



Spatial patterns of bacteria show that members of higher taxa share ecological characteristics

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PS.15.001 MODELING TEMPORAL DYNAMICS OF VAGINAL BACTERIAL COMMUNITIES IN HEALTHY WOMEN

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The beneficial effects of the indigenous microbiota on women's health are numerous and poorly characterized. Significant alterations or disruptions of the vaginal microbiome, such as in bacterial vaginosis, may increase a woman's risk to preterm labor and acquisition of infections. We sought to develop a mathematical model of temporal variations in the composition and abundances of indigenous bacterial populations in the human vagina and determine associations with environmental, behavioral, and life history characteristics. The Bayesian approach presented here has a hierarchical framework, which can be divided into two main parts. First we model the lower level of the hierarchy, which includes changes in the presence/ absence of bacterial phylotypes and their relative abundance. We suggest a mixture model, combining a Bernoulli distribution describing presence and absence of each phylotype and a Poisson distribution describing the corresponding abundances. In the second part we implement the metadata into the model, which includes environmental, behavioral, and life history aspects using a state space model in conjunction with a generalized linear model. This approach allows us to detect dependencies between bacterial community structures and the metadata. The models will be applied to a longitudinal data set obtained by 454 pyrosequencing of 16S rRNA genes based on vaginal swab samples and questionnaires addressing environmental, behavioral, and life history aspects, both provided every 3rd day from 39 woman over a period of 15 weeks. Preliminary results suggest that the temporal dynamics of the bacterial communities are personalized, that is there are no obvious patterns in changes in the vaginal bacterial communities over time among woman but rather the dynamics are individual to each woman.

Abstract Category

15 Microbial Ecology and Ecological Theory

PS.15.002 NUTRIENT CYCLING INCREASES THE PERSISTENCE OF A MODEL MICROBIAL ECOSYSTEM

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Nutrient cycling is key feature of microbial ecosystems but from a theoretical point of view, the consequences of nutrient cycling for ecosystem dynamics remain poorly understood. Our aim is to use mathematical modeling to study the effects of nutrient cycling on the dynamics and persistence of simple model microbial ecosystems.

We have used computer simulations to study a simple mathematical model for a two-species, nutrient-cycling, microbial ecosystem. We compare this nutrient cycling model to the equivalent

one-species model system, without nutrient cycling. Our simulations include randomness due to the births and deaths of individual microbial cells, so are relevant to environmental communities inhabiting very small niches.

Unexpectedly, we find that the birth-death random noise in our simulations can cause population oscillations, in both the one-species and two-species models. Small communities are highly susceptible to extinction. We compare the average time to extinction (persistence time) for the one-species and two-species models. We find that nutrient cycling leads to increased ecosystem persistence, and that in environments where the resource supply is very intermittent, it may even be beneficial for a population to divert nutrients from its own growth to sustain the other partner in the cycle.

Simple mathematical models have great potential for shedding light on the fundamental behaviour of microbial ecosystems. We discuss the implications of our results for real environmental microbial ecosystems, from both an ecological and an evolutionary perspective.

Abstract Category

15 Microbial Ecology and Ecological Theory

**PS.15.003 RESISTANCE AND RESILIENCE OF BACTERIAL COMMUNITIES
DEPEND ON DISTURBANCE STRENGTH AND FREQUENCY**

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Disturbances are important factors controlling biodiversity and ecosystem functioning. Even though bacteria are key components of ecosystems, systematic knowledge about how they respond to different types of perturbations is unknown. More specifically, little is known about their resistance and resilience in response to variations in disturbance intensity and frequency. We therefore implemented a transplant experiment with dialysis bags to investigate how the strength and frequency of a perturbation (an increase in salinity), affects the composition and functioning of aquatic bacterial communities. To investigate the effect of disturbance strength, microbial communities were exposed to six different salinity treatments (0, 1, 3, 5, 10, 20 psu). Dialysis bags filled with freshwater were moved from the control tank (0 psu) to the different disturbance treatments and incubated for 24 h. Afterwards the bags were moved back to the control tank and incubated for 36 h. To investigate the effect of disturbance frequency, another experiment was performed using the same set-up. Here, the dialysis bags were swapped between the control and the 20 psu treatment at different frequencies (0, 1, 2, 3 or 4 times over a 64 h period). In both experiments, water samples from the bags were taken before and after disturbance exposure to obtain a measure of resistance of the communities, and after the second incubation in the control tank to obtain a measure of resilience. For each sample, bacterial abundance, activity and community substrate utilization profile were measured. Moreover, bacterial community composition was determined by t-RFLP of the 16S rRNA gene. With these data we will test 1) how resistant and resilient bacterial communities are in terms of the measured functional properties as well as community composition, 2) whether resistance decreases with increasing disturbance rates and 3) whether resilience is higher in less disturbed communities.

Abstract Category
15 Microbial Ecology and Ecological Theory

PS.15.004 ARE SPECIES COHESIVE? WHAT MICROBIOLOGISTS AND ZOOLOGISTS CAN LEARN FROM ONE ANOTHER

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Evolutionary biologists have viewed species as cohesive groups of organisms, but it is not clear that either the macroorganisms or the bacteria form cohesive species. Here I address, through theoretical and bioinformatics approaches, whether species-like ecotypes (ecologically homogeneous populations) of bacteria are subject to these three modes of cohesion: speciation-quashing cohesion (preventing divergence), niche-transcending cohesion (sharing of adaptations), and intra-population cohesion (elimination of within-species diversity). Bacteria are not subject to speciation-quashing cohesion by recombination; theory of recombination-selection balance shows that recombination is too rare to prevent divergence in niche-specifying adaptations. Likewise, animals show little speciation-quashing cohesion, as interbreeding populations can usually diverge without bound in their niche-specifying adaptations. Genome comparisons show that bacteria share niche-transcending genes among ecologically distinct populations while maintaining their niche specificity; the difference between bacteria and animals is that sharing of niche-transcending genes is limited to close relatives in animals but not in bacteria. While most models of bacterial species assume intra-population cohesion, this is not yet proved; recent genome comparisons indicate that some bacterial species are not subject to intra-population cohesion. Species studies of animals and plants focus on the evolution of barriers to recombination, which emphasizes the end of niche-transcending cohesion and de-emphasizes the origins of ecological divergence. Species studies in bacteria instead focus on the origins of irreversible divergence, since there are no phylogenetic limits on the ability of bacteria to acquire niche-transcending genes. If zoologists were to follow the lead of bacteriology in de-emphasizing niche-transcending cohesion, this would allow them to focus on the origins of diversity.

Abstract Category
15 Microbial Ecology and Ecological Theory

PS.15.005 CO-AGGREGATION MAY FAVOUR THE SURVIVAL OF GRAZING-VULNERABLE BACTERIA IN FRESHWATER HABITATS

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Aggregation is a successful anti-predator strategy for freshwater bacteria against the smallest and most effective protistan predators (nanoflagellates). We enriched for grazing-resistant bacterial phenotypes by exposing natural microbial communities from a lake to predation by the voracious interception-feeding nanoflagellate *Poterioochromonas*. Aggregates larger than the predators were sorted out by flow cytometry and plated on low-nutrient agar to obtain bacterial strains that were able to aggregate or to co-aggregate with others. A number of strains from different

bacterial taxa were isolated, identified, and tested in batch co-cultures with *Poteroochromonas*. A wide spectrum of different responses was observed: besides aggregating strains, there were also edible, non-aggregating ones, albeit with different nutritional quality for the predator. Since all strains were derived from sorted aggregates, we hypothesized that some of the non-aggregating strains were able to co-exist with aggregate forming ones, thereby obtaining refuge against the predators. This was tested in batch culture experiments with predators and defined mixes of grazing-vulnerable and aggregate forming strains and subsequent analyses by fluorescence in situ hybridization combined with microscopy and flow cytometry. The survival of an edible strain was significantly favoured in co-culture with an aggregating strain (as compared to pure culture), providing evidence for the advantage of co-aggregation as a means to escape nanoflagellate predation. Interestingly, predators also seemed to profit from the simultaneous presence of aggregating and non-aggregating strains, possibly because the refuge within the aggregates allowed for a continued production of free-living, edible cells by the non aggregating strain. The here described mechanisms might be important both for the maintenance of grazing-vulnerable bacterial populations in freshwaters and for their importance as food for bacterivores.

