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► To cite this version:

Mireille Morisson, Florence Vignoles, Katia Feve, Sophie Leroux, David Gourichon, et al.. Development of polymorphic markers in quail by next generation sequencing. 32nd Conference of the International Society of Animal Genetics (ISAG), Jul 2010, Edinburgh, United Kingdom. 2010, Proceedings of the 32nd International Conference on Animal Genetics. hal-01193847

HAL Id: hal-01193847

<https://hal.science/hal-01193847>

Submitted on 4 Jun 2020

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P4042 Development of Polymorphic Markers in Quail by Next Generation Sequencing

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Molecular genetic analyses in quail will benefit greatly from a higher density of genetic markers. We chose therefore to obtain high numbers of SNP (Single Nucleotide Polymorphism) by high-throughput sequencing (Titanium 454 GS-FLX, Roche) of two main types of reduced representations of the genome: restriction digested fractions of genomic DNA and EST (Expressed Sequence Tag), representing the expressed genes. The genomic fractions were generated as AFLP (Amplified Fragment Length Polymorphism) fragments and the expressed ones by preparing cDNA libraries from two tissues: embryo and brain. To optimize the information content of the SNP detected for subsequent analyses, libraries were prepared from individuals selected in the two lines involved in a QTL cross and each individual in the AFLP library was tagged. Sequencing runs produced 399,189 sequence reads from cDNA, and 1,107,451 from genomic fragments, covering over 433 Mb of sequence in total and allowing the detection of 17,400 putative SNP. Further analyses using the tags information will allow the estimation of heterozygosity in the F1 males.

Besides the interest of the production of a large number of new SNP, this technology should allow to sequence GC rich regions corresponding to the smallest microchromosomes for which there is no or few sequence in chicken. The comparison of the quail sequences with the chicken genome assembly will allow a virtual mapping of the SNP obtained, based on the high synteny conservation between these two avian species.

P4043 Progress in catfish genomics: aiming for impact at the pond bank

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Catfish (*Ictalurus* sp.) represents the largest segment of the modest domestic aquaculture industry in the United States. While demand continues to grow for safe, local, and sustainable food sources, catfish producers have been sidelined by lack of profitability tied to poor feed efficiency, high disease mortality, and uneven product quality. Simultaneously, competition with imported catfish and tilapia have limited market share and pricing flexibility. Molecular tools and genetic improvement of broodstock can help to address the industry's need for a high-quality, low-cost standardized product. Much of the last decade has been spent in the creation of genetic and genomic resources necessary for identification of QTL and realization of marker-assisted selection in catfish. These efforts are nearing fruition, but much work remains to accurately characterize and capture important phenotypic trait variation. Here, I will outline current progress in catfish genomics in the areas of map integration, whole-genome sequencing, transcriptome profiling, bioinformatics, and catfish species identification (market substitution). I will also highlight promising research areas and approaches that are likely to have economic impacts at the pond bank in the near-term.

P4044 Genetics of global gene expression patterns and gene networks affecting muscling in sheep

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This study investigated the genetics of gene expression traits (etraits) affecting rib eye muscle depth in sheep. Samples from 40 progeny born to high and low muscling sires (based on estimated breeding values; EBVs) were subjected to microarray based transcription profiling and genotyped using the ovine SNP 50k chip. Unsupervised clustering revealed significant genetic structure associated with the gene expression data. We next analyzed differential gene expression (DE) patterns between high and low muscling EBV groups and applied weighted gene coexpression network analyses (WGCNA) to detect hub genes unique to low and high EBV groups. Identified genes from DE profiling and WGCNA were subjected to functional annotation and GO analyses. There were distinct DE patterns between the muscling groups and distinct gene networks that were predictive of muscling. For the high vs. low EBV contrasts, 2,058 genes were statistically significant (BH-adjusted $p \leq 0.05$). The high and low EBV groups each contained 11 modules (with 64-491 genes and 130-482 genes, respectively). The biological processes most impacted by sire EBV were *miRNA processing*, *development* and *negative regulation of metabolic processes*. Based on several filtering criteria and GO analyses, we identified 10 and 25 genes that are unique candidate biomarkers for high and low muscling phenotypes, respectively. Finally, we targeted specific lists of etraits from these biomarkers and conducted association mapping using SNPs within cis-acting genomic regions of etraits. Preliminary results reveal genetic networks underlying muscling phenotypes. This is the first report of a 'systems genetics' approach for a muscling trait in sheep.

P4045 Genetic dissection of a complex trait: White markings in the Franches-Montagnes horse population

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A steady rise of white facial and leg markings has been observed during the domestication process of several species. In horses, the basic coat color has a significant influence on the expression of white markings with chestnut horses typically having more extended white markings than bay or black horses. We applied a whole-genome SNP association mapping approach using DNA from 53 Franches-Montagnes horses with extended white markings (cases) and 64 horses with little white markings (controls). The horse DNAs were genotyped with the equine Illumina 60k SNP genotyping microarray. The analysis identified three loci of strong association influencing the expression of white markings. One of these loci is the *MC1R* gene, which determines the basic coat color (bay vs. chestnut). The other two loci were located in a region on ECA 16 containing the *MITF* gene and a region on ECA 3 containing the *KIT* gene. The analysis revealed an epistatic interaction of the basic coat color and the quantitative expression of white markings. However, these interactions between the genotype at *MC1R* and genotypes at *MITF* and *KIT* are incomplete and not fully understood so far. For the subsequent fine-mapping the number of analyzed horses was enlarged to 384 Franches-Montagnes horses. Using the Illumina GoldenGate assay 96 polymorphisms spread over 2 Mb intervals each were genotyped for the *KIT* and the *MITF* locus, respectively. In addition the coding sequences of the *KIT* gene and the *MITF* gene were sequenced, but did not contain any obvious functional variants. We present the latest fine-mapping data regarding the *KIT* and *MITF* loci.