be attributed to effect of GA on thermoregulation and selection of body temperature, which might affect metabolic rate, general activity and hence indirectly growth. We tested this possibility by monitoring growth of control and castrated males in the male-larger gecko *Paroedura picta* kept in the thermal gradient. We did not find any differences between treatment groups in growth rate and final body size. Castration affects neither oxygen consumption nor foraging activity of experimental geckos. In conclusion, GA seems to have neither direct nor indirect effect on the ontogeny of SSD in geckos and the evolutionary changes in SSD in this group cannot be connected to evolutionary changes in GA metabolism.

Poster session B - GEN 2000

Genetic relatedness does not predict the queen's successor in the primitively eusocial wasp, *Ropalidia marginata* (52335)

Saikat Chakraborty, Thresiamma Varghese, Shantanu Shukla, Javaregowda Nagaraju, K P Arunkumar, Raghavendra Gadagkar.

Centre for Ecological Sciences, Indian Institute of Science; Laboratory of Molecular Genetics, Centre for DNA Fingerprinting and Diagnostics, Hyderabad 500001; Deceased.

Ropalidia marginata is a tropical paper wasp in which queens and workers are morphologically indistinguishable. Colonies consist of a single docile queen and up to 100 functionally sterile workers. Once the queen is dead or experimentally removed, one of the workers increases her aggression and eventually becomes the next queen. The chance of a worker succeeding the queen has been shown to be uncorrelated with her body size, dominance rank, ovarian or mating status, but imperfectly correlated with her age. Here we investigate whether genetic relatedness predicts the queen's successors. We first estimated pair-wise genetic relatedness using polymorphic microsatellite markers. Next, we constructed models based on successors i) being most closely related to the queen, ii) being most closely related to the immediate predecessor queen, iii) having the highest relatedness to the majority of the workers and iv) having the highest average relatedness to all the workers. We predicted up to five successors based on each of these models after performing experiments to determine up to five successors in experimental colonies. The predictions of none of the models matched the experimental results. Thus genetic relatedness does not predict the queen's successors in this species.

Phylogenetic (in)stability of G and B matrices in Acridid grasshoppers (52336)

Anasuya Chakrabarty, Holger Schielzeth.

Bielefeld University.

Adaptive evolution is influenced by the fitness landscape and by the amount of heritable variation. But traits do not occur in isolation, since they are often genetically correlated due to pleiotropy or linkage disequilibrium. This causes non-independent inheritance of trait variation and influences the response to selection. The additive genetic variance-covariance matrix G efficiently summarizes the underlying genetic architecture and dependencies among traits. The size and structure of G can act as a constraint to adaptive evolution if the leading eigenvector of G (g_{max}) is not aligned with the selection vector. We estimate and compare the additive genetic covariance structure of five morphological and five song traits in three Acridid grasshopper species in order to assess the degree of phylogenetic stability of the G matrix. G matrices might diverge by genetic drift or by selection. Knowledge about the phylogenetic relationships among the three species allows us to ask if closely related species are more similar in the G matrices and if species divergence is biased towards g_{max} . Furthermore, we explore the structure of the matrix B , a submatrix of G that summarized cross-sex genetic covariances. This sheds light on sex-specific genetic variation and the evolution of sexual dimorphism in grasshoppers.

Fishery-induced selection: what can be learned from introduced salmonids in Sierra Nevada Lakes? (52337)

Sébastien Nusslé, Stephanie Carlson.

University of California Berkeley.

Size-selective fishing is expected to trigger evolutionary responses. However, the potential for fishery-induced selection to significantly modify population characteristics is controversial and not yet well understood. In this study, we analyzed data from over 30 populations of brook trout and rainbow trout that were completely removed from lakes in California's Sierra Nevada during the course of a habitat restoration program. We estimated fishery selection on body length in replicate populations, and related the strength of fishery selection to population- and habitat-specific characteristics. Even though "non-selective fishing gear" was used in removal efforts, we found that fishing was more likely to remove larger individuals. Due to this size selectivity, we observed a dramatic decline in the mean and variability of fish length within a few months across populations. The magnitude of this decrease can be linked to population-specific parameters, such as initial size distribution and local environmental factors (e.g. lake size, elevation). Our study demonstrates that size-selective fishing not only

affects population structure by removing the largest individuals, but also that the environment can mediate the impact of fishing.

Poster session B - GEN 2000

Experimental reduction of penis length reduces male reproductive success in a bug (52444)

Liam Dougherty, David Shuker.

University of St Andrews.

Animal genitalia are some of the most elaborate and fastest evolving traits we know of. It is now clear in many species that genital morphology in both males and females has been shaped by sexual selection. However, it has historically been difficult to confirm correlations between morphology and fitness, as genital traits are complex and manipulation tends to impair function significantly. The seed bug *Lygaeus simulans* has a long, coiled intromittent organ (or processus) that is threaded into the female spermathecal duct during mating. The processus is a hollow, sclerotized tube, and thus can be shortened easily by cutting. We confirm that there is significant selection acting on male processus length in *L. simulans* by experimental shortening of the processus prior to mating, and show that males with shortened processi have significantly reduced reproductive success. Importantly though, the sperm transfer function of the processus is not impaired by the manipulation itself. Such manipulation of a genital trait directly involved in sperm transfer has been reported only once before in the literature to our knowledge. We thus present rare, direct experimental evidence that an internal genital trait functions to increase reproductive success.

Poster session B - GEN 2000

Phylogenetic origins of the avian MHC Class IIB (52445)

Julien Goebel, Reto Burri, Marta Burri-Promerová, Luca Fumagalli.

Department of Ecology and Evolution, Laboratory for Conservation Biology, Lausanne University; Department of Evolutionary Biology, Evolutionary Biology Centre, Uppsala University ; Department of Medical Biochemistry and Microbiology, Biomedical Centre, Uppsala University.

Gene duplication is thought to be one of the primary sources of adaptive evolution. The major histocompatibility complex (MHC) multigene family is a well-known example of an important ecological novelty coming from duplication events. It encodes genes involved in the vertebrates' adaptive immune response and stands for the most polymorphic genetic system known to date in vertebrates. Its frequent gene duplications and losses result in a marked variation in gene number and genomic organization between vertebrates. Mammalian MHC Class II β chain (MHCIIB) paralogs evolve independently and their duplication history can be traced back over tens of millions of years. Recent studies on birds report also strong

evidence for the persistence of two ancient MHCII B lineages (DAB1 & DAB2) over at least 100 million years, unequally distributed between bird species. We isolated and recovered MHCII B genes from species all over the avian phylogeny. We figured out mechanisms that broke the duplication signal by reconstructing avian MHCII B recombination and selection histories, and assessing its concerted evolution pattern. Thus, we could identify gene regions that reflect the history of the duplication. We reconstructed the phylogenetic history of avian MHCII B and provided an accurate estimate for the origin of the two ancestral lineages.

Poster session B - GEN 2000

Role of gamete and propagule dispersal in shaping the genetic distribution of sessile organisms (52489)

Valeria Montano, Samuel Neuenschwander, Jerome Goudet.

University of Lausanne; University of Lausanne; University of Lausanne.

Dispersal employs different strategies in sessile and motile organisms. Among terrestrial plants, complex dispersal behaviours, involving multiple traits (dispersal syndrome) and interaction with vector species, are well known in relation to seed dispersal. During the life cycle of sessile organisms, dispersal may also happen at a previous stage, i.e. during gametic production. These two dispersal stages (gamete and propagule) contribute differently to the spatial and temporal distribution of genetic variation. In fact, a new genetic variant introduced into a population may be carried in higher number of copies by n propagules than by n gametes. Moreover, the two processes are likely to drive temporal fluctuations in the distribution of genetic variation. Here, we perform a simulation study of the differential role of gametic and propagule dispersal in shaping allele distribution, using a simple model of sessile organism facing two dispersal stages.

Poster session B - GEN 2000

Individual experience affects how zebra finch males attend to physical properties of nest materials (52508)

Alexis J. Breen, **Eira Ihalainen**, Eric Bowman, Susan D. Healy.

University of St Andrews.

Nest building is almost ubiquitous among bird taxa but the nest produced is immensely varied. Within a single species the materials used to construct the nest can also vary enormously, but we currently know very little of how birds 'know' what kind of a nest to build. For a century, nest building has been assumed to be 'instinctive' but recent evidence shows construction behaviour to be experience-dependent. We tested whether birds choose structurally suitable building materials based on their own experience with those materials or whether they have rules for selecting what to build with. In a laboratory experiment, we first tested male zebra finches' (*Taeniopygia guttata*) initial preference for four types of material

that differed in length and/or rigidity (the male selects and deposits the material at the nest site). The males then built using one of these materials, after which their preference was tested for the second time. The changes in the males' preferences suggest that their choices depend on their building experience in a way that indicates they attend to physical properties of nest materials in a hierarchical fashion.

Poster session B - GEN 2000

Does phenotypic integration constrain morphological diversification? A phylogenetic comparative study (52524)

Masahito Tsuboi, Niclas Kolm.

Uppsala University, Evolutionary Biology Centre, Department of Ecology and Genetics/Animal Ecology; Stockholm University, Department of Zoology/Ethology.

Organisms need their parts to be integrated to function as a coherent whole, while a degree of modularity between functionally independent subunits is a ubiquitous feature of organismal design. Though theory predicts that the degree of phenotypic integration and modularity can influence the direction and the rate of evolutionary processes (the phenotypic integration hypothesis), empirical evidence is still scarce. Here, we investigated the key theoretical prediction that phenotypic integration constrains morphological diversification using craniofacial morphology of Lake Tanganyika cichlids, a well-known model system of morphological adaptation. We first employed geometric morphometrics to quantify the degree of phenotypic integration and modularity within cichlids' craniofacial system. Then, by explicitly taking phylogeny into consideration, we investigated the rate of morphological diversification in relation to the level of phenotypic integration. Specifically, we focus on four functionally significant traits in the cichlids' cranium; oral jaw morphology, brain size, eye size, and cheek muscle size. The result will be interpreted and discussed in light of the phenotypic integration hypothesis.

Poster session B - GEN 2000

POPULATION STRUCTURE OF THE COCONUT CRAB BIRGUS LATRO (DECAPODA: ANOMURA: COENOBITIDAE) FROM CHRISTMAS ISLAND IN THE INDIAN OCEAN (52533)

Christiana Anagnostou, Christoph D. Schubart.

Department of Evolutionary Ecology and Genetics, Zoological Institute; Biologie I, Institut für Zoologie, Universität Regensburg, D-93040 Regensburg, Germany.

There is increasing evidence for a lower degree of population connectivity and a higher degree of self-recruitment in marine species with planktonic larvae than expected under a passive dispersal model, giving rise to population sub-structuring. We assessed the genetic and biometric population structure of a terrestrial anomuran crab species with marine

planktonic larvae, the coconut crab *Birgus latro* on Christmas Island (Indian Ocean) using seven polymorphic microsatellite markers and morphometry. Adult individuals were sampled at five different locations (\triangleq subpopulations), with 20 individuals per location. A number of biometric measurements were taken as well as haemolymph and tissue samples for DNA extraction and subsequent microsatellite analysis. Results of genetic structuring analyses do not suggest an obvious population subdivision: Global and pairwise F_{ST} values were low; Bayesian methods and a principal component analysis did not reveal any population sub-structuring. The results of a population assignment test using estimated allele frequencies were ambiguous depending on the statistical method (17% versus 90% of individuals assigned to the subpopulation where they had been sampled), probably due to the low sample size. Regarding the biometric measurements, significant differences among some of the subpopulations could be detected. In conclusion, *B. latro* may so far be considered as a single management unit on Christmas Island.

Poster session B - GEN 2000

The role of kinesin in the regulation a quantitative colour trait (52570)

Jesper Fogelholm.

IFM Biology.

The genetic regulation of coat colour is one of the most studied gene systems to date, with ~150 genes known to be involved. Currently, however, all have Mendelian, rather than quantitative, effects. Using QTL mapping in two intercross chicken populations we identify a 2Mb region associated with the intensity of red colouration. This region contained a selective sweep (fixed in domestic birds), with five genes in close proximity. Expression of Kinesin-like-protein7 was found to strongly correlate with intensity of red colouration in feathers from juvenile Red Junglefowl x White Leghorn backcross individuals, as well as from separate adult RJF x WL intercross individuals. Microarray analysis of all genes in the QTL interval using multiple intercross individuals revealed KIF7 to be the sole candidate correlating with feather coloration. To the best of our knowledge this is the first time that a gene regulating a quantitative colour trait has been identified. Strikingly a kinesin has been shown to be involved in red colouration in butterflies from the *Heliconius* family. If this is the same mechanism at work, it suggests that this is functionally conserved, with 550 m.y.o to the last common ancestor, the Urbilaterian.

Poster session B - GEN 2000

Explaining the variation in gestation length and weaning age across mammals (52596)

Renske Gudde, Andrew Meade, Jeffrey Joy, Chris Venditti.

University of Reading; University of British Columbia.

Mammalian length of gestation and weaning period differ remarkably. Furthermore, it has recently been suggested that these traits are coupled; when gestation length increases, lactation time decreases and vice versa. We studied the variation in gestation length and weaning age for 491 species of four mammalian orders, artiodactyls, carnivores, primates and rodents, and within these orders on the family level. By calculating the rate of evolution of these traits, we are able to explain when and how this variation has evolved, what other life history traits affected gestation length and weaning age and if they are indeed coupled traits. We found that the rates of gestation length and weaning age are affected by different life history traits and vary highly among orders (and families within orders). For example, in artiodactyls gestation length depends on the age of sexual maturity, the rate of gestation length is affected by litter size and neonatal body mass, weaning age is determined by litter size and maximum longevity and the rate of weaning age evolution by diet. Finally, the rates of evolution suggest that gestation length and weaning age are coupled in primates, but not in the other orders.

Poster session B - GEN 2000

Colonization pathways, genetic diversity and inbreeding depression in non-native lizards (52602)

Sozos Michaelides, Geoffrey While, Tobias Uller.

University of Oxford ; University of Tasmania; Lund University.

Studying biological invasions may further our understanding of how ecological and evolutionary processes shape patterns of diversity within species and communities. The ability of non-native species to persist and adapt to new environments is expected to rely on their genetic diversity. To understand what shapes their genetic structure we need to have a detailed knowledge of their colonization history. In this study, we used Bayesian clustering, approximate Bayesian computation methods and network analyses to reconstruct the origin and colonization pathways of 23 populations of the wall lizard *Podarcis muralis* in England. We then inferred how genetic diversity is affected by the origin(s) and admixture of distinct genotypic lineages. Our analyses show that established populations in southern England originate from at least nine separate sources from native populations in France and Italy. Genetic diversity was significantly lower in the non-native populations but mixed-origin populations had higher genetic diversity than single origin populations. The loss of genetic diversity was accompanied by increased hatching failure in non-native populations. This study thus demonstrates the importance of understanding colonization history for understanding the persistence and adaptation of non-native species.

Poster session B - GEN 2000

Relation between sex specific hormones (testosterone, progesterone) and sex specific traits in the Barn owl (*Tyto alba*) (52625)

Paul Béziers, Alexandre Roulin, Wolfgang Goymann.

Department of Ecology and Evolution, University of Lausanne, Building Biophore, 1015 Lausanne, Switz; Max-Planck-Institut für Ornithologie, Abteilung für Verhaltensneurobiologie, D-82319 Seewiesen, Germ.

Natural selection exerted on a given trait shared by both sexes can act differently in males and females. Given that sexual dimorphic traits are commonly under control of sexual hormones, it is likely that sexual selection acting on sexually antagonistic traits indirectly acts on sexual hormones or, alternatively, that sex hormones are directly responsible for sexual conflicts. We examined whether blood-circulating levels of testosterone and progesterone in barn owl nestlings (*Tyto alba*) were sex specifically related to melanin-based traits. Colour traits that are known to be under antagonistic sexual selection in this species. This study shows that nestlings displaying female specific traits, so large eumelanic spots and dark pheomelanic traits, had higher levels of progesterone than nestlings displaying male specific traits. And inversely, nestlings sired by males with male specific traits, so small eumelanic black spots, had higher levels of testosterone than nestling displaying female specific traits. Our results suggest that plumage traits in barn owls seems to signal the levels of sex hormones and thereby support the association found between melanin-based traits and sex-specific behavior in barn owls. These results also support the idea that sexual antagonistic selection observed in coloration may also exist for sex hormones

Poster session B - GEN 2000

No evidence for reproduction-lifespan tradeoffs in females of a *Drosophila* long-lived insulin-signaling mutant, under varying exposure to males (52684)

Irem Sepil, Pau Carazo, Stuart Wigby.

University of Oxford; University of Valencia.

Across a broad range of taxa, similar factors mediate female lifespan: mating, reproduction and high levels of insulin-signaling all tend to reduce longevity. Although lifespan extension in insulin signaling mutants are often accompanied by reduced fecundity, exceptions to this pattern have been reported. This conflicts with life-history theory, which predicts an obligate trade-off between reproduction and lifespan. However, studies of long-lived mutants tend to be conducted under specific mating conditions, and often fail to consider other factors such as egg-adult viability, which may mask potentially important fitness effects. We varied the exposure to males of robustly long-lived *Drosophila melanogaster* females, in which key insulin producing cells are ablated. Ablated females always lived longer, had decreased fecundity but higher egg-adult viability than controls. However ablated females that received intermediate levels of exposure to males showed the highest increase in lifespan and no overall decrease in reproductive success. Lifespan extension under continuous exposure to males was likely mediated by reduced mating rates of the ablated females. Our results conflict with life-history theory, and instead suggest that optimal exposure to males and reduced insulin signaling result in maximal lifespan and reproduction for females.

Poster session B - GEN 2000

Evolution of multiple trade-offs in a predator-prey system (52685)

Noemi Woltermann, Lutz Becks.

Community Dynamics Group, Dept. Evolutionary Ecology, Max Planck Institute for Evolutionary Biology.

Trade-offs are often perceived as a gain in one trait combined with a loss in another and are often used to explain the maintenance of intra- and interspecific variation. They are however typically viewed to occur between two different traits and little is known about the evolution of trade-offs between a higher numbers of traits. Here we present results from a study where we followed the evolution of traits in the green-algae *Chlamydomonas reinhardtii* when evolving with and without predation by a rotifer (*Brachionus calyciflorus*). After 6 months, we isolated several clones from each evolving population and measured algal growth rates and palatability, survival of the predator when feeding on the evolved clones, as well as diversification (morphology) and colony formation of the isolates. We found lower growth rates, more colony forming genotypes, and lower rotifer survival rates for the isolates from the predation treatment. We found however no difference in diversification between treatments. Testing for multidimensional trade-offs, we found that different strategies evolved. Overall we show that (I) trade-offs evolve repeatedly but different with and without predation, (II) the evolution of traits depends on the genetic background of the ancestor and (III) colony formation evolves as defense against predation.

Poster session B - GEN 2000

Hybridization capture using RAD-seq probes: a novel technique improving data quality and among-sample overlap (52689)

Camille Pitteloud, Tomasz Suchan, Anna Kostikova, Nadezhda S. Gerasimova, Nadir Alvarez.

University of Lausanne; InsideDNA Ltd., United Kingdom; School of Biology, Lomonosov Moscow State University.

Development of next-generation sequencing brought new dynamics into evolutionary biology, allowing a dramatic increase in the representation of loci and specimens in population genomics studies. The most frequently used technique to reduce genome complexity in a reproducible manner is restriction-associated-DNA sequencing (RAD-seq). However, restriction site heterogeneity in RAD-seq can cause imbalanced loci representation and complicate data processing. In addition several sources of noise identified in RAD-seq can make data analysis more difficult. Here we describe a novel method, which improves among-sample locus overlap and strongly reduces stochastic variations in sequences outputs. The technique relies on the capture of shotgun Illumina libraries by molecular biotin-labelled probes that anneal to streptavidin beads. While probes generation can be PCR-based, using baits made of RAD-seq libraries allows whole genome scanning and avoids biases encountered in standard procedures. The method also applies well to historical DNA, characterized by high contaminant load that can thus be filtered prior to sequencing. The

approach described here offers extensive flexibility of applications and substantially improves RAD-seq potential in producing high-quality data.

Poster session B - GEN 2000

Tracing the invasion history of Europe's worst slug pest (52736)

Miriam A. Zemanova, Eva Knop, Gerald Heckel.

Institute of Ecology and Evolution, University of Bern, Switzerland; Swiss Institute of Bioinformatics, Lausanne, Switzerland.

Invasive species are one of the major threats to global biodiversity. The slug *Arion vulgaris* (syn. *lusitanicus*) is considered one of the hundred most invasive species in many European countries and a major agricultural pest but its origin and routes of expansion are contentious. Its apparent spread over the last decades is probably still ongoing in several parts of Europe. Here we trace the invasion history of *A. vulgaris/lusitanicus* by analyzing mitochondrial and nuclear markers in 32 populations covering its entire European distribution. Our results show that there is very little genetic differentiation between different European locations with a main mtDNA haplotype shared by individuals from 20 countries. Most populations in Eastern Europe have fairly low levels of nuclear diversity which is consistent with a very recent arrival of the species there. Genetic diversity of *A. vulgaris/lusitanicus* is highest in Western and Central European populations, but the common suggestion of an Iberian origin of the invasive slug is not supported by our data. Additionally, there is clear evidence of a strong human impact on the invasion history of this species. It is likely that human activities will also contribute to further range expansion of *A. vulgaris/lusitanicus* in the future.

Poster session B - GEN 2000

Transcriptome profiling of a key morphological innovation: the propelling fan of the water walking bug *Rhagovelia obesa* (52740)

M. Emilia Santos, Abderrahman Khila.

Institute of Functional Genomics of Lyon.

The invasion of new habitats often requires the evolution of key novel traits that facilitate the exploitation of the new environment. The mechanisms and selective forces underlying the emergence of such evolutionary novelties are largely unknown.

In *Rhagovelia* sp. (water-walking insect) the evolution of an elaborate swimming fan on the mid-legs increases water resistance against leg movements, increasing their propelling function. This trait allowed the *Rhagovelia* group to conquer and diversify on running water surfaces; a niche inaccessible for other water-walking insects. The genes underlying the fan development are unknown.

Here, we report a comparative analysis of the full transcriptomes of *Rhagovelia obesa* and *Limnoporus dissortis*, another water walking insect without propelling fans. We also provide a characterization of gene expression levels between developing mid-legs (with fan) against forelegs and hind-legs (without fan) in *R. obesa*.

This approach has allowed the identification of a list of genes associated with the evolution of this novel phenotype. Finally, we provide evidence that both co-option of pre-existing genes and lineage specific genes might be involved in the evolution of novel phenotypes. Studying the developmental genetic and adaptive bases of this phenotype will help understand the mechanisms through which novel morphological adaptations emerge under specific environmental pressures.

Poster session B - GEN 2000

Artificial selection for genital size impacts brain morphology (52783)

S  verine D. Buechel, Alexander Kotrschal, Isobel Booksmythe, J. Scott Keogh, Michael D. Jennions, Nicolas Kolm.

Stockholm University; Australian National University.

The vertebrate brain is one of the most energetically costly organs. Investment into the brain may therefore be prone to trade-offs with other costly traits. Indeed, comparative and experimental studies have shown negative associations between brain size and several other organs. For sexual traits however, evidence remains inconclusive. A recent experimental study even showed positive associations between brain size and male traits; male guppies selected for large brains had higher expression of several sexually selected traits including longer genitalia. Brain size and male sexual traits may be positively associated through at least two mechanisms. First, via selection on a third trait, for instance overall body condition; individuals with larger brains may be better at foraging and thus secure more or better quality food allowing for greater investment in costly sexual traits. Second, a genetic correlation between brain size and sexual traits may be generated through pleiotropy or linkage disequilibrium. Here we test for genetic linkage between brain size and male genitalia length by comparing brain morphology of male mosquitofish (*Gambusia holbrooki*) artificially selected for long and short genitalia length. We discuss our findings in the light of the many exiting recent advances in brain evolution research.

Poster session B - GEN 2000

How leaf mimicry of Kallima butterflies evolved? (52794)

Takao K Suzuki, Shuichiro Tomita, Hideki Sezutsu.

National Institute of Agrobiological Sciences.

Leaf mimicry provides a textbook example of adaptation and is also a historically contentious subject that has spurred criticism of modern evolutionary synthesis. Although Darwin and Wallace (and subsequent evolutionary biologists) argued for the gradual origin of leaf mimesis, the lack of direct experimental evidence has allowed antagonists to produce alternative evolutionary scenarios (e.g. saltation) for leaf mimesis. Here we examine whether the evolutionary process of leaf wing patterns of butterflies (Kallima) was gradual or sudden, and how the evolutionary changes that generated these features accumulated over long time periods. First, comparative morphological analyses indicated that Kallima leaf patterns are decomposed into the homologous pattern elements which 45 closely related species share, suggesting that the pattern elements have been inherited across species. Next, we used Bayesian phylogenetic methods to estimate the ancestral wing patterns, and revealed that the leaf pattern has evolved through several intermediate states from a non-mimetic ancestor. Finally, we estimated the temporal order of character-state changes in the pattern elements by which leaf mimesis evolved. In summary, our study provides the first evidence for gradual evolution of leaf mimicry.

Reference: Suzuki et al. (2014) Gradual and contingent evolutionary emergence of leaf mimicry in butterfly wing patterns. BMC Evol Biol 14:229

Poster session B - GEN 2000

Reproductive isolation between sibling species of seaweeds: the case of two *Lessonia* species along the Chilean coast (52918)

Florence Tellier, Claudia Hurtado, Nicole Badilla, Mauricio Orostica, Natalia Valderrama, Sylvain Faugeron, Myriam Valero.

Facultad de Ciencias, Universidad Catolica de la Santisima Concepcion; Programa de Magister en Ecologia Marina, UCSC (Concepcion, CL); School Ocean Sciences, Bangor University (UK); UMI EBEA 3614, Pontificia Universidad Catolica de Chile (Santiago, CL); UMI EBEA 3614, Evolutionary Biology and Ecology of Algae, CNRS, UPMC Sorbonne Université (Roscoff FR).

In seaweeds, reproductive isolation among closely-related species has been studied in only a few models. Here we focused on Laminariales, large brown seaweeds (kelps). *L. berteroana* and *L. spicata* are cryptic and closely-related species that show a parapatric distribution along the Chilean coast (north and south of 29-30°S), but the overlapping region (29-30°S) is very peculiar as it is composed of successive monospecific patches. Of five contact zones between adjacent patches, four zones showed a complete spatial segregation, and the species range limits correspond to unsuitable areas (200m to 50km long). The last contact zone showed coexistence of species along ~150 m of coastline. Using nuclear markers, we did not find evidence of any interspecific gene flow between patches separated by 1.5 km of unsuitable habitat. This contrasted with the large proportion of hybrids which have been obtained in controlled conditions. Furthermore, the contact zone where both species coexist (currently under study) presented some evidence of temporal isolation (different peaks of reproduction and recruitment). Up to 40% of the fixation discs (i.e. holdfasts) are shared among individuals from distinct species. The role of the different reproductive barriers (intrinsic and extrinsic; prezygotic and postzygotic) will be discussed.

The total evidence approach with sampled ancestors (52927)

Alexandra Gavryushkina, Tracy Heath, David Welch, Tanja Stadler, Alexei Drummond.

The University of Auckland; Iowa State University; ETH Zurich.

The evolutionary studies greatly rely on phylogenetic trees. Although there have been developed a number of methods to infer phylogenies there are still problems that require attention. One such problem is the dating of species phylogenies using the fossil evidence. A promising method is the 'total-evidence' approach, where molecular and morphological data of extant and fossil species are jointly used to infer species divergence times and macroevolutionary parameters. However current implementations of the method need to be improved in several aspects. In a Bayesian framework, an important component is the tree prior model which describes the tree branching process. Previous attempts to apply the total-evidence approach have used tree prior models that do not account for the possibility of fossil samples to be direct ancestors of other samples, that is, other fossils or extant species. Recently, Heath et al and Gavryushkina et al applied the fossilized birth-death model that explicitly models the sampling process and naturally allows for sampled ancestors to estimate divergence times based on molecular data and fossil occurrence dates. Here we present a method to analyse morphological and molecular data in a unified Bayesian framework with models that account for sampled direct ancestors. We apply this method to extant penguins and their fossil ancestors.

Transcriptomic changes characterizing inbreeding depression in a wild population of Alpine ibex (*Capra ibex*) (52966)

Kasia Sluzek, Lukas Keller, Andreas Wagner.

Institute of Evolutionary Biology and Environmental Studies, University of Zurich.

When natural populations crash, matings between kin inevitably become more frequent due to shrinkage of the pool of breeding individuals. If the population fails to promptly recover, inbreeding will further accumulate over successive generations at low population size. Inbred individuals experience inflated genome-wide homozygosity leading to the expression of deleterious, recessive alleles and as a consequence, often show depressed fitness. However, the magnitude of inbreeding depression is highly variable amongst individuals of comparable inbreeding coefficients, implying that it is a complex phenomenon not purely determined by global homozygosity levels.