Abstract Category

15 Microbial Ecology and Ecological Theory

PS.15.006 CONSERVATION OF GENE REGULATION IN *BURKHOLDERIA*

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Understanding the common functions and regulatory features of larger groups (e.g., genera and families) enables extension of data from specific lab strains to more diverse natural assemblages. The rapid accumulation of genome sequences compels this expanded focus. We have begun deciphering the common properties of *Burkholderia*- a versatile group that thrives in diverse ecological niches including soils, water, protozoa, insects, plants, and animals. Using *Burkholderia thailandensis* as a model system, we applied comparative genomics, high-throughput experiments, and informatics to build a functional map of the genome and extend information across the genus. With this combined approach, we a) revised *Burkholderia* species gene maps to improve consistency across the genus; b) used these maps to compare the conservation of orthologous genes and corresponding intergenic regions, c) obtained ~170 global gene expression profiles for *B. thailandensis* under a wide range of growth conditions; d) used these profiles to validate operon structure and predict transcriptional regulatory interactions; e) experimentally identified DNA binding sequences for transcriptional regulatory proteins; f) and transitively mapped the information gained from *B. thailandensis* to closely related species. Our collection of *B. thaliandensis* Affymetrix gene expression data is comparable in size to the landmark collections for *Shewanella* and *E. coli*. Our aggregate data has substantially increased our understanding of gene regulation in *B. thaliandensis*, and has generated experimentally testable hypotheses about gene regulation in this and closely related species. We are now poised

to validate regulatory features conserved across the *Burkholderia* genus, and to identify regulatory divergence associated with speciation and niche specialization.

Abstract Category

15 Microbial Ecology and Ecological Theory

PS.15.007 DYNAMICS OF BACTERIAL COMMUNITY SUCCESSION AND INTERACTION IN A CHEMOSTAT MODEL

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Chemostat models on phenol were constructed to investigate the basis of bacterial ecosystem. Analyses of bacterial community structure using both culture-dependent and -independent methods revealed that the succession of dominant bacteria occurred in a chemostat enrichment added soil as a inoculum; first dominant bacterium was genus of *Pseudomonas*, next were *Ralstonia* and *Acinetobacter*, and final was *Variovorax*. Interestingly, kinetic parameters for phenol of the enrichment changed from low KS and high KI values to high KS and low KI values with oscillation, which corresponded to these parameters of strains isolated from the chemostat; *Pseudomonas* strains exhibited low KS and high KI values and *Variovorax* strains exhibited high KS and low KI values. How does the *Variovorax* become dominance in the culture? We thought that there is a clue for understanding microbial ecosystem. A mixed chemostat model culture was established with *Pseudomonas* sp. C8, *Ralstonia* sp. P-10, and *Variovorax* sp. chemo24. These λ values of strains C8, P-10, and chemo24 were 0.0155, 0.0556, and 0.147, respectively. The λ value was calculated according to dominating theory (Hansen & Hubbel 1980 Science 207:1491), which demonstrated that the bacterium exhibiting lower λ value become dominance. These population densities were monitored with real-time PCR targeting the gene coding α subunit of phenol hydroxylase. Bacterial succession was observed and chemo24 became dominance in the culture. Their interaction was evaluated by measuring the growth curve under the addition of supernatant or not. The supernatant of C8 strongly suppressed the growth of P-10 and chemo24, while each supernatant of P-10 and chemo24 hardly affected the growth of all three strains. Interestingly, the mixed supernatants of C8 and P-10 enhanced the growth of chemo24. This research demonstrated that bacterial interaction is an important key factor for microbial ecosystem.

Abstract Category

15 Microbial Ecology and Ecological Theory

PS.15.008 CROSSING ECOSYSTEM BOARDERS: A MICROBIAL COMMUNITY TRANSECT STUDY FROM THE TERRESTRIAL SHORELINE TO THE FRESHWATER COLUMN OF A LAKE.

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Terrestrial and aquatic ecosystems are two connected neighboring biomes linked via nutrient flows, water run-off, ground water, and flooding events. Environmental studies on microbial turnover and total carbon and nitrogen yields indicate sensitivities to environmental and climate changes. Hence it is important to understand the diversity and ecology of the microorganisms involved. Earlier studies from globally dispersed sites suggest that each of these biomes harbor a characteristic microflora mediating carbon and nitrogen turnover. In the present study we assess microbial dispersal along a horizontal transect from the terrestrial shoreline across the littoral of a lake towards the pelagic zone in a temperate Swedish freshwater lake, lake Erken, east of Uppsala. We have sampled soil cores on the shoreline and collected sediment and water samples in the littoral and open water. For each sampling site, pH, carbon and nitrogen contents were determined along with temperature and oxygen levels in the open water. These variables allowed determine the environmental context of the microbial community in this study. We here applied the modern TITANIUM pyro-sequencing technology to identify the bacterial and archaeal community, using the 16S rRNA gene sequence and the ITS region for the fungal community respectively. The data allow drawing a picture on the phylogenetic connectivity of microbial communities in geographically close terrestrial and aquatic environments. This study is incorporated in a project of the Uppsala Microbiomic Center (UMC) investigating microbial communities at terrestrial and aquatic sites, and their importance in chitin degradation.

Abstract Category

15 Microbial Ecology and Ecological Theory

PS.15.009 COMMENSALISM AND NICHE ADAPTATION IN *Escherichia coli*

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Commensalism and pathogenesis are important evolutionary and ecological adaptations that enable organisms to exploit new and different habitats. *Escherichia coli* is capable of existing as a free-living organism and as a commensal or pathogen in the colons of mammals and birds. The genome of the pathogenic strains of this species contains several genetic elements such as pathogenic islands and plasmids that encode an array of virulence factors. Surprisingly, the commensal strains also have some of these pathogenic elements in their genomes. The aim of the present research is to explore the evolutionary mechanisms that allow *Escherichia coli* to adapt to different niches. Using Pulsed Field Gel Electrophoresis, Southern blots, Multilocus Sequence Typing and dot-blot of several virulence factors, we surveyed a collection of 153 isolates. These isolates include wild mammalian and avian hosts as well as environmental isolates from mud, water and from healthy and diseased humans. Great variability in chromosome size and number of plasmids was found throughout the sample whereas no remarkable differences were found among commensal and pathogenic strains. We also obtained high levels of genetic diversity together with intermediate levels of recombination and genomic rearrangements. Defined genetic structures and a wide distribution of virulence factors were also detected in the isolates. All above suggests that *E. coli* presents considerable genome plasticity and genetic diversity which allows this species to adapt to different ecological niches. Furthermore, due to the astonishing

genetic information harbored, commensal strains carry out an important role in the evolution of the pathogenesis acting as a reservoir of potentially adaptive factors.

