response of the mammary gland of goats, one of the target organs of small ruminant lentivirus is local and independent of the systemic.

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Key Words: gen=e expression, SRLV infection, cytokines

P6007 Cell-type dependent immune response post porcine reproductive and respiratory syndrome virus infection. M. J. Pröll, C. Neuhoff, C. Grosse-Brinkhaus (Institute of animal science, University of Bonn, Bonn, Germany), M. A. Müller, C. Drosten (Institute of Virology University of Bonn Medical Centre, Bonn, Germany), M. J. Uddin (School of Veterinary Science, The University of Queensland, Gatton campus, Gatton, Gatton, Australia), D. Tesfaye (Institute of animal science, University of Bonn, Bonn, Germany), E. Tholen, and K. Schellander (Institute of Animal Science, University of Bonn, Bonn, Germany)

The porcine reproductive and respiratory syndrome (PRRS) is one of the most important diseases of the global swine industry. The understanding of the responses to porcine reproductive and respiratory syndrome virus (PRRSV) as well as of the genetic elements and functions involved in the immune response to PRRSV was lacking. Therefore the aims of this study were to investigate the expression profiles and protein profiles of candidate genes which have a high impact on the host's disease response to PRRSV in different respiratory cell types of two pig breeds (Pietrain and Duroc). To improve the understanding of genetic components and functions in the responses to PRRSV as well as to characterize changes in the immune gene expression a RNA-sequencing analysis of PRRSV infected Pietrain and Duroc lung DCs was performed and differently expressed candidate genes were obtained. The gene expression analyses of these candidate genes were done by qRT-PCR at six time points (0 h, 3, 6, 9, 12, 24 hpi) in three respiratory cell types: dendritic cells (DCs), pulmonary alveolar macrophages (PAMs) and trachea epithelial cells. Additionally, the cytokine concentrations of four (IFN-γ, IL-8, IL-1β and TNF-α) cytokines in cell culture supernatants were measured and were set in relation to the cytokine gene expression profiles. The gene expression trends with regard to 24 hpi proceeded for all respiratory cells contrarily. Investigations of the differently expressed genes showed a common reduced expression trend of the cytokines and chemokines for lung DCs. Other trends could be detected for PAMs as well as for trachea epithelial cells. There were more up-orientated gene expression trends for PAMs in comparison to the common down-orientated gene expression trends for lung DCs. Furthermore, the cytokine concentrations varied between Pietrain and Duroc and between DCs, PAMs and trachea epithelial cells. In conclusion, these various cell-type responses to PRRSV showed that there were different cell-type susceptibilities to PRRSV. With regard to time point 24 hpi the expression profiles of lung DCs led to the suggestion that these cells did not have enough power to stimulate other immune reactions. In contrast, PRRSV infected PAMs seemed to have enough capacity to give necessary signals to the immune system. These observed cell-type dependent differences should be taken into account for following investigations about immunity traits in pig breeding and about more effective vaccines.

Key Words: PRRSV, dendritic cells, pig

P6008 Genomic basis of Lipomatous Myopathy in Piedmontese beef cattle. S. Peletto (Istituto Zooprofilattico Sperimentale del Piemonte, Liguria e Valle d'Aosta, Torino, Italy), M. T. Capucchio (Università degli Studi di Torino, Torino, Italy), M. G. Strillacci (Università degli Studi di Milano, Milano, Italy), C. Boin (Istituto Zooprofilattico Sperimentale del Piemonte, Liguria e Valle d'Aosta, Torino, Italy), E. Biasibetti (Università degli Studi di Torino, Torino, Italy), P. Modesto (Istituto Zooprofilattico Sperimentale del Piemonte, Liguria e Valle d'Aosta, Torino, Italy), F. Schiavini (Università degli Studi di Milano, Milano, Italy), P. L. Acutis (Istituto Zooprofilattico Sperimentale del Piemonte, Liguria e Valle d'Aosta, Torino, Italy), and A. Bagnato (Università degli Studi di Milano, Milano, Italy)

In Piedmontese cattle breed, the sporadic detection of lipomatous myopathy (LM) is reported. The disease expression consists in degeneration/infiltration of the muscular tissue characterized by replacement of myofibers with adipose tissue. The aim of this study was to investigate the existence of genetic loci associated with LM in Piedmontese cattle breed through a genome-wide association study based on DNA pooling design. Samples used for the study were collected from the meat cutting plant of a local consortium, pairing cases and controls within farm. Samples of different muscles (diaphragm, superficial and deep pectoral, intercostal, sternocleidomastoid group and vastus lateralis) were histopathologically and enzymatically classified as cases and controls. Pools were constructed after evaluations of DNA integrity, purity and total concentration. Equal amounts of DNA were