In order to explore the functional underpinnings of inbreeding depression further, we are performing RNASeq on individuals from the ancestral population of Alpine ibex in the Gran Paradiso National Park, Italy.

This population has passed through at least two severe bottlenecks and has previously been shown to exhibit inbreeding depression for a set of fitness-related traits, including body mass, horn length and parasite load. Thus, it constitutes an ideal model for studying the gene expression changes underlying this conservation-relevant syndrome in a natural context.

Poster session B - GEN 2000

Spatial patterns in a human controlled population, the Swedish moose (*Alces alces*) (52972)

Lovisa Wennerström, Nils Ryman.

Dept. of Zoology, Stockholm University.

The moose (*Alces alces*) is the most intensely managed game species in Fennoscandia; approximately one third of the population, c. 16,000 animals, is harvested annually through hunting. Thus, the anthropogenic impact on the species' evolution is high. Despite the obvious risk of human-induced selection and the socio-economic importance of the moose, there are knowledge gaps with respect to its intraspecific diversity and genetic structure. To delineate the current spatial genetic landscape and the population history of the Swedish moose we used allozyme variability from over 20,000 georeferenced moose collected all over Sweden in combination with information from 12 microsatellite loci and mitochondrial DNA sequences. We combined individual-based and traditional statistical approaches with coalescence based simulations. The results indicate a complex history with bottlenecks and recent expansions. We show that the Swedish moose population is separated into two major genetic groups with a transition zone of sharp allelic shifts between them. This genetic structure has been stable for at least 30 years, despite extensive harvest. The divergence is not reflected in the mtDNA variation, however, and we conclude that the population structure of moose occurred after post-glacial immigration to Scandinavia, and is possibly affected by human hunting and harvest induced selection.

Poster session B - GEN 2000

Differentially expressed genes in *Anguillicola crassus*-infected European eels (53550)

Seraina E. Bracamonte, Michael T. Monaghan, Klaus Knopf.

The occurrence of invasive parasites has increased dramatically in recent years and several of them are implicated in the decline or extinction of their newly acquired host species. The parasitic swim bladder nematode of eels, *Anguillicola crassus*, has been introduced into the European eel population in the early 1980s and is considered to be one of the factors involved in the decline of its new host. Despite its devastating effect on the host, little is known about the processes affected during host response to an infection with *A. crassus*. Here we identify pathways that are important during the early stage of an *A. crassus* infection in European eels. We experimentally infected 3 European eels with *A. crassus* nematodes and compared the

transcriptome of infected and uninfected individuals for differentially expressed genes at three days post infection.

Poster session B - GEN 2000

The Avian Transcriptome Response to Malaria Infection (53551)

Elin Videvall, Charlie K. Cornwallis, Vaidas Palinauskas, Gediminas Valkiūnas, Olof Hellgren.

Department of Biology, Lund University, Lund, Sweden; Department of Biology, Lund University, Lund, Sweden; Institute of Ecology, Nature Research Centre, Vilnius, Lithuania; Institute of Ecology, Nature Research Centre, Vilnius, Lithuania; Department of Biology, Lund University, Lund, Sweden.

Malaria parasites are highly virulent pathogens which infect a wide range of vertebrates. Despite their importance, the way different hosts control and suppress malaria infections remains poorly understood. With recent developments in next-generation sequencing techniques, however, it is now possible to quantify the response of the entire transcriptome to infections. We experimentally infected Eurasian siskins (*Carduelis spinus*) with avian malaria parasites (*Plasmodium ashfordi*), and used high-throughput RNA-sequencing to measure the avian transcriptome in blood collected before infection (day 0), during peak parasitemia (day 21 postinfection), and when parasitemia was decreasing (day 31). We found considerable differences in the transcriptomes of infected and uninfected individuals, with a large number of genes differentially expressed during both peak and decreasing parasitemia stages. These genes were overrepresented among functions involved in the immune system, stress response, cell death regulation, metabolism, and telomerase activity. Comparative analyses of the differentially expressed genes in our study to those found in other hosts of malaria (human and mouse) revealed a set of genes that are potentially involved in highly conserved evolutionary responses to malaria infection. By using RNA-sequencing we gained a more complete view of the host response, and were able to pinpoint not only well-documented host genes but also unannotated genes with clear significance during infection, such as microRNAs. This study shows how the avian blood transcriptome shifts in response to malaria infection, and we believe that it will facilitate further research into the diversity of molecular mechanisms that hosts utilize to fight malaria infections.

Poster session B - GEN 2000

The genetic handicap principle: a severely deleterious mutation can be tolerated if the genome-wide mutation load is sufficiently low (53592)

Konstantin Popadin, Peischl Stephan, Sailani Reza, Letourneau Audrey, Santoni Federico, Garieri Marco, Nikolaev Sergey, Meyer Diogo, Excoffier Laurent, Antonarakis Stylianos E..

University of Geneva Medical School, Department of Genetic Medicine and Development; University of Lausanne, Center for Integrative Genomics; Institute of Ecology and Evolution,

Computational and Molecular Population Genetics (CMPG); Stanford University, Stanford School of Medicine; University of Sao Paulo, Department of Genetics and Evolutionary Biology.

Every human genome harbors hundreds of slightly-deleterious mutations. Even though most of these mutations have each a small effect, their cumulative effect (mutation load) could substantially reduce the fitness of an individual. Here we investigate an interaction between a severely deleterious mutation and the mutation load, formulating the genetic handicap principle: an individual bearing a severely deleterious variant (genetic handicap) is viable only if the genome-wide mutation load is sufficiently low. We develop a population-genetic model, which predicts that live-born individuals carrying a handicap mutation (causing, for example, 50-90% probability of miscarriage) show a reduction (5-20%) in their number of slightly-deleterious mutations as compared to controls. To test this prediction, we used data on trisomy of chromosome 21 (T21), a frequent chromosomal abnormality in humans which is associated with high miscarriage rates. Three genetic lines of evidence support the view that live-born T21 individuals have passed through the strong embryonic selection and thus have decreased load of slightly-deleterious mutations. We conclude that the negative fitness consequences of severe mutations such as trisomy can be partially compensated by a reduced genome-wide load of slightly-deleterious mutations and thus the approach can help to uncover a composition of mutation load.

Poster session B - GEN 2000

Transmission, genome size and the evolution of symbiosis (53702)

Roberta M. Fisher, Henry Lee, Stuart A. West.

Oxford University.

Symbiosis between bacteria and their hosts is a potential between-species major evolutionary transition in individuality. Bacterial symbionts are found in a diverse range of hosts, but the degree to which they benefit their hosts varies. A major hypothesis to explain this variation has been transmission route, with vertical transmission of clonal symbionts leading to higher levels of cooperation than horizontal transmission. It has also been suggested that horizontal transmission may be particularly beneficial in changeable or stressful environments. Here, we test the hypothesis that transmission mode and environment determine how much symbionts should benefit their hosts using a phylogenetically controlled comparative analysis of studies measuring host fitness on removal of their symbiont(s). We find (1) vertically transmitted symbionts are more beneficial than horizontally transmitted ones and have smaller genomes, (2) but horizontally transmitted symbionts are relatively more beneficial in stressful versus unstressful environments, (3) that nutritional symbioses are more beneficial to hosts than defensive ones, and (4) mutual dependence leads to a reduction in genome size compared to where there is no dependence. Our results show that to understand the evolution of symbiosis we need to consider multiple aspects of transmission mode, host-symbiont dependence and ecology.

Fine-scale genetic structure reflects sex-specific dispersal strategies in a population of sociable weavers (51573)

Rene E. van Dijk, Rita Covas, Claire Doutrelant, Claire N. Spottiswoode, Ben J. Hatchwell.

University of Sheffield, UK; CIBIO, Portugal; CEFÉ-CNRS, France; University of Cambridge, UK.

Dispersal is a critical driver of gene flow, with important consequences for population genetic structure, social interactions and other biological processes. Limited dispersal may result in kin-structured populations in which kin selection may operate, but it may also increase the risk of kin competition and inbreeding. Here, we use a combination of 20 years of data from >6500 birds and molecular genetics to examine dispersal patterns and their consequences for the population genetics of the sociable weaver (*Philetairus socius*), which exhibits cooperation at various levels of sociality from nuclear family groups to their unique colonial nests. We found that both sexes are philopatric, but that dispersal is female-biased, with females dispersing further and to less-closely related destination colonies than males. This pattern of dispersal is reflected by isolation by distance in terms of genetic relatedness and significant genetic variance among colonies, especially among males. Crucially, significant relatedness extended beyond the level of the colony for both sexes. Such fine-scale population genetic structure has probably played an important role in the evolution of cooperative behaviour in this species, but it may also result in a significant inbreeding risk, against which female-biased dispersal alone is unlikely to be an effective strategy.

Evolution of parasite interactions and virulence: from within-host growth to epidemiological feedbacks and back again (51695)

Mircea Sofonea, Samuel Alizon, Yannis Michalakakis.

Université de Montpellier; CNRS.

Many hosts are infected by several parasite genotypes at a time. Within these coinfecting hosts, parasites cooperate through public goods and compete through spiteful interactions. At between-host level, parasites also compete through transmission so the combinatorial diversity of cotransmission routes complicates the epidemiology and makes it difficult to predict the evolution of virulence. We introduce a new framework to model multiple infections that circumvents and goes beyond the co/super-infection dichotomy owing to explicit within-host dynamics and free cotransmission network. We use analytical solutions and numerical simulations to investigate how within-host dynamics affect the evolution of virulence and reciprocally how epidemiological feedbacks affect the evolution of within-host interactions.

Decisions of Group Size with Respect to Social Dilemmas and Between-Group Competition (51698)

Stephen Heap, Mikael Puurtinen.

University of Jyväskylä; University of Jyväskylä.

The interplay of cooperation and conflict drive the evolution of organization and complexity in biological systems, bringing individuals into groups and promoting new levels of individuality. Group size is inherently part of this dynamic, yet studies typically involve small groups of constant size and thus provide only limited scope. Important trade-offs may exist, such that larger groups can have advantages over smaller groups in between-group conflict, yet also experience a weakening of their cooperative bonds due to larger individual incentives to free-ride. Our research uses a public goods game, in which human participants are exposed to a dilemma between individual and cooperative interests. The players can also define their preferred group size, and vote for whether their group competes, cooperates or ignores other groups. We discuss the nature of the trade-offs underlying decisions of group size and the implications that our results have for the emergence of population structures that support cooperation in light of human social evolution and the major evolutionary transitions. Our study thus provides an initial experimental investigation into an expanded realm of inquiry that involves not only the interdependence of cooperation and conflict, but also the self-organized structuring of the population that occurs alongside these principles.

The Evolution of Antibiotic Resistance in Bacterial Colonies (51791)

Isabel Frost, Kevin Foster, Craig MacLean.

University of Oxford.

The evolution of antibiotic resistance is one of the major challenges facing society. However, the vast majority of research into antibiotics focuses on solitary cells that are swimming in liquid. In reality, bacteria often live in dense and diverse communities where social interactions are central to their phenotypes. We have been studying how growth in colony biofilms impacts resistance evolution in the pathogen *Pseudomonas aeruginosa*. Our strain carries a clinical plasmid conferring resistance to streptomycin, which is inactivated intracellularly, and carbenicillin, which is broken down extracellularly and so has more potential for “social” effects where one cell influences the fitness of another. We compete resistant and susceptible strains in varying concentrations of one, or the other, antibiotic. This reveals that susceptible strains can exploit and outcompete resistant strains in the presence of antibiotic, but only for carbenicillin, which has extracellular effects. We also show that this effect depends on the different genotypes being mixed. When different strains make single genotype patches within colonies (high genetic relatedness), the resistant strains are always selected. In sum, we show that antibiotic resistance can be a social trait and this can lead to

the counter intuitive outcome that there are conditions where antibiotics will favor susceptible, rather than resistant, genotypes.

Poster session B - GEN 2000

Social microbial immunity: experimental test with *Pseudomonas aeruginosa* bacterium and lytic bacteriophages (51806)

Ville-Petri Friman, Pierre Moreau, Sandra Andersen, Stephen Diggle.

Imperial College London; Technical University of Denmark; University of Nottingham.

The relative benefit of cooperation often increases with the group size. However, group living exposes populations to pathogens and parasites, and as a counter defence, social groups have evolved several altruistic tactics that require cooperation to work efficiently. Here we studied this link with bacteria and their infective parasites, bacteriophages. *Pseudomonas aeruginosa* bacterium cooperates by secreting and responding to quorum sensing (QS) signal molecules. Thus, we hypothesized that QS genes might be linked to resistance genes against bacteriophages. We found that QS-positive strains reached higher densities in the presence of bacteriophages and that this was due to higher rate of resistance evolution. While non-signaling, QS-negative, cheaters benefited from the presence of QS-positive strain in the presence of phages, non-signaling and non-responding double mutants did not. This result suggests that phage resistance was socially regulated. Moreover, we found that PQS QS-system was especially important in the presence of phage, and that pyoverdine receptors can have a dual function in iron uptake and phage receptor with clinical *P. aeruginosa* isolates. These results suggest that phage resistance can be socially regulated with *P. aeruginosa*, and that intra-specific social interactions could also drive trophic level interactions in microbial communities.

Poster session B - GEN 2000

Is vocal similarity used to assess relatedness in cooperative breeders? (51833)

Amy E. Leedale, Ben J. Hatchwell.

University of Sheffield.

Animal societies are often composed of relatives, and kin selection is widely invoked to explain cooperation in such groups. Strong selection pressure for effective kin recognition is therefore likely to occur in cooperative species. However, the mechanisms involved are poorly understood. Kin can be discriminated from non-kin using vocalisations in several cooperatively breeding birds, but in some species, individuals can also distinguish between kin of varying relatedness. The mechanism that permits this refined discrimination remains undetermined, but may involve a gradient-based assessment of relatedness through phenotype-matching. We explored how similarity in contact calls may be used to assess kinship in the long-tailed tit *Aegithalos caudatus*, a species where learned calls provide

information on kinship. By analysing the calls of all adults in a well-studied long-tailed tit population, in which patterns of relatedness are known, we describe how call variation among individuals correlates with relatedness. We discuss whether call similarity could act as a reliable recognition cue for refined discrimination among different degrees of kinship. This could be used to modify helping behaviour to fit Hamilton's rule or as an inbreeding avoidance mechanism. This research contributes to our understanding of recognition systems and how they influence adaptive decisions in social animals.

Poster session B - GEN 2000

Evolution of informed dispersal : the effect of information transmission (51836)

Ryosuke Iritani.

Kyushu University.

Dispersal, defined as any movement causing gene flow across space, is one of the most fundamental phenomena in ecology and evolution. In particular, informed dispersal, in which individuals use, carry, and transmit information that affects the decision making of dispersal, has recently begun to gather attention both in theory and nature. Because the availability of information exhibits variation, it may generate phenotypic plasticity of dispersal. In the present talk, I introduce several ecological scenarios of information acquisition including vertical transmission, horizontal transmission, individual learning, and so on. I will classify the life-historical scenarios of transmission process/timing that might generate disruptive/stabilizing selection on dispersal, and also predict what scenarios are expected to generate phenotypic plasticity (conditional dispersal) or not (unconditional). I use neighbor-modulated approach to capture the effect of information transmission among relatives in subdivided populations.

Poster session B - GEN 2000

Stable eusociality through maternal manipulation (51872)

Mauricio González-Forero.

University of Lausanne.

Eusociality involves workers that devote their lives to help. One hypothesis posits that eusociality evolves because workers are manipulated by nestmates into helping. This hypothesis is problematic because manipulated workers could evolve resistance to manipulation, destabilizing eusociality. Resistance can fail to evolve when it is costly, but resistance might be relatively costless if manipulation occurs via queen pheromones, a common way in which worker reproduction is suppressed. Using mathematical models, I find that stable eusociality can evolve from maternal manipulation with costless resistance because of the evolution of maternal reallocation of resources. I study the coevolution of maternal

manipulation, costless resistance, and maternal resource allocation. With an initially limited ability of offspring to resist manipulation, the mother evolves to reduce her maternal care toward recipients of help. The mother simultaneously evolves to reallocate the freed resources into producing offspring that she does not raise and that thus disproportionately benefit from help. Hence, manipulated workers result helping highly benefiting recipients, rendering resistance disfavored. The outcome is reproductive division of labor with sterile workers that are maternally induced and have no incentive to resist. I further find that this process yields stable eusociality under broader conditions than when manipulation is absent.

Poster session B - GEN 2000

Disgusting or refreshing? Do offspring benefit from feces sharing in the European earwig? (51945)

Maximilian Körner, Janina M.C Diehl, Joel Meunier.

Department of Evolutionary Biology, Institute of Zoology, Johannes-Gutenberg University Mainz.

Sociality only evolves when the benefits of group-living outweigh the benefits of solitary life. In family life, it is assumed that parents mostly mediate the benefits of group-living through parental care. However, recent studies revealed resource sharing among mobile siblings, which could play a key role in the early evolution of family life. Here we investigated whether mobile offspring (nymphs) benefit from food sharing through allo-coprophagy in the European earwig, *Forficula auricularia*. We tested whether access to feces produced by siblings or the mother affects nymph survival in presence/absence of food. We found that access to sibling, but not maternal feces, enhanced offspring survival under food deprivation. We then conducted a food choice experiment to reveal whether nymphs prefer food to feces, and if they discriminate between feces produced by related and unrelated nymphs and mothers. We found that offspring preferred food over feces while still consuming some feces in presence of food. Without food, however, nymphs showed no preference between sibling or mother feces. Overall, our results show defecation having possibly meaningful effects on group living by mediating beneficial interactions. More generally, they show that feces release and sharing possibly play an important role in the evolution of sociality.

Poster session B - GEN 2000

Cooperative bacteria in stationary phase are immune to cheating (51951)

Melanie Ghoul, Stuart West, Ashleigh Griffin.

University of Oxford.

Microbial cells rely on cooperative behaviours that can breakdown as a result of exploitation by cheats. Despite cheats invading, cooperation dominates microbial life. A continuing challenge is to determine how natural cooperative populations resist cheating and to what

extent experimental studies give insight into microbial life outside of laboratory cultures. First we illustrate the importance of defining cheating correctly in evolution studies of social behaviours. We show that whether a strain is a cheat depends on the costs and benefits associated with the social and abiotic environment and not the absolute expression of a cooperative trait. In nature bacteria exist as established populations in a non-growing state similar to the stationary phase of laboratory cultures. A limitation with experimental bacterial studies is that cheating is often tested for in competition assays initiated with cooperator populations at a low density - in lag phase. Here, we use the production of pyoverdine, an iron scavenging siderophore, as a public good in the bacteria *Pseudomonas aeruginosa*, to test how the growth stage of a cooperative population affects a cheat's invasive ability. We show that a strain's ability to cheat correlates with the rates of pyoverdine production, which varies with the bacterial growth stage.

Poster session B - GEN 2000

Eco-evolutionary dynamics of social dilemmas (52059)

Chaitanya Gokhale, Christoph Hauert.

New Zealand Institute for Advanced Study, Massey University; Department of Mathematics, University of British Columbia.

Social dilemmas are an integral part of social interactions ranging from microbial populations to human societies. Cooperative interactions such as the secretion of expensive extracellular products or blood donations, are costly to the actor but provide potentially vital benefits to recipients. Both costs and benefits often depend non-linearly on the number and types of individuals involved – as captured by idioms such as 'too many cooks spoil the broth' where additional contributions are discounted, or 'two heads are better than one' where cooperators can synergistically enhance the group benefit. Interaction group sizes often depend on the size of the population and hence on ecological processes. This results in feedback mechanisms between ecological and evolutionary processes, which jointly affect and determine the evolutionary trajectory. Only recently became such combined processes experimentally tractable in microbial social dilemmas. Here we analyse non-linear social dilemmas in eco-evolutionary settings where the population fluctuates in size and the environment can change over time. We find that combining these traditionally independently studied processes has the potential to routinely reveal highly complex dynamics, which are infrequent when studied in isolation but possibly quite common in nature. One particularly interesting outcome is the evolutionary feasibility and maintenance of cooperation at high densities in ecologically fluctuating populations.

Poster session B - GEN 2000

The co-evolution of social institutions, demography, and large-scale human cooperation (52070)

Simon Powers, Laurent Lehmann.

University of Lausanne.

Human cooperation is typically coordinated by institutions, which determine the outcome structure of the social interactions individuals engage in. Explaining the Neolithic transition from small- to large-scale societies involves understanding how these institutions co-evolve with demography. Yet nearly all previous evolutionary models have assumed that social interactions, such as cooperation and punishment, are carried out in an entirely uncoordinated and unilateral manner. Consequently, very little work has studied the evolutionary origin of social institutions, and none has considered how they co-evolve with aspects of human demography such as carrying capacity. We address this using a demographically explicit model of institution formation in a patch-structured population. Each patch supports both social and asocial niches. Social individuals create an institution, at a cost to themselves, by negotiating how much of the costly public good provided by cooperators is invested into sanctioning defectors. The remainder of their public good is invested in technology that increases carrying capacity, such as irrigation systems. We show that social individuals can invade a population of asocials, and form institutions that support high levels of cooperation. We then demonstrate conditions where the co-evolution of cooperation, institutions, and carrying capacity creates a transition from small- to large-scale social groups.

Poster session B - GEN 2000

Family living - an overlooked social system in the evolutionary history of cooperation (52159)

Szymon Drobniak, Michael Griesser.

University of Zurich.

Cooperative breeding represents one of the major challenges in evolutionary biology. In spite of understanding its ultimate causes we still lack proper understanding of how a prerequisite of cooperation - namely delayed post-natal dispersal - evolved. Here we suggest a novel approach by considering the third social system category, expanding currently bi-categorical classification into cooperatively and non-cooperatively breeding species. Using a large sample of extant species we demonstrate that family living, i.e. delayed post-natal dispersal of offspring without further reproductive cooperation, represents a distinct social system that should not be merged together with non-family living species. Family-living species differ substantially from non-family living ones in terms of their life history, i.e. they exhibit much lower levels of initial reproductive investment. Using this life-history trait we derive a new classification, based on the time the offspring stays with their parents beyond nutritional independence, which successfully classify bird species into family and non-family living ones. This new approach will substantially expand our understanding of how delayed dispersal evolved. Moreover, since reproductive cooperation occurs almost exclusively in families, family living is likely to represent an important intermediate state in the evolution of cooperation.

Poster session B - GEN 2000

The evolution of anti-social rewarding and its counter-measures in public goods games (52160)

Miguel dos Santos.

Department of Ecology and Evolution, University of Lausanne.

Cooperation in joint enterprises breaks down when self-interests are in conflict with collective benefits, causing a tragedy of the commons. In such dilemmas, the possibility for contributors to invest in pool-reward funds which will be shared exclusively among contributors, can be powerful for averting the tragedy, as long as the second-order dilemma (withdrawing contribution to reward funds) can be overcome, e.g. with second-order sanctions. In human societies however, wrong-doers can also pool their effort to reward each other, and profit from productive joint enterprises of their own. The present research reveals the vulnerability of pool-rewards to the presence of reward funds raised by defectors and shared among them. Such 'anti-social rewarding' causes a cooperation breakdown, even when second-order sanctions are possible. Escaping this social trap requires the additional condition that coalitions of defectors fare poorly compared to pro-socials, with either better rewarding abilities for the latter, or reward funds that are contingent upon the public good produced beforehand, allowing groups of contributors to invest more in reward funds than groups of defectors. Future experiments on pool-reward funds should allow anti-social rewarding in order to fully understand how positive incentive mechanisms can enhance human cooperation in collective action dilemmas.

Poster session B - GEN 2000

Cooperating to Exclude Competitors in Natural Bacterial Populations (52174)

John Bruce, Stuart West, Ashleigh Griffin.

University of Oxford.

All bacteria produce antagonistic compounds, such as bacteriocins, which are important determinants of intraspecific competition. Both theory and experimental studies have shown that production of these toxins is important for the invasion and defence of niches, as well as providing a mechanism to maintain diversity. However, the relevance of antagonistic behaviours to the diversity and distribution of strains in natural bacterial populations is unknown. Here, we sampled and genetically characterized natural populations of *Pseudomonas fluorescens* from soil at multiple sites in a local park and constructed a network of antagonistic interactions between strains. We find that genetically diverse strains coexist at very local, centimetre, scales and demonstrate that antagonism is attenuated locally, within-sites, and more prevalent between-sites. These results suggest that these genetically diverse populations of *P. fluorescens* are adapted to their local social environment: they are resistant to an array of locally produced toxins. This may be the result of limited dispersal in local populations, or alternatively, antagonistic interactions may reinforce boundaries between populations and deter invasion by conspecifics. This raises both theoretical and empirical questions concerning how antagonistic traits, through their influence on population structure, will coevolve with cooperative traits.

Evolution of an artificial ecosystem (52239)

Yu Liu.

Uppsala University.

We made an agent-based model with the purpose to study that why some specific interactions or food webs would emerge, what the most important underlying mechanism is, whether there are general patterns for a ecosystem to evolve, etc.

In the model, the system consists of 'microbes' and 'substances'. Each kind of microbes digests and excretes specific substances (a simple rule decides what substances it excretes according to what it digests). The metabolic path is recorded in their 'genes' which could mutate. Reproduction happens when microbes have enough food to digest, while death happens when they starve.

There are some primary results till now. Firstly, there are patterns from the simulations which could be find in the real world, totally emerging from the very simple model, even though we did not assume any priori fitness functions. Secondly, the artificial system seems to have seral stages, like a young forest grows to an old forest. Thirdly, since we know how each individual behaves, we could explain various patterns (population structure, trophic level, etc.) of the artificial ecosystem from the individual level.

Natural and experimentally induced queen succession in the tropical social wasp *Ropalidia marginata* (52252)

Paromita Saha, M. C. Shilpa, Sruthi Unnikrishnan, Shantanu Shukla, Souvik Mandal, Anjan Nandi, Aniruddha Mitra, Raghavendra Gadagkar.

Centre for Ecological Sciences, Indian Institute of Science, Bangalore, India.; Evolution Génomes Comportement Ecologie, Centre National de la Recherche Scientifique, France.

Insect societies are hallmarks of cooperation because one or a few queens monopolize reproduction and several non-reproductive workers cooperatively raise brood. However, the loss of the queen exposes a colony to potential reproductive conflict, which is resolved only after a new queen takes over. We study queen succession in natural and experimental colonies of the primitively eusocial wasp *Ropalidia marginata* to understand the proximate behavioural strategies involved in the resolution of this conflict. Experimental queen removal always results in one worker becoming hyper-aggressive and taking over the colony as its next queen. Here we show that even during natural queen turn-over, one and only one worker becomes hyper-aggressive and takes over as the next queen, without any scramble competition. Unlike in the case of experimental queen removal however, during natural queen turn-over, aggression of the successor may begin before the loss of the old queen and may decline more rapidly. As might be expected, the successor begins to lay eggs sooner after a natural queen

turn-over as compared to experimental queen removal. Because queen succession is expected to be more prevalent in tropical perennial species, we expect natural selection to have favoured such an orderly queen succession without scramble competition.

Poster session B - GEN 2000

Cooperation mediates density-dependent dispersal and colonization efficiency in a ciliate (52280)

Staffan Jacob, Priscilla Wehi, Alexis Chaine, Delphine Legrand, Nicolas Schtickzelle, Michele Huet, Jean Clobert.

CNRS Moulis; Landcare Research Manaaki Whenua, New Zealand; Earth and Life Institute & Biodiversity Research Centre, Belgium.

Theory predicts that low dispersal is required for the evolution of cooperation because it maintains high within-groups relatedness. However, limited dispersal also increases kin competition and can therefore negate the benefits of cooperation. Theoretical work has suggested that conditional dispersal, when individuals can adjust their dispersal decisions to the local context, might resolve this paradox. We tested the hypothesis that density-dependent dispersal decisions should differ between six genotypes of the unicellular *Tetrahymena thermophila* differing in cooperation strategy. Furthermore, we investigated whether cooperation strategy affects post-dispersal colonization efficiency from single founder cells or several cells (akin to group dispersal). We found that density-dependent dispersal decisions and dispersers' phenotype differed between genotypes' cooperation level. Cooperative lines decreased dispersal rate with density, whereas dispersal rate in low cooperative lines was low at extreme densities and high at intermediate densities. Moreover, colonization efficiency after dispersal of cooperative genotypes was low for single founder cells compared to less cooperative lines, and as efficient as less cooperative lines when colonization occurred from several cells. Thus, kin cooperation during transience and/or settlement may exist for high cooperative lines. Our results demonstrate that cooperation strategy governs both density-dependent dispersal decisions and the subsequent colonization success.

Poster session B - GEN 2000

The Evolution of Cooperation through Genetic Niche Hiking (52330)

Sarah Hammarlund, Brian Connelly, Katie Dickinson, Benjamin Kerr.

University of Washington; University of Oxford.