Abstract Category

15 Microbial Ecology and Ecological Theory

PS.15.010 A WHOLE LANDSCAPE IN A SINGLE MICROTITRE PLATE - THE DYNAMICS OF MICROBIAL DIVERSITY OF ARTIFICIALLY COUPLED ECOSYSTEMS WITH INCREASING DISPERSAL

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The emergence or the persistence of a high microbial diversity in natural ecosystems results in the balance between the probability of having the best adapted species of the local niche, and the colonization of new species through immigration from neighboring communities. Designing microbial microcosms seemed well adapted to delineate the respective role of the competitive exclusion at the local scale and the immigration events at the regional scale according to the theory of island biogeography. We started from an activated sludge of a domestic wastewater treatment plant as inoculum. It was repeatedly grown in either commercially available 96 wells microplates with 31 substrates (EcoPlate Biolog) or custom designed microplates. The productivity of each community was monitored on line with a microplate absorbance reader. The community structure and genetic diversity were assessed after each growth by CE-SSCP fingerprinting profiles. Successive inoculations allowed us to follow the dynamics of about 100 generations. In order to gradually increase the immigration pressure, we added increasing amounts of cells from neighboring wells (with bacteria having different history) for the successive inoculations. The inoculum diversity first decreased then stayed constant at equilibrium, but differed according to the substrate used (as expected by the niche theory). The immigration from the regional pool induced a larger diversity as compared with the undisturbed communities, but a slightly lower performance. These results were in accordance with the island biogeography theory; the dispersal of non adapted species increased the apparent local diversity but encountered unfavorable conditions. We were able to follow the dynamics of many communities in parallel with a perfect control of environmental conditions. This smart experimental set up allowed us manipulating artificial ecosystems to test whether some fundamental ecological theories applies to microbes.

Abstract Category

15 Microbial Ecology and Ecological Theory

PS.15.011 RESISTANCE AND RESILIENCE IN MICROBIAL ECOLOGY, THEORETICAL CONSIDERATIONS APPLIED TO IMPACTS OF MERCURY ON SOIL MICROBIAL COMMUNITIES

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Resilience of soil microbial communities is a major concept for managing ecosystems' durability. While it appears somehow difficult to give an estimation of the ecological resilience of an ecosystem, resilience can be easily defined as the time required for an ecosystem to recover from a stress while its resistance, the amount of perturbation tolerated. This is the bases of the engineering resilience concept. However, when applied to microbial communities, this concept must integrate the return to a steady state of multiple descriptors simultaneously. These descriptors may be as diverse as relative species composition and/or multiple functional activities. In addition, these descriptors may be more or less correlated, which increases the complexity of the task.

We thus developed a multivariate based estimation of microbial communities' resilience and resistance, which was validated on ECOLOG-based multiple substrate degradation analysis and biodiversity measurement using DGGE in tropical soils: Tropical soil samples were submitted to different levels of mercury and their functional diversity and genetic structure were followed for one month using ECOLOG plates and DGGE patterns, respectively. Dynamics of soil microbial community's global recovery were obtained by (i) performing Principal component (PCA) and factor analysis (FA) on the quantitative (ECOLOG) and qualitative (DGGE patterns) descriptive variables, respectively, and (ii) calculating an Euclidian distance between the individual's (the soil samples) projections using their factorial (or principal component) coordinates and (iii) representing the evolution of this distance during time.

While a sigmoid shape of this distance curve indicates an irreversible shift of ecological parameters, a dome shape allows the estimation of the resistance and the engineering resilience of a complex microbial community as the height and the width of the dome.

Abstract Category

15 Microbial Ecology and Ecological Theory

PS.15.012 RECOVERY OF METHANOTROPHS FROM DISTURBANCE: POPULATION DYNAMICS; EVENNESS; AND FUNCTIONING

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Earth's biodiversity is declining forcing humankind to consider how ecosystems' stability and services will change in future. Prokaryotic microbes can catalyze all biogeochemical cycles and have been assumed to be functionally redundant and virtually inextinguishable. However, recent work indicates that microbes may well be sensitive to environmental disturbance. Functional guilds like methane oxidizing bacteria with a well-defined substrate usage are prime candidates to study potentially endangered microbial functions. We simulated disturbance-induced mortality by mixing native with sterilized paddy soil in two ratios, 1:4 and 1:40, representing moderate and severe die-offs. Disturbed microcosms were compared to an untreated control. Recovery of activity and populations was followed over four months by process measurements, pmoA-qPCR, pmoA-based T-RFLP, and a pmoA-based diagnostic microarray (pmoA: gene encoding a subunit of the methane monooxygenase). Methanotrophs showed a remarkable resilience even over-

compensating for die-offs, yet resulting in a decreased evenness. Evenness of a microbial community has been found to be important for their functioning under environmental stress. Here, we show that upon disturbance different growth rates may lead to an uneven community that nevertheless is functioning better than the control. Linking microbial diversity or evenness to functional resilience should consider not only population structure but also population dynamics and controls of activity. While paddy soil methanotrophs supported by high methane concentrations have been found to be resilient, methanotrophs in upland soils living at extremely low methane concentrations was found to be vulnerable. We suggest that the energy flow through a microbial population and its effect on quantitative population dynamics plays a key role deserving increased attention in biodiversity-ecosystem-functioning studies.

Abstract Category

15 Microbial Ecology and Ecological Theory

PS.15.013 AGING WELL: METHANOTROPHIC POTENTIAL AND COMMUNITY STRUCTURE ALONG A PADDY SOIL CHRONOSEQUENCE OF 2000 YEARS.

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Given that rice paddies are anthropogenic methane sources and the inevitable need to increase rice production to sustain human population growth, it is pertinent to identify the effects of long term agriculture on the selection of methanotrophs. Methanotrophs play a crucial role in mitigating methane emission from rice paddies. Here, we analyzed the methanotrophic community along a chronosequence of paddy soils from China covering recently reclaimed sites to paddies under permanent culture since 2000 years (Cheng et al. 2009, *Geoderma* 151, 31-41). Fresh soil was incubated under 10 vol.% CH₄ atmosphere. Temporal changes in activity and population dynamics were followed by methane uptake measurement, pmoA-based T-RFLP and group-specific quantitative PCR (pmoA: gene encoding a subunit of the methane monooxygenase). Maximum potential methane oxidation rate was positively correlated to soil age. Long-term agriculture also imposes a selection pressure on different groups of methanotrophs. More evident in the ancient soil, type Ib methanotrophs were observed to multiply in correspondence with increasing methane uptake, while other groups showed a relatively constant community composition. Long term agriculture shapes the microbial community, selecting for sub-populations of methanotrophs and allows for an elevated level of potential methane oxidation.

