



Whole genome re-sequencing of the MeLiM porcine model for cutaneous melanoma

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Equine osteochondrosis (OC) is a juvenile osteoarticular pathology characterized by a local failure of cartilage maturation, leading to dissection of an articular flap or to subchondral cysts development in joints. With an incidence of 10 to 30%, OC is a major concern in terms of animal health care and economy. Many factors have been suggested including nutrition, trauma and genetics. The aim of our study is to bring new insight into molecular mechanisms and biological process involved in OC susceptibility. We performed a comparative study focused on histology, proteome and microtranscriptome of normal cartilage and subchondral bone from healthy and OC affected foals. Proteomic analyses of cartilage have long been impaired because of technical challenges related to their biochemical properties. We have developed an efficient method to characterize the proteome of cartilage and bone and compare healthy and OC foals. Our study highlighted several modulated proteins involved in extracellular matrix structure and dynamics, chondrocyte metabolism as well as bone mineralization. In addition, a SOLIDTM RNA-Seq strategy was followed to establish the cartilage and bone miRNA catalogs and define a set of modulated miRNAs. Taken together, our findings point out the heterogeneous nature of OC and suggest that both cartilage and bone defects may be involved in the physiopathology.

Key Words: equine osteochondrosis, proteomic, microtranscriptome

P5019 Genome-wide association study for immunity traits in French Large White pigs. J. Estelle^{*1,2}, L. Flori¹, Y. Gao^{1,2}, M. P. Sanchez¹, J. P. Bidanel¹, and C. Rogel-Gaillard¹, ¹INRA, Laboratory of Animal Genetics and Integrative Biology, Jouy-en-Josas, France, ²University of Wisconsin-Madison, Department of Nutritional Sciences, Madison, USA.

Improving robustness and resistance to pathogens is a high priority in most livestock species, particularly in pigs. We study immunocompetence in French Large White pigs and have previously shown that the levels of a wide range of both innate and adaptive immunity traits (ITs) are heritable. Our aim is now to dissect the genetic architecture of these ITs' by performing a genome-wide association study (GWAS) on 325 animals using the Illumina PorcineSNP60 beadchip. Significant associations have been found for a large number of various traits, as white blood cells subpopulations, specific antibody levels after vaccination or phagocytosis and in vitro cytokine production. The functional annotation provided by GWAS results will allow us to identify putative relevant candidate genes to be further studied. Since many animals have also been analyzed for blood transcriptome, we will combine genetic variations and

gene expression profiles to go deeper in the detection of candidate genes underlying the studied ITs. A further step will be to relate heritable traits that qualify immunocompetence to disease resistance/susceptibility. In conclusion, our overall results provide new data on the genetic control of ITs and should contribute to evaluate the feasibility of including health traits in future selection schemes.

Key Words: pig, GWAS, immune response

P5020 Whole genome re-sequencing of the MeLiM porcine model for cutaneous melanoma. J. Estelle^{*1,2}, D. Esquerre^{3,4}, O. Bouchez^{3,4}, S. Vincent-Naulleau^{1,2}, P. Wahlberg^{1,2}, and E. Bourneuf^{1,2}, ¹INRA, UMR1313 GABI, Jouy-en-Josas, France, ²CEA, DSV/iRCM/SREIT/LREG, Jouy-en-Josas, France, ³INRA, UMR444 LGC, Castanet-Tolosan, France, ⁴GeT-PlaGe, Genotoul, INRA, Castanet-Tolosan, France.

The Melanoblastoma-bearing Libechov minipig (MeLiM) has been selected for spontaneous melanoma occurrence and provides an excellent model to study these cutaneous tumors. QTL and genome-wide association analyses have already evidenced genomic regions potentially harboring causal polymorphisms. To help fine-mapping these regions, we have resequenced the whole genome of 2 MeLiM individuals and 2 pools of healthy and sick animals. Globally, over 700 Gb of paired-end sequences were generated on a HiSeq2000 instrument. QC-filtered reads were aligned to the reference genome (Sscrofa v10.2) and provided a read depth > 30X for each of the samples. Variant calling on the 2 MeLiM individuals identified more than 12 million variants (~10 million SNPs) between MeLiM sequences and the reference genome (Duroc). Finally, a Fisher's exact test was performed to compare the reads supporting the reference or an alternative (MeLiM allele) event in the 2 pooled groups; the frequency of the reference allele should be lower in the sick pool than in the healthy individuals' pool. Results identified over one hundred thousand MeLiM variants with significant allele frequency differences on the 2 pools and provide a short-list of potential causal variants for porcine cutaneous melanoma.

Key Words: melanoma, pig, whole genome sequencing

P5021 Case-control study for Salmonellosis confirms genetic resistance in commercial chickens. M. S. Fife^{*}, N. S. Salmon, and K. Billington, *Institute for Animal Health, Compton, Berkshire, UK.*

Systemic Salmonellosis in chickens causes a typhoid-like infection and destruction of the spleen and liver of infected animals. Resistance to this disease is a genetically determined complex trait. We previously identified, and recently refined a novel resistance QTL