Cooperation is evolutionarily paradoxical. When individuals pay a cost to benefit others, cooperators are at a competitive disadvantage relative to non-cooperators ("defectors"). Most solutions to this paradox involve a scenario where cooperators disproportionately benefit from cooperation (e.g., via interactions with kin). Here we model the evolution of cooperation under circumstances where such positive assortment occurs but is not sufficient to ensure

cooperator success. Our scenario begins with an exogenous stress, where stress tolerance is completely unrelated to cooperation. This stress (1) thins the population, after which growth can lead to clustering of like types, and (2) creates opportunities for adaptation to the stress itself. In structured, adapting populations, cooperator-rich populations reach larger population sizes; consequently, cooperative lineages experience more mutational opportunities to adapt to the stressful conditions, which allows cooperators to competitively displace defectors. Such displacement can occur even as the population structure erodes. In analogy with genetic hitchhiking, we call this process "genetic niche hiking," where an otherwise deleterious allele for cooperation can increase in frequency due to an association with the "niche" it creates. We explore this process in detail using an agent-based computational model and discuss genetic niche hiking in the context of exoenzyme production in bacteria.

Poster session B - GEN 2000

Social evolution and antibiotic resistance in *Pseudomonas aeruginosa* infections (52350)

David Crosse, Melanie Ghou, Ashleigh Griffin.

University of Oxford.

Antibiotic resistance is a global health crisis. As pathogenic bacteria are social organisms, social evolutionary theory needs to be applied to this problem. Beta-lactam antibiotics (a major class which includes the penicillins) are often resisted by beta-lactamase, an extracellular enzyme. Beta-lactamase is potentially a public good: cooperative producers could therefore be vulnerable to exploitation by non-producing cheats. *Pseudomonas aeruginosa* is an opportunistic pathogen that uses beta-lactamase for resistance. It causes chronic lung infections in cystic fibrosis (CF) patients, where it is the primary cause of morbidity and mortality. In this study we assay beta-lactamase production in sequential isolates from 17 CF patients to look for potential cheats, and we test whether high beta-lactamase producers can cross-protect a coexisting non-producer. As non-producers are themselves vulnerable to antibiotics, their maintenance in a bacterial population would be of considerable clinical significance.

Poster session B - GEN 2000

Brood discrimination in the ant *Formica exsecta* (52449)

Unni Pulliainen, Nick Bos, Patrizia d'Ettorre, Liselotte Sundström.

University of Helsinki; Université Paris 13.

In social insects, the ability to recognize and discriminate nestmates from non nestmates plays an important part in maintaining colony integrity and protecting the colony and its resources from unrelated intruders and social parasites. Typical colony intruders are adult individuals, and thus recognition among adults is highly developed and precise. However, whether ants

can recognize and discriminate brood of different origins is less clear. From a fitness point of view it would naturally be beneficial for a colony to accept nest mate brood. Accepting alien worker destined brood, especially pupae, might not be harmful either, and it might even be beneficial, as in some cases alien workers, adopted as brood, successfully integrate into adoptive colonies. However, accepting alien sexual brood should be avoided as these individuals may use colony resources without contributing to the colony, and instead act as social parasites. We investigated whether worker ants are efficient in discriminating brood, and whether the discrimination rules differ among brood of different castes. We answer these questions using behavioural assays coupled with chemical analysis in the ant *Formica exsecta*.

Poster session B - GEN 2000

Facilitation and kin selection in a Patagonian dominant tree (52490)

Irène Till-Bottraud, Alex Fajardo, Cristain Torres.

Univ. Grenoble Alpes, Laboratoire d'Ecologie Alpine (LECA), F-38000 Grenoble, France; CNRS, LECA, CNRS F-38000 Grenoble, France; Centro de Investigación en Ecosistemas de la Patagonia (CIEP) Conicyt-Regional R10C1003, Universidad; Laboratorio de Genómica y Biodiversidad, Departamento de Ciencias Básicas, Universidad del Bío Bío, .

In plant ecological theory, beneficial interactions occur mostly under stressful conditions (facilitation; in the context of the “stress gradient hypothesis”). Facilitation is commonly described as an interspecific interaction in which at least one of the species benefits from the interaction. Among individuals of the same species and the same cohort, the interaction is reciprocal and all individuals benefit from the interaction (cooperation). We studied one such case of facilitation in *Nothofagus pumilio*, a dominant tree species in Patagonia. The edge of post-fire even-aged second-growth forests is composed of merged trees. We showed that seedlings growing in clusters at the edge of the forest facilitate each other (greater survival than alone) by sheltering each other from the strong winds. Merging of the seedlings occur at a later stage. We found that merged stems were more closely related than on average in the population. We also showed, in an experiment where seedlings were planted in clusters, that mortality over 7 years lead to significantly higher than average relatedness within the clusters, indicating selection for kin individuals. This situation is thus an example of kin cooperation in plants, with facilitation being a prerequisite for kin selection.

Poster session B - GEN 2000

A dynamic model of reproductive decisions in primitively eusocial insects (52529)

Piret Avila, Lutz Fromhage.

University of Jyväskylä.

Cooperative breeding has arisen numerous times in the Hymenoptera, but the role of time- and context-dependent decision rules in this context is still incompletely understood. To study this topic, we developed a stochastic dynamic game model of the behaviour of a seasonal cooperatively breeding insect with alloparental care, in which dispersing females must decide between founding a nest or joining an existing nest as a helper. We assume that the dominant female in a nest does all the reproduction; that establishing a nest takes time and effort before any sexual offspring can be produced; and that helpers can inherit the nest if the dominant dies. We assess the relative importance of indirect and direct fitness effects in the decision making process and the degree to which evolved helping behaviour is mutualistic or altruistic. We also study the degree to which environmental constraints, effort of nest establishment and average within-group relatedness affect optimal decisions of females and expected group size.

Poster session B - GEN 2000

Queen signal evolution in social Hymenoptera (52698)

Jelle van Zweden.

KU Leuven.

Social Hymenoptera have long been a model to study the evolution of cooperation. They are characterized by a reproductive division of labour, whereby queens perform most of the reproduction and workers help to raise offspring. Queen pheromones, which signal the presence of a fertile queen and reduce reproduction in the workers, are thought to play a key role in regulating this altruistic system. Progress in the study of queen pheromones has been slow, since very few had been identified up until a few years ago. Their evolutionary history, therefore, remained unknown. Recently, however, we identified sterility-inducing queen pheromones in several species of ant, wasp and bee. Moreover, by synthesizing existing data of compounds that characterize female fertility in species of social Hymenoptera, we find that these are strikingly conserved in lineages of *Lasius* ants and Vespinae wasps, as well as across at least three independent origins of eusociality. Wasps, ants and some bees all appear to use non-volatile, saturated hydrocarbons to advertise fertility and reduce worker reproduction. These results suggest that queen signals follow very similar evolutionary trajectories from solitary ancestors, and argue against rapid evolution that would result from queen-worker arms races ensuing from manipulative queen control.

Poster session B - GEN 2000

Does cooperation mean kinship in spatially discrete nests within an ant colony? (52707)

Duncan Procter, Michael Hofreiter, Joan Cottrell, Kevin Watts, Elva Robinson.

University of York; Universitat Potsdam; Forest Research.

Ant colonies are often one of the first examples people give of kin selection in action, with the classical description of a colony in one nest (monodomy) with highly related workers and a single queen (monogyny). However this is very often not the case. As well as the well-studied phenomenon of multiple queens in each nest (polygyny), colonies can be split between spatially discrete nests (polydomy). Polydomous colonies are defined by social connections between discrete nests, and in many species multiple colonies live side by side. This begs the question, what causes these polydomous colonies to keep a social connection with some nests and not others? Is this colony really a good example of kin selection after all or is it merely two nests cooperating for some other reason? The red wood ant *Formica lugubris* is polygyne and polydomous in the UK. Using 20 triplets of nests, two of which were from the same colony and the third from a neighbouring separate colony we used analysis of worker movement, resource transfer and relatedness of nests to put this definition of a polydomous colony into an evolutionary perspective and ask whether kinship does determine cooperation in this situation.

Poster session B - GEN 2000

The rise and fall of cooperative breeding in birds – the role of life-history and ecology for evolutionary transitions to and from cooperative breeding (52795)

Michael Griesser, Szymon M Drobniak, Shinichi Nakagawa.

University of Zurich; University of Otago.

Understanding cooperation in animal societies is a key question of evolutionary biology. Yet theory and comparative studies so far contrasted cooperative breeders with non-cooperative breeders. This approach neglects that non-cooperative breeders are a heterogeneous group encompassing both non-family and family living species, however, cooperation primarily takes place within families. Using a phyla-wide dataset in birds, we show that evolutionary transitions occur from pair-living to family living, and from there to cooperative breeding, in both directions along this axis. Moreover, the transition patterns differ across different lineages, where life-history parameters and ecology play a key role in influencing whether lineages remain asocial whether they evolve family living, or whether they also evolve cooperative breeding. For example, most precocial lineages evolve family living but never evolve cooperative breeding, confirming that particularly altricial species benefit from cooperative breeding. Overall, our results provide an important conceptual advancement, showing that understanding family living might be crucial to resolve the evolution of cooperative breeding.

Poster session B - GEN 2000

Resource competition and population structure makes social learning models more biologically relevant (52855)

Marco Smolla, Tobias Galla, Tucker Gilman, Susanne Shultz.

*Computational and Evolutionary Biology, Faculty of Life Sciences, University of Manchester;
Complex Systems and Statistical Physics Group, School of Physics and Astro, University of
Manchester.*

The success of humans in colonising virtually every terrestrial habitat is based on cumulative culture. Its fundamental mechanism is social learning (gaining information by interacting with or observing others), which is widespread in the animal kingdom. A recent social learning strategies tournament (Rendell et al., 2010, Science) found that the most competitive strategies almost entirely rely on social learning; a surprising result, which contradicts empirical findings that show most animals opt for asocially and not socially acquired information.

By using an agent-based model relying on resource competition and population structure, we can show that environmental conditions, such as strength of competition, number of resources, environmental stability, evenness of resource values, and network properties strongly influence the success of social learning.

Our model is more biologically relevant than earlier models that rely on arbitrary learning costs and neglect resource competition, which is omnipresent in nature. We believe our model will not only help us to better understand the evolution of social learning, but also shed light on the evolution of cumulative culture in humans.

Poster session B - GEN 2000

Comparison of Public and Private Partner Selection Models in Cooperation and Coordination Games (52881)

Pedro Mariano, Davide Nunes, Luís Correia.

BioISI - Dep. de Informática, Faculdade de Ciências, Universidade de Lisboa.

We have been investigating how public and private partner selection models promote cooperation and diversity in a population of evolving agents using well know games such as Prisoner's Dilemma, Stag Hunt, Snowdrift, Public Good Provision, Centipede, Ultimatum, Battle of Sexes, and Give-and-Take. Our models are generic in the sense that they only use the payoff obtained by the selecting agent to update its partner selection policy.

Both partner selection models are able to promote cooperation compared to random partner selection. As for diversity in coordination games, only the public partner selection had partial success. We have observed groups of agents with different ways to play the game during many iterations of the evolutionary algorithm, but in the long run, only one strategy profile prevails.

In ongoing work we are investigating other ways to promote diversity in cooperation and coordination games. One avenue of research consists in having in the chromosome all the parameters of the partner selection models. In previous work, some of the parameters were externally defined.

P. Mariano and L. Correia. Partner selection delays extinction in cooperative and coordination dilemmas. In F. Grimaldo and E. Norling, editors,

A selfish genetic element influences sperm precedence patterns in house mice (51706)

Andreas Sutter, Anna K. Lindholm.

University of Zurich.

Multiple mating by females is taxonomically wide-spread, which extends male-male competition beyond pre-copulatory contest. Sperm precedence patterns are typically species-specific, and males are predicted to tailor their investment according to whether they mate in the favoured or disfavoured role. Selfish genetic elements (SGEs) that favour their own transmission at the cost of the entire organism often target male gametogenesis, with potential consequences on optimal male reproductive strategies.

The t haplotype in house mice is the best-known SGE in a vertebrate. It exhibits strong transmission ratio distortion in males by influencing spermatogenesis and male carriers are strongly disadvantaged in sperm competition compared to wild type males. Here, we investigated sperm precedence patterns in sperm competition trials involving males with a t haplotype. We found that sperm precedence patterns depended on whether t males were involved in sperm competition. Competition between t carriers resulted in a reversal of the species-typical first male precedence and the optimal timing of ejaculation was different for t heterozygous and wild type males. Nevertheless, males did not tailor their copulatory behaviour depending on their t haplotype status.

We discuss these findings in the light of genomic conflict and constraints arising from the genetic control of copulatory behaviour.

Prezygotic segregation distortion in female and male zebra finches *Taeniopygia guttata* (51707)

Ulrich Knief, Holger Schielzeth, Hans Ellegren, Bart Kempenaers, Wolfgang Forstmeier.

Max Planck Institute for Ornithology, Department of Behavioural Ecology and Evolutionary Genetics; Bielefeld University, Department of Evolutionary Biology; Uppsala University, Department of Evolutionary Biology.

At least three processes can lead to an apparent departure from fair Mendelian segregation: (early) viability selection, biased gene conversion and segregation distortion. Here we conduct a genome-wide scan for transmission distortion in a captive population of zebra finches (*Taeniopygia guttata*) using 1,302 single nucleotide polymorphisms followed by confirmatory analyses on independent samples from the same population. In the genome scan we found

weak but significant distortion at three linked loci on chromosome Tgu2 and we were able to replicate this finding in each of two follow-up datasets (overall transmission ratio = 0.567, 95% CI = 0.536–0.600, based on 1,101 informative meioses). Although the driving allele was preferentially transmitted by both heterozygous females (ratio = 0.560, 95% CI = 0.519–0.603) and heterozygous males (ratio = 0.575, 95% CI = 0.531–0.623) we could rule out (early) viability selection and biased gene conversion as possible mechanisms, because the bias remained the same in clutches in which all eggs were analyzed (ratio = 0.564, 95% CI = 0.521–0.606) and could be verified over several megabases. Thus, we here describe a prezygotically active segregation distorter operating equally effectively in female and male meioses.

Poster session B - MAX 412

Retrotransposon-mediated origin of loci functioning under alpine conditions in the autotetraploid *Biscutella laevigata* (51795)

Rimjhim Roy Choudhury, Christian Parisod.

University of Neuchâtel.

Transposable elements (TEs), long considered as junk DNA, harbor regulatory sequences potentially affecting host genes in response to stresses and environmental challenges. Accordingly, bursts of TE activity after whole genome duplication (WGD) events may have a substantial evolutionary impact by fostering the origin of phenotypic novelties and supporting lineage diversification. In this study, we explore the hitchhike of TE sequences in duplicated genomes and their co-option for plant regulation to stress response. We focus on functional TE-gene sequences in natural populations of the alpine mustard *Biscutella laevigata*, including highly dynamic autopolyploid genomes and their diploid progenitors. We thus mined the transcriptome of *B. laevigata* to characterize putatively functional TE-gene co-transcripts and, out of 530 TE transcripts, we identified 17 chimeras joining large gene and TE parts. These transcripts were highly expressed as compared to random TE insertions and mostly contain element binding sites having potential relation with drought and cold challenges in alpine areas. Genotyping across populations and other Brassicaceae highlight their origin and evolution. Further studies linking genotype to phenotype will bring significant advances in our understanding of the mechanisms generating evolutionary-relevant variation from burst of transposition.

Poster session B - MAX 412

Revisiting the selfish conflict theory of mitochondrial inheritance (51862)

Joshua Christie, Timothy Schaerf, Madeleine Beekman.

The University of Sydney.

For almost four decades, uniparental inheritance of mitochondria (UPI) has been explained by the selfish conflict theory. This hypothesis states that UPI evolved to prevent the spread of selfish mitochondria, which replicate quickly but produce energy inefficiently. UPI is thought to prevent the spread of selfish mitochondria by causing segregation of such mitochondria into unfit cells that are purged from the population. UPI, however, so efficiently purges selfish mitochondria that it is subject to negative frequency-dependent selection: when UPI is common, selfish mutants are rare; when selfish mutants are rare, UPI is no longer advantageous. As a result, UPI does not go to fixation in mathematical models under realistic assumptions. Clearly, we require a new explanation for UPI that is consistent with population genetic theory. Empirical evidence may hold the key. It has recently been shown that merely mixing two different but normal mitochondrial haplotypes within a cell (heteroplasmy) can cause dysfunction. Using a mathematical model, we show that selection against heteroplasmy can lead to the evolution of UPI under a wide variety of assumptions and parameter values. Thus, we suggest that selection against heteroplasmy explains the evolution of UPI.

Poster session B - MAX 412

The evolution of metazoan genomes and highly conserved SINE domains (51881)

Andrea Luchetti, Eva Satovic, Miroslav Plohl, Barbara Mantovani.

*Department of Biological, Geological and Environmental Sciences - University of Bologna;
Division of Molecular Biology, Ruder Boskovic Institute - Zagreb.*

Short interspersed elements (SINEs) are non-autonomous retrotransposons with modular structures: a small RNA-related head, a body and an AT-rich tail. Despite their high turnover rate and de novo emergence, the body may retain highly conserved domains (HCD) among different SINE families: in metazoan, up to seven HCD-SINEs have been recognized. Interestingly, two HCD-SINEs (CORE- and Deu-SINEs) have been repeatedly subject to exaptation in mammalian genomes, becoming part of gene regulatory networks. Analyzing molluscan transcriptomes and genomic sequences we characterized four new HCD-SINE families, whose insertion site analyses suggest recent activity. Two HCDs were previously found in chordates' SINEs: the V-domain (here found in gastropods, bivalves and chitons), and the CORE-domain (here found in bivalves and gastropods). A CORE-SINE has been further identified in the horseshoe crab and one more family isolated in snails retains the cephalopods' Ceph domain. Tracking the ancestry of HCDs in the metazoan phylogeny revealed that some of them date back to the Radiata-Bilateria and the Protostomia-Deuterostomia splits. We suggest that the evolutionary conservation of HCD may account for the high SINE diversity ("module exchange" model) and for their long-term inheritance in metazoan genomes.

Poster session B - MAX 412

Horizontal gene spread through bacterial host altruism (51971)

Tatiana Dimitriu, Dusan Misevic, Sam Brown, Ariel Lindner, Francois Taddei.

*Imperial College London; Institut National de la Santé et de la Recherche Médicale;
University of Edinburgh.*

In bacteria, plasmids and other mobile genetic elements often confer crucial phenotypes such as antibiotic resistance, providing strong benefits to their hosts. However, the fitness consequences of horizontal transfer itself are less clear. Indeed, transfer can be interpreted as a parasitic trait because of its costs to the host, but also as a trait benefiting host populations through the sharing of a common gene pool. Here we show that costly plasmid donation is an altruistic act when it spreads beneficial genes, and can be specifically maintained by kin selection mechanisms. We first show mathematically that donor ability can be selected when relatedness among donors and recipients is high, ensuring high frequency of transfer towards kin. We further experimentally demonstrate that sufficiently high relatedness can be achieved through either kin discrimination or population structure, both mechanisms being likely to occur in natural environments. Our work shows that horizontal gene transfer can be promoted by bacterial hosts themselves and not only by mobile genetic elements. Moreover, preferential transfer among kin combined with the fitness benefits brought by beneficial plasmids can lead to a mutualistic association between high transfer strains and beneficial plasmids.

Poster session B - MAX 412

PGE in the citrus mealybug: is the maternal victory complete? (52156)

Andrés G. de la Filia, Laura Ross.

Institute of Evolutionary Biology, The University of Edinburgh.

Genetic conflict has been brought up to explain the striking diversity of genetic systems. Among these, paternal genome elimination (PGE) is found in several insects, including citrus mealybugs (*Planococcus citri*). In males, the paternally inherited genome, under control of the maternal half, is first heterochromatinized and discarded later during spermatogenesis. PGE is therefore a whole-genome form of meiotic drive, as sperm only contain maternally inherited chromosomes. However, paternal genomes can sometimes escape germ-line elimination and/or silencing, suggesting an evolutionary arms race between maternal and paternal genomes. This study investigates if paternal genomes have evolved adaptations against PGE that could be unveiled by exposing paternal genotypes to different maternal backgrounds by analyzing F1 and F2 of intraspecific and interspecific crosses (with *P. ficus*). Paternal line inheritance was assessed via microsatellite analysis, while transcriptome data for whole F1 males and F1 testis samples was generated to evaluate whether paternal alleles can escape inactivation and if expression patterns differ in testes. Our results provide a solid ground to study potential PGE suppressors and thus increase our knowledge of how PGE is maintained and lost, eventually casting more light on the involvement of male-female conflict in the evolutionary dynamics of genetic systems.

Poster session B - MAX 412

Dynamics of transposable elements in the genome of *Taraxacum officinale* apomictic lineages. (52214)

Julie Ferreira de Carvalho, Peter Van Dijk, Koen Verhoeven.

Netherlands Institute of Ecology (NIOO KNAW), Wageningen, The Netherlands; Keygene, Wageningen, The Netherlands.

Asexual species are considered as evolutionary dead-ends with reduced probability of fixing advantageous mutations and enhanced accumulation of deleterious mutations due to inefficient purging. Therefore, active transposable elements (TE) might accumulate in asexual lineages, which could be further promoted if TE silencing mechanisms associated with meiosis and gametogenesis are circumvented in asexuals.

To gain more insight into the dynamics of TEs under asexuality, we used apomictic dandelions as a model system to evaluate: (1) TE activity differences during gametogenesis and plant development and (2) the involvement of TEs in early evolutionary divergence between plants from a single apomictic lineage. We used an RNA-Seq approach, comparing gene expression levels between reproductive cells and somatic tissue and between leaf tissues of five apomictic natural accessions sampled around Central Europe.

Our results suggest main differences in the level of gene expression between reproductive cells and vegetative tissue suggesting activation of TEs coupled with activation of silencing enzymes during gametogenesis. Heritable gene expression differences between apomictic clone members were dominated by TEs and TE associated genes. Specifically, some protein domains (transposase and transcriptase-like proteins) are differentially expressed between clone members suggesting a possible role in early stages of evolutionary divergence in this species.

Poster session B - MAX 412

Transposable element dynamics mediated by piRNA pathway in response to environmental changes (52345)

Marta Marialva.

Instituto Gulbenkian de Ciência.

Heritable phenotypic variation is the raw material for evolution by natural selection. To fully understand evolutionary change, we must study the processes that drive the formation of new genetic variants. Transposable elements, genomic sequences with the ability to move, are an important source of adaptive genetic variation. In order to understand what make transposable elements move we explored to what extent biotic and abiotic environmental factors impact their activity during *Drosophila melanogaster* oogenesis. It is known that environmental stresses can induce transposon jumping, and that the piRNA pathway inhibits transposition in the germline. We connected these two observations by looking at the expression of transposons and at piRNA pathway activity in the germline of females under different environmental conditions. We concluded that abiotic (temperature) and biotic (symbiont) factors affect transposable element activity synergistically, and propose that Piwi, a key protein in the piRNA pathway, mediates those responses.

Parasitic plasmids increase bacterial mutation rates and antibiotic resistance (52357)

Fredrik Inglis, Jenna Gallie, Martin Ackermann.

Washington University in St. Louis; ETH Zurich; ETH Zurich.

Plasmids play a pivotal role in bacterial evolution and ecology, acting as reservoirs of genetic material that allow for rapid adaptation to novel environments. However, as many bacteria inhabit fluctuating environments, under various environmental conditions plasmids may provide little or no benefit to their host cell, and because there is often a fitness cost associated with plasmid carriage, they should be selected against. Under these conditions plasmids no longer act as beneficial sources of genetic information, but can instead be viewed as genetic parasites exploiting their bacterial host. It has previously been shown that coevolution with parasites is an important evolutionary factor that can drive rapid and extensive changes in both host and parasite. As bacteria are constantly evolving in the presence of plasmids, we were curious to investigate how bacteria respond when coevolving with a parasitic plasmid. After coevolving *Escherichia coli* carrying a ColE1-type plasmid for 120 generations, we found that mutations in two different bacterial genes caused a drastic loss in plasmid carriage. Interestingly mutations in these two genes also conferred high levels of antibiotic resistance through an increase in bacterial mutation rate and changes to RNA polymerase. This suggests that mutations associated with plasmid carriage and loss can lead to large pleiotropic effects in the host.

Evolutionary dynamics of meiotic drive elements in the fungus *Podospora anserina* (52565)

Eric Bastiaans, Duur K. Aanen, Alfons J. M. Debets, Jesper Svedberg, Hanna Johannesson.

Uppsala University; Wageningen University.

Natural selection may favour selfish genetic elements in the genome that harm the individuals carrying them. One class of such selfish genetic elements consists of meiotic drivers, also referred to as segregation distorters. Although meiotic drive is widespread in nature and has been identified in a wide range of eukaryotes, there is a profound lack of empirical insight into the evolutionary causes and consequences of this phenomenon.

We introduce the ascomycete fungus *Podospora anserina* as a novel system for the study of the evolutionary dynamics of meiotic drive. In *P. anserina* several meiotic drive elements that cause spore killing are present at a high frequency in natural populations. Spores carrying the Spore killer allele inhibit the development of spores not carrying the allele. We are using six different Spore killers found in a large collection of natural isolates from the Netherlands to study the dynamics of Spore killing. We will combine experimental and genomic approaches

to I) Identify the six yet unidentified Spore killer elements of *P. anserina*, II) Investigate the evolutionary dynamics of the different Spore killers by comparative genomics, and III) Experimentally investigate population biology of *Podospora* Spore killers, i.e., under which conditions they may invade a population.

Poster session B - MAX 412

Differential introgression of retrotransposons in a natural hybrid zone between wild wheats (52670)

Natacha Senerchia, François Felber, Christian Parisod.

University of Neuchâtel; Musée et Jardins botaniques cantonaux vaudois.

Interspecific hybridization leads to new interactions among divergent genomes, revealing the nature of genetic incompatibilities having accumulated during and after the origin of species. Conflicts associated with misregulation of transposable elements in hybrids expectedly resulted in their activation and genome-wide changes that may be key to species boundaries. Repetitive genomes of wild wheats have diverged under differential dynamics of specific long terminal repeat retrotransposons (LTR-RTs), offering unparalleled opportunities to address the underpinnings of plant genome reorganization and speciation under the influence of selfish sequences.

The investigation of a natural hybrid zones between *Aegilops geniculata* and *Aegilops triuncialis* revealed that conflicting LTR-RTs presented asymmetrical introgression and specific reorganization among natural hybrids. Specific reorganization of those LTR-RTs among viable hybrids indicated that they may represent genome-wide incompatibilities shaping species boundaries zones.

Moreover, experimental reciprocal F1 hybrids between those species assessed restructuring and epigenetic repatterning in relation to the strength of reproductive isolation. Asymmetrical reorganization of LTR-RT families predicted to cause conflicting interactions matched differential survival of F1 hybrids. In particular, non-random sequence losses and methylation appeared coherent with the necessary repression of incompatible loci in sustaining hybrid viability, confirming and LTR-RTs may foster species integrity in face of gene flow.

Poster session B - MAX 412

Transposable elements in animals of varying age and reproductive mode (52785)

Jens Bast, Ina Schaefer, Mark Maraun, Stefan Scheu, Ken Kraaijeveld.

*University of Lausanne, Department of Ecology and Evolution, Lausanne, Switzerland;
Georg-August-University Goettingen, J.F. Blumenbach Institute, Goettingen, Germany;
University of Amsterdam, Department of Animal Ecology, Amsterdam, The Netherlands.*

The prevalence of sexual reproduction among eukaryotes is a central question in evolutionary biology. Genetic models predict the early demise of parthenogenetic lineages through accumulation of transposable elements (TEs), due to reduced efficiency of purifying selection. However, asexual reproduction should align the interests of hosts and TEs, leading to a decrease in TE abundance and activity given sufficient time. This predicts accumulation of deleterious TEs in newly arisen asexual lineages but a lower TE load in asexuals that have persisted for prolonged periods as compared to sexuals. To investigate this hypothesis, we analyzed the TE content of three animal groups of varying phylogenetic age using whole genome data. Overall, there was no evidence for TE accumulation in independent lineages that recently switched to asexuality (Leptopilina and Daphnia). However, certain TE families (Gypsy) were more abundant in these asexuals. By contrast, species under prolonged asexuality (oribatid mites), harbored only few and mostly inactive TEs. This suggests, that early extinction of asexual populations is unlikely to be caused by an overall expansion of TE copies in their genomes, but potentially by certain TE types if not contained. Furthermore, TEs might be cleared from asexual species over time in at least some cases.

Poster session B - MAX 412

Major QTL of a morphological lock-and-key mechanism in *Drosophila santomea* and *Drosophila yakuba* (51579)

Alexandre E. PELUFFO, Isabelle NUEZ, Rosina SAVISAAR, Vincent DEBAT, David L. STERN, Virginie ORGOGOZO.

Institut Jacques Monod, CNRS-Université Paris Diderot/Sorbonne Paris Cité, Paris, France; ISySEB Département Systématique et Evolution, MNHN, Paris, France; Janelia Farm Research Campus, Howard Hughes Medical Institute, Ashburn, USA.