Abstract Category

15 Microbial Ecology and Ecological Theory

PS.15.014 MICROBES AND MICROBIAL PATTERNS AS SENTINELS FOR GROUNDWATER ECOSYSTEM ASSESSMENTS

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Healthy aquifers deliver important ecosystem services, e.g. the purification of infiltrating water and its storage in high quality. Nowadays, environmental policy started to consider groundwater not only a resource but a living entity. For a comprehensive protection and management of groundwater ecosystems, the assessment of its ecological status is necessary, but ecological groundwater quality criteria have not defined so far. Aquifers are ecosystems harbouring a vast diversity of microorganisms which are involved in almost all geochemical processes occurring in the subsurface. Besides, microbes are characterised by short generation times and high metabolic rates when compared to classical indicator organisms such as invertebrates, providing a fast reaction to environmental changes. Subsurface microorganisms and microbial patterns are thus believed to represent ideal sentinels of groundwater ecosystem status. Within the framework of a current research project several aquifer systems located in geographically distinct areas of Germany are under investigation. The focus is on the development of an ecologically sound concept for the assessment of groundwater quality and ecosystem health. Our central working hypothesis is that in low dynamic habitats microbial communities reflect the in situ environmental conditions and their biomass, activity and diversity may serve as sensitive criteria for short-term dynamics in aquifers. Linking biodiversity patterns with environmental data is still a challenge for ecologists. Our first results indicate that groundwater microbial community patterns successfully mirror impacts from land use (e.g. agriculture) resulting in an elevated bacterial biodiversity atypical for pristine systems. The application of multivariate statistical approaches, such as multivariate regression trees and aggregated boosted trees, useful for the identification of indicator species/groups is introduced.

Abstract Category

15 Microbial Ecology and Ecological Theory

PS.15.015 IN SITU ABUNDANCE AND DISTRIBUTION OF HYDROCARBON-DEGRADING SRB AT MARINE GAS AND OIL SEEPS

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Hot spots of sulfate-reduction (SR) occur in anoxic marine sediments, where methane, short-chain alkanes or oil components dominate. In methane seeps, SR is tightly coupled to anaerobic oxidation of methane (AOM). In contrast, in sediments with natural oil seepage methane-dependent SR drops to less than 10% of total SR rates as an indicator for non-methane hydrocarbon degradation by sulfate-reducing bacteria (SRB). Although several SRB have been described to be capable of hydrocarbon degradation it is still unknown which SRB are relevant in the environment.

Here, we describe the distribution and abundance of SRB at marine oil and gas seeps as detected by CARD-FISH.

Non-aggregated Deltaproteobacteria made up between 4% and 23% of total single cells while SRB of the Firmicutes were close to the detection limit. SRB of the *Desulfosarcina/Desulfococcus* (DSS) branch strongly dominated gas as well as oil seeps with up to 17% of total single cells, indicating a major role in hydrocarbon degradation. Of these, members of SEEP-SRB1, including the sulfate-reducing partners of methanotrophic archaea but also members of unknown metabolic functions were abundant with up to 35% but only at gas seeps. Other DSS cells seemed to be highly diverse indicating the presence of numerous diverse

and specialized but low abundant SRB (e.g. relatives of str. BuS5) rather than the presence of a dominant subgroup or single species. SEEP-SRB-2, -3, and -4 as well as relatives of aromatics-degrading *Desulfobacterium anilini* were detected in remarkable numbers of up to 5% of total cells. cDNA-based clone libraries were constructed for ribosomal (16S) and functional genes (*aprA*, *dsrA*). Clone sequences confirmed our previous results, showing most sequences affiliated to the DSS branch, SEEP-SRB groups 1 and 2, *Desulfobacterium anilini* and *Syntrophobacterales*. The active sulfate-reducing community is currently further analyzed by stable-isotope probing and NanoSIMS.

Abstract Category

15 Microbial Ecology and Ecological Theory

PS.15.016 ENERGY FLOW AND DISTURBANCE SHAPE METHANOTROPHIC COMMUNITIES

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Methane is next to water vapor and carbon dioxide the third most important greenhouse gas. The largest single sources are natural wetlands and wetland rice fields. In wetland rice fields, aerobic methanotrophs play a key role oxidizing methane before it is released to the atmosphere. However, it has been shown that methanotrophs are affected by nitrogen fertilization, a common agricultural practice in rice fields. We tested two hypotheses: (1), nitrogen fertilization has an inhibitory effect, and (2), methanotrophs are more resilient at high energy flows. We used microcosms supplementing a thin layer of water-saturated paddy soil from below with methane and from above with air. We used two different source strengths of methane resulting in a different flux into the oxic-anoxic boundary, and, hence, different energy flows through the community. Ammonium-based fertilization was applied at high and low energy flows. We analyzed the different communities with a *pmoA* specific microarrays (*pmoA*: gene encoding a subunit of the methane monooxygenase), and used ordination and indicator species to unravel the effects of energy flow and fertilization. Different energy flows had a significant influence on the methanotrophic community, while fertilization had not. Fertilization did not affect methane oxidation activity. Indicator species analysis revealed the genus *Methylobacter* and an environmental cluster strictly affiliated with paddy soils as indicative for high energy flows. Based on these results we rejected the first (effect of fertilization), but could support the second hypothesis (energy flow). We suggest that methanotrophs are adapted to particular environments, and that changes in the energy flow have major effects for the community structure.

Abstract Category

15 Microbial Ecology and Ecological Theory

PS.15.017 THE ROLE OF MICROBIAL COMMUNITIES IN SOIL FOOD WEBS

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A growing body of food web theory studies the paradoxical idea that herbivory can have positive feedbacks on nutrient flow to plants. In more detail, the relationships between root grazing herbivores, microbial pathogens and microbial decomposers may heavily influence plant primary production. By developing a theoretical model combined with glasshouse experiments using dune grasses, ectoparasitic nematodes and dune microbial inoculum, we tested the idea that plants, microorganisms and plant herbivores are in a delicate balance between maximizing nutrient mineralization, inhibiting microbial pathogens and maintaining plant biomass. Microbial enemies of nematodes can control population size of root grazing nematodes, thus protecting the plant from overgrazing. Individual plant species have their own local microbial flora, and this flora interacts with grazing nematodes to affect their population size as well as plant growth. However microbial nematode control is dependent on plant and nematode species, and the mechanisms responsible for this variation have not been established. In fact, nematode grazing activity may stimulate microbial growth through mineralization of nutrients and increased availability of root carbon. In our research, we are resolving the mechanisms of interaction between root herbivores, microorganisms (the microbial loop including protozoa and bacteria) and the plant host. Specifically, we focus on the microbial loop for its critical role in nutrient mineralization. In the past, both positive and negative feedbacks between microorganisms and herbivorous nematodes have been established. Our research describes an unexplored interaction network in soil food webs where herbivorous nematodes and the microbial loop positively affect nutrient availability and plant productivity.

Abstract Category

15 Microbial Ecology and Ecological Theory

PS.15.018 USING ECOLOGY FOR THE UNDERSTANDING AND RATIONAL DESIGN OF BACTERIAL CONSORTIA FOR THE BIODEGRADATION OF WASTE METAL WORKING FLUIDS.