pooled from individuals for the constitution of 4 pools (2 independent biological replicates for cases and 2 for controls). Technical duplicates were also built and all pools genotyped with the Illumina BovineHD BeadChip three times each, for a total of 24 chip array positions. SNPs positions were based on the UMB 3.1 bovine assembly. The B-allele frequencies for each array replicate were obtained from the Illumina Genome Studio software® and used in a specific pipeline in R software to perform a multiple marker test. The test statistic used for each SNP was *Ztest = Dtest/SD(Dnull)* where Dtest is the difference of the B-allele frequencies means among tails and Dnull is the difference of the B-allele frequency means within tails. The test statistic was distributed as X^2 with one degree of freedom under the null hypothesis of equal allele frequencies. The analysis was performed after excluding the 5% of SNPs showing the highest BAF variability from the replicate arrays within tail as well as the monomorphic SNPs. A total of 123 significant SNPs were identified on the 29 bovine autosomes, and 57 on the X chromosome. A subset of the identified markers falls inside or nearby the genes *LARGE*, *PDZRN3* and *DMD*. The biological role of these genes in the onset of LM has been identified looking at the known functions of the encoded proteins on the GeneCards database. In particular, a strong association has been identified on the X chromosome with the *DMD* gene, coding for dystrophin and being responsible for Duchenne muscular dystrophy in humans.

Key Words: Myopathy, Piedmontese, GWAS

P6009 Focus on atherosclerosis and the pig as a model to identify genes affecting cholesterol and other plasma lipid levels. P. Karlskov-Mortensen, S. D. Frederiksen, S. D. Pant, S. Cirera, C. B. Jørgensen, C. S. Bruun, T. Mark, and M. Fredholm (Department of Veterinary Clinical and Animal Sciences, Faculty of Health and Medical Sciences, University of Copenhagen, Copenhagen, Denmark)

Cholesterol is a ubiquitous steroid and a vital component of cellular membranes in vertebrates. At the same time, subendothelial deposition of cholesterol and other lipoproteins is the culprit of atherosclerotic lesions leading to a range of cardiovascular diseases which together represent the most frequent causes of death in the industrialized world. The balance between plasma levels of low-density lipoprotein cholesterol (LDL-C) and high-density lipoprotein cholesterol (HDL-C) is critical for disease development. A high level of LDL-C is atherogenic whereas a high level of HDL-C is cardio protective. Heritability of LDL-C and HDL-C levels in humans are estimated to be up to 70%. However, loci identified by large-scale genome-wide screens in humans explain only a small fraction of the genetic variation. Few GWAS and QTL mapping studies have been performed in mice to identify loci affecting blood lipid levels. More often, spontaneous dyslipidemic and genetically engineered mice models have been used to study the effect of dyslipidemia associated genes identified in human GWAS studies. Here we employ the pig as a full size animal model for atherosclerosis. The pig has a close similarity to humans in physiology, organ development and disease progression. We have established F2 pedigrees using Göttingen Minipig as the parental boar line and Duroc and Yorkshire as parental sow lines. Whereas Duroc and Yorkshire represent lean, fast growing production breeds, the Göttingen Minipig is an obesity prone pig breed often used in studies of obesity, diabetes and metabolic syndrome. Levels of LDL-C, HDL-C and several other blood lipids were measured at two age points in a total of 564 F2 animals. GWAS, LD and haplotype analyses identified seven loci with effect on different blood lipid levels. Five of these loci are clustered in a 12 Mb region on chromosome 3. Interestingly, the haplotypes associated with an atherosclerosis protective blood lipid profile are in general found to originate from the Göttingen Minipig.

Key Words: pig, GWAS, atherosclerosis

P6010 Identification of novel genetic variants in the equine collagenous lectin genes through targeted, next generation re-sequencing. R. S. Fraser (Department of Pathobiology, University of Guelph, Guelph, ON, Canada), A. Meyer (Ontario Institute for Cancer Research, Toronto, ON, Canada), L. G. Arroyo (Department of Clinical Studies, University of Guelph, Guelph, ON, Canada), J. D. Hammermueller, and B. N. Lillie (Department of Pathobiology, University of Guelph, Guelph, ON, Canada)

Infectious diseases are an important source of welfare and economic burden in horses. Collagenous lectins are a family of soluble pattern recognition receptors that play an important role in innate immune resistance to infectious disease. Through recognition of carbohydrate motifs on the surface of pathogens, some collagenous lectins can activate the lectin pathway of complement, providing an effective means of defense. They may also opsonize, agglutinate, or directly neutralize pathogens. Genetic polymorphisms in collagenous lectins have been shown in other species to predispose animals to a variety of infectious diseases. In this case-control study, we used a high-throughput, targeted