The recently discovered *D. santomea* is endemic to the African island of São Tomé where it hybridizes with its closest relative species *D. yakuba* (0.5-1 million year divergence). One of the prezygotic barriers limiting gene flow between these two species is a lock-and-key mechanism acting at the level of genitalia morphology. In *D. yakuba*, male spiny ventral branches contact female protective pockets during copulation. In *D. santomea* the ventral branches have a rounded shape and female pockets are absent. Interspecific mating induces female wounding or sperm leakage. The difference in ventral branch shape provides a unique opportunity to tackle the question of 1) rapid morphological evolution in genitalia and 2) the genetic basis of adaptive morphological evolution.

To identify the loci involved in this key evolutionary change in male ventral branches, we performed a QTL mapping with 400 progeny individuals from an interspecific backcross. Individuals were phenotyped using geometric morphometric methods and genotyped at a fine scale genome-wide resolution using Multiplexed Shotgun Genotyping. We identify one major QTL with a very strong signal in a small autosomal region and are now performing introgression mapping to identify specific genes.

Poster session B - MAX 412

BayeScEnv: A new Fst-based method to uncover local adaptation using environmental variables (51617)

Pierre de Villemereuil, Oscar E. Gaggiotti.

Laboratory of Alpine Ecology, Université Joseph Fourier; Scottish Oceans Institute, University of St Andrews.

Genome scan methods, which aim at detecting selection using dense genotypic markers, can be separated into two main families: (i) Fst-based methods that detect outlier loci based on genetic differentiation and, (ii) Environmental methods that detect significant correlations between environmental factors and allele frequencies.

Because no method of the first family takes advantage of environmental information, we decided to develop a new method that combine two existing Bayesian approaches, BayeScan (Foll & Gaggiotti, 2008) and GESTE (Foll & Gaggiotti 2006). This method aims at revealing signatures of local adaptation by explaining locus-specific patterns of genetic differentiation in terms of environmental "differentiation". Just as BayeScan, it is based on the F-model (Gaggiotti & Foll, 2010), but unlike it, BayeScEnv explicitly models local adaptation in order to distinguish it from spurious locus-specific effects (high mutation rate, background selection).

A simulation study shows that BayeScEnv has a lower False Discovery Rate than BayeScan, although it has a lower power. Overall, it represents a better compromise between false positives and power than its predecessor. We illustrate the use of this new method with an application to a Human Single Nucleotide Polymorphism (SNP) dataset. The comparative interest of each method is then discussed in the conclusion.

Poster session B - MAX 412

Genotyping museum samples from extinct vs extant populations to identify genes affecting adaptation (51647)

Toby Fountain, Marko Nieminen, Jukka Sirén, Swee Wong Chong, Ilkka Hanski.

University of Helsinki.

The application of Next Generation Sequencing to ecological model species facilitates the study of adaptation in natural populations. The ecological dynamics of the Glanville fritillary metapopulation in the Åland islands in SW Finland have been studied for over 20 years, producing a unique understanding of these dynamics across a large heterogeneous area. Recently, the full genome has been published along with two experimental RNAseq datasets. We selected 272 SNPs within genes indicated as under likely selection for increased or reduced flight capacity in RNAseq experiments, along with putatively neutral markers, and genotyped 10,000 individuals from three regions in Åland. We also genotyped 119 individuals from museum collections sampled between 50 and 150 years ago from extinct and extant populations across the Baltic. We used the F-model to calculate population and locus-specific drift values for the museum samples in comparison with a contemporary reference population. This approach has strengthened evidence that a subset of loci previously identified as candidate markers may be under selection in natural populations, with the majority in genes

related to flight and host plant use. We discuss the significance of incorporating ecological, demographic and phenotypic data with a candidate gene approach to investigate loci under selection.

Poster session B - MAX 412

Validating SNPs underlying local adaptation in lodgepole pine (51700)

Kimberly J. Gilbert, Nicholas K. Ukrainetz, Sally N. Aitken, Michael C. Whitlock.

University of British Columbia; BC Ministry of Forests, Land and Natural Resource Operations.

Detecting the loci that underlie local adaptation is a difficult task, but one which is highly sought after. Methods for identifying such loci include environment-allele correlations, FST outlier tests, and genome-wide association studies (GWAS). However, these methods are subject to false positives from neutral processes that may leave behind signatures of selection on the landscape. In this study, I aim to validate the identification of selected SNP loci underlying adaptation to climate conditions in the lodgepole pine, a common timber tree in British Columbia. A larger study at the University of British Columbia has identified such selective SNPs from the aforementioned methods, using samples collected across the provinces of BC and Alberta and grown as seedlings in varying induced climates under growth chamber conditions. My study has sampled natural-growing, mature (>40 year-old) trees from the long-term, large-scale Illingworth provenance trials. I use these samples to assess whether lifelong selection on individuals leads to the same selective SNPs being identified in populations adapted to specific climate conditions, therefore serving to validate the selection of loci underlying local adaptation.

Poster session B - MAX 412

Boosting inference power by gathering time-serial data: an example from influenza virus (51753)

Claudia Bank, Jeffrey Jensen.

School of Life Sciences, EPFL; Swiss Institute of Bioinformatics.

The recent genomics revolution has provided us with novel means to study the processes that drive evolution at the molecular level. High-throughput genome sequencing enables us to survey genetic variation over multiple generations at modest costs, and new technical developments allow for the extraction and sequencing of DNA from ancient specimens. As compared with genome scans from a single time point, genomic time-serial data obtained from natural populations or generated by experimental-evolution approaches dramatically increase the power to investigate the mechanisms that drive evolution. Here, we use time-sampled whole-genome SNP data from a mutation-accumulation experiment in influenza H1N1 under various environmental conditions (represented by different antiviral drug

treatments) to identify loci involved in adaptation, and discuss their potential functional role in the evolution of drug resistance. We further point out the limits and challenges of current approaches to time-serial selection inference, and lay out a roadmap for future developments.

Poster session B - MAX 412

Females with long legs: signatures of selection in the genome of the South African bee genus *Rediviva* (51783)

Belinda Kahnt, Antonella Soro, Michael Kuhlmann, Robert J. Paxton.

Martin-Luther-University Halle; The Natural History Museum, London.

The great phytodiversity of the South African Succulent Karoo is thought to be due to the close interaction and reciprocal adaptation of plants and their pollinators. *Rediviva* bees and their *Diascia* host plants represent a particularly fascinating example of such a co-evolutionary relationship. In order to collect oil from the long spurs of its host plant, *Rediviva* females have evolved a unique adaptation: elongated forelegs, which show not only inter- but also intraspecific variation and are significantly correlated with spur length of *Diascia* hosts. We aim to understand the genetic underpinning of leg length in *Rediviva*. We RAD (Restriction-site-Associated DNA) sequenced 60 individuals from two adjacent populations of *Rediviva longimanus*, significantly differing in leg length, and use these data to: i) characterise SNPs ii) identify regions under selection using an F_{ST} -outlier approach; iii) sequence F_{ST} -outliers found in coding regions of *R. longimanus* in the sympatric *R. intermixta* and *R. macgregori*, species with shorter forelegs, and iv) test for signatures of selection by analysis of the KA/KS ratio. Results of our studies not only inform processes of adaptation and speciation in co-evolving pollinator-plant systems but are also of great relevance for the conservation management of both endemic genera.

Poster session B - MAX 412

QTL mapping of stress related traits in the model brown alga *Ectocarpus siliculosus* (51789)

Komlan Avia, Fiona Lerck, Stephane Mauger, Susana Coelho, Pierre Boudry, Myriam Valero, Mark Cock.

Algal Genetics Group, LBI2M UMR 8227 CNRS-UPMC, Station Biologique Roscoff, France; Evolutionary Biology and Ecology of Algae, UMI 3614, Station Biologique Roscoff, France; Unité Physiologie Fonctionnelle des Organismes Marins, UMR 6539 LEMAR, IFREMER Plouzane, France.

Brown algae are complex photosynthetic organisms with a very different evolutionary history to green plants. They are dominant species in rocky coastal ecosystems. They are economically important as food products, animal feed, fertilizer, source of polysaccharides or other important extracts, or even biofuel resources. Despite their importance, many aspects of

these organisms are still poorly understood. The filamentous brown alga *Ectocarpus siliculosus* has been proposed as a general model for the brown algae and its genome has been sequenced.

As sessile organisms, brown algae require high levels of tolerance to various abiotic stressors (osmotic pressure, temperature, salinity, light) and previous studies showed that an important proportion of the expressed genes are regulated in response to hyposaline, hypersaline or oxidative stresses.

Using double digest RAD sequencing method, a denser genetic map has been constructed and QTL for stress-related primary and secondary phenotypes have been mapped. These first results of QTL mapping in *Ectocarpales* are discussed in the light of the peculiar as well as common characteristics of these species relative to other algae and land plants.

Poster session B - MAX 412

Distribution of chromosome identical-by-descent block length as an integrating multilocus approach in population genetics (52162)

Mathieu Tiret, Frédéric Hospital.

INRA Jouy en Josas.

In population genetics, incorporating NGS data requires to consider multiple loci at once, and hence take account of multiple levels of linkage disequilibrium. Here we address this from the identity by descent (IBD) relationship: two chromosome tracts are said to be IBD if they are copies of a same ancestral chromosome without having undergone any mutation nor recombination. Because of recombinations, all the genome cannot remain IBD for the whole population, and so genomes split into blocks of IBD zones and non-IBD zones. We study the length distribution of such IBD blocks over time in a neutral context.

Using the theory of junctions (Fisher, 1954), and a Wright-Fisher model with recombination, we derived an approximation of the average IBD block length in a population, which depends only on heterozygosity, population size and time. Under this approximation, there is a transient phase during which the average length is constant. Since the duration of this phase increases with population size, we conclude that average IBD block length should remain constant in large populations.

Poster session B - MAX 412

Identification of Arctic population of *Mytilus* mussels based on SNP markers (52228)

Malgorzata Zbawicka, Lis Bach, Jakob Strand, Roman Wenne.

Institute of Oceanology; Aarhus University .

Mussels *Mytilus* are widespread in northern and southern hemispheres and are known to inhabit subarctic and arctic regions, where must conform to extremely harsh environmental conditions. The *Mytilus* species are very important component of marine coastal ecosystems. Information of genetic biodiversity have importance for biogeography, and environmental monitoring studies related to global climate changes.

Molecular markers based on single nucleotide polymorphisms (SNPs) were used for study the population structure and identifying the geographical origin of the Arctic mussels.

Genotyping of SNPs was performed using the Sequenom MassARRAY iPLEX platform.

Sixty six polymorphic SNPs were used to genotype *Mytilus* spp. samples, consisting of 700 individuals, collected from Greenland, Iceland, and Spitsbergen. Reference samples from North America and Europe were used. The highest heterozygosity was observed in the populations from a Greenlandic fjord, at Maarmorilik, and in sample from Spitsbergen, and the lowest in Savissivik in Northwest Greenland. Correspondence Analysis, Structure and fixation index values based on SNPs very clearly show diversity among and within the studied populations. The outlier detection was carried on to identify candidate loci that might be under selection. The obtained results indicate the high potential of the SNPs markers in the study of population structure and admixture level of mussels of the genus *Mytilus* in the Arctic

Poster session B - MAX 412

Eco-evolutionary dynamics in response to seasonal adaptation in *Drosophila* (52253)

Subhash Rajpurohit, Alan Bergland, Martin Turcotte, Jonathan Levine, Dmitri Petrov, Paul Schmidt.

University of Pennsylvania; Stanford University; ETH Zurich.

In temperate populations of *D. melanogaster*, the rapid and cyclical adaptation to seasonality is driven by multiple genes and phenotypes. Using an experimental orchard with insect enclosures, we generated large outbred populations from fully sequenced, inbred lines and manipulated the rate of evolution in response to changing seasonal parameters. We examined how the adaptive response to seasonality over the agricultural growing season determines fundamental aspects of population ecology and, in turn, how changing ecological dynamics affect the subsequent evolutionary response. Our data demonstrate a predictable genomic and phenotypic adaptive response to seasonality, and that this adaptive response results in a faster rate of population growth and a higher carrying capacity. The differential density between treatments over time was associated with evolutionary change in several traits that affect fitness in a density-dependent fashion. These experiments suggest a fundamental interplay between ecological and evolutionary dynamics in natural populations that inhabit seasonal environments.

Poster session B - MAX 412

The power to detect selection from gene frequencies variation in 10 generations (52384)

Jean-Noël Hubert, Frédéric Hospital.

INRA Jouy en Josas.

Available strategies to identify targets of selection in the genome include population genomics and especially bottom-up analyses seeking footprints of selection. Various methods developed through this scope allowed detecting even small cumulative effects of selection over large timescales. By contrast, looking for selection in small populations undergoing a strong directional selection during only a few generations, as it may be the case in selection experiments or in response to rapidly changing environments, received a limited attention. We propose to address this issue by coupling a diallelic Wright-Fisher model to a maximum-likelihood approach. Individual-based simulations, performed under this approach with 10-generation long scenarios, indicated that detecting selected SNPs by following the variation of allele frequencies over a very short period of strong directional selection is feasible. Importantly, the initial situation at each considered SNP in terms of allele frequency and linkage disequilibrium, in addition to the selection intensity, was shown crucial to get enough power of detection. Our maximum-likelihood estimation seems adapted for inferring selection due to rapid adaptation, in particular those caused in the course of selection experiments.

Poster session B - MAX 412

Hybrid zones as natural laboratories to study adaptation in host-parasite systems: the Murine cytomegalovirus in the European house mouse hybrid zone (52531)

Joelle Gouy de Bellocq, Stuart J.E. Baird, Jaroslav Pialek.

Institute of Vertebrate Biology, ASCR.

When hosts and their parasites co-diverge during isolation, their secondary contact creates a natural laboratory for investigating loci underlying adaptation in host-parasite systems. We sampled mice across a 145-km transect in the Bavaria-Bohemia region of the hybrid zone between *Mus musculus domesticus* and *Mus musculus musculus* to investigate the occurrence and the genetic structure of a common herpesvirus of mice, the Murine cytomegalovirus (MCMV). We screened 319 lung samples collected from 97 localities by nested-PCR. 133 were positive, and for these we sequenced 6 genes distributed across the genome and analysed their genetic structure. The two mouse taxa carry different strains of MCMV. Four genes located centrally in the MCMV genome and involved in the viral life cycle were structured in close accordance with the host genetics. In contrast, genes located at both extremities of the genome and involved in the subversion of the host immunity have recombined and introgressed. This result lets us glimpse the potential of parasite genomic studies in host hybrid zones for identifying potential candidate genes underlying adaptation. Sequencing of a sample of MCMV genomes will provide a more detailed picture of the introgressive viral genes.

Local adaptation in osmoregulatory physiology in sticklebacks (52585)

Jacquelin De Faveri, Mehedi Hasan, Satu Kuure, Sanna Lehtonen, Surjya Dash, Scott McCairns.

University of Helsinki.

Organisms living in high and low salinity environments face opposing physiological demands in order to survive the challenges posed by environmental salinity. Earlier studies of three-spined stickleback (*Gasterosteus aculeatus*) have suggested that populations residing in low salinity regions of the Baltic Sea have become locally adapted to their native salinity conditions. However, the physiological and functional genetic basis of this adaptation has remained unstudied. For example, signatures of selection have been detected in several genes related to osmoregulation, yet their functional role has not been validated. In this study, we integrate candidate gene expression and comparative kidney cell morphology to explore the physiological underpinnings of adaptation to low salinity environments in Baltic three-spined stickleback. A factorial common garden experiment revealed a high degree of plasticity in kidney cell morphology and candidate gene expression in the population residing in high salinity regions of the Baltic Sea. In contrast, the native low-salinity population showed little changes in response to differences in environmental salinity, suggesting canalization of key osmoregulatory traits.

Genome wide approach to detect positive selection on the plant pathogen fungal genus *Colletotrichum* (52610)

Ana Vieira, Diogo N. Silva, Octavio S. Paulo, Dora Batista.

COBIG2, CE3C, Faculdade de Ciências, Universidade de Lisboa, Lisboa, Portugal; CIFIC /Biotrop/Instituto de Investigação Científica Tropical, Oeiras, Portugal.

Natural selection leaves imprints on DNA, offering the opportunity to identify functionally important regions of the genome. Currently, with the rapid accumulation of genome sequences and the development of powerful statistical methods to detect signatures of adaptation, it is possible to pinpoint genomic regions under selection. Recent studies have shown the importance of looking for genes under positive selection in pathogens, since this allows to better understand the co-evolution dynamics of host-pathogen interactions and aid in the pursuit of effective strategies to control diseases. The fungi *Colletotrichum* spp. are listed in the "Top 10" of the most economically devastating groups of plant pathogens, causing severe diseases in a vast range of crops throughout the world, and have been associated with several cases of emergent plant diseases in new hosts. In this study, we used a genome-wide approach to screen for positive selection across as many orthologous as possible from the six full genome sequenced species of the *Colletotrichum* genus, adapted to different hosts and

representing different lifestyles (*C. graminicola*; *C. higginsianum*; *C. orbiculare*; *C. acutatum* var. *fiorinae*, *C. sublineola* and *C. gloeosporioides*). New candidate genes are being identified and functions putatively involved in different adaptive processes will be discussed. Funded by FCT grant SFRH/BD/89397/2012.

Poster session B - MAX 412

Mapping of quantitative trait loci (QTL) for fitness-related traits in the house sparrow (52630)

Henrik Jensen, Ingerid Hagen, Anna Billing, Henrik Pärn, Bernt Rønning, Thor Harald Ringsby, Bernt-Erik Sæther, Sigbjørn Lien, Arild Husby.

Norwegian University of Science and Technology; Norwegian University of Life Sciences; University of Helsinki.

A major challenge in evolutionary biology is to understand the genetic processes and mechanisms that enable populations to adapt to environmental changes. The recent revolution in high-throughput molecular methods has made development of large numbers of molecular markers, genetic maps, and even whole-genome sequencing affordable also in non-model species. This allows study of the genetic architecture of quantitative traits by use of quantitative trait locus (QTL) mapping in natural populations, which will provide invaluable information to improve our understanding of the genetics of adaptation. Here, we used genomic resources recently developed for the house sparrow (*Passer domesticus*) to genotype more than 6000 Single Nucleotide Polymorphisms (SNPs) with known position, in ca. 2000 individuals from long-term studies of a set of natural populations in northern Norway. QTL mapping of fitness-related morphological traits was carried out by Genome Wide Association Studies (GWAS) and identified QTL for some of the morphological traits. Variation in the allele frequencies of SNPs within these QTL was then examined across generations and populations. By relating these patterns to the observed spatio-temporal phenotypic variation as well as the strength and direction of phenotypic selection we are starting to understand some genetic mechanisms for adaptation in these populations.

Poster session B - MAX 412

Identifying the Loci of Selection in a 30-Year Long Selection Experiment for Longevity in *Drosophila melanogaster* (52650)

Kathrin I. Garschall, Daniel K. Fabian, Martin Kapun, Robert Arking, Christian Schlötterer, Thomas Flatt.

Department of Ecology and Evolution, University of Lausanne, Lausanne, Switzerland; Institute of Population Genetics, University of Veterinary Medicine Vienna, Vienna, Austria; Department of Genetics, University of Cambridge, Cambridge, United Kingdom; Department of Biological Sciences, Wayne State University, Detroit, USA.

To study the mechanistic basis of the evolution of longevity, we have recently performed whole-genome sequencing of experimental replicate populations of *Drosophila melanogaster* that have been undergoing selection for postponed senescence for over 30 years. Based on our analysis of highly differentiated single nucleotide polymorphisms (SNPs) between longlived selection and non-selected control lines, we have identified numerous candidate genes as potential targets of selection for increased lifespan. For example, a particularly interesting set of genes, strongly genetically differentiated between selection and control lines, are involved in innate immunity. In support of their functional relevance, we find that the evolved lines outperform controls in pathogen infection assays, and preliminary qPCR data suggest that selection lines differ substantially from the controls in the expression of several immune genes. Here we aim to complement and extend these findings by applying transcriptomic (RNA-seq) analyses to this long-term selection experiment. Comparing these gene expression data to our DNA sequence data allows to substantially refine our list of candidate loci for further functional experimental testing.

Poster session B - MAX 412

Seed dormancy contributes strongly to local adaption in *Arabidopsis thaliana* (52672)

Froukje M. Postma, Jon Ågren.

Uppsala University.

Seed dormancy is a key life-history trait in plants, but its role in local adaptation remains poorly known. We examined the genetic basis and adaptive significance of seed dormancy in a reciprocal transplant experiment using 220 Recombinant Inbred Lines (RILs) derived from a cross between two populations of *Arabidopsis thaliana* from the northern and southern limits of its native range (Italy and Sweden). We mapped QTL for seed dormancy and fitness (number of fruits produced per seed planted) using seeds matured at the respective field site and planted at the time of seed dispersal, in one year in Italy and in three years in Sweden. The local genotype had higher fitness than had the non-local genotype at both sites in all years. We found strong divergent selection on seed dormancy between the two sites, with temporal variation in the strength of selection in Sweden. We detected 6 dormancy QTL of which 4 overlapped with fitness QTL. The dormancy QTL with the strongest effect was significant at both field sites and collocated with the dormancy gene *DOG1*. The results demonstrate that genetically based differences in seed dormancy play an important role in adaptive differentiation among natural populations of *A. thaliana*.

Poster session B - MAX 412

Dertermination of the selection process acting on the PGM in *Alevinella Pompejana* (52673)

BIOY Alexis, LE PORT Anne Sophie, MARY Jean, JOLLIVET Didier.

The Pompeii worm occurs exclusively on hydrothermal-vent chimneys along the East Pacific Rise (EPR). This environment is considered as one of the most extreme and variable in temperature. Previous works on the phosphoglucosyltransferase revealed that diversifying selection acts on the frequencies of isoforms 78, 90 and 100 between thermal habitats at small spatial scales. Both protein stability and thermal optimum of enzyme activity were clearly different between isoforms. Allozymes also displayed a clinal distribution from North to South with an abrupt replacement of isoform 100 by isoform 78. In the present study, alleles encoding these isoforms were completely sequenced from northern and southern individuals. The distribution of highly divergent alleles without recombination on both sides of the EPR are likely the result of balancing selection combined with spatial isolation. Only two non-synonymous mutations (EQ) located in the exon 3 explain the polymorphism of charge. Directional mutagenesis allowed us to mutate allele 100 into the two other alleles and to overexpress them to explore the additive effect of the mutations over the biochemical properties of the enzyme in the face of temperature. Results are coherent with those obtained on native proteins and showed the direct effect of mutations on the protein thermostability.

Poster session B - MAX 412

Lipocalin Gene Expression Divergence in *Drosophila melanogaster* and *Drosophila simulans* (52696)

Banu Sebnem Onder, Nazli Ayhan, Pinar Güler.

Hacettepe University; Aix Marseille University.

Environmental stressors are among the strongest forces of natural selection. When organisms encounter with an environmental stress, the characters of organisms are shaped by evolutionary adaptive mechanisms to buffer these factors. Studies with Lipocalin genes have shown that stress responsive signal pathways are important for regulation of the lipocalin genes expression and metabolic adaptation of the organism to environmental challenges. Besides, lipocalin gene family is evolutionarily conserved from flies to vertebrates. Here, we present analyses of expression divergence in adults of two recently diverged species of *Drosophila*. Depending on the aging and dietary stress, single-gene expression of lipocalin genes NLaz, GLaz and Karl was quantified. We found different gene expression responses between two species in different age intervals and under dietary stress. *D. melanogaster* showed up-regulation with age in all lipocalins, whereas *D. simulans* showed different age-related expression patterns. Further, we found that malnutrition could affected lipocalin expression patterns reveal the differences between species. Results of this experiment showed that the present lipocalin genes might be differ within sibling species in terms of function or regulation.

Poster session B - MAX 412

Efficient detection of novel nuclear markers for Brassicaceae by transcriptome sequencing (52715)

Reinhold Stockenhuber, Stefan Zoller, Rie Shimizu-Inatsugi, Felix Gugerli, Kentaro K. Shimizu, Alex Widmer, Martin C. Fischer.

University of Zurich, Institute of Evolutionary Biology and Environmental Studies; ETH Zürich, Genetic Diversity Center; WSL Swiss Federal Research Institute; ETH Zürich, Institute of Integrative Biology.

The lack of DNA sequence information for most non-model organisms impairs the design of primers that are universally applicable for the study of molecular polymorphisms in nuclear markers. Next-generation sequencing (NGS) techniques provide a powerful approach to overcome this limitation. We present a flexible and inexpensive method to identify large numbers of nuclear primer pairs that amplify in most Brassicaceae species. We first obtained and mapped NGS transcriptome sequencing reads from two diverged Brassicaceae members, *Cardamine hirsuta* and *Arabis alpina*, onto the *Arabidopsis thaliana* reference genome, and then identified short conserved sequence motifs bioinformatically. From these, primers were developed and tested successfully on 30 Brassicaceae taxa. Sequence analysis and phylogenetic reconstruction with a subset of these markers on different levels of phylogenetic divergence in the mustard family were compared with previous results and corroborate the usefulness of our newly developed primer pairs, e.g., for phylogenetic analyses or population genetic studies. We identified 2,334 universally applicable primer pairs, targeting 1,164 genes, which provide a significant and readily usable genomic resource that will help addressing novel questions in the Brassicaceae family.

Poster session B - MAX 412

Local adaptation at the transcriptomic level in European populations of *Daphnia* (52811)

Mathilde Cordellier, Suda Ravindran, Ann-Kathrin Huylmans, Alberto Lopez, Klaus Schwenk, John Parsch.

Universität Hamburg; Ludwig-Maximilians-Universität München; Westfälische Wilhelms-Universität Münster; Universität Koblenz-Landau.

Simultaneously phenotype and genotype, gene expression profiles are heritable, thus providing a substrate for evolution. In species with little or no gene flow between populations such as permanent *Daphnia* populations, local adaptation can lead to distinctive gene expression profiles within a single species. Selection drivers as diverse as parasitism, predation and heavy metal pollution were already shown to cause rapid genetic shifts in *Daphnia*.

In this study, we inferred the intra-specific variation at the transcriptome level in *Daphnia galeata*. A large scale RNAseq experiment was conducted on 24 clonally propagated genotypes from four European lakes. In total, 72 libraries were sequenced and long reads generated for assembly purposes. The de novo assembly was made using the EvidentialGene pipeline and used as a reference for the differential expression analysis. Candidate genes

exhibiting differential expression patterns between populations were relatively few, partly due to the high variation within populations. Expression levels of these candidate genes will be correlated with fitness measurements and sequence variation, in order to establish a link between phenotype and genotype. The outcome of this study will allow us to understand the genetic background of rapid adaptation to environmental changes in a key species of aquatic ecosystems.

Poster session B - MAX 412

Genotype and phenotype in a changing ocean: can standing genetic variation in stress responses rescue mussel populations from the negative impacts of climate change? (52826)

Sarah E Kingston, Jenna Watling, Benjamin Eisenberg, David Carlon.

Bowdoin College.

As physical and chemical features of the ocean change in response to the changing climate, marine calcifiers face the biochemical and physiological challenge of maintaining calcium carbonate shell structure in a more acidic environment. A key component to understanding organismal response to this multifactorial stressor is linking underlying genetic variation to phenotypic variation in stress response. We take advantage of the genomic gradient across the blue mussel hybrid zone (*Mytilus edulis* and *Mytilus trossulus*) in the Gulf of Maine to link genetic variation with variance in calcification rates in response to lower pH, higher temperatures, and reduced food availability. Intertidal blue mussels were collected from midcoast Maine up to Cobscook Bay and subjected to a 14-day exposure in a laboratory common garden treatment of climate stress (20°C, pH 7.8, and low food availability). The control treatment simulated ambient Harpswell Sound summer conditions (17°C, pH 8.1, and high food availability). Interestingly, the climate stress treatment rendered significantly greater variation in calcification rates (change in buoyant weight) than the control treatment, while the means did not vary significantly. The calcification rate phenotypes were then linked to underlying genomic variation through a next generation sequencing-based SNP assay and genome-wide association survey.

Poster session B - MAX 412

Phylogenomics provides insights on the adaptive evolution of rust fungi (52957)

Diogo N. Silva, Sebastien Duplessis, Pedro Talhinhos, Helena Azinheira, Octávio S. Paulo, Dora Batista.

Computational Biology and Population Genomics Group, Science Faculty, University of Lisbon; Centro de Investigação das Ferrugens do Cafeeiro/BioTrop, IICT; Institut National de la Recherche Agronomique, UMR 1136 INRA/Université de Lorraine; Université de Lorraine, UMR 1136, INRA/Université de Lorraine.

In this work, we employed a phylogenomics approach focused on single-copy genes shared by 38 Basidiomycota species to search for signatures of natural selection during the evolutionary origin of the rust fungi (Pucciniales). We identified 1006 orthologs that were screened for positive selection acting specifically at the basal branch of the rust fungi. In total, 1103 positively selected codon sites were uncovered across 185 genes (18%), which is a surprisingly high proportion given the fact that these genes are conserved across the Basidiomycota. To further assess the adaptive impact of the positively selected sites on the evolution of rust fungi, sites were sorted depending on whether they remained unchanged or continued diverging throughout the diversification of rust fungi. While the majority of the positively selected sites (78%) remained unchanged and, therefore, represent prime candidates to help us understand the early divergence of rust fungi, the remaining 22% of the sites continued to diverge and may represent candidates contributing for the origin of rusts and species-specific traits. We will discuss the functional categories enriched for each type of the positively selected genes as well as the usefulness and impact of genome-wide screens of positive selection. Funded by FCT PTDC/AGR-GPL/119943/2010 and SFRH/BD/86736/2012.