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Bacteria can be found in short term associations, established communities or may be deliberately assembled for a specific purpose. In these circumstances there will be a relationship between the diversity of bacteria present and their net effects such as biodegradation, and nutrient cycling. Many of these effects are ecosystem functions providing services such as bioremediation of wastes or promoting plant growth. In various situations these effects are important for an extensive list of services including human health, rumen function, or the local sewage plant. In all of these we are interested in the relative significance of the different ways in which bacterial diversity influences the activity of systems. Our aim is to study the impact of bacterial diversity by identifying the variance in effects due to different species identities, species richness and interactions among species. We will present results using the random partitions design (1, 2) that show the relative contribution of bacterial identities, diversity and interactions to the bacterial anaerobic reduction of metal working fluid. Our results show the potential for the rational design of biological systems using microbial ecology and ecological theory to establish communities effective in the biodegradation of metal working fluids and the generation of biogas (3). Metal

working fluids are lubricating coolants, extensively employed for manufacture of metal products. They are chemically complex (oils, amine propoxylate, biocides), toxic in nature, with high chemical oxygen loading (COD 20,000-50,000 mg/l), which makes their safe disposal problematic. 1) Bell, T., Newman J. A., Silverman B. S., Turner S. L., and Lilley A. K. 2005. *Nature* 436. 2) Bell T., Lilley A.K., Hector A., Schmid B., King L, and Newman J.A. 2009. *Am. Nat.* vol 174. 3) Curtis, T.P., Head I.M., Graham, D.W. 2003. *Environmental Science and Technology*.vol 65

Abstract Category

15 Microbial Ecology and Ecological Theory

PS.15.019 CURVE-BASED COMMUNITY FINGERPRINT DATA ANALYSIS IN THE FOLLOW-UP OF ECOLOGICAL SUCCESSION AND EVALUATION OF TREATMENT EFFECTS

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Community fingerprinting techniques produce data from large environmental sample numbers at a reasonable cost, enabling statistically valid study design. The technical details of fingerprinting methods are discussed actively; less attention has received the subsequent data processing step necessary to refine the fingerprint images into reproducible, representative and ecologically significant information on the phenomena.

Here we describe the possibilities of exploratory and hypothesis-driven analysis of fingerprints as curves (electropherograms) instead of binary or semi-quantitative peak data. To exemplify community succession and the effects of different treatments we utilise length heterogeneity PCR fingerprint and background data from a 21-week contaminated soil bioremediation experiment (10 sampling times and three treatments: oil+plant, unvegetated ctrl, uncontaminated ctrl). Pearson correlation was used for similarity, cluster and canonical analyses. Averaged fingerprints enabled recognition of community changes. The taxa responsible for the community shifts were identified by sequencing.

The 180 bacterial community fingerprints grouped into three clusters. Contaminated soils separated from the Unaltered Cluster into the Oil-Degrader Cluster mostly due to the rapid growth of *Aquabacterium*, an r-strategist whose relative abundance correlated with oil degradation rate. Short fragments were characteristic of the Developed Cluster and comprised likely K-strategic *Alfaproteobacteria*. On week 21 these were indifferent in all three treatments, demonstrating community recovery from the contamination.

Both similarity and diversity approaches showed that oil addition induced a rapid but reversible shift in the bacterial community. The gradual effect of the growing plant was less pronounced but also significant. Curve-based fingerprint analysis avoided the caveats and subjectivity of peak binning and quantitation, but enabled sensitive and equally extensive data analysis.

Abstract Category

15 Microbial Ecology and Ecological Theory

PS.15.020 INSIGHTS INTO THE IRON-OXIDIZING ZETAPROTEOBACTERIA: IS EVERYTHING EVERYWHERE?

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The *Zetaproteobacteria* represent a novel class of *Proteobacteria* found predominantly at sites of microbially mediated iron oxidation in marine environments. The chemoautotrophic, neutrophilic Fe-oxidizing representative isolate for this novel class, *Mariprofundus ferrooxydans*, was isolated from Fe-oxide encrusted microbial mats at Loihi Seamount, Hawaii. To date, environmental clones from the *Zetaproteobacteria* have been shown to be dominant at numerous sites with iron-rich microbial mats, including Loihi Seamount, Juan de Fuca Ridge, Tonga Arc and the Southern Mariana Backarc Spreading Center. However, no attempts at describing the phylogenetic relationships of these geographically distinct clones have yet been made. For this study, 66 full-length (>1300bp) small subunit rRNA gene sequences representing 228 *Zetaproteobacteria* clones were identified using the Ribosomal Database Project seqmatch algorithm. Aligned sequences were grouped into operational taxonomic units (OTUs) based on a minimum similarity of 97% (DOTUR). Sequences were also analyzed via principle component analysis (PCA) and analysis of molecular variance (AMOVA) to see if any regional/environmental trends could be correlated to *Zetaproteobacteria* OTU distribution. Seven OTUs contained clones from more than one geographic region. Three of these were widely distributed throughout the Pacific Ocean. The published representative *Zetaproteobacteria* isolates (*M. ferrooxydans* JV-1 and PV-1) grouped as the tenth most abundant OTU, and were found to be endemic to Loihi Seamount. Several other OTUs were also found to be endemic. PCA and AMOVA provided support for *Zetaproteobacteria* biogeography. Ultimately, in order to gain a more detailed understanding of *Zetaproteobacteria* biogeography we need—in addition to further sampling from more diverse geographic regions—more isolates from the dominant OTUs identified by this study.

Abstract Category

15 Microbial Ecology and Ecological Theory

PS.15.021 BIOGEOGRAPHIC PATTERNS IN *THERMOCOCCUS* ISOLATES FROM HYDROTHERMAL VENT SYSTEMS OF THE PACIFIC

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In terrestrial environments islands can be geographically isolated from one another leading to the divergence of populations. In marine environments hydrothermal vent systems and the organisms associated with them can exist as island-like ecosystems dispersed along plate boundaries and geographically isolated from one another over vast stretches of the seafloor. While geographic isolation is commonly accepted as an evolutionary force in the divergence of macroorganisms

the significance of geography in the structuring of microbial diversity remains unclear. *Thermococcus* are an Archaeal genus of hyperthermophilic microorganisms, found to have ubiquitous distribution in hydrothermal habitats. Although *Thermococcus* are anaerobic they can withstand exposure to oxygen and cold temperatures, allowing them to survive outside of hydrothermal habitats and resulting in high dispersal potential. DNA analysis of *Thermococcus* isolates from the Juan de Fuca Ridge, Gorda Ridge, East Pacific Rise, Mid-Atlantic Ridge, Loihi Seamount, and Mariana Arc, were used to determine the relationship between geographic distribution and relatedness. Amplified fragment length polymorphism (AFLP) analysis was used to resolve genomic differences at the species and strain level in 85 *Thermococcus* isolates, allowing for the detection of biogeographic patterns. Population genetic analyses were used to test for geographic genetic structure in isolates at varying geographic scales. AFLP fingerprints and population genetics analyses differentiated isolates from different regions thus supporting the pattern of endemic populations resulting from geographic isolation, while raising new questions about distinct lineages observed and the identification of putative ecotypes.

Abstract Category

15 Microbial Ecology and Ecological Theory

PS.15.022 MODELING NICHE PARTITIONING OF *SYNECHOCOCCUS* SPECIES IN YELLOWSTONE HOT SPRING MICROBIAL MATS

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We are developing a theory of niche structure for *Synechococcus* species inhabiting microbial mats in the effluent channels of Yellowstone alkaline siliceous hot springs, basing both modeling and microbiological approaches on the physical, chemical and biological realities of this community. Most mathematical speciation models assume that a predetermined Gaussian curve describes how fitness relates to an environmental parameter. In contrast, we developed a procedure that optimizes the shape of the fitness curve subject to given environmental parameters (e.g., temperature fluctuation). Our model output for one parameter (e.g., temperature) was not a Gaussian curve with mean value at the parameter average. Rather, it was a flattened u-shaped curve with maxima at the parameter extremes, possibly resulting from longer exposure times at the extremes than at the average. Given the improbability of bimodal temperature optima in a single organism, these results suggest that two species may be better than one in a fluctuating environment, i.e., fluctuations in environmental conditions may lead to niche partitioning. We have used our model to perform competition experiments between two hypothetical species where the first species has Gaussian fitness and the second species has fitness represented by a sum of two Gaussian curves. We have observed combinations of curve width and separation that allow the second species to outcompete the first, further supporting our niche partitioning theory. We are currently considering two fluctuating environmental parameters and incorporating temperature and light data we have empirically measured in situ into our model. In addition, we have cultivated numerous *Synechococcus* isolates and have characterized them as to species, using *psaA* sequence variation and an evolutionary simulation, Ecotype Simulation. Studies of the isolates' temperature and light adaptations will allow us to test the accuracy of our model results.

Abstract Category
15 Microbial Ecology and Ecological Theory

PS.15.023 TOWARDS THEORETICAL MICROBIAL ECOLOGY: HOW MUCH DO WE BENEFIT FROM BORROWING GENERAL PRINCIPLES OF MACRO-SCALE ECOLOGY?

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It is commonly accepted that modern microbial ecology remains mostly descriptive science with limited ability to predict microbial performance and translate microbiological data (e.g. 16S rRNA survey) into macro-scale perspectives of biogeochemical processes at ecosystem to landscape levels. It is further assumed that ecological theory has been shaped mostly by plant and perhaps animals ecologists, while microbial ecology lags behind. In this presentation, I will analyze the applicability to soil microbial communities of several principles, concepts and 'laws' firmly established in general ecology: the concept of ecosystem and carrying capacity, Liebig's 'Law of Minimum, Shelford's "Tolerance Law", 'Alle principle' etc. It will be shown that some of the listed 'laws' are empirical generalizations of limited theoretical value. Actually they can be derived as particular cases of more general solutions generated by non-linear dynamic theory developed for microbial populations. Modern molecular microbial ecology combined with kinetic experiments in continuous culture gives excellent opportunity to create more refined mathematical description of population dynamics than those used for plants and animals. Simpler life cycle of microbial populations, high growth rates, perfect control of environmental conditions and support by advanced molecular tools gives real chance to improve the bases of general ecological theory by using certain microbial communities as model examples. On the other hand, we will greatly benefit from borrowing mathematical tools and concepts carefully developed in plant and animals ecology to characterize bio-morphological structure of natural populations, such as age-dependent structure, differentiation, genetic heterogeneity, etc. Another important lesson which plant ecologists can teach us is the theory of community dynamics: understanding and prediction of community evolution and ecological succession induced by perturbations

Abstract Category
15 Microbial Ecology and Ecological Theory

PS.15.024 SPATIAL PATTERNS OF BACTERIA SHOW THAT MEMBERS OF HIGHER TAXA SHARE ECOLOGICAL CHARACTERISTICS

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Whether bacteria display spatial patterns of distribution and at which level of taxonomic organisation such patterns can be observed are central questions in microbial ecology. Here we investigated how the total and relative abundances of eight bacterial taxa at the phylum or class level were spatially distributed in a pasture by using quantitative PCR. Geostatistical modelling was used to analyse the spatial patterns of the taxa distributions. To test whether the spatial distributions of the different taxa were related to soil heterogeneity, we performed exploratory analyses of relationships between abundance of the bacterial taxa and key soil properties. The distributions of the relative abundance of most taxa varied by a factor of 2.5 to 6.5 and displayed strong spatial patterns at the field scale with autocorrelation ranging between 2 to 37 m. These spatial patterns were taxon-specific and correlated to soil properties, which indicates that members of a bacterial clade defined at high taxonomical levels shared specific ecological traits in the pasture. Overall, the present study showed spatial patterns of distribution of bacteria both at the meter scale and at high taxonomical levels of organisation. Such spatial patterns allow comprehensive observations and predictions of bacterial occurrence in nature, hence helping in the generation of hypotheses concerning the mechanisms generating and maintaining bacterial diversity. The taxa-specific spatial patterns observed here suggest that, in a given environment, ecological traits are shared at high taxonomic levels within the domain Bacteria. This is a piece of evidence that the 16S rRNA gene tree divisions are not only based on evolutionary theory, but also have an ecological reality

Abstract Category

15 Microbial Ecology and Ecological Theory

PS.15.025 THE NEBRASKA SANDHILLS ALKALI LAKE ECOSYSTEM: FITTING A NULL OR NICHE BASED MECHANISM OF SELECTION

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Understanding the forces that shape microbial community structure and function is an important research topic in microbiology. Contained within the Nebraska Sandhills are numerous small lakes, many of which are highly alkaline. A unique combination of climate, geology, and hydrology has resulted in extreme alkaline-saline and freshwater lakes being in close proximity to each other. Because the lakes are in close proximity, microbes freely exchange by animal movement as well as by wind. Thus, assuming water chemistry is a strong selective force, we hypothesized that community structure would correlate to water chemistry (Niche-based mechanisms). The aim of this study was to survey the diversity of microbes in lakes over space and time by pyrosequencing 16S tag rRNA amplicons as a preliminary investigation into the distribution patterns of microbial taxa. DNA was extracted from 16 samples obtained from different lakes (spatial) and at different times in two seasons (temporal). The samples were amplified with 6-base tags and sequenced using the Roche 454 technology. Sequences were processed through the Ribosomal Database Project pyrosequencing pipeline. Taxa richness, abundance, and co-occurrence between samples were then calculated. Four taxa comprised between 70 - 95% of the most abundant Genera in each sample. Across all 16 samples, there were 166 total unique Genera, of which 31 were abundant (upper quartile abundance) and 135 were rare (less than 0.1% abundance). While there were differences in diversity between samples, these differences did not correlate to pH, alkalinity, salinity, location, or time. The

structure of the lake communities is simple in that there were relatively few abundant Genera. Although our data showed clear differences in community structure between samples, there was no correlation between a presumed selective force and structure. This data suggests that gamma-community structure best fits a null rather than a niche model.

Abstract Category

15 Microbial Ecology and Ecological Theory

PS.15.026 TESTING MACROECOLOGICAL IDEAS USING MICROBIAL COMMUNITIES

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Macroecology aims to determine and explain large-scale patterns in nature. Ideas from macroecology, such as species-area relationships, lie at the heart of conservation and population ecology. Many studies have focused on the nature of the patterns without determining explanations of the mechanisms that produce the patterns. While macroecological-like patterns have been detected in microbial communities most studies are hampered by incomplete sampling of the community and the broad-brush, whole community approach that is often used by microbial ecologists. This is in contrast to ecology, where effective sampling is commonplace and studies are usually focused on taxonomic groups at the family level or lower.

We have avoided these problems by analysing patterns in the distribution of specific microbial populations at the genus level and by exploiting high-throughput sequencing technology to completely sample the community. Using the sulfate-reducing bacterial genus *Desulfobulbus* and the methanogenic archaeal genus *Methanosaeta* as models we have analysed microbial distribution using functional gene markers along an estuarine gradient. Pyrosequence data from 30 sediment samples from 10 sites has been used to determine the distribution patterns of these genera in comparison to traditional microbial ecological analyses. We show clear, distinct distribution patterns for these genera with >98% coverage of the community at all 10 sites. We also use this data to determine what macroecology patterns, such as species-area relationships, heritability of occupancy and nestedness, are present in the data. Excitingly, the ability to experimentally manipulate microbial communities opens up the possibility of testing proposed mechanisms behind macroecology patterns in a way that is not possible with larger organisms. Therefore, microbial ecology could lead the way in the move beyond patterns to mechanisms in macroecology.