Poster session B - MAX 412

Analysis of allele-specific expression in a putative pathogenesis-related gene of coffee leaf rust (52964)

Inês S. Modesto, Andreia Luoreiro, Renata Martins, Ana Paula Pereira, Vítor Várzea, Octávio S. Paulo, Dora Batista, Célia Miguel.

iBET, Instituto de Biologia Experimental e Tecnológica, Apartado 12, 2781-901 Oeiras, Portugal; CIFC-Biotrop, IICT, Quinta do Marquês, 2784-505 Oeiras, Portugal; CoBiG², Ce3C, FCUL, Campo Grande, 1749-016 Lisboa, Portugal; ITQB-UNL, Av. da República, 2780-157 Oeiras, Portugal.

Hemileia vastatrix is a rust fungus responsible for one of the main devastating diseases of Arabica coffee. Durable coffee resistance has been hampered by the high capacity of *H. vastatrix* to adapt, driven by the dynamic of host-pathogen co-evolution. In this scenario, it is pressing to understand the mechanisms underlying adaptation in *H. vastatrix* populations. In a previous study, population genetic variation was analyzed for a set of pathogenesis-related candidate genes activated during the early stages of *H. vastatrix* infection as identified from a 454-transcriptomic dataset. For one such genes, a pattern of very divergent alleles particularly related with coffee hosts was found revealing a clear structuring of genetic variation with a probable adaptive significance. Allele-specific expression has been detected as common and widely distributed along several taxa, leading to phenotypic variation, and underlying adaptation. In a first attempt to elucidate its functional activity, we investigated the candidate gene expression profile in different rust isolates bearing contrasting allelic compositions, along the different stages of the infection process, using real-time PCR to discriminate putative allelic asymmetric expression. The differential expression profiles obtained will be discussed concerning putative causal relations between allelic variants and pathotypes, and their possible adaptive significance.

Finding the genes which make great tits innovators (52967)

Veronika Laine, Toni Gossmann, Kees van Oers, Kyle Schachtschneider, Ole Madsen, Kai Zeng, Jon Slate, Marcel Visser, Martien Groenen.

Netherlands Institute of Ecology (NIOO-KNAW); University of Sheffield; Wageningen University.

For more than 50 years the great tit (*Parus major*) has been a prime model species for ecological, behavioural and evolutionary studies. Studies of learning and cognition in great tits suggest that this species displays an unusual propensity for behavioural plasticity and social learning in response to environmental challenges. Here we sequenced to high coverage, de novo assembled and annotated the genome of the great tit. Furthermore, we sequenced the methylome of two tissues, RNA of eight tissues and whole genomes of 29 additional individuals to identify genomic regions under positive selection in this species. These regions show an increased level of CpG methylation, decreased non-CpG methylation, and an overrepresentation of genes related to learning and cognition, traits which seem to be important in recent adaptive evolution of great tits. These observed patterns raise interesting questions regarding neuronal epigenetic regulation and the potential role of methylation in learning, memory and experience-induced plasticity.

Comparative phylogenetic analysis of sex allocation evolution in the hermaphroditic flatworm genus *Macrostomum*. (51713)

Jeremias Brand, Toon Janssen, Dita B. Vizoso, Lukas Schärer.

Zoological Institute, University of Basel, Vesalgasse 1, CH-4051 Basel, Switzerland; Nematology Research Unit, Department of Biology, Ghent University, K.L. Ledeganckstraat 35, 9000 Ghe.

In simultaneous hermaphrodites sex allocation is the decision about relative investment into male versus female reproduction. Sex allocation is strongly influenced by the intensity of sperm competition, which can vary drastically between species. In species with traumatic insemination (sperm injection through the body wall with an intromittent organ) sperm competition is likely to follow a fair-affle model and may therefore be high as injected sperm are swimming through the tissue in the search of eggs. Conversely, in species with copulation (insertion of an intromittent organ into a female sperm receiving structure) sperm are more likely to compete with related sperm due to the possibility for sequential sperm displacement and cryptic female choice. Here we present results from work combining photomicrographic documentation of field collected worms and a molecular phylogeny of 50 species of *Macrostomum*. We estimated relative gonad size, since it has previously been shown to be a useful proxy for sex allocation in *Macrostomum*, and evaluated its distribution across the phylogeny to test whether sex allocation is free to evolve or phylogenetically constrained in this genus. Furthermore, we measured qualitative and quantitative traits of male and female

sexual organs to map their phylogenetic distribution and investigate whether combinations of these traits are phylogenetically correlated to sex allocation.

Poster session B - MAX 413

**Do females produce more sons when mating with more attractive males?
(51757)**

Isobel Booksmythe, Brian Mautz, Jacqueline Davis, Shinichi Nakagawa, Michael Jennions.

University of Zurich; Uppsala University; University of Cambridge; University of Otago; Australian National University.

Do females produce more sons when mating with more attractive males? Early support for this prediction has become less clear-cut over time. Rapidly accumulating empirical studies are broadening the range of taxa, mating systems, attractive traits and moderating factors included in tests of the hypothesis. Additionally, theoretical advances have questioned whether sex allocation in response to mate attractiveness should be either expected or empirically detectable. We used meta-analysis for a quantitative review of the empirical literature on this topic. The mean effect size was very small, but statistically significant in the predicted direction. It was not, however, robust to correction for an apparent publication bias towards significantly positive results. We also examined the strength of the relationship using different indices of male attractiveness. Of these, ornamentation and body size predicted the proportion of sons produced, but again these effects were very small. Our study provides weak support for a relationship between male attractiveness and the offspring sex ratio, but highlights the need for more powerful empirical tests. Ultimately, we need more direct experimental tests of whether females produce more sons when mated to more attractive males, that also provide evidence this occurs because sons have higher mean fitness than daughters.

Poster session B - MAX 413

**Divorce and infidelity are associated with skewed adult sex ratios in birds
(51949)**

Tamas Szekely, Andras Liker, Robert Freckleton.

University of Bath; University of Pannonia; University of Sheffield.

Adult sex ratio (ASR) is a fundamental concept in population demography, and recent theory suggests that ASR plays a central role in social behaviour, mating systems and parental care. Unbalanced ASRs are predicted to influence pair-bond and mating behaviour since the rarer sex in the population has more potential partners to mate with than the more common sex. Here we use phylogenetic comparative analyses to test whether ASR is related to three major aspects of mating behaviour: divorce, social polygamy and pair-bond infidelity. ASR is strongly correlated with long-term pair-bonds since divorce rate is higher in species with

female-biased sex ratio, indicating that mate change by pair members and/or breaking of pair-bonds by unmated individuals is more frequent when females outnumber males. Short-term pair-bonds are also associated with ASRs: males are more commonly polygamous when females outnumber males, and conversely, females are more polygamous when males outnumber females. Furthermore, infidelity increases with male-biased ASR in socially monogamy, suggesting that male coercion and/or female willingness to cheat the partner are facilitated by male-biased ASR. Our results provide the first comprehensive support for the proposition that ASR influences multiple aspects of pair-bonds and mating behaviour in wild populations.

Poster session B - MAX 413

Socially sensitive gene expression analysis of seminal fluid proteins in a simultaneously hermaphroditic marine flatworm (51984)

Bahar Patlar, Steven Ramm.

Bielefeld University.

The ejaculate often contains many seminal fluid proteins that are transferred along with sperm during mating. Since it is known that these proteins function in diverse ways to maximize male reproductive success, often exerting strong effects on female reproductive physiology and behaviour, the study of SFPs has become a central concern of sexual conflict research. Considering that production of seminal fluid is costly, we expect individuals to strategically invest in SFP production according to the level of sperm competition. This study examines the impact of social environment on SFP production in the simultaneously hermaphroditic marine flatworm *Macrostomum lignano*. It is well known that individuals of *M. lignano* kept in larger social groups invest more in male reproductive traits than individuals in smaller social groups, presumably as a consequence of sperm competition and as predicted from sex allocation theory. Thus, we predict that the transcriptional activity of seminal fluid genes in worms will also differ between large versus small social group sizes. Moreover, by measuring seminal fluid gene expression in multiple inbred lines, we can assess genetic variation for expression plasticity of these genes, i.e. to test for genotype-environment interaction effects as a response to differing social environments.

Poster session B - MAX 413

Maladaptive sex ratio manipulation in invasive *Artemia franciscana* (51999)

Eva JP Lievens, Gil Jorge Barros-Henriques, Yannis Michalakis, Thomas Lenormand.

CEFE, CNRS Montpellier; MIVEGEC, CNRS Montpellier.

Sex allocation theory is often hailed as the most successful area of evolutionary theory, and sex allocation traits are typically expected to respond quickly to changing selection pressures. Here, we demonstrate that this is not always true. We studied French populations of the sexual

brine shrimp *Artemia franciscana*, which invaded from the Americas in the 1970s (200-500 *Artemia* generations ago). Since then, *A. franciscana* has coexisted with a native parthenogenetic species, *Artemia parthenogenetica*. First, we report the regular occurrence of extremely male-biased sex ratios in natural populations of invasive *A. franciscana*, and we show that the extent of male-biasing is predicted by the proportion of *A. parthenogenetica* in the population. Second, we experimentally prove that both native-range and invasive-range *A. franciscana* overproduce sons when exposed to an excess of females, without distinguishing between conspecific and parthenogenetic females. We conclude that *A. franciscana* have an ancestral ability to plastically ‘correct’ skews in the population sex ratio, which has persisted unchanged in the invasive range despite being maladaptive in the presence of *A. parthenogenetica*. This study demonstrates that although sex allocation is a key life-history parameter with large effects on fitness, it is still subject to constraints that may dramatically slow adaptation.

Poster session B - MAX 413

Testing for cytonuclear conflict over sex allocation in a simultaneously hermaphroditic flatworm (52043)

Nikolas Vellnow, Dita B. Vizoso, Lukas Schärer.

University of Basel, Zoological Institute, Evolutionary Biology, Basel, Switzerland.

Uniparental inheritance of cytoplasmic genes creates a potential for cytonuclear conflict over sex allocation. In particular, maternally inherited cytoplasmic genes in simultaneous hermaphrodites may be selected to reduce allocation towards male gametes. This can lead to the spread of cytoplasmic male sterility mutations and a consequent transition to gynodioecy, as found in many plant species. Curiously, gynodioecy seems to be rare or absent in animals. Here we provide a quantitative test for cytonuclear conflict over sex allocation in the simultaneously hermaphroditic flatworm *Macrostomum lignano*. We generated replicate crosses of 15 different pairs of inbred lines ($2 \times 15 = 30$ independent lines), resulting in F1 offspring for each cross that had either of the two lines as the maternal parent. This design allows to compare the sex allocation of individuals with the same nuclear genome, but presumably different cytotypes. A preliminary analysis revealed significant effects of the nuclear genome, but no significant effects of cytotype on sex allocation, indicating absent or weak cytonuclear conflict. Analyses to evaluate the power of the experimental design are underway, but we hypothesize that the relatively small mitochondrial genome in animals compared to plants may be a reason why mutations that bias sex allocation arise less often in animals, leading to weaker cytonuclear conflict.

Poster session B - MAX 413

Identifying the selective pressures underlying offspring sex-ratio adjustments to test a priori predictions: a case study (52048)

Thomas Merkling, Etienne Danchin, Jorg Welcker, A. J. Mark Hewison, Alexander S. Kitaysky, John R. Speakman, Scott A. Hatch, Pierrick Blanchard.

Université Toulouse 3 Paul Sabatier; CNRS; ENFA; UMR 5174 EDB; Australian National University; Research School of Biology; Norwegian Polar Institute; University of Alaska Fairbanks, Institute of Arctic Biology; INRA, UR035, CEFS; University of Aberdeen, Institute of Biological and Environmental Sciences; State Key Laboratory of Molecular Developmental Biology, Institute of Genetics and Devpt Biolgy; U.S. Geological Survey, Alaska Science Center; Institute for Seabird Research and Conservation.

Despite how crucial information on the benefits and costs of producing males or females is to correctly predict and interpret offspring sex-ratio results, it is currently lacking for vertebrates. However, one should ideally identify the underlying selective pressures before examining sex-ratio variation itself. Therefore, we did so in our study species, the black-legged kittiwake (*Rissa tridactyla*), and examined the underlying assumptions of two plausible sex allocation models: the 'cost of reproduction hypothesis' and the 'Trivers-Willard hypothesis'. Using data from a long-term feeding experiment, we found stronger support for the former: rearing sons was energetically more costly for parents (higher energy expenditure and baseline corticosterone levels) than rearing daughters. Then, we made a priori predictions based on this difference in rearing costs and used a multiyear dataset to compare the explanatory power of six variables. Surprisingly, none of the 'classic' variables, such as food availability, were important predictors of offspring sex-ratio variation. Rather, pair-bond duration was the only important predictor, with a quadratic effect on sex-ratio that we interpreted in the light of the 'cost of reproduction hypothesis'. Future sex-ratio studies will certainly benefit from a more systematic investigation of the selective pressures occurring in a given species.

Poster session B - MAX 413

The genetic architecture of sex allocation in a simultaneous hermaphrodite (52181)

Steven A. Ramm, Dita B. Vizoso, Lucas Marie-Orleach, Mathias Kölliker, Lukas Schärer.

Bielefeld University; University of Basel.

In simultaneous hermaphrodites, individuals can gain reproductive success through both male and female sex functions, and sex allocation (SA) describes the balance of investment into these two routes to fitness. Although it is clear that simultaneous hermaphroditism may have important consequences for the operation of sexual selection and sexual conflict, predicting the evolutionary response to the resulting selection pressures also requires knowledge of the underlying genetic architecture of sexual traits. We aimed to estimate relevant quantitative genetic parameters in a simultaneously hermaphroditic model system, the free-living flatworm *Macrostomum lignano*, using a three-generation breeding design involving over 1200 individuals. We measured a suite of male and female reproductive traits in two social environments favouring different SA, to estimate: 1) the heritabilities and within- and between-sex function genetic correlations for these traits, and 2) the magnitude of gene-by-environment interaction effects on SA. Parallel studies are aiming to identify the genomic basis of SA plasticity in this species, meaning we can now begin to piece together the

complex ways in which hermaphroditism might impact upon the expression and evolution of sexual traits. We can thus test the generality of current conclusions about the genetics of sexual traits based almost entirely on studying species with separate sexes.

Poster session B - MAX 413

Sex role decisions of a simultaneous hermaphrodite: young and small snails choose to be male first (52225)

Yumi Nakadera, Elferra M. Swart, Jeroen J. P. Maas, Joris M. Koene.

Animal Ecology, Ecological Sciences, VU University Amsterdam, the Netherlands; Evolutionary Biology, Bielefeld University, Germany; Applied Biology, HAS University of Applied Sciences, the Netherlands.

Many simultaneous hermaphrodites choose to mate as male or female upon copulation, contrasting with pre-determined mating roles in separate-sexed species. This sex role decision in simultaneous hermaphrodites reflects their sex allocation at the behavioral level, and allows to examine reproductive strategies between different life stages or conditions. It is widely believed that larger individuals prefer to act as females, because they have higher reproductive resources, and produce more eggs. Hence, previous studies predominantly focused on effects of body size on sex role decisions, but have excluded or ignored other confounding traits, such as age. Therefore, we examined the effect of age and size on sex role decisions in a freshwater snail species, *Lymnaea stagnalis*. We paired snails of different types (young/old or small/large) to see which individuals act as male first. Our results show that young and small individuals tend to perform the male role first. Furthermore, small snails allocated proportionally more to their male function, based on weight of reproductive organs. However, large and/or old individuals did not perform better as females, in terms of egg production and reproductive allocation. These findings suggest that the behavioral output of sex allocation requires further attention to understand reproductive strategies in simultaneous hermaphrodites.

Poster session B - MAX 413

Does local resource competition select for less female biased sex ratios under local mate competition in spider mites? (52590)

Alison Duncan, Celine Devaux, isabelle Olivieri, Sara Magalhães.

University of Montpellier 2; University of Montpellier 2; University of Montpellier 2; University of Lisbon.

Sex allocation decisions pertain to parental investment in male versus female offspring. Local mate competition (LMC) occurs in sub-divided populations, in which closely related males compete for mates. LMC selects for mothers to produce a lower proportion of sons, which acts to reduce competition between related males as well as to increase the number of mates

per son. However, this prediction relies on the absence of competition among sisters for resources (LRC), which is achieved by the dispersal of females following mating. We thus expect the offspring sex ratio to be less female biased under both strong LMC and LRC (between females), than under LMC alone. We will present results of a selection experiment testing these predictions by comparing how high and low levels of female dispersal (mimicking LRC levels) under strong LMC impacts the evolution of female sex allocation behaviour in the spider mite *Tetranychus urticae*.

Poster session B - MAX 413

Local mate competition: the role of population viscosity, fecundity, and mating system. (52874)

Antonio M. M. Rodrigues, Andy Gardner.

University of Cambridge; University of St Andrews.

The extremely successful interplay between theoretical and empirical research into the sex ratio has been a touchstone for the study of evolution by natural selection. Central to the study of the sex ratio is local mate competition (LMC). LMC theoretical and empirical work have shown that females should produce female-biased sex ratios to prevent competition for mates among related males. Two independent extensions of LMC theory have produced two important predictions that have been the focus of extensive empirical testing: both population viscosity and variation in fecundity among breeding mothers have no impact upon the number of sons each mother produces. We will show under which conditions these two predictions hold. Specifically, we will show how the conjunction of population viscosity and variation in fecundity among breeders on the one hand, and deviations from the monogamous mating system on the other hand, can break down these two invariance results. Our study highlights the need for further work on the impact of population viscosity and of individual quality on sex allocation in particular, and on social evolution in general.

Poster session B - MAX 413

Sex allocation, plasticity and the preference for the male role in simultaneous hermaphrodites (52935)

Maria Cristina Lorenzi, Massimiliano Santi, Stefania Meconcelli.

*Laboratoire d'Ethologie Expérimentale et Comparée, University of Paris13, France;
Department of Life Sciences and Systems Biology, University of Turin, Italy.*

Simultaneous hermaphrodites have both male and female functions. According to theory, sexual selection should favor hermaphrodites that shift their reproductive resources between sexual functions depending on mating-group size. Although often tested at the population level, sex allocation theory has been rarely tested exposing the same individual to different levels of mating opportunities in subsequent time periods, thus really testing individual

plasticity.

We tested individual plasticity in female allocation in iteroparous, simultaneously hermaphroditic polychaete worms that are obligate outcrossers and alternate sex roles in subsequent reproductive events. We exposed focal hermaphrodites to weekly changes in mating opportunities, varying either their opportunities to mate as both males and females or competition for the male role (controlling for density). Finally, we exposed worms to simulated weekly changes in mating opportunities by manipulating chemical signals hermaphrodites use to assess partner and/or rival numbers.

Results showed that wherever either real or simulated opportunities to mate as males, hermaphrodites produced fewer eggs, irrespective of density, suggesting no preference for the female role.

These results support theoretical predictions on sex allocation plasticity in hermaphrodites, and show that hermaphrodites may have a preferred sex role. These results have implications for understanding the evolutionary transitions hermaphroditism/separate sexes.

Poster session B - MAX 413

Experimental evolution of male harm and female resistance in *Callosobruchus maculatus*. (51666)

Eduardo Rodriguez-Exposito, Francisco Garcia-Gonzalez.

Doñana Biological Station, Spanish Research Council CSIC; Centre for Evolutionary Biology, School of Animal Biology, Nedlands, University of Western Australia.

The interests of the two sexes when it comes to reproduction are expected to diverge in species that are not genetically monogamous. This sexual conflict can lead to sexually antagonistic coevolution. Theory suggests that the intensity of sexual selection and sexual conflict should modulate this coevolutionary process, but empirical evidence for sexually antagonistic coevolution is limited to a few species. The bean beetle *Callosobruchus maculatus* is a common model system in the study of sexual conflict. The genitalia of males in this species exhibit spines that damage the female reproductive tract. As a result, females are expected to develop counter-adaptations to minimize the costs imposed by mating, and indirect evidence for this evolutionary response comes from comparative studies across species in the genus. We have used experimental evolution to assess the evolution of male harm and female resistance in populations of bean beetles in which sexual selection and conflict was present or absent. Divergence in male harmful adaptations was analyzed by investigating fitness (Lifetime Reproductive Success) in females from outside the selection experiment that were mated to males from the selection treatments. The impact of sexual selection and conflict on the evolution of female resistance was also assessed.

Poster session B - MAX 413

Investigating the contribution of different developmental and breeding ecologies to mediating sexual conflict in laboratory populations of *D. melanogaster*. (52015)

Avani Mital.

Jawaharlal Nehru Centre for Advanced Scientific Research.

Inter-locus sexual conflict arises over traits that are expressed during reproductive interactions between the two sexes and have different fitness consequences for them. Reproductive fitness is determined by traits expressed in adults, largely shaped by their developmental ecology. Ecological changes experienced by an organism during development as well as in the adult stage influence reproductive traits. Many studies have examined the impact of different adult ecologies (levels of intra-sexual competition) on sexual conflict, using experimental evolution. Our work focuses on studying differences in sexual conflict between two types of lab-adapted *D. melanogaster* populations that experience different ecologies, both during development and as adults during breeding; one is selected to a) develop faster, and b) reproduce sooner, than the other. Our results suggest a large contribution of reduced body size (a correlated response to selection on rapid development) to changes in sexual conflict. Additionally, we are attempting to determine the effect of different breeding ecologies on sexual conflict, given large differences in mating and courtship rates between our experimental populations. To understand the specific roles played by these selection pressures, we are also studying populations experiencing completely relaxed selection for rapid developmental, but either 'control' or 'selection' breeding ecology.

Poster session B - MAX 413

Intralocus sexual antagonism in a hermaphroditic flatworm (52056)

Anna K. Nordén, Jessica K. Abbott.

Section for Evolutionary Ecology, Department of Biology, Lund University.

Sexual antagonism occurs when the same allele for a gene has opposite fitness effects for females and males. Although generally studied in sexual organisms, sexual antagonism may occur in hermaphrodites and may be one means to maintain genetic variation. To investigate this, we measured the response to sex-limited evolution in populations of the flatworm *Macrostomum lignano* (a free-living flatworm) to determine if hermaphrodites can evolve sex-differentiated chromosomes. A GFP locus incorporated into the worm's DNA is used as a dominant sex-determining gene by letting it pass through either eggs ('female' treatment) or sperm ('male' treatment) in each generation. After ten generations we measured the response in each treatment with a fitness assay. Additionally, we used a standard paternal half-sib design to measure sexually antagonistic genetic variation in *M. lignano*, allowing us to look at the heritability of fitness via male and female sex roles. We present data on the response to sex-limited experimental evolution as well as the heritability of fitness via male and female sex roles. Preliminary data suggest that sexually antagonistic genetic variation in populations of *M. lignano* is heritable, and that there is a negative relationship between the heritability of fitness via male and female sex roles.

The demographic consequences of evolution of female polymorphisms in damselflies (52065)

Yuma Takahashi, Suzuki Noriyuki, Masakado Kawata.

Tohoku University; Rissho University.

The effect of evolutionary changes in traits and phenotypic diversity on ecological dynamics has received much theoretical attention. However, the mechanisms and demographic consequences in the natural condition are largely unknown. Theoretical model incorporating key features of the sexual interaction suggests that the evolution of female-limited color polymorphism in damselflies can alter demographic dynamics by relaxing sexual conflict. Field data and mesocosm experiments using a damselfly *Ischnura senegalensis* demonstrates that the evolution of increased phenotypic diversity reduces overall fitness costs to females from sexual conflict, which in turn increases productivity, density and stability of a population. Here we analyzed the further ripple effects the evolution of female color polymorphisms on demographic dynamics, such as distribution range and extinction risk, in some damselfly genera. Irrespective of genus, polymorphic species have wider distribution ranges than monomorphic species. The extinction risks of polymorphic species were lower than that of monomorphic ones. Our study suggests that increased phenotypic diversity can enhance population sustainability and thereby influence community dynamics and macroevolutionary processes.

Female limited X-chromosome evolution reveals non-additivity of sexually antagonistic traits (52099)

Jessica Abbott, Katrine Lund-Hansen, Edward Morrow.

Lund University; University of Sussex.

The concept of sexual antagonism has become key to our understanding of sex chromosome evolution, with the X chromosome being of particular interest for a number of reasons. X-linked loci are known to contribute to the evolution of complex traits, the X is expected to be a hotspot for sexual antagonism, and there are clear predictions regarding the dominance properties of X-linked sexually antagonistic loci. We have therefore carried out a female-limited X-chromosome (FLX) evolution experiment in *Drosophila melanogaster*, where expression of the wildtype X has been restricted to females for over 30 generations with the help of an FM balancer chromosome. We had two aims with this experiment: to quantify the nature and magnitude of the response to sex-specific selection on the X, and to determine whether X-linked sexually antagonistic loci are preferentially non-additive in nature. We found that a number of traits that have previously been characterized as sexually antagonistic responded to the selection, including fitness, body size, and gene expression. By comparing females that were heterozygous and homozygous for the evolved X's we also show that many

traits showed evidence of non-additivity. We thereby confirm many of the predictions about the genetic architecture of X-linked traits.

Poster session B - MAX 413

Divergence of *Drosophila melanogaster* populations in female sensitivity to sex-peptide (52107)

Kristina Wensing, Claudia Fricke.

Institute for Evolution and Biodiversity, University of Münster.

Sexual conflict is hypothesised to be an important driver of divergence in reproductive traits between conspecific populations. Female *Drosophila melanogaster* pay a fitness cost due to multiple mating that is mainly caused by receipt of the sex-peptide. This short peptide is produced in the male accessory gland and transferred to the female at mating. Previous research has shown that females can evolve resistance against male harm however the extent to which *D. melanogaster* populations might diverge in their sensitivity to sex peptide has not been studied before. Here I fill this gap in our knowledge by testing for divergence in female resistance to sex-peptide by phenotypically comparing cost of mating effects in different *D. melanogaster* populations. I exposed females of three different populations continuously to standardised males unable to produce sex-peptide or control males throughout their whole life. I measured survival, lifetime reproductive success, and mating frequency and used those variables to calculate and compare a fitness index across the different populations. Divergence in female sensitivity to sex peptide between the different populations may reflect differences in patterns of sexually antagonistic coevolution, underlying genetic variance and/or mating dynamics.

Poster session B - MAX 413

“Exploring the Genetic Basis of Intralocus Sexual Conflict in *Drosophila*” (52175)

Tanya Pennell.

University of Sussex.

Males and females often optimise fitness differently, and can therefore require differential gene expression to reach their respective optimal trait values. When this cannot be achieved, an evolutionary tug-of-war ensues between the sexes, where they select for different alleles at the same genomic locus (known as intralocus sexual conflict, IASC). This acts to maintain alleles in a population that have opposite fitness effects for male and females. Although fitness effects of IASC have been quantified, its genetic basis remains largely unexplored.

We use hemiclonal analysis to create 223 lines of *Drosophila melanogaster*, where a genomic haplotype is shared between individuals within a line. This will enable us to quantify the sex-

specific fitness consequences of expressing such haplotypes, and to identify the level of IASC that exists in our laboratory adapted population. Combined with whole-genome sequencing data from each line, we can also perform a genome-wide association study to identify genes associated with IASC.

Furthermore, I explore how environmental change can impact the level of IASC within our population. This could provide an insight into selection pressures that affect sexually antagonistic genes, and how this might subsequently alter the dynamic of conflict resolution.

Poster session B - MAX 413

Are males in old age still competitive? Age-dependent sexual conflict in *Drosophila melanogaster* (52180)

Hanna Ruhmann, Claudia Fricke.

Institut for Evolution and Biodiversity.

In most species males and females have divergent reproductive strategies. When traits are favored by one sex but cause fitness costs in the other sex, sexual conflict can occur. Evidence is accumulating that not just female but also male age influences reproductive success. We are interested in studying how ageing might affect the expression of a sexual antagonistic trait in males and how this might alter sexual conflict dynamics.

We conducted studies to investigate the reproductive success of ageing males in *Drosophila melanogaster* with a special focus on accessory gland proteins and their known induced phenotypic responses. We focused on the sex peptide and ovulin, as particularly sex peptide is involved in mediating sexual conflict between the sexes. Using the ELISA method we quantified how much of these proteins males of different ages transfer to females and detected significant differences between the ages.

We determined that the ability to gain a first mating with a virgin female, to prevent females from remating and the competitive power of a male changes significantly over his lifetime. Hence age significantly affects male reproductive success, however this decrease is not constant across male age and already shows a first dip in intermediate aged males.

Poster session B - MAX 413

Sexually antagonistic genetic variation in a simultaneous hermaphrodite (52237)

Tim Janicke, Elodie Chapuis, Stefania Meconcelli, Nicolas Bonel, Patrice David.