Abstract Category

15 Microbial Ecology and Ecological Theory

PS.15.027 THE RELEVANCE OF NEUTRAL THEORY TO MICROBIAL ECOLOGY

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Neutral theory is based on the premise that all individuals are ecologically equivalent. Consequently individual species numbers fluctuate as a result of random birth and death events. In Hubbell's model the distribution of abundances in a community is derived from a combination of this stochastic population dynamics and immigration events from a metacommunity (Hubbell 2001). Neutral theory has been successfully if controversially applied in macrobiology. We will discuss its relevance to microbiology. We will address one of the major objections to neutrality by showing how neutral dynamics can be achieved through trade-offs that allow species to have different life history properties but the same deterministic fitness (Parsons and Quince Theor. Pop. Biol. 2007). This 'quasi-neutrality' generates neutral stochastic dynamics without the assumption of identical individuals. We will illustrate this with the example of bacteria in a chemostat. We go on to use this model to investigate whether environmental fluctuations will swamp the stochastic signature from random birth and death events in this system. We conclude with a discussion of effective population sizes in microbial communities given spatial structure and consequently how neutral theory can explain the dramatic variation in microbial species richness that is observed across environments.

Abstract Category

15 Microbial Ecology and Ecological Theory

PS.15.028 NOT ONLY WHO IS THERE, BUT ALSO WHO IS ACTIVE: HOW COMMUNITIES RESPOND TO ENVIRONMENTAL STRESS?

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Drought and the associated rewetting events are common stressors for microorganisms in soil. Yet little is known regarding how sensitive communities are to such perturbations. In soils, most microorganisms are dormant most of the time, but rewetting events should provide ideal conditions for some groups of microbes to respond and grow quickly. Identifying microbes that are active under these kinds of episodic is an ongoing challenge in microbial ecology. Who grows? How fast? To answer these questions, we characterized bacteria that actively grow following rewetting a dry soil, and following multiple dry/wet cycles. Our study site is a California grassland, with a Mediterranean climate, with long hot summer. We used bromodeoxyuridine (BrdU) to label actively growing cells. BrdU, a thymidine analog, is incorporated into newly synthesized DNA, which is then isolated from total DNA by immunocapture. Incubations were conducted to (1) assess the response of bacterial community 12h, 24h and 48h after a rewetting event, and (2) evaluate the impact of multiple cycles coupled with substrate additions. To evaluate differences between the actively growing and total communities we did initial screening using T-RFLP of 16S rRNA genes; and followed it up with pyrosequencing. Bacteria that can grow rapidly following rewetting are a small group, distinct from the overall community. The response to multiple stress cycles was dependent on substrate availability. Developing the links between community composition and function require

characterizing the composition of communities active under specific conditions and the biological processes they carry out.

Abstract Category

15 Microbial Ecology and Ecological Theory

**PS.15.029 TEMPORAL SCALING OF MARINE BACTERIOPLANKTON
ASSEMBLAGE COMPOSITION**

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Perhaps the simplest descriptor of the biodiversity of an ecosystem is its species richness. However, it can be far from simple to characterize species richness of a system as richness depends not only on sampling methodologies, but the size of the area sampled and the duration of the sampling period. This is especially true of communities as diverse as bacterial communities. The species-area relationship (SAR), the positive relationship between the number of species observed and the size of the area sampled, has received perhaps the most attention of any pattern of diversity. The temporal scaling of species diversity has received considerably less attention than spatial scaling. The species-time relationship (STR), the temporal analogue of the SAR, describes the positive relationship between the number of species observed and the time span over which the community is observed. The STR provides a baseline understanding of the temporal scales over which richness varies in a given area and is central to our understanding of community assembly and colonization dynamics. Here we examine the temporal scaling of marine bacterioplankton monthly for 6 years at multiple depths of the San Pedro Ocean Time Series (SPOT) station in the Southern California Bight. Samples were compared using automated ribosomal intergenic spacer analysis (ARISA) fingerprints. In particular, we find that marine bacterioplankton do exhibit a significant taxa-time relationship. Turnover in community composition over time increases with depth as shown by an increase in the slope of the TTR with depth. Finally, the observed turnovers through time of bacterial communities are relatively low but do not differ from those observed for a range of other taxa.

Abstract Category

15 Microbial Ecology and Ecological Theory

**PS.15.030 AQUATIC BACTERIA, LAKES, AND WATER COLUMN OVERTURN: A
MODEL MICROBIAL SYSTEM FOR DISTURBANCE ECOLOGY**

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Microbes, their processes, and their interactions with each other and with their environments are essential for life. However, a theoretical backbone for microbial ecology is lacking. To help address this, we borrowed the principles of disturbance ecology that were developed in larger-scale systems, and applied them to a model microbial experimental ecosystem. The model

system included lakes, planktonic bacteria, and water column mixing as the disturbance. Mixing is a disturbance because it disrupts physical and chemical gradients known to structure microbial communities in both space and time. We conducted a whole-ecosystem experiment during which we imposed an unprecedented disturbance on microbial communities by artificially mixing a temperate lake during peak summer thermal stratification. We observed real-time environmental responses to the lake mixing using environmental sensors, including profiled water temperature and dissolved oxygen, and analyzed water for carbon, nutrients, and a suite of respiration products. We fingerprinted the bacterial communities using automated ribosomal intergenic spacer analysis and 454 tag-pyrosequencing. Then, we performed multivariate analyses of community composition, diversity, and structure to determine the robustness of the bacterial communities to the mixing disturbance. The artificial mixing radically increased the bottom-lake temperature and exposed the microorganisms to novel physical conditions. Despite the novelty of the post-mixing environment, we found that the communities were not resistant but surprisingly resilient to the disturbance. This reveals an incredible robustness of the lake bacterial communities to unpredictable perturbation. Our results suggest that we may be able to predict microbial community responses to disturbances. This has application for understanding microbial components of global change and human wellness, and for advancing a general ecological theory for microbes.

Abstract Category

15 Microbial Ecology and Ecological Theory

PS.15.031 ANALYSIS OF BACTERIAL METACOMMUNITY ASSEMBLY AND INTERNAL DISPERSAL MECHANISMS

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The metacommunity framework predicts the spatial distribution of community patterns based on the relative importance of environmental factors, dispersal, competition and stochastic processes. However, in microbial ecology there is a debate whether pure spatial factors play any role shaping communities' biogeographic distribution or whether, according to the "everything is everywhere" concept, only species sorting through local conditions is relevant. In this study we assess this question by investigating the factors shaping a rock-pool metacommunity. For this, 50 pools were sampled in an area of approx 5000 m² on the Baltic Sea Coast. Local environmental conditions were identified measuring various abiotic (e.g. salinity, nutrient content) and biotic (e.g. phytoplankton biomass, zooplankton abundance) parameters. For the description of the spatial characteristics, a detailed map was created and spatial statistical tools were applied to the data. Bacterial community structure was determined using both TRFLP and 454 sequencing of the 16S rRNA gene. As salinity (ranging from 0 to 12 psu) was the main factor influencing microbial community composition, the data set will be further used to 1) identify the contribution of different taxa to this pattern, 2) assess the factors influencing the metacommunity structure of halotolerant bacteria, and 3) of halosensitive and halodependent groups in the fresh and saline pools, respectively. In addition, a transplant experiment was performed to examine the mechanisms of internal dispersal between fresh and saline pools. Here tanks were filled with water from two similar pools differing only in salinity, and dialysis bags were used to transfer the communities and the mixes of the two communities to their own and to the alien

environment. Survival and competition between the two communities will be assessed using bacterial abundance and activity data, and community structure determined as described above.