Centre d'Ecologie Fonctionnelle et Evolutive, CNRS-UMR 5175 ; IRD, UMR 186 "Résistance des plantes aux bioagresseurs"; Department of Life Sciences and Systems Biology, Università di Torino; Departamento de Biología, Bioquímica y Farmacia, Universidad Nacional del Sur, Bahía Blanca.

Simultaneous hermaphrodites express both sex functions at the same time offering unique forms of sexual conflict to arise. These include conflicts over the sex role that both interacting individuals adopt when mating and the manipulation of the partners' sex allocation by the sperm donor. Over the last two decades, significant strides have been made in characterizing these and other sexual conflicts in simultaneous hermaphrodites but until now very little is known about intra-locus sexual conflicts in these organisms, which are thought result from opposing fitness effects of an allele when expressed in a sperm donor and a sperm recipient. Here, we report an empirical test of intra-locus sexual conflict in the simultaneously hermaphroditic freshwater snail *Physa acuta*. We explored pre- and post-copulatory reproductive performance of the male and female sex function and tested for sexually antagonistic genetic variation of several fitness components. This was done under varying levels of food availability using a full-sib breeding design.

Poster session B - MAX 413

Intralocus sexual conflict and the evolution of sexual dimorphism - a large scale approach (52312)

Maja Tarka, Christophe Pelabon, Thomas F. Hansen, Bernt-Erik Sæther.

Center for Biodiversity Dynamics, Norwegian University of Science and Technology (NTNU), Trondheim, ; Centre for Ecological and Evolutionary Synthesis, University of Oslo, Oslo, Norway.

Males and females often have different adaptive peaks due to differences in reproductive roles. However, most traits are controlled by the same genes in both sexes, which manifests as strong cross-sex genetic correlations. Such correlations are expected to hamper the independent evolution of each sex towards its adaptive peak, causing intralocus sexual conflict. Mitigation or resolution of intralocus sexual conflicts can be achieved by a decreased cross-sex genetic correlation and hence the evolution of sexual dimorphism. However, very few studies have investigated the relationship between sexual dimorphism and the strength of cross-sex genetic correlations. Furthermore, genomic imprinting and differences in genetic variance among sexes could also explain the evolution of sexual dimorphism despite strong cross-sex genetic correlation, but these hypotheses have never been broadly tested. We investigate these different hypotheses using published data on sexual dimorphism and additive genetic variances and cross-sex covariances. In these analyses, we take particular care of using proper standardization methods and accounting for errors of the estimates.

Poster session B - MAX 413

Parallelism in sex-biased gene expression (52361)

Kirsten M Jalvingh, Zoe Dumas, Tanja Schwander.

University of Lausanne.

Sexually antagonistic selection can cause gene expression differences between males and females in order to help resolve genetic conflict. The type of genes that can be subject of sexually antagonistic selection range from genes associated with sex-specific tissues to genes related to life-history and behavior. However, some genes may display similar sex-biased expression across related species, while others are under sexually antagonistic selection only in isolated species. In this study we explore sex-biased gene expression in the Timema clade of stick insects. Using RNA-seq we quantify sex-biased gene expression in four different species in the same clade, to detect parallel and divergent patterns in gene expression differences between males and females. This allows us to examine which gene networks are consistently associated with sex-biased gene expression and which ones are subject to species-specific sexual selection.

Poster session B - MAX 413

Not a fair share; female house finches build and protect the nest from parasites using cigarette refuse, butt... (52385)

Montserrat Suárez-Rodríguez, Constantino Macías Gracia.

Instituto de Ecología, Universidad Nacional Autónoma de México.

Several species exhibit phenotypic traits which apparently represent recent adaptations to urban environments. One potential adaptation in *Passer domesticus* and *Carpodacus mexicanus* is the use of discarded cigarette butts to line their nests and thus reduce ectoparasite load. In *C. mexicanus* butts in nests promote growth but also genotoxic damage to nestlings. As parents are in contact with butts during nest construction and attendance, we predicted that they also exhibit genotoxicity at an intensity that should co-vary with exposure, itself a function of 1) amount of cigarette butts brought to the nest, and 2) parental behaviour. Analyses of blood samples taken at four times between egg-laying and chick fledging revealed that damage in female *C. mexicanus*, which do all the building, is positively associated with the amount of cigarette butts in the nest, and is greater shortly after building the nest than later on. Males, which do not participate in nest-building, showed much less genotoxic damage. It is uncertain whether genotoxicity has long-term negative consequences for short-lived passerines, but if it does, then the way parental roles are partitioned between sexes in this species would mean that the cost of this urban antiparasite strategy is largely borne by the females.

Poster session B - MAX 413

Do asymmetric paternal effects on offspring size reveal male manipulation of maternal investment? (52386)

Yolitz Saldivar Lemus, Constantino Macías García.

Instituto de Ecología, Universidad Nacional Autónoma de México.

Where embryos can influence maternal investment, paternal genetic manipulation may evolve, prompting the evolution of maternal countermeasures. A way of detecting such coevolution is to examine crosses between populations, as asymmetric embryonic growth may occur upon secondary contact if the coevolution is no longer matched. Appropriate models include matrotrophic fish, where maternal investment is an important component of life history. We sought evidence of asymmetry in reciprocal crosses between two distant populations of the Amarillo fish (*Girardinichthys multiradiatus*): Zempoala (Z) and San Matías (M). Whereas offspring from M females and Z males were indistinguishable from their controls (M-M), offspring from Z females and M males were bigger and heavier than their controls (Z-Z). Hybrid vigor cannot explain this difference, since M-Z offspring were smaller than those of Z-M. It is also unlikely that Z females found M males more attractive and thus preferentially invested on their offspring, because females from both populations prefer sympatric males. Our data agree with expectations if antagonistic coevolution in M promoted enhanced male epigenetic manipulation of female reproductive allocation coupled with enhanced female resistance, in comparison with Z. This preliminary conclusion calls for evaluation of the pattern of expression of genes responsible for embryonic growth.

Poster session B - MAX 413

Temporal dynamics of sex-biased gene expression in an annual plant (52412)

Guillaume Cossard.

University of Lausanne.

Most flowering plants are hermaphroditic, but separate sexes have recurrently and independently evolved in about half of angiosperm families. The separation of sexes in plants, as in animals, is associated with two potentially related processes: the frequent evolution of sex chromosomes; and the evolution of sex-biased expression. Both processes are thought to allow a divergence in phenotype between males and females, either by confining sexually antagonistic genes to the non-recombining region of sex chromosomes, or through the differential expression of the same genes between sexes. A key question of the latter process concerns when during development differential gene expression first becomes evident. This is particularly interesting in plants that lack a germ line: divergence in phenotype might be expected to show itself most strongly only during and after flowering, particularly if secondary sexual dimorphism is the outcome of different sex allocation patterns between the sexes. Here, we report dynamic patterns of sex-biased gene expression in meristematic tissues using RNAseq, from the seedling stage through to the onset of flowering in the dioecious herb *Mercurialis annua*. We highlight two key results: (I) sexual dimorphism in gene expression occurs prior to flowering; (II) at reproductive stage, the number of male-biased genes dramatically increases.

Poster session B - MAX 413

When caring evens out between the sexes (52452)

Isabel Salome Keller, Olivia Roth.

GEOMAR.

Sexual immune dimorphism evolved upon a resource allocation trade-off between investment into immune defence and sex-specific life-history traits. In conventional parental investment roles males maximize their fitness by allocating resources towards sexual selection while females need to elongate their life span to achieve the same gain. The larger this differential allocation between males and females the more pronounced the display of sexual immune dimorphism.

We suggest sexual immune dimorphism to depend on parental investment and thus to diminish if both sexes provide a similar degree of parental investment. Using biparental and maternal mouth-brooding cichlids of Lake Tanganyika we examined the correlation between immune competence and parental investment strategies. Predicting that biparental mouth-brooding species will have a less distinct immune dimorphism than maternal mouth-brooding species consequential to the mentioned resource allocation trade-off. Cellular immune parameter measurements and immune gene expression of three biparental and four maternal mouth-brooding species suggest sexual immune dimorphism to disappear in biparental mouth-brooders and a generally higher immune competence baseline than in maternal mouth-brooders. Those results imply that parental investment levels out sexual immune dimorphism and that strength of immune system might be coupled to parental investment levels.

Poster session B - MAX 413

Is sexually antagonistic selection causing the replacement of a sex chromosome system in *Podisma pedestris*? (52461)

Hannes Becher, Richard A Nichols.

Queen Mary University of London, School of Biological and Chemical Sciences.

We describe the identification of sex chromosome-linked markers in *P. pedestris*, in order to address key questions about the evolution of sex chromosomes, by studying their penetration through hybrid zones. This species has an ancestral X0 sex chromosome system, and a derived neo-X/neo-Y system produced by an X-to-autosome fusion event. The analysis of sex-chromosome clines in the hybrid zone can reveal if neo-Y chromosomes have been subject to sexually antagonistic selection, which would fuel their penetration into the ancestral race. Thus, we can ask if we are witnessing the replacement of a sex chromosome system in this alpine grasshopper driven by this form of selection.

Poster session B - MAX 413

Pollen dispersal affects the evolution of sexual dimorphism (52503)

Jeanne Tonnabel, Agnès Mignot, Ophélie Ronce, Isabelle Olivieri.

University of Lausanne; Institut des Sciences de l'Evolution de Montpellier; Institut des Sciences de l'Evolution de Montpellier; Institut des Sciences de l'Evolution de Montpellier.

Sexual antagonist selection is deeply studied in animals. Whether the same selective pressures, such as male-male competition, also shape sexual dimorphism in plants is open to question. Here, we test the hypothesis that male-male competition in plants can be mediated by pollen dispersal strategies which contrasted evolution can consequently affect the evolution of sexual dimorphism. Conversely to wind-pollinated species, we expect, in insect-pollinated species, that males displaying morphologies more similar to females would be more efficient competitors due to insect recognition mechanisms. Using a newly reconstructed phylogeny for the genus *Leucadendron* (Proteaceae) and robust methods that account for phylogenetic uncertainty, we show that both the degree of sexual dimorphism and pollen dispersal strategies are convergent across the evolutionary history of the genus. By comparing models of trait evolution including, or not, correlated evolution, we show that insect-pollinated species tend to evolve decreased sexual dimorphism compared to wind-pollinated ones. This macro-evolutionary study suggests that pollen dispersal strategies through male-male competition can affect sexually antagonist selection. At the micro-evolutionary scale, we are currently studying sexually specific selective gradients in a population of the species *Leucadendron rubrum* using genetic and spatial data to estimate male and female fecundities.

Poster session B - MAX 413

The architecture of sexually antagonistic genetic variation (52720)

Karl Grieshop.

Uppsala University .

Intralocus sexual conflict (IaSC) is an emergent property of having two sexes sharing one genome. Because males and females experience different selection pressure(s), there exist sexually antagonistic (SA) loci at which alternative allelic variants are favored oppositely between the sexes. Despite growing interest over recent decades, answers to some of the most basic questions regarding IaSC remain unclear. We previously documented a population of the seed beetle, *Callosobruchus maculatus*, to be dominated by SA genetic variation (having a negative intersexual genetic correlation for fitness). We have now generated a panel of inbred lines from that SA population, with which we have performed a diallel cross—the most powerful quantitative genetic approach to partitioning variance among its many origins. The data generated from this breeding design will provide insight to several of the voids in our understanding of IaSC, such as the extent to which the underlying genetic architecture for fitness is shared between the sexes, the extent to which that shared genetic architecture is SA, whether or not variances in the additive genetic contribution to fitness are different between the sexes, and the process by which IaSC might maintain genetic variation for fitness.

Poster session B - MAX 413

Males increase their fitness with high MHC diversity whereas females do not: sexually antagonistic selection on immunity genes? (52734)

Jacob Roved, Dennis Hasselquist, Bengt Hansson, Helena Westerdahl.

Lund University.

Host-pathogen interactions has rendered much recent interest, with a number of hypotheses proposed to explain the complex dynamics and selection patterns on hosts and their pathogens. The highly polymorphic genes of the major histocompatibility complex (MHC) have been assigned a major role in the evolution of host defense against pathogens. Heterozygosity in MHC genes has been hypothesized to be favorable conferring protection to a wider range of pathogens. The recent development in DNA sequencing techniques now enables screening of MHC genes also in animals with many loci and high diversity. We have used massively parallel amplicon sequencing to investigate the impact of within-individual MHC class I variation on Darwinian fitness in a wild population of great reed warblers (*Acrocephalus arundinaceus*). The number of MHC alleles per individual predicted relative offspring survival, but with opposite effects between the sexes, suggesting sexually antagonistic selection. Males showed a significant positive relationship between MHC allelic diversity and the proportion of recruiting offspring, whereas in females this relationship tended to be negative. A possible explanation for the sexual antagonism could be that females with high MHC allelic diversity are more susceptible to autoimmune reactions, which may have adverse effects on parental care and maternal effects.

Poster session B - MAX 413

Evolutionary consequences of male attraction to warning patterns in mimetic butterflies. (52895)

Richard Merrill, Chris Jiggins.

University of Cambridge; University of Cambridge.

The warning patterns of *Heliconius* butterflies are a textbook example of ecological adaptation. Because predators learn to associate particular patterns with unpleasant experiences, an individual's risk of predation decreases as the local density of its warning pattern increases. However, *Heliconius* warning patterns are known for their diversity and the establishment of entirely new phenotypes is paradoxical under strict number-dependent selection. During periods of relaxed selection, drift may allow new variants to rise above a threshold density until mimicry selection takes over. Here, I consider an alternative hypothesis. We have shown that male *Heliconius* use warning patterns as a mating cue. As a result, mated females may suffer fitness costs if these cues lead to harassment by males during oviposition or foraging. I present a series of experiments testing whether novel patterns may allow females to resist costs imposed by males. In addition, individual-based simulation models, informed by the ecology and genetics of *Heliconius*, imply that male harassment could have played an important role in the diversification of warning patterns. Sexually antagonistic selection appears to be a viable alternative (or addition) to genetic drift to explain the evolution of novel warning patterns in *Heliconius* butterflies.

Evolution of interacting reproductive behaviours in burying beetles (*Nicrophorus vespilloides*) (51749)

Nick Royle, Mauricio Carter, Alastair Wilson, Emma Davey, Allen Moore.

University of Exeter; University of Georgia.

Reproductive behaviours involve social interactions not just between males and females (inter-sexual), but also between individuals of the same sex (intra-sexual). Social interactions provide the potential for Indirect Genetic Effects (IGEs), which occur when genes expressed in one individual affect how genes are expressed in an interacting individual and can affect how traits evolve. However, few studies have considered IGEs arising from both inter-sexual and intra-sexual interactions simultaneously. Here we use experimental populations of burying beetles (*Nicrophorus vespilloides*) that have experienced directional selection on mating rate for 18 generations to test for the presence of IGEs on male reproductive behaviour under different male-male competitive scenarios. Males selected for high mating rate are more socially sensitive to male-male competition than males from lines selected for low mating rate. We found that Direct Genetic Effects (DGEs) are more important sources of genetic variation in mating rate of males than the genetics of social partners (IGEs), but the reverse is true for resource-holding (dominance) behaviours (IGEs are more important than DGEs). Our results highlight the importance of considering social context in order to understand how reproductive traits evolve in species with intra-sex competition.

Once-a-year coordinated dispersal in subsocial beetles reduces inbreeding rate (51890)

Ally Harari, Hadass Steinitz, Martin Tremmel, Daphna Gottlieb, Yael Lubin.

The Volcani Center; 2. Haifa University, Israel ; 3. Ben Gurion University of the Negev, Israel.

Sub-social female beetles of the haplodiploid palm-seed borer, *Coccotrypes dactyliperda*, enter a date seed and establish a colony in which up to five generations may overlap and sisters help tend the young. In most cases, females that leave their natal seed are already mated, but if virgin, the foundress lays a small clutch of eggs that develop into males. After mating with her son, her daughters mate with their brothers, thus a high rate of inbreeding is common. In accordance with Hamilton's (1967) LMC prediction a highly female-biased sex ratio is expected. However, once-a-year, in various populations and coinciding with the high availability of date seeds dropping from the trees, the beetles' behavior is completely changed: Single-sex cohorts of males or females are produced and larvae do not share the typical, common breeding gallery, but each bores its own tunnel and pupates in its own excavated cell. Beetles leave the seed as virgins, outbreed on the way to or in a new seed and,

again, in accordance with Hamilton's (1967) LMC prediction, produce significantly less female biased offspring in the following generation.

Poster session B - MAX 413

Kin selection and male-male competition: geographic variation in male-male lethal fighting in a social spider mite (51936)

Yukie Sato, Martijn Egas, Maurice Sabelis.

University of Tsukuba; University of Amsterdam.

Inclusive fitness theory predicts that the intensity of male-male fight over mates varies with relatedness of the males. Specifically, assuming that competition among males is local, the relationship between aggression and relatedness is predicted to be dome-shaped. However, this prediction has rarely been tested in natural populations. Here, we study the relation between relatedness and male-male aggression in colonies of the social spider mite *Stigmaeopsis miscanthi*. This mite forms colonies on Chinese silver grass, constructs woven nests on the undersurface of grass leaves, and lives within the nests in kin groups. Inside nests, males may kill rival males to establish their own harem. Male-male aggression varies among populations. We measured male-male aggression in 25 mite populations across a wide geographic range between Taiwan and Japan, using winter harshness as a proxy of genetic relatedness among nest members in this mite species. Our results show that male-male aggression peaks at intermediate relatedness. This result conforms qualitatively to predictions from inclusive fitness models that incorporate local competition, thereby highlighting the importance of the scale of competition.

Poster session B - MAX 413

Learning to tell the differences: When can mate-choice copying facilitate hybridisation? (52019)

Gonçalo S. Faria, Inês Fragata, Pedro Simões, Sofia G. Seabra, Marta A. Santos, Margarida Matos, Susana A. M. Varela.

CE3C – Centre for Ecology, Evolution and Environmental Changes, FCUL.

Mate-choice copying (MCC) by females occurs when they obtain information about the performance of a male, increasing or decreasing their preference for that male, accordingly. MCC has been suggested to cause reproductive isolation between populations with different mate preference traditions. However, the opposite scenario can also occur, if invader individuals copy the choices of natives, leading to hybridization events. We studied the hybridization hypothesis using different populations of *Drosophila subobscura*, originated from the extremes of the species European latitudinal cline: Portugal (PT) and the Netherlands (NL). Half of the females received positive social information about a male from their own population and the other half about a male from a control (lab) population. At generation six,

we saw that females had an innate preference for the males of their own population, and that they did not copy. Only after four more generations of convergent adaptation in the lab, PT females, but not NL, started to copy. This suggests that MCC does not facilitate hybridization at an early phase after invasion, and that it may be selected in nature only under specific ecological and social contexts, supporting the hypothesis that MCC is most advantageous when males are phenotypically similar.

Poster session B - MAX 413

The effect of relatedness structure and sexual conflict on the evolution of inbreeding avoidance and preference (52096)

Alexander Duthie, Jane Reid.

University of Aberdeen.

When selecting mates, individuals are widely assumed to avoid breeding with relatives, but theory highlights that inbreeding can increase an individual's inclusive fitness. Inclusive fitness theory predicts sexual conflict over inbreeding such that avoiding inbreeding is often beneficial for females, but not males. Nevertheless, predictions concerning inbreeding conflict are limited by highly restrictive assumptions regarding relatedness structure within populations. We first extend previous theory to show that relatedness structure affects whether inbreeding conflict is predicted when individuals choose mates. We then model a small population of potentially inbreeding individuals in which inbreeding conflict is resolved either in favour of females or males under conditions of biologically realistic relatedness, inbreeding depression in offspring survival, and negative direct selection. We show that inbreeding avoidance often evolves when inbreeding conflict is resolved in favour of either sex. In contrast, inbreeding preference is predicted to be rare and, counter-intuitively, restricted to populations in which inbreeding conflict is resolved in favour of females. Interestingly, this suggests that inbreeding conflict may arise where females benefit by actively preferring inbreeding but males benefit by mating randomly. We thereby provide new predictions regarding sex-specific evolution of inbreeding avoidance and preference and their dependence on resolutions of sexual conflict.

Poster session B - MAX 413

Sexual conflict over laying patterns in the burying beetle *Nicrophorus vespilloides* (52117)

Lucy Ford.

University of Edinburgh.

Asynchronous hatching (when the offspring from a single reproductive event hatch over an extended period of time) occurs in the burying beetle *Nicrophorus vespilloides*, an insect which provides parental care. Sexual conflict occurs when males and females have conflicting

optimal reproductive strategies. Each parent will try to minimise the amount of parental care it provides, at the expense of the other parent, as long as the total care provided is sufficient for the brood to survive. The sexual conflict hypothesis for the evolution of asynchronous hatching predicts that females may adjust laying patterns to increase male parental effort relative to female effort. To investigate the influence of laying pattern on the duration of care provided, I produced synchronous (20 larvae at 0h, with 0h being the time at which the caring individuals' larvae begin to hatch) asynchronous (10 larvae at 0h, 10 larvae at 24h) and highly asynchronous (10 larvae at 0h, 10 larvae at 48h) broods experimentally. The broods were raised with males either present or absent, and the time of desertion was recorded for each parent. I assessed the fitness consequences for the parents and offspring were using measurements of longevity, parental mass change and offspring pronotum width.

Poster session B - MAX 413

Indirect Genetic Effects on Reproductive Behaviour and Morphology (52166)

Lucas Marie-Orleach, Nadja Burri, Pierick Mougnot, Aline Schlatter, Dita B. Vizoso, Lukas Schärer.

Evolutionary Biology, Zoological Institute, University of Basel, Basel, Switzerland.; General and Systematic Zoology, Museum and Zoological Institute, Ernst Moritz Arndt University of Gr.

The trait values expressed by an individual depend on both its genes and the encountered environmental conditions. Because the latter often encompass social interactions with conspecifics, an individual's phenotype may possibly be affected by the specific genotypes of its partners (i.e., "indirect genetic effects"), and can potentially result in a conflict of interest between the social partners. In two experiments where we crossed distinct genetic lines of the free-living flatworm *Macrostomum lignano* we found clear evidence of indirect genetic effects on morphological and behavioural reproductive traits. The genetic line of the partner significantly affected the focal's testis size — which varied up to 2.4-fold — and its propensity to copulate and to perform the postcopulatory suck behaviour that has been postulated to be involved in sexual conflicts over the fate of received ejaculate. Interestingly, we found not indirect genetic effects on copulation duration, a trait compounded from both partners. Overall, our results show that the expression of reproductive traits can be affected by the genotype of social partners. We discuss how such indirect genetic effects are expected to alter the evolutionary trajectories of reproductive traits and mediate the interplay between social evolution and sexual selection.

Poster session B - MAX 413

Epigenetic machinery underlying paternal genome elimination in *Planococcus citri* (52210)

Stevie Anne Bain, Laura Ross.

Paternal genome elimination is a genomic imprinting phenomenon found among several insect species, including the citrus mealybugs (*Planococcus citri*). In sons, the paternally inherited set of chromosomes is silenced and then eliminated from the germline. Since males can only pass on their genetic information through daughters, it is in their interest to female-bias their offspring's sex ratio. However, females have a genetic transmission advantage through sons, as sons can only pass on their maternally inherited chromosomes to any offspring they sire. Thus, a sexual conflict occurs. In an evolutionary context it seems most likely that a maternal factor underlies the process of PGE, since females benefit from a transmission advantage and males suffer a disadvantage. Genomic imprinting in *P. citri* appears to be regulated by the same epigenetic machinery involved in mammalian silencing and imprinting (histone modifications and methylation), but the molecular details remain poorly understood. Here we study the parent-of-origin specific epigenetic modifications involved using whole genome bisulphite sequencing and immunostaining for histone modifications throughout development. These data help to understand how paternal and maternal chromosomes are distinguished in order to allow elimination of only those paternally inherited by sons.

Poster session B - MAX 413

Sexual antagonism, cryptic bias, and the evolution of social hormones in bank voles (52397)

Mika Mikkonen, Esa Koskela, Eija Lönn, Tapio Mappes, Phill Watts.

University of Jyväskylä; Simon Fraser University; University of Oulu.

Recent evidence indicates that sexual conflict can result in adaptive production of offspring that will minimize the associated fitness costs. However, little is still known about how individuals optimize their reproductive investment in light of the antagonistic fitness effects on offspring sex. To test this question, we bred male and female bank voles (*Myodes glareolus*) to produce offspring that differed in the length of the arginine vasopressin receptor (*avpr1a*) and oxytocin receptor (*oxtr*) promoter-associated microsatellites because these allele lengths regulate their expression. These hormones and receptors affect a variety of socio-reproductive behaviours. We measured the reproductive success and survival of animals with contrasting genotypes in field enclosure experiments (focusing on the effects of *avpr1a* and *oxtr* separately), where the social environment was manipulated (density and operational sex ratio). By mapping the parental origins of the alleles in the offspring, we found that both *avpr1a* and *oxtr* are selected towards sex-specific optima, indicating they are sexually antagonistic. Furthermore, cryptic sex-ratio bias according to the allele length reduced the associated fitness costs through biased production of the more beneficial sex. We will discuss how sexual antagonism and cryptic bias maintain genetic variation in genes important for modulating social behaviours in reproduction.

Poster session B - MAX 413

The role of male-male relatedness on sexual interactions in *Drosophila melanogaster* (52505)

Sally Le Page, Irem Sepil, Pau Carazo, Stuart Wigby.

University of Oxford; University of Valencia.

The importance of relatedness in social interactions has long been known, yet it is only recently that the ideas of kin selection have been applied to the field of sexual selection. Male *Drosophila melanogaster* display a 'sexual altruist' strategy, competing less frequently over females when competing against their brother than against an unrelated male. However, when two brothers and one unrelated male are simultaneously presented to the (unrelated) female, the unrelated male has a paternity advantage – an unexpected and as yet unexplained phenomenon.

To determine the evolutionary stability of this advantage, we are disentangling the potentially conflicting effects of male-male competition and female choice that can occur at both the pre- and post-copulatory stages. Whilst we are increasingly seeing effects of relatedness on sexual interactions, it is not yet known whether *D. melanogaster* use genetic cues or familiarity/environmental cues to discriminate between individuals.

The preliminary data suggest that unrelated males do not experience a mating advantage in a sequential mating system, which may make the 'sexual altruist' strategy more stable, and we are currently elucidating the mechanisms of kin recognition in this species.

Poster session B - MAX 413

Is dispersal a good strategy? Sibling competition, dispersal and fitness outcomes in humans (52605)

Aïda Nitsch, Charlotte Faurie, Virpi Lumma.

Institute for Advanced Study in Toulouse; University of Montpellier 2, Institute of Evolutionary Sciences of Montpellier; University of Sheffield.

Determining the fitness consequences of dispersal and its interplay with sibling interactions is pivotal for understanding the evolution of family living. On the one hand dispersal, could be a strategy to avoid sibling competition, thereby increasing access to competing resources. On the other hand, dispersal could mainly benefit philopatric individuals through a decrease of the intra-familial competition in the natal territory. These two explanations of dispersal imply different fitness outcomes between philopatric and dispersing siblings. Moreover, the intensity of intra-familial competition is likely to influence the fitness outcomes of each strategy. However, studies investigating the fitness outcomes of dispersal according to the intensity of intra-familial competition are lacking. Using a large demographic dataset on humans from preindustrial Finland (n=4,000), we investigated the fitness consequences of dispersal on different indicators of lifetime reproductive success according to sex-specific birth rank. Contrary to our predictions, the negative effect of same-sex elder siblings on reproductive success was similar between philopatric and dispersing individuals for both

males and females. Overall, these findings do not support the hypothesis that the costs and benefits of dispersal vary with intra-sex birth rank. This study has important implications for the evolution of family dynamics, dispersal and sibling interactions.

Poster session B - MAX 413

Male and mutual sexual imprinting: what strategy is the best? (52617)

Miguel Gomez.

University of Manchester.

Sexual imprinting occurs when individuals acquire a preference for mates with a trait observed on a member of the parental generation. Sexual imprinting can have different strategies, depending on which group of the parental generation individuals imprint on. Different strategies have different effects on males and females. When female imprinting evolves, imprinting on their fathers trait allow females to choose the fittest mate. However, the way in which male and mutual sexual imprinting evolves is not well understood. We developed a model to analyse under which circumstances male and mutual sexual imprinting evolves, and which strategies allow individuals to choose the fittest mate. We found that for males, maternal imprinting is the most likely strategy to evolve. When mutual imprinting evolves, is more likely that both sexes imprint on their fathers. We discuss the importance of male and female imprinting interaction, sex-specific recognition and fitness gains in the evolution of the sexual imprinting strategies. Finally, we suggest variability in the population as a novel way for mutual imprinting to evolve.

Poster session B - MAX 413

Molecular mechanisms of post-copulatory sexual selection in a leaf-cutting ant (52669)

Joanito Liberti, Ryan Dosselli, Morten Schiøtt, Boris Baer, Jacobus J. Boomsma.

Centre for Social Evolution, University of Copenhagen; Centre for Integrative Bee Research, University of Western Australia.

The queens of polyandrous lineages of ants combine promiscuous mating with strict sexual partner commitment when storing sperm for a life-time of up to two decades without re-mating. This poses the evolutionary dilemma that sperm competition may benefit queen fitness just before sperm enters the spermatheca, but will decrease her life-time reproductive success when it continues after irreversible storage. In an earlier study it was shown that this dilemma in the ant *Atta colombica* is resolved by initially allowing mutual sperm incapacitation between ejaculates, but terminating that via secretions of the queen sperm storage organ*.

We used a controlled artificial insemination experiment and transcriptomics/ proteomics

techniques to identify genes and proteins mediating the interaction between rival ejaculates and between the sperm and seminal fluid components of ejaculates with spermathecal fluid. This allowed us to unravel a set of proteins that mediate post-copulatory sexual selection in an experimentally predictive manner.

* Den Boer, S.P.A., Baer B. & Boomsma J.J. (2010): Seminal fluid mediates ejaculate competition in social insects. *Science* 327, 1506-1509.

Poster session B - MAX 413

An explicit test for the relative role of pre- versus postcopulatory inbreeding avoidance in an acridid grasshopper (52840)

Michael Haneke-Reinders, Holger Schielzeth, Tim Schmoll, Klaus Reinhold.

Department of Evolutionary Biology, University of Bielefeld.

Matings between relatives often lead to inbreeding depression that is ultimately caused by the expression of recessive deleterious alleles. Kin-recognition is an important mechanism to avoid inbreeding. We already know inbreeding avoidance by kin-recognition in many vertebrates but kin-recognition is also observable in insects like ants, bees (social context) and field crickets (mating context). Although grasshoppers often occur in high densities, the avoidance of inbreeding may also be important due to limited dispersal and large family sizes. Here we investigated simultaneously the relative roles of pre- versus postcopulatory mechanisms of inbreeding avoidance in the rufous grasshopper *Gomphocerus rufus*. We caught grasshopper nymphae in the field and bred full siblings under controlled laboratory conditions. With the F1-generation we performed a double-mating experiment: We offered each female a full-sibling or an unrelated male and (if copulation occurred) we offered a second male of the alternative type after one week and analyzed mating behavior (copulation propensity, latency and duration) and paternity allocation using microsatellite analysis. Matings with two unrelated males served as controls. Furthermore, our double-mating experimental design also allows to test for sex-specific repeatabilities in traits like copulation duration where it is unclear by which sex they are controlled.

Poster session B - MAX 414

The ups and downs of interlinked public goods traits (51672)

Adin Ross-Gillespie, Zoé Dumas, Rolf Kümmerli.

University of Zurich; Swiss Federal Institute of Aquatic Science and Technology (EAWAG); University of Lausanne.

Public goods cooperation is vulnerable to freeloaders, which, under appropriate conditions, can drive the loss of an otherwise beneficial trait. Yet, many organisms juggle multiple interlinked public goods and the interactions between these multiple traits can rather

complicate their evolutionary trajectories. We explored conceptually how different forms of linkage between two public goods traits (i.e. uni- or bidirectional stimulation or repression) could influence one another's selection. We then tested some of our predictions in the context of the bacterium *Pseudomonas aeruginosa*'s production of two different iron-scavenging siderophores, whose regulation is known to be hierarchically ordered. We tracked production of the two siderophores in lines experimentally evolved for ~300 generations under different iron-limitation regimes that favour different expression profiles. Strong iron limitation led to decreases in the dominant siderophore (due to freeloaders) and increases in the secondary siderophore (due to derepression), while under moderate iron limitation, the reciprocal pattern did not arise: only the secondary siderophore significantly decreased its expression. Our results confirm that the nature of regulatory inter-connections between public goods traits can significantly modulate the course of their evolution, yet also suggest how we might predict the impacts such complexities will have on phenotypic divergence and community stability.

Poster session B - MAX 414

Molecular and Genetic Mechanisms Underlying Parallel Loss of Seasonal Photoperiodism in Sticklebacks (51941)

Asano Ishikawa, Jun Kitano.

National Institute of Genetics.

In temperate regions, organisms can use photoperiods to reproduce during favorable seasons. When surrounding environments are stable across seasons, some organisms lose their seasonality and elongate their breeding periods. We are investigating the molecular and genetic mechanisms underlying loss of seasonality by using different ecotypes of threespine stickleback. Ancestral marine ecotypes show seasonal migration, whereas derived freshwater ecotypes do not migrate and instead elongate their breeding periods. Our laboratory experiments revealed that maturation of testes is triggered by a shift to long photoperiod in marine populations, but is independent of photoperiods in multiple freshwater populations. Whole transcriptome analysis showed that thyroid hormone-stimulating hormone beta 2 (TSH β 2) exhibit the highest response to photoperiodic changes in marine populations, but that this response was lost in multiple freshwater populations. TALEN-mediated TSH β 2 knockout sticklebacks showed abnormality in testis development, consistent with previous studies showing a substantial role of TSH β 2 in photoperiod-dependent reproduction. In some freshwater populations, cis-regulatory mutations explained some of the difference in TSH β 2 response. To investigate the adaptive significance of loss of seasonality, we plan to manipulate TSH β 2 response by genetically modifying the cis-regulatory region of TSH β 2 and measure the fitness under various environments.

Poster session B - MAX 414

Competition between symbiont species – a mechanism for trait loss? (52012)

University of York.

Poster session B - MAX 414

David Monnin, Natacha Kremer, Clément Berny, H  l  ne Henri, Adeline Dumet,
Yann Voituren, Emmanuel Desouhant, Fabrice Vavre.

Symbioses are long-term inter-specific interactions that form a continuum ranging from parasitism to mutualism. Reactive oxygen species (ROS) are molecules able to mediate symbiotic relationships since they can affect the physiology of both host and symbionts. Although detrimental to many cellular components when in excess, ROS also play a role as part of the immune response to infection by microorganisms. As a consequence, the oxidative homeostasis, i.e. the balance between ROS and antioxidant molecules, may be a key factor underlying the evolution of symbioses. As a dramatic example, the dependence of *Asobara tabida* (Hymenoptera) to *Wolbachia* for oogenesis may be due to a breakdown of oxidative homeostasis resulting from the adaptation of the host to its symbiont (tolerance). Using *Drosophila melanogaster* as a model, we show that experimental manipulations of oxidative homeostasis can decrease *Wolbachia* density and reduce the cost of infection. This suggests that tolerance evolution in insect-*Wolbachia* symbioses can involve a modulation of oxidative homeostasis. Because of the multifarious effects of ROS, any adaptation involving a modulation of oxidative homeostasis is likely to have many side effects, potentially rendering the host maladapted to the absence of its symbiont, or even completely dependent upon it.

The genetic architecture of sexual trait decay (52226)

Casper J. van der Kooi, Christoph Vorburger, Tanja Schwander.

*Department of Ecology and Evolution, University of Lausanne; EAWAG, ETH Zürich;
Department of Ecology and Evolution, University of Lausanne.*

Changes in life history can induce a shift in selection pressures and thereby render formerly adaptive traits non-functional. Consequently, these non-functional traits are expected to decay, either because the traits are released from selection (i.e. neutral) or because investment can be costly (e.g. in terms of resource investment). In asexual lineages, the traits formerly involved in sexual reproduction are non-functional and often decay, yet it remains unknown whether this decay is the result of many mutations with small effects or few mutations with large effects.

The aim of this study is to infer the level of sexual trait decay and its genetic architecture in asexual lineages of the parasitoid wasp *Lysiphlebus fabarum* (Hymenoptera: Braconidae). Using the few males that are occasionally produced by asexual females, we introgress alleles from the asexual into sexual lineages and perform mating assays to test the sexual functionality of females. The genetic architecture of decayed sexual traits and various morphological traits is inferred from classical genetic crosses in combination with a mapping approach based on RAD sequencing. Our findings on the genetic architecture of decayed sexual traits are compared with the genetic architecture of other traits.

Evolutionary shifts in chemical communication: The loss of a sex pheromone (52288)

Jan Buellesbach, **Thomas Schmitt**.

Jena School for Microbial Communication; Department of Animal Ecology and Tropical Biology, Biocenter, University of Würzburg.

The evolution and maintenance of intraspecific communication channels constitutes a key feature of sexual communication that requires tight coordination between the senders and receivers of sexual cues. However, in the emerging Hymenopteran model organism *Nasonia*, we were able to detect an unexpected loss of function in an apparently ancestral female sexual cue. Generally in *Nasonia*, female cuticular hydrocarbons (CHC) function as species-specific sexual cues, enabling males to detect, discriminate and prefer conspecific females. In females of *N. giraulti* though, one of the most recently diverged *Nasonia* species, CHC profiles displayed a dramatic shift, greatly contrasting the genetic divergence in the *Nasonia* species complex. These findings are further complemented by the apparent loss-of-function of female CHC as sexual cues in this species, whereas *N. giraulti* males retain their perception capabilities as demonstrated by their reaction to heterospecific female CHC. This constitutes

one of the first reports of an apparent deviation from an intact communication system due to an evolutionary shift and a loss-of-function in the signaller, which the receiver did not adapt to. The implications of these findings are discussed in the light of the genetic basis of CHC variation and the potential evolutionary processes underlying and enabling such a shift.

Poster session B - MAX 414

Recent diversification events in *Bicyclus* butterflies are generally linked with trait loss (52487)

Oskar Brattstrom, Kwaku Aduse-Poku, Ullasa Kodandaramaiah, David C Lees, Paul M Brakefield.

Cambridge University - UK; IISER, Thiruvananthapuram - India.

Males of many butterflies have androconia that are specialised wing scales important in courtship and are prime candidates in understanding speciation. Having traditionally been linked with scent communication, recent studies suggest that they also have additional, as yet unknown roles.

The subtribe Mycalesina shows an extraordinary complexity of androconia, especially in the African genus *Bicyclus*. Mapping these traits across more than two hundred taxa suggests that divergence in androconial number between sister species typically happened through loss. This can be detected as androconia are often arranged as groups of functional units. The more developed structures, such as hairpencils, appear to be fully reduced almost immediately. Less conspicuous units, such as scale patches, disappear more gradually leaving microscopic evolutionary fossils on the wings that help to reveal the ancestral state.

When new androconial traits arise they usually represent a reoccurrence of a type of androconia common within the subtribe. Looking back at older phylogenies where rates of loss and gain were estimated without knowledge of microscopic structural remains these showed a higher rate of gain than of loss. In general, it appears that complex novel traits arise rarely amongst Mycalesina, and when lost they are replaced by more general traits.

Poster session B - MAX 414

Differential gene expression associated with evolutionary loss of a metabolic trait (52578)

Mark Lammers, Ken Kraaijeveld, Peter H. Neleman, Jacintha Ellers.

Animal Ecology, VU University Amsterdam.

Over the last decade there has been increased appreciation for the fact that evolutionary changes are frequently associated with the loss of phenotypic characters. However, the evolutionary trajectories leading to trait loss are poorly understood, particularly the genetic

changes associated with this important evolutionary process. Parasitoid wasps form an excellent model system to discover unifying principles that link phenotypic trait loss with molecular decay in the genome, because of the repeated loss of a key metabolic trait in parasitoids, the loss of de novo lipogenesis. Although parasitoids are capable of utilizing dietary carbohydrates to meet immediate energy demands, the conversion of such carbohydrates to long-term storage in the form of lipids is impaired even in the presence of excess carbohydrates. Here we present the results of a gene expression experiment to unravel regulatory changes associated with trait loss. We show major changes in the transcription of enzymes in the fatty acid biosynthesis pathway, among others, in the non-lipogenic parasitoid *Nasonia vitripennis* compared to a species capable of lipogenesis, *Drosophila melanogaster*. These results suggest gene regulation as a potential molecular mechanism underlying trait loss.

Poster session B - MAX 414

Males of a small marine fish reduce the use of one of two courtship signals as a response to aquatic noise (52753)

Karen de Jong, Adrian Klein, Katja U. Heubel.

University of Tübingen; University of Bonn.

The increasing levels of background noise in our oceans may hamper acoustic communication under water. However, because behaviour is often flexible, animals may be able to change their signals to overcome the loss of signal efficacy. Males of a small marine fish, the two-spotted goby (*Gobiusculus flavescens*), use two different acoustic signals to attract females. We found that when we added experimental noise to an aquarium in a repeated measure design males responded by reducing the use of one of these signals, but not of the other. As a noise source, we used a submersed electromotor which produced a constant noise with a dominant frequency that partly overlapped with the two-spotted goby calls, thus interfering with the signal while allowing us to see when sounds were made. Males reduced the use of the signal that was most overlapped by the noise source, suggesting that they are able to adapt their acoustic signals to the acoustic environment. The reduction of one of the courtship signals may, however, lead to different choices in females and therefore affect the direction or strength of sexual selection.

Poster session B - MAX 414

Gene flow-selection balance and the response of metapopulations to climate change (51590)

Michael L. Logan, M. C. Duryea, Orsolya Molnar, Benji Kessler, Ryan Calsbeek.

Stellenbosch University; University of Lund; University of Brazil; Dartmouth College.

Progress towards understanding the impact of climate change on natural populations has been hampered by a lack of an evolutionary perspective. Critically, most models assume that populations exist in isolation, ignoring the fact that nearly all populations are connected by some degree of dispersal. This is an important shortcoming because the maintenance of genetic and phenotypic diversity, which are needed for a successful response to climate change, are in large part determined by the balance between natural selection and gene flow. Here, we use the brown anole lizard, *Anolis sagrei*, to examine how variation in the thermal environment across an island archipelago drives local adaptation in the face of pervasive gene flow. Despite high levels of island connectivity, thermal optima for locomotor performance in each population closely matched the local thermal environment, suggesting local adaptation. Moreover, gene flow was highest between islands with similar thermal environments, irrespective of island area or isolation. These results are consistent with the view that exceptionally strong natural selection can overwhelm the homogenizing effects of gene flow, and that spatial variation in selection generates an 'adaptive reservoir' that may buffer species against the negative effects of climate change.

Poster session B - MAX 414

The role of life history traits in mammalian invasion success (51668)

Isabella Capellini, Joanna Baker, William Allen, Sally Street, Chris Venditti.

University of Hull; University of Reading; University of Hull; University of Hull; University of Reading.

Why some organisms become invasive when introduced into novel regions while others fail to even establish is a fundamental question in biology, with strong implications given the huge impact of invasive species on biodiversity and economy. A central concept in invasion biology is the sequential nature of invasions along an 'invasion pathway'. Barriers at each stage should filter species along the invasion pathway, but no study to date has investigated the whole pathway in a single taxon at the global scale. Here we demonstrate how life history traits support population growth across the entire pathway in mammalian invasions at the global scale. Human mediated introductions considerably bias which species have the opportunity to become invasive, as mammals producing larger and more frequent litters over longer reproductive lifespans are far more likely to be introduced. Subsequently, highly productive mammals with longer reproductive lifespan establish self-sustaining populations. Established species that spread exhibit higher reproductive output. Greater productivity thus supports population growth and invasion success, with barriers at each invasion stage filtering species with progressively higher fecundity.

Poster session B - MAX 414

Temperature-dependent benefits of bacteria for the hatching success of resting eggs of *Daphnia magna* (51710)

Alexandra Mushegian, Elodie Burcklen, Dieter Ebert.

Universität Basel.

The “seed bank” of resting eggs of *Daphnia magna* and other crustaceans is recognized as an important biotic reservoir affecting the dynamics of aquatic ecosystems, but little is known about the effects of interspecies interactions on the hatching success of these eggs. We performed a series of laboratory experiments manipulating temperature and bacterial environment of resting eggs of *Daphnia magna*. Unexpectedly, at elevated temperatures ($>25^{\circ}\text{C}$), resting eggs with no live bacteria on their surface or in their environment had reduced hatching success and correspondingly higher rates of severe morphological abnormalities compared to eggs with bacteria in their environment. These results highlight the complexity of the ecological dimensions of animal development, and indicate that activities of environmental bacteria might be important to consider when predicting the effects of environmental change.

Poster session B - MAX 414

Empirical evidence that natural selection is not the only mechanism of adaptive evolution (51712)

Pim Edelaar, Adrian Baños-Villalba, David Quevedo-Colmena, Graciela Escudero.

University Pablo de Olavide.

Is natural selection really the only mechanism capable of deterministically driving adaptive evolution? We studied grasshoppers which locally adapt in colour to that of natural soils. A novel, urban habitat has narrow pavements of different colours which are colonised by divergent, cryptic grasshopper populations. We experimentally excluded plasticity as driving the observed divergence. Capture-recapture studies and simulations show that natural selection is also not able to maintain the observed degree of divergence. Manipulation of grasshopper colour using synthetic hormones resulted in the predicted, adaptive change of preferred habitat, both in a small-scale lab assay and a true-scale field experiment. Hence together these data show that individuals, given their colour, preferentially settle and stay on those novel substrates which provide them greater crypsis. Common-garden experiments showed that colour is partly genetically determined. Finally, males detect females over just a few meters, such that choice of type of pavement indirectly leads to assortative mating by colour. We therefore conclude that genetically variable individuals have chosen to colonise those novel habitats to which they were pre-adapted, thereby creating genetically diverged, locally adapted populations. Thus, habitat choice can deterministically drive adaptive evolution, and could do so even if natural selection didn't act.

Poster session B - MAX 414

Do opposites attract or detract? Direct conflicts between genetic and environmental influences on body size in North American *Drosophila* (51794)

Michelle Taylor.

University of Exeter.

Populations of a species often differ in key traits. Differences can be explained by genetic variation, plastic responses to the environment or a mixture of the two. However, it is rarely known whether genetic and environmental influences produce the same or different outcomes in trait variation. In the most extreme cases, where genetic and environmental influences directly contradict each other, this may result in maladapted traits across species distributions. We examined this issue by investigating temperature-size relationships in populations of *D. pseudoobscura* from North America. We used a selection of isolines from each of three populations and reared them in four temperatures that represented the range of environmental temperatures across their geographic range. We found that individuals from all populations had larger wing sizes when reared at colder temperatures, conforming to well-known geographic patterns of temperature and size. However, we also found that flies originating from Northern populations, who routinely experienced a cooler climate, were consistently smaller than their Southern, warmer climate conspecifics when reared under equal conditions. This revealed a direct conflict between genetic and environmental influences on wing size, which may impact on population fitness across the species range.

Poster session B - MAX 414

The determination of the sensitive parameters to analyze the uncertainty of the terrestrial ecosystem (51811)

Guodong Sun.

LASG, Institute of Atmospheric Physics, Chinese Academy of Sciences.

In this study, we present a new approach to ascertain the subset of those relatively more sensitive and important parameters among the physical parameters. The Lund–Potsdam–Jena (LPJ) dynamical global vegetation model was utilized to test the validity of the new approach. The results imply that nonlinear interactions among parameters play a key role in the uncertainty of numerical simulations in arid and semi-arid regions of China compared to those in northern, northeastern and southern China. The uncertainties in the numerical simulations were reduced considerably by reducing the errors of the subset of relatively more sensitive and important parameters. The results demonstrate that our approach not only offers a new route to identify relatively more sensitive and important physical parameters but also that it is viable to then apply “target observations” to reduce the uncertainties in model parameters.

Poster session B - MAX 414

Predation pressure accelerates evolutionary response to temperature change (51850)

Michelle Tseng, Mary I. O'Connor.

University of British Columbia; University of British Columbia.

Given the projected increase in mean global temperature, there is a pressing need for research that examines whether organisms can evolve fast enough to adapt to changing climate. While a handful of studies have demonstrated rapid adaptation to temperature, they have all been performed on single species systems and thus their relevance to natural settings is limited. Virtually all organisms live in a community setting, thus understanding how trophic interactions mediate the evolutionary response to environmental change can improve predictions of evolutionary trajectories in nature. Here we report experimental evidence that predation pressure by Dipteran predators (*Chaoborus americanus*) accelerated the evolutionary response of *Daphnia pulex* (a freshwater crustacean) to temperature change. Populations selected with predators also evolved elevated phenotypic plasticity to temperature. Together these results reveal that biotic interactions not only modify but enhance evolutionary responses to environmental temperature change.

Poster session B - MAX 414

Determinants of connectivity in the marine environment: a multispecies approach (51877)

Abigail Cahill, Didier Aurelle, Emilie Boissin, Aurélien De Jode, Emilie Egea, Zinovia Erga, Romain David, Sophie Dubois, Jean-Baptiste Ledoux, Anne Chenuil.

Aix-Marseille Université; Institut Méditerranéen de Biodiversité et d'Ecologie Marine et continentale (IMBE) UMR 7263.

An important step in studying responses to global change is determining the patterns and scale of connectivity among populations. Gene flow and selection are expected to be important and opposing forces governing a species' capacity to respond to changing conditions. In marine invertebrate species, adults are often sessile and populations exchange individuals via dispersal of gametes and larvae. This leads to a general pattern where species that have a long larval period are expected to be more connected than those without larval dispersal. However, in the northwestern Mediterranean Sea (Marseilles, France), even species with relatively long-lived larvae and high dispersal potential show a surprising number of genetic breaks over a small spatial scale (approx. 250 km). We compiled data on genetic patterns, habitat, and life history traits in nine species spanning five phyla. Using a comparative approach and current modeling techniques, we hoped to understand what factors (life history, habitat, environment, etc.) best explain the number and placement of these genetic breaks. By using data from a single area, we minimized the effects of sampling at different sites and instead focused on traits that may influence connectivity, and ultimately local adaptation and responses to global change in these species.

Poster session B - MAX 414

Mapping genetic and species diversity of pollinators to the ecosystem service of pollination across changing landscapes (51975)

Panagiotis Theodorou, Josef Settele, Christoph Bleidorn, Oliver Schweiger, Ivo Grosse, Tomás E. Murray, Robert J. Paxton.

Martin-Luther-University Halle-Wittenberg; University of Leipzig; Helmholtz Centre for Environmental Research – UFZ Halle; National Biodiversity Data Centre, Ireland; German Centre for Integrative Biodiversity Research (iDiv), Halle-Jena-Leipzig.

Animal pollinators, especially wild bees, are a critical component of our terrestrial ecosystems by providing essential pollination services to many wild and crop plants. However, during the last decades numerous reports have shown declines in numbers of both wild and managed pollinators that can have major ecological and economic consequences. The relationship between species diversity and ecosystem function has been clearly demonstrated in experimental microcosms and field plots with respect to primary productivity but rarely explored across other trophic levels or ecological interactions, including pollination. Moreover, the relationship between flower visitor species diversity and pollination service provision shows little consensus across studies. Here, we study the degree to which genetic diversity of pollinators can predict the ecosystem service of pollination. Using sites that differ in their land use, we map population genetic diversity to community species diversity and their relationship to the ecosystem service of pollination. We use high-throughput DNA sequencing for species diversity assessment and Illumina-based RAD-sequencing for genetic diversity assessment. By incorporating urban/rural paired sites into our experimental design we test whether genetic diversity of functional pollinators is enhanced in structurally complex habitats, including warmer urban sites, and identify potential evolutionary responses of pollinators to climate change.

Poster session B - MAX 414

Photosynthetic Pathways and Selective Herbivory: A Phylogenetic Comparative Approach (52029)

Erik van Bergen, Russell Hall, Paul Brakefield, Colin Osborne.

University of Cambridge; University of Sheffield.

Mycalesine butterflies have radiated dramatically in Africa, Madagascar and Asia and produced more than 300 extant species. Their larval host plants are nearly always grasses. A major driving process could have been the ability of mycalesine butterflies to invade the empty niches that arose as a result of the evolution of the C4 photosynthetic pathway and the worldwide expansion of C4 grasses in open environments.

In theory, C4 photosynthesis should exert a strong influence on trophic interactions. C4 leaves are predicted to have higher physical resistance leading to higher harvesting and processing costs. In addition, the digestibility and nutritional values of C4 foliage are lower. These expectations led to the hypothesis that herbivores should develop more slowly and have lower fitness on C4 than on C3 leaves (Caswell hypothesis).

Here we test this hypothesis by measuring establishment and growth rates of one species of mycalesine butterflies on a set of 80 different grass species, representing the multiple origins

of C4 photosynthesis together with C3 sister taxa. We aim to investigate if and how herbivore fitness and early development is affected by photosynthetic pathway and evolutionary history of the hosts and test the relative importance of the nutritional value and physical resistance of the grasses on these two herbivore fitness traits.

Poster session B - MAX 414

Plastic response of a long-lived shorebird to extreme climatic events (52061)

Liam Bailey, Martijn van de Pol.

Australian National University; Netherlands Institute of Ecology.

Global climate change is expected to increase the frequency and magnitude of previously rare climatic extremes, with potentially negative consequences for affected populations. Phenotypic plasticity may facilitate rapid adaptation to extreme climatic events, but the occurrence of a plastic response will be dependent on an extreme climatic event exhibiting reliable cues, which may not always be the case. As such, the occurrence of plasticity as a response to extreme climatic events still requires empirical assessment. Here, we monitor the nest-site selection process of the long-lived Eurasian oystercatcher (*Haematopus ostralegus*) in response to increasingly frequent and more extreme high tides, using data covering the past 20 years. We show that the average nest elevation of the population has increased over time as tidal patterns have changed; however, we found this trend was driven most strongly by changes in selection, with low elevation territories being abandoned and left unoccupied, rather than intra-generational changes in nest-site selection. Our results suggest that phenotypic plasticity does not provide a means for the Eurasian oystercatchers to adapt to changing patterns of extreme climatic events. This represents one of the first attempts to empirically test the efficacy of phenotypic plasticity as a response to extreme climatic events.

Poster session B - MAX 414

Climate change responses in canopy-forming seaweeds (52151)

Alexander Jueterbock, Galice Hoarau.

University of Nordland.

Canopy-forming seaweeds provide foundational habitat for diverse ecosystems along temperate rocky shores. The seaweeds' centers of adaptive potential in ancient glacial refugia - rich in genetic variation and uniqueness - are highly threatened with extinction from current climate change. To predict the impact of climate change on seaweed meadows in the temperate and sub-polar regions of the northern hemisphere, we used a multidisciplinary approach, integrating Niche Modeling (biogeographic effect), heat-stress experiments (physiological plasticity), and population genetics (evolutionary responsiveness). Our models predicted that suitable seaweed-habitat will open up in the southern Arctic. At the same time, some species of

seaweeds are

likely to disappear in southern Europe before year 2200 - changes that would largely disturb species interactions and ecosystem services. Population-specific heat-stress responses in performance and heat-shock protein gene expression suggested local thermal adaptation in the seaweed *Fucus serratus*. The seaweed's physiology, however, is likely insufficient to prevent the predicted habitat loss at its southern distributional edge, where we recorded significant loss of allelic richness (>12%) over the past decade; along with a 90% decline in abundance. The remaining key question is whether evolutionary responses, which we recorded in microsatellite outlier-loci, could save the seaweed's center of adaptive potential.

Poster session B - MAX 414

Broadness of thermal tolerance is linked to decreased virulence in fish pathogen - does climate change alter disease epidemics? (52168)

Roghaieh Ashrafi.

Longer summers associated with climate change are expected to lengthen the period of environmentally borne disease outbreaks. By changing the thermal tolerance of naturally occurring opportunistic pathogens climate change could also alter the virulence of the pathogens. Here, using a multi-locus sequence analysis, temperature dependent growth experiment and virulence experiment, we show that the fish pathogen *Flavobacterium columnare* trades off virulence with thermal tolerance breadth. High virulence was associated with reduced ability to tolerate a wide range of temperatures. Moreover, ca. 80 clones sampled over ten years across Finnish fish farms seem to be derived from two ancestral lineages and have semi-clonal and epidemic population structure. However, genotypes were independent from the geographic origin and year of analysed isolates. Thermal tolerance data showed no relationship based on geography but genotypes explained thermal tolerance differences in *F. columnare* isolates. Our results suggest that the link between thermal tolerance and virulence in *F. columnare* can effectively lead in to the changes of the virulence and disease outbreaks when climate warming proceeds.

Poster session B - MAX 414

Phenotypic responses of a water flea population to rapid environmental change (52182)

Miia Mannerla, Laura Sartamo, Anu Vehmaa, Ulrika Candolin.

University of Helsinki, Department of Biosciences, Helsinki, Finland; University of Helsinki, Department of Environmental Sciences, Lahti, Finland; Tvärminne Zoological Station, University of Helsinki, Hanko, Finland.

A powerful way to reconstruct past responses of populations to human-induced environmental changes is to investigate their fossils. Cladocera (water fleas) have been shown to undergo changes in morphology in response to changes in the environment, and to leave subfossils that

provide valuable material for long term studies of phenotypic changes. We investigated how a common Baltic Sea cladoceran, *Eubosmina maritima*, has phenotypically changed in response to eutrophication during the past decades. Sediment cores from sites with different eutrophication history have been sampled, and fossils from sediment layers from periods before, during and after the most severe eutrophication have been measured. We will present our results on how morphological changes (such as changes in overall size of the organism and in the length of appendages) correlate with eutrophication induced changes in the food web (such as primary production and predator community). The results will reveal the magnitude and rate of phenotypic responses of this common species to past environmental changes, and thus help to predict its future success in the face of new challenges.