Abstract Category

15 Microbial Ecology and Ecological Theory

PS.15.032 DESPITE LONG TERM COMPOST AMENDMENTS, SEASONAL CHANGES ARE MAIN RUDDERS OF SOIL FUNGAL AND BACTERIAL COMMUNITY IN A VINEYARD

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Organic matter depletion is a serious problem in soil ecosystem. A great consideration has been given to possible utilization of compost in agriculture. Nevertheless organic amendments can influence soil microorganisms which play a pivotal role in sustainability of agricultural system. In a productive Tuscan vineyard soil annually amended since 2001 with 50 Kg ha⁻¹ N, 30 kg ha⁻¹ P, 70 kg ha⁻¹ K (NPK thesis), or 15 Mg ha⁻¹ compost (C thesis), or 25 kg ha⁻¹ N 15 kg ha⁻¹ P 35 Kg ha⁻¹ plus 15 Mg ha⁻¹ compost (C+ ½NPK thesis), bacterial and fungal populations of both bulk soil and rhizosphere of grapevine (*Vitis vinifera*) have been analysed. Differentially treated soils were sampled in three positions along two diverse plants in early summer (July), mid-summer (August), and before harvest (October) and community genetic fingerprints were generated by 16SrDNA and ITSrDNA Multiplex Terminal Fragment Length Polymorphism (M-TRFLP). In bulk soil, multivariate Multi Dimensional Scaling (MDS) ordination method highlighted a significant effect induced by seasonal variations, while compost or NPK treatments showed no significant differences between microbial communities at any time. In grapevine rhizosphere, temporal separation obtained by MDS was even stronger for bacterial population, due to modulation of the rhizosphere effect, while fungal community didn't show any treatment or time effect. Nevertheless, univariate analysis by ecological indices showed an increase in species richness in rhizosphere fungal population long-term fertilized with NPK. Obtained results suggested that soil microbial populations in productive ecosystems may be more sensitive to environmental changes induced by temporal variation and also show a certain degree of resilience to different agricultural practices.

Abstract Category

15 Microbial Ecology and Ecological Theory

PS.15.033 TESTING THE INSURANCE HYPOTHESIS WITH STREAM DENITRIFYING BACTERIA: ARE DIVERSE COMMUNITIES MORE RESILIENT TO DISTURBANCE?

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Ecological theory suggests diverse communities are more resilient to disturbance than species poor communities. This idea, known as the insurance hypothesis, has been tested for artificially assembled, but not naturally occurring microbial communities. We set out to determine whether

denitrification rates of diverse denitrifying bacteria communities from a forested stream are more resilient to disturbance than species poor denitrifying bacteria communities from an urban stream. Denitrification removes harmful excess nitrogen and is, therefore, a critical ecosystem service.

We inoculated microcosms with inoculum from our urban or forested study stream. We used presence-absence data from terminal restriction fragment length polymorphisms of nitrite reductase genes to estimate community diversity. Microcosms were assembled in media containing known amounts of nitrite. There were two experimental treatments: a chemical stress (AgNO_3 and NaCl) and a temperature stress ($+10^\circ\text{C}$) treatment. Microcosms were incubated anaerobically (20 hrs) and nitrite concentrations measured to estimate denitrification rates.

Species poor urban communities removed more nitrite than diverse forested communities (one-way ANOVA, $F(1,90)=7.48$, $p=0.008$). With pollutant stress, species poor communities suffered a reduction in nitrite removal capacity (one-way ANOVA, $F(1,88)=17.11$, $p=8.062\times 10^{-5}$), while diverse communities were not affected. With temperature stress, species poor and diverse communities removed comparable amounts of nitrite (one-way ANOVA, $F(1,83)=2.77$, $p=0.099$). With both pollutant and temperature stress, species poor communities again suffered a reduction in nitrite removal capacity (one-way ANOVA, $F(1,84)=4.06$, $p=0.047$). These results suggest that, while species poor urban communities show higher levels of denitrification under non-stressful conditions, they may be less resilient to disturbance than diverse forested communities.

Abstract Category

15 Microbial Ecology and Ecological Theory

PS.15.034 NICHE SELECTION OF TILLAGE MEDIATES THE IMPORTANCE OF STOCHASTIC MICROBIAL COMMUNITY ASSEMBLY

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To understand forces driving the pattern of community diversity and composition has long been a central task in ecology but so far no consensus has been reached. Both niche and neutral theories have been proposed to explain the community assembly based on attempts focusing on conspicuous macroorganisms, however, little is known about microorganisms despite their ecological importance. To fill this gap, we analyzed soil samples from agricultural land at KBS LTER experimental site (Hickory Corners, MI, USA) by microarray-based GeoChip, a high-throughput genomics technique, to characterize soil microbial communities at the whole-community-wide scale and the functional gene level to investigate the impact of tillage. Comparing tillage and non-till treatments at high fertilizer level, tillage significantly decreased the community richness (detected gene number) and diversity indexes of Shannon-Weaver and Simpson ($p<0.05$). The detrended correspondence analysis (DCA) for functional gene composition was able to separate tillage and non-till samples clearly. Moreover, tillage samples

clustered tightly but non-till samples were scattered in the DCA profile. By multi response permutation procedure (mrpp), the dissimilarities within tillage and non-till groups were 28.7 and 45.1, respectively, calculated by overall weighted mean of group mean distances. The higher within-group dissimilarity of non-till samples might be attributed to stochastic ecological drift and priority effects. The tillage practice could be regarded as an environmental filter for niche selection to decrease the species pool of regional community in neutral theory and lead to less divergent communities in different locations. These results imply that tillage practices mediate the importance of stochastic processes in soil microbial community assembly. Combined, niche-based processes and stochastic-neutral processes were jointly responsible for community assembly and their relative importance may vary.

Abstract Category

15 Microbial Ecology and Ecological Theory

PS.15.035 TRADE-OFF BETWEEN OXYGEN AND IRON ACQUISITION IN THE BACTERIAL CELLS AT THE AIR-LIQUID INTERFACE

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Many aerobic microorganisms can colonize at the air-liquid interface and form biofilm-like structure, pellicle. Although pellicle formation is considered to provide the fitness advantage for aerobes due to the accessibility for both gaseous (oxygen) and liquid (nutrient and water) phases, contribution of pellicle on the fitness is still unclear. In this study, the fitness effect of pellicle formation was investigated and the physiological characterization of pellicle cells was performed. All experiments were performed with a pellicle-forming facultative aerobe, *Pseudomonas aeruginosa* PAO1 and its derivatives in LB medium at 37 °C under static condition. At first, a pellicle deficient mutant ($\Delta psl\Delta pel$) was constructed. The total productivity (biomass) of the mutant was reduced compared to the wild type in static culture, suggesting the fitness advantage of pellicle formation in static environment. Since the fitness advantage seemed to be caused by the oxygen availability, the effect of an alternative electron acceptor in liquid phase on the pellicle formation was examined. Supplementation of medium with nitrate resulted in the decrease of pellicle mass. On the other hand, supplementation of medium with iron dispelled the negative effect of nitrate on the pellicle formation. Promotion of anaerobiosis by nitrate probably invoked the intraspecies competition for iron between aerobic and anaerobic subpopulations, causing the decline of pellicle formed by aerobic subpopulation. Transcriptome analysis revealed that the iron uptake system was highly upregulated in the pellicle cells. The result indicates that the pellicle cells are under condition of low iron availability and therefore the acquisition of iron would be crucial factor for the growth at the air-liquid interface. Thus, while pellicle formation could provide the fitness advantage for aerobic bacteria, there is a nutritional trade-off between oxygen and iron acquisition in the niche at the air-liquid interface.

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