Poster session B - MAX 414

Do the number of niches limit diversification? (52194)

Louis du Plessis, Tanja Stadler.

ETH Zürich.

The amazing biodiversity of life on earth emerges through the evolution of new species. Although diversification is a constantly ongoing process, the rates at which species arise and go extinct are far from constant. Diversity-dependent speciation postulates that speciation is limited by the number of free niches that can be occupied by novel species. Many adaptive radiations show an initial increase in the speciation rate followed by a subsequent slowdown. Although this appears to support diversity-dependence, it is possible that slowdowns are caused by alternative explanations [1].

We implemented a model within the BEAST 2 framework that quantifies diversity-dependent speciation by modeling diversification as a birth-death process with an explicit dependence of the speciation rate on the number of free niches. We look for evidence of diversity-dependent speciation among monomorphic clades within the global bird phylogeny [2]. We further use simulations to explore whether or not the observed slowdowns in the speciation rate can be explained by sampling biases or geographic factors.

[1] Moen D, Morlon, H, “Why does diversification slow down?” Trends Ecol Evol (2014)..

[2] Jetz et al., “The global diversity of birds in space and time” Nature (2012).

Poster session B - MAX 414

Experimental evolution of metal tolerance in changing environments (52213)

Florien A. Gorter, Mark M. G. Aarts, Bas J. Zwaan, J. Arjan G. M. de Visser.

Wageningen University.

Directional environmental change is a ubiquitous phenomenon, with climate change as a notorious example. To investigate the effect of different rates of change on evolution, we grew *Saccharomyces cerevisiae* for 500 generations in the presence of (i) constant high, or (ii) gradually increasing, concentrations of cadmium, nickel or zinc. We anticipated that, depending on the nature of underlying genotype-by-environment interactions (GxE), these regimes would result in different evolutionary dynamics and endpoints. More specifically, we considered the consequences of magnitude versus reranking GxE. Both types of GxE predict that gradual change, as opposed to abrupt change, delays fitness increase, but only under reranking GxE may evolution under both regimes lead to different endpoints. Our data show that gradual change delays fitness increase compared to abrupt change, but fitness of evolutionary endpoints is the same under both regimes. For cadmium this is due to smaller fitness differences at low metal concentrations (magnitude GxE), while for nickel different isolates are selected at different concentrations (reranking GxE). Whole-genome sequencing uncovered SNPs and structural changes that provide additional support for our hypotheses. Our findings imply that the rate of environmental change and the nature of the stressor are crucial determinants of evolutionary dynamics and outcomes.

Poster session B - MAX 414

Phenotypic variation between core and edge populations of a range expanding plant species (52311)

M. Nicky Lustenhouwer, Jennifer L. Williams, Jonathan M. Levine.

Institute for Integrative Biology, ETH Zurich; Department of Geography, University of British Columbia.

Population spread lies at the heart of biological invasions and range shifts with climate change. Spreading populations may evolve rapidly, driven by selection for higher dispersal and fecundity at the invasion front, local adaptation and/or serial founder events. We studied phenotypic variation between range core and edge populations of *Dittrichia graveolens*, a Mediterranean annual plant species that is currently spreading into Switzerland. In a common garden experiment in Switzerland, field-collected seeds were sown from 3 Swiss populations from the expanding range edge and from 4 southern and 9 central French populations from the range core. We found a strong latitudinal gradient in phenology, with plants from the central French and Swiss populations flowering on average 3 weeks earlier than plants from southern France. The Swiss populations had the highest germination, biomass and fecundity in our Swiss common garden, followed by the central and southern French populations. No clear differentiation in dispersal ability was found. The high germination and fecundity of range edge populations in Switzerland could contribute considerably to their spread velocity. Local adaptation should therefore not be discounted as a force increasing the invasion velocity of spreading populations, even in the absence of dispersal evolution.

Poster session B - MAX 414

Heterosis and inbreeding depression in alpine populations of *Arabidopsis thaliana* (52334)

Marie Roumet, Widmer Alex.

ETH Zürich; ETH Zürich.

Climate warming is pushing species ranges upwards in elevation. This problem raises interest in studies focusing on adaptation at range margins and on how changes in connectivity among populations may affect their evolutionary trajectory.

The model species *Arabidopsis thaliana* is a common species in the central European part of its range, where it occurs from sea level up to about 2000m above sea level. In alpine regions, *A. thaliana* populations are typically small and isolated. Focusing on 6 populations located along an altitudinal gradient in the Swiss Alps, we used controlled crosses to (i) investigate the evolutionary consequences of genetic drift and, (ii) discuss how inter-populations gene flow could affect their evolutionary trajectories.

We frequently observed a fitness reduction associated to selfing (inbreeding depression) and a positive effect outcrossing (heterosis), implying that genetic drift caused the accumulation and fixation of deleterious recessive mutations. We also reported cases where inter- and intra-populations crosses caused reduced hybrid fitness. This last result suggests that the selfing mating system and small effective size of alpine populations of *A. thaliana* favour the accumulation of genetic incompatibilities; it also highlights the risks associated to gene-flow and the introduction of novel genetic variation into a local pool.

Poster session B - MAX 414

Environmental variation affects fitness and energetics in nectar-feeding butterflies (52354)

Kristjan Niitepõld, Carol Boggs.

University of Helsinki; University of South Carolina.

Changes in environmental conditions alter the availability and distribution of resources, which can lead to changes in population dynamics. When available resources are limited, individuals have to allocate their finite resources among different life-history traits such as movement, foraging, maintenance, and reproduction. We used nectar-feeding butterflies as our study system and subjected butterflies to nutritional stress at different life stages. In addition, we forced butterflies to fly to see how increased energy expenditure affected life-history. We recorded a large number of traits such as egg production, food intake, body mass and lifespan, as well as resting and flight metabolic rate throughout the entire adult life. We found that butterflies conserved their flight capacity when food was scarce. This highlights the importance of flight for butterflies. However, forced flight elevated the rate of metabolic senescence, suggesting that flight is physiologically costly. Flight did not affect reproduction, whereas adult food restriction clearly reduced reproductive output. Interestingly, the strength of the decrease in fecundity differed between species, reflecting life-history strategies and egg composition. Mechanistic studies of resource allocation under stress are therefore needed to

build a comprehensive understanding of how environmental changes affect species-specific population dynamics of natural populations.

Poster session B - MAX 414

Evolutionary Potential in the Face of Catastrophic Change (52451)

Carol Eunmi Lee, Marijan Posavi, Gregory Gelembiuk, Jane Remfert, Guy Charmantier, Mireille Charmantier-Daures.

University of Wisconsin; Université de Montpellier.

How can we assess whether populations have the potential to evolve in response to catastrophic environmental change, such as biological invasions, oil spills, or climate change? To what extent are populations constrained from undergoing an evolutionary response? And would independently derived populations show evidence of parallel evolution? This talk summarizes key results from several studies, including laboratory selection experiments and comparative studies that document rapid evolutionary responses to crude oil from the Deep Horizon Gulf oil spill, salinity changes during biological invasions, and temperature shifts in coastal environments. In particular, invasive populations are striking in their capacity to extend their ranges into novel habitats. Analyzing populations that can invade, relative to those that cannot, point to the nature of the native range in shaping the evolutionary potential to undergo habitat shifts. A history of temporal fluctuations in the native range, along with mechanisms promoting the maintenance of genetic variation, might serve as critical factors.

Poster session B - MAX 414

Is hotter always smaller? Evolutionary response of *Daphnia* to global warming. (52469)

Marcin Dziuba, Slawek Cerbin, Lukasz Wejnerowski.

Adam Mickiewicz University.

Daphnia will undergo strong alterations due to climatic changes. One of the threats for freshwater herbivores like *Daphnia* is temperature-mediated prevalence of filamentous cyanobacteria with more frequent and longer blooming events. Cyanobacterial filaments pose a great threat to this key-stone herbivore. According to hotter is smaller rule, global warming should reduce the average size of *Daphnia*, which is advantageous in the presence of filaments. We hypothesized that under simulated global warming conditions *Daphnia* will be smaller; the size reduction should be advantageous in coping with cyanobacterial filaments. In order to verify our hypotheses we conducted life-history experiments, where *Daphnia* clones from artificially heated lakes and closely spaced non-heated lakes were exposed to filamentous *Cylindrospermopsis raciborskii*. Our research provided an evidence for a possibility of evolutionary adaptations to prevalence of filamentous cyanobacteria. *Daphnia* from heated lakes differed in life strategy – under the pressure of the filaments they grow

bigger in order to produce more offspring with the cost of shorter life span. This is in conflict with Hotter is smaller rule, but for organisms, which brood size is limited by body size it is advantageous to grow larger when they pay cost of shorter lifespan.
Research funded by MNiSW no. DI2012014242

Poster session B - MAX 414

Simulating predicted environmental changes in freshwater ecosystems: how do altered conditions affect *Daphnia* populations and host-parasite interactions? (52530)

Manja Saebelfeld, Jörg Sareyka, Laëtitia Minguez, Mark O. Gessner, Justyna Wolinska.

Leibniz-Institute of Freshwater Ecology and Inland Fisheries (IGB), (Berlin, DE); Berlin Institute of Technology (TU Berlin), Berlin, Germany; Freie Universität Berlin (FU Berlin), Berlin, Germany.

Changes in climatic conditions have been recorded at a global scale over the past decades and are expected to continue in the future. Direct consequences for lake ecosystems include altered thermal stratification, nutrient availability, organic matter turnover and oxygen concentration. This can massively affect primary production and thus have great impact on food web interactions and biodiversity. Another effect of climate change comprises shifts in the disease prevalence within populations since host susceptibility and parasite infectivity are often sensitive to environmental variation. To study effects of climate change on freshwater communities we will use the zooplankter *Daphnia* and their microparasites as a model system. Our main objectives are to assess effects of predicted global stressors on (i) the intra- and interspecific diversity of *Daphnia* populations and (ii) the spread of infectious diseases. Thus, laboratory and large-scale field experiments in enclosures will be conducted. The enclosure experiments will be conducted in a unique mesocosm system (LakeLab) consisting of 24 experimental units (1270 m³ each) located in Lake Stechlin (Germany). From this, conclusions could be made on how an ongoing climate change will affect biodiversity and trophic cascades in lakes.

Poster session B - MAX 414

The Great American Biotic Interchange: studying biological invasions in deep time (52558)

Juan D. Carrillo, Carlos Jaramillo, Marcelo R. Sánchez-Villagra.

Paleontological Institute and Museum - University of Zurich; Smithsonian Tropical Research Institute.

During most of the Cenozoic, South America (SA) was an island continent with an endemic mammalian fauna. This isolation ceased during the late Neogene after the formation of the Isthmus of Panama and the establishment of a land connection with North America (NA). As

result, one of the greatest biological experiments of biota exchange at a continental scale took place, the Great American Biotic Interchange (GABI). The GABI begins during the late Miocene (~10–7Ma), the number of GABI participants rapidly increases after ~5Ma and this trend continues during the Pleistocene. We investigate biogeographic patterns in South America when the first immigrants are recorded and we review the temporal and geographical distribution of fossil mammals during the GABI. We support a differentiation between tropical and temperate mammal faunas in SA at least since the middle Miocene. The GABI can be used as a model to study biological invasions at a continental scale and geologic time. The fossil record and the distribution of extant mammals suggest that mammals with NA origin dominate in temperate zones whereas mammals with SA origin dominate in the tropics supporting a strong niche conservatism of temperate and tropical mammals in the continent.

Poster session B - MAX 414

Phylogenomics method for ranking populations of the endangered Anadromous Atlantic Salmon (*Salmo salar*) for conservation management. (52577)

Laurelene Faye, Arne Mooers.

SFU.

In an Age of Extinction, wildlife managers need tools to help conserve and manage genetic resources for the future. Wild Atlantic salmon (*Salmo salar*) is at risk across its range, and so genetic prioritization would seem prudent. Recently, Volkmann and his colleagues developed a new tool allowing the ranking of populations by conservation importance, integrating phylogenomic and environmental data. This state of the art approach is to build phylogenetic networks and score each population by its relative distinctiveness or evolutionary isolation. In a first time, we will simulate dynamic metapopulations using QuantiNemo software in order to identify which indices of genetic distance are most robust for prioritizing populations for conservation for a widely distributed stream species under different management scenarios. Then, using collected *S. salar* genomic-scale SNP and microsatellite data we will test this tool and construct the phylogenetic network of 50 populations representing all the legally designated at-risk Designatable Units (DUs) in Canada. We hypothesize that some populations may be currently under-evaluated regarding their contribution to present and future *S. salar* genetic diversities. Such populations might be prioritized both for more active research into the genetic basis of local adaptation, and for conservation by managers, immediately.

Poster session B - MAX 414

Why would a hybrid clone outcompete its parental species? (*Daphnia galeata* × *longispina* species complex) (52581)

Johanna Griebel, Sabine Giessler, Monika Poxleitner, Amanda Navas Faria, Mingo Yin, **Justyna Wolinska**.

Leibniz-Institute of Freshwater Ecology and Inland Fisheries (IGB); Ludwig-Maximilian-University Munich, Germany; School of Life Science, Fudan University, China; Free University, Berlin, Germany.

In natural communities of cyclical parthenogens, rapid response to environmental change is enabled by switching between two reproduction modes. While long periods of asexual reproduction allow some clones to outcompete others, sexual reproduction restores genetic variation in such systems. Moreover, sexual reproduction may result in the formation of interspecific hybrids. We observed that the *Daphnia* community of a small lake was consistently dominated by a single *D. galeata* × *D. longispina* hybrid clone. Furthermore, in artificial communities consisting of many clones (parental species and hybrids), this special hybrid clone took over within about ten generations. Neither the fitness assay conducted under different temperatures, and under crowded and non-crowded environments, nor the carrying capacity test revealed any outstanding life history parameters of this hybrid clone. However, under simulated winter conditions, the hybrid clone eventually showed a higher survival probability and higher fecundity compared to parental species. Enhanced overwintering possibilities as parthenogenetic lineages might explain the successful establishment of hybrids in the natural community within the *D. longispina* complex. In extreme cases, a superior hybrid genotype might be the only remaining clone after cold winters. Novel traits, such as enhanced overwintering, might promote establishment of hybrids in nature.

Poster session B - MAX 414

Genetic variability in the wild is influenced by microhabitat characteristics in *Drosophila subobscura* (52599)

Zorana Kurbalija Novicic, Marija Savic Veselinovic, Bojan Kenig, Aleksandra Patenkovic, Mihailo Jelic, Marina Stamenkovic-Radak, Marko Andjelkovic.

Institute for Biological Research, University of Belgrade, Serbia; Faculty of Biology, University of Belgrade, Serbia; Serbian Academy of Sciences and Arts, Belgrade, Serbia.

While it is predicted that many populations are able to shift their geographic ranges to track global change, the question remains of the potential of populations to adapt to rapid change in their microhabitats. The aim of the present research is to understand the microevolutionary processes across natural populations and to detect the actual degree of local adaptation through the dynamic interaction between selective pressures and gene flow. The research consists of two levels: i) assessing genetic diversity of natural populations of *Drosophila subobscura* inversion polymorphism, mtDNA variability and microsatellites, ii) assessing the habitat diversity by defining the microclimatic conditions of each selected habitat across several environmental parameters across small geographic scale. Results showed that populations of this species are genetically diverse, even on a small geographical scale. Different chromosomal gene arrangements have been found to be differently favored in various microhabitats. The results of this study will provide the additional information about the adaptive character of inversion polymorphism, and help us answer questions about the evolutionary potential of the populations in the wild.

Evolutionary history counts in population response to thermal stress in inbred and outbred lines of *Drosophila subobscura* (52604)

Aleksandra Patenković, Marija Tanasković, Zorana Kurbalija Novičić, Bojan Kenig, Marina Stamenković-Radak, Marko Anđelković.

Institute for Biological Research “Siniša Stanković”; Faculty of Biology, University of Belgrade, Belgrade, Serbia; Serbian Academy of Sciences and Arts, Belgrade, Serbia.

Ongoing climate change and landscape alterations represent a serious threat for existence of many species. Temperature, one of the most important factors with large influence on biological processes, can act synergistically with genomic stress, leading to significant decrease of fitness and deterioration of population survival especially in isolated populations challenged with habitat fragmentation. Therefore, the consequences of temperature stress on population level must be study in combination with genomic stress.

We analyzed wing size and shape of inbred and outbred lines of *Drosophila subobscura* from two ecologically different habitats, reared under 16°C and 22°C temperature. The results showed statistically significant difference in wing size between homozygote and heterozygote groups, with both cold and heat thermal treatments decreasing wing size. Statistically significant difference between heterozygotes groups may be contributed to maternal effect. Differences in a capacities of populations to adapt to thermal stress, reflects different population histories that these populations have experienced: one in polluted urban part of Belgrade under anthropogenic influence, other in natural unpolluted resort with stable microclimatic conditions.

The obtained results suggest that for predicting the consequences of environmental changes, it is necessary to take into account the population history, as well as the degree of genomic stress.

Spatial distributions of genetic diversity and local adaptation in metapopulations on heterogeneous landscapes (52834)

Etsuko Nonaka.

Metapopulation Research Group, Department of Biosciences, University of Helsinki.

Existing theories of population genetics for spatially subdivided populations often assume a constant genetic variance across local populations for mathematical tractability. Genetic diversity is a key ingredient determining evolutionary potential of populations, especially under changing environments. It can be temporally and spatially variable and influenced by selection, gene flow, and genetic drift. In heterogeneous landscapes, spatial habitat structure influences such evolutionary as well as demographic processes and determines gene flow and the prevalence of genetic drift, resulting in heterogeneous spatial distributions of genetic

diversity. We developed an eco-evolutionary model of a metapopulation living in a heterogeneous landscape to investigate 1) the effects of dynamic vs. constant genetic diversity on local adaptation, and 2) how landscape structure may affect the spatial distributions of genetic diversity. The results suggest that dynamic genetic diversity can produce different patterns of local adaptation than when it is kept constant at the mean value. Long-term averages of genetic diversity and the degree of local adaptation can be well predicted by population size and types of immigrants, which are in turn predicted largely by patch area and connectivity. Frequent extinction and colonization events can obscure this relationship.

Poster session B - MAX 414

Evolutionary trade-off in thermal adaptation and its effect on responses of animals to global climate change (52936)

Karin Maldonado, Natalia Lopez-Morgado, Gabriela Piriz, Francisco Bozinovic, Pablo Sabat.

Departamento de Ciencias Ecológicas, Universidad de Chile; Departamento de Ecología, LINC-Global, CAPES, Pontificia Universidad Católica de Chile.

The effect of global warming on species' geographic ranges has attracted much attention and concern from researchers in recent decades. In this sense, it has suggested that limits of animals' distribution may be set according to their physiological tolerance or phenotypic plasticity in response to climate. Nevertheless, it has proposed that species that evolved greatest physiological tolerances have done so at the expense of tolerance's phenotypic plasticity. Such evolutionary trade-off in thermal adaptation, may cause that extant more thermo tolerant species would paradoxically be most likely to be at threat by increasing temperatures. Due to thermal tolerances and metabolic rates are strongly influenced by environmental temperatures and linked to species' geographic distribution, those variables have been widely used to study the effect of global change. In the present study, we examined thermal tolerances (CTmin, CTmax) and metabolic scopes (BMR, Msum), together with their acclimatory capacities, in rodents (*Phyllotis darwini*) from the northernmost and the southernmost limit of their distribution in Chile. We found a significant relationship between physiological tolerance and phenotypic plasticity; however, this pattern differed in relation to the trait analyzed. The results suggest that more studies are needed to establish generalizations about the existence of an evolutionary trade-off on thermal adaptation.

Poster session B - MAX 414

Niche conservatism and evolutionary range expansion in mycalesine satyrine butterflies (52987)

David Lees, Erik van Bergen, Kwaku Aduse-Poku, Brattström Oskar.

Cambridge University.

A spectacular Old World radiation of mycalesine butterflies resulted in largely monophyletic radiations in major tropical biogeographic regions, each of 70+ species. A robust phylogeny and distribution records across Mycalesina allows us to compare niche models between regions, both at species and higher clade level, examining the extent that phylogenetic niche conservatism (PNC) may constrain climatically realized niches. In African *Bicyclus* for example, nested sets of early diverging lineages are relatively restricted to W.African rainforests as expected under PNC, whereas in more distal parts of the evolutionary radiation, dramatic expansion occurred into savannah environments, likely driven by Miocene climatic change favouring adaptation to a C4 photosynthetic pathway in their grass hostplants. This contrasts to the genus *Heteropsis* in Madagascar, where radiations have largely occurred within humid forest regions, and early diverging lineages are widespread. Projecting the fundamental niches using surfaces at the same spatial scale confirms clearcut differences within the Afrotropics. These models help to understand the varying extent to which a process of sequential colonization of land masses and archipelagos may have happened with, or been limited by, PNC. Present inference illuminates the potential of range expansion or contraction for future climate scenarios, including predicted movements along latitudinal/elevational gradients.

Plenary MON MAX 350/351

The genomic basis of sexual dimorphism (53360)

Judith Mank.

University College London.

Sexual dimorphism is arguably the most pervasive form of intra-specific diversity in the animal kingdom, and the prevalence of sexual dimorphism in animals prompted Darwin's conjecture of sexual selection as a force distinct from natural selection. Central to the study of sexual dimorphism is the question of how divergence occurs between the sexes within a species when so much of the genome is shared. In many cases, phenotypic sex differences are the result of transcriptional dimorphism, and integrating genome and transcriptome data offers a powerful tool for understanding the evolution of sexual dimorphism. I'll discuss recent studies testing the relationship between sex-specific selection and phenotypic sexual dimorphism with genome and transcriptome evolution. These studies reveal the ways that selection navigates evolutionary constraints and sexual conflicts to create both inter- and intra-sexual phenotypic diversity. These observations and approaches are also valuable for understanding many other forms of intra-specific phenotypic variation.

Plenary TUE MAX 350/351

Dissecting the evolutionary ecology of reproductive strategies in the wild (53363)

Jane Reid.

University of Aberdeen.

Reproductive strategies enacted by individual organisms define social interactions and influence allele and genotype frequencies in subsequent generations, and thereby shape the course of evolution. However, evolutionary ecologists still do not fully understand the evolution or persistence of widespread reproductive strategies, including biparental inbreeding and multiple mating. Progress remains limited because reproductive strategies and fitness have not been comprehensively measured in wild populations experiencing natural social and environmental variation. Furthermore, field studies typically estimate phenotypic associations between reproductive strategy and fitness components rather than directly estimating key genetic (co)variances that could drive or constrain evolution. I applied quantitative genetic analyses to comprehensive pedigree, reproductive strategy and fitness data from socially monogamous but genetically promiscuous song sparrows (*Melospiza melodia*), to estimate genetic (co)variances that could underlie micro-evolution of extra-pair reproduction and inbreeding. Analyses revealed substantial additive genetic variance in the degrees of extra-pair reproduction expressed by females and males, with divergent negative and positive genetic covariances with fitness components. The degree of biparental inbreeding also showed substantial additive genetic variance, but sex-specific selection was weak despite inbreeding depression in offspring fitness. These analyses provide new insights into evolution of reproductive strategies, and illustrate explicit test of key evolutionary hypotheses in nature.

Plenary WED MAX 350/351

Social evolution in microbes: from model systems to the microbiome (53520)

Kevin Foster.

University of Oxford.

Since Darwin, evolutionary biologists have been fascinated by cooperative behaviour. Honeybee workers labour their whole life without reproducing, birds make alarm calls, and humans often help each other. Much less attention has been paid to the microbes. They exist all around us and inside us, and it has become clear that microbes commonly live in densely interacting communities that have major effects on animals and plants. But what determines if microbes are cooperative towards each other and their hosts? We study this question by combining theory with experimental systems, including pathogenic bacteria, budding yeast and the mammalian microbiome. We find that single-genotype patches naturally emerge in microbial communities, which favours strong cooperation by kin selection. By contrast, interactions between genotypes can be strongly competitive. Bacteria strains are often at war and we find that they can rapidly detect incoming attacks and respond in kind. Microbial interactions then follow the same evolutionary principles that were first understood through the study of animal behavior. However, one unusual and fascinating property of microbes is that an entire ecosystem can lie within another evolving organism: a host. This raises the possibility that hosts will act as ecosystem engineers that change the rules of microbial interaction for their own benefit.

How do proteins evolve? (53508)

Dan Tawfik.

Weizmann Institute of Science.

New proteins evolve via genetic processes of duplication and diversification. We investigate the mechanisms, driving forces and intermediates that underlie these processes, thus giving rise to new proteins, with new structures and functions.

I will describe two recent, unpublished studies:

- Coevolution of transcriptional and protein regulation. Duplication, giving rise to paralog genes, is the most common mechanism for evolutionary innovation. The divergence of transcriptional regulation of paralogs is routinely recorded. However, no evolutionary trait evolves on its own. I will show a case study, indicating why and how promoters and the proteins whose transcription they drive coevolve.
- The birth of a new protein. Alongside paralogs, orphan genes comprise more than a third of all genomes. But is the 'birth' of a new, globular, structured protein a feasible event? We reconstructed in the laboratory the de novo emergence of a functional, globular protein by cooption of a short sequence motif from an existing protein belonging to a different fold. Folding efficiency, or foldability, and not the stability or function of the native state, was the key parameter under evolutionary selection.

Plenary FRI MAX 350/351

Digging for genes that affect behavior (53507)

Hopi Hoekstra.

Understanding which genes affect fitness-related behaviors, and how they work in the brain, remains a major challenge in biology. To address this goal, we are capitalizing on natural variation in behavior within and between species of deer mice (genus *Peromyscus*). In this talk, I will focus on an innate behavior – burrowing, an intriguing and complex animal architecture – to explore the genetics and neurobiology of behavioral evolution.

Presidential address FRI MAX 350/351

Supergenes, sex and sociality (53608)

Laurent Keller.

department of ecology and evolution.

Understanding the genetic basis of evolutionary adaptations is a central focus of modern evolutionary biology. Recent studies have uncovered a panoply of complex phenotypes,

including locally adapted ecotypes and cryptic morphs, divergent social behaviours in birds and insects, as well as alternative metabolic pathways in plants and fungi. In this talk I will show how the occurrence of such adaptive alternative phenotypes can be generated and maintained by either phenotypic plasticity or supergenes (i.e. ,clusters of tightly linked loci). I will in particular discuss the case of alternative forms of social organization being controlled by social chromosomes having similar properties as sex chromosomes.

JMS Prize 2014 MAX 350/351

The Time-Scale Of Recombination Rate Evolution In Great Apes (53364)

Laurie Stevison, August Woerner, Jeffrey Kidd, Joanna Kelley, Krishna Veeramah, Kimberly McManus, Great Ape Genome Project, Carlos Bustamante, Michael Hammer, Jeffrey Wall.

University of California San Francisco.

We recently completed three linkage-disequilibrium (LD)-based recombination maps generated using whole-genome sequencing of 10 Nigerian chimpanzees, 13 bonobos, and 15 western gorillas, collected as part of the Great Ape Genome Project (Prado-Martinez et al. 2013). We also identified species-specific recombination hotspots in each group using a modified LDhot framework, which greatly improves statistical power to detect hotspots at varying strengths. Using species-specific PRDM9 sequences to predict potential binding sites in hotspot regions as compared to match cold spot regions, we identified an important role for PRDM9 in predicting recombination rate variation in multiple great ape species. While previous research showed that PRDM9 is not associated with recombination in western chimpanzees (Auton et al. 2012), we attribute this lack of signal to higher population-level diversity at the PRDM9 locus in this group. Additionally, we show that fewer hotspots are shared among chimpanzee subspecies than within human populations, further narrowing the time-scale of complete hotspot turnover. We quantified the variation in the biased distribution of recombination rates towards recombination hotspots across great apes, highlighting similar distributions across great apes with Europeans as an outlier. Further, we found that pairwise comparisons of broad-scale recombination rates decay more rapidly than pairwise nucleotide divergence between species. We also compared the skew of recombination rates at centromeres and telomeres between species and show a skew from chromosome means extending as far as 10-15 Mb from chromosome ends. Our study is the first to analyze within- and between-species genome-wide recombination rate variation in several close relatives.

JMS Prize 2015 MAX 350/351

Mathematical adventures in sex and disease evolution (53375)

Matthew Hartfield.

University of Toronto.

John Maynard Smith Lecture Abstract

Mathematical modelling has always played an important role in elucidating evolutionary phenomena. Here, I present an overview of various models I've worked on during my career. First, it has been postulated that sexual reproduction is beneficial by recombining genomes, thus re-creating optimal genotypes. This hypothesis has faced renewed interest due to the ability to test hypotheses using next-generation sequence data. I will show how strong selection for recombination, that can potentially maintain costly sex, appears if acting over hundreds of sites subject to selection. Major benefits to sex and recombination arise through disentangling beneficial mutations from deleterious backgrounds. Finally, I will also discuss my research into disease emergence. Specifically, I investigate how the spread of existing strains hampers the ability of mutated pathogens to emerge, by limiting the available pool of susceptible individuals.
