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Footrot is a polymicrobial disease of sheep in which *Dichelobacter nodosus* and *Fusobacterium necrophorum* often play major roles, and it results in severe lameness with hoof separation from the underlying tissue. Economic losses have been estimated at more than $20 million per year in the UK, which is the country with the best analysis; globally, footrot in the 975 million sheep outside the UK certainly has much higher costs. There are a variety of treatment and prevention methods, but many are labor-intensive and expensive. Genetic footrot resistance and/or resilience would be a valuable tool to advance control especially because it could help in prevention without the need for exposure. A sample of 251 US sheep including Katahdin, Blackbelly, and various European-influenced crossbred sheep from 9 farms with footrot issues were scored for hoof condition. A large subset (200) were genotyped with the OvineHD array (>600,000 SNP per animal), and 51 others were genotyped with the Ovine50K array (>50,000 SNP) and then imputed up to create a uniform genotype data set. Mixed models were used for genome-wide association, and they accounted for farm and genotype-derived principal components in addition to a random term for the genomic relationship matrix. Genome-wide significant loci were observed on ovine chromosomes 1, 3, 16, 17, and 18 including loci near genes involved in the immune response and in hoof development. This is the first study to report multiple genome-wide significant loci associated with ovine footrot. These results provide a strong foundation for future work toward discovering functional mutations underlying footrot susceptibility. With additional research, these data will improve tools for selectively breeding healthy sheep.

Key Words: footrot, sheep, resistance, susceptibility, genome-wide association

OP161   **Genomic background of heat stress in Assaf sheep.** M. J. Carabaño*[1], I. Ureña[1], J. H. Calvo[2], M. A. Jiménez[3], M. Ramon[4], C. Díaz[1], F. Freire[3], and M. Serrano[1], *[1]INIA, Madrid, Spain, [2]CITA-ARA-ID, Zaragoza, Spain, [3]ASSAF.E, Toro, Spain, [4]IRIAF, Valdepeñas, Spain.*

Extreme weather events pose a challenge for animal production in the Mediterranean area. Highly selected breeds are expected to be more susceptible than local breeds to environmental challenges. This study aimed at researching the genetic background of heat stress response in the Spanish Assaf population using milk recording information and meteorological data from weather stations. A total of 1.1 million of milk, protein and fat test day records from 150,000 ewes were used to generate pseudo-phenotypes that characterize individual heat stress response. Pseudo-phenotypes were obtained by fitting a random regression model, which included environmental effects (herd-year and season of lambing, parity and days in milk combination and number of lambs born) and a random regression on heat load for each ewe. Heat load was the average of the test day and the 3 previous days for daily average values of a temperature-humidity index (THI). A quadratic Legendre polynomial regression was used to describe individual responses. For rams, pseudo-phenotypes were obtained from a weighted average of their daughters pseudo-phenotypes. Genotypes of a custom 50K SNP Affymetrix microarray for 1,091 rams and 766 ewes were used in the genome-wide association study (GWAS) with the GCTA software. For milk, fat and protein yields, associations at the genome level ($p_{Bonferroni} < 0.01$) were found in chromosomes 5, 13, 17, 26 and X. Three known genes were annotated in these regions. *ADRB3* β 3-adrenergic-receptor (OAR26) is an obesity gene that is involved in the regulation of energy balance and a variety of physiological functions by increasing lipolysis and thermogenesis. *ZNF182* Zinc Finger Protein 182 gene (OARX) has roles in various cellular functions, including cell proliferation, differentiation and apoptosis, being also, a high regulator of transcription. In mouse, variation at this gene has been related with decreased food intake. *PPEF1* protein phosphatase with EF-hand domain 1 gene (OARX) suppresses genotoxic stress response via de-phosphorylation of *PDCD5*. In *Arabidopsis thaliana*, this gene is involved in heat stress tolerance.

Key Words: heat stress, GWAS, sheep

OP162   **Functional fertility genomics in sheep (*Ovis aries*).** K. Pokharel*[1], J. Peippo[1], M. Honkatukia[2], M.-H. Li[3], and J. Kantanen[1], *[1]Natural Resources Institute Finland, Jokioinen, Finland, [2]Nordgen – The Nordic Genetic Resources Center, Ås, Norway, [3]Chinese Academy of Sciences (CAS), Beijing, China.*

In sheep, ovulation rate and litter size are complex, economically important traits affected by endocrinological, genetic and environmental conditions. We have analyzed factors affecting fecundity of the highly prolific native Finnsheep and less prolific cosmopolitan Texel breeds and searched for related structural and functional changes in their genomes. Total of 31 ewes representing the breeds and their F1-crossbreds were included in the study. Experiments were focused on 2 different time points during the establishment of pregnancy: follicular growth phase (*first phase*) and early pregnancy before implantation (*second phase*). In the first phase, one ovary from each ewe was surgically removed during follicular growth phase of the estrus cycle for transcriptomic study. The second set of tissues representing second phase was collected from pregnant ewes in the slaughter house. Approximately 21000 genes and 531 miRNAs were expressed in the data set with few miRNAs differentially expressed between the breed groups. We observed a cluster of miRNAs on ovine chromosome 18 that is homologous to the one present on Human chromosome 14. We identified several putative markers (e.g., GDF9 V371M mutation) and genes (e.g., CST6, MEPE, and HBB) with expression level significantly different between the breed groups. Meanwhile several genes including those that were differentially expressed between the breeds lacked annotations. We observed that CA5A was found to be always upregulated in F1 cross-bred ewes compared with both pure-breeds. Our data suggested a role of imprinting in the fertility performance in F1-ewes. Taken together; our results will improve the knowledge of important fertility traits as well as genomics of sheep reproduction in general.

Key Words: RNA-Seq, ovary, corpus luteum, endometrium

OP163   **Genetic diagnosis of sex chromosome aberrations in sheep based on parentage test by microsatellite DNA and analysis of X- and Y-linked markers.** J. A. Bouzada*, J. M. Lozano, M. R. Maya, A. Trigo, L. B. Pitarch, T. Mayoral, and E. Anadón, *Laboratorio Central de Veterinaria, Algete (Madrid) Spain.*

Autosomal chromosome aberrations have little impact on animal breeding since the carriers usually show abnormal body conformation and are thus promptly eliminated by breeders. In contrast, anomalies involving sex chromosomes are more tolerated by species due to random X chromosome inactivation of one of the 2 X chromosomes in all somatic cells for gene dosage compensation and the fact that Y chromosome carries few genes. Hence most carriers often show a regular body conformation but abnormal sex development, mainly in females, causing sterility (most of cases) or subfertility. A reliable survey at an early stage is therefore required because detection and characterization of sex chromosome aberrations in newborn has important economic effects. It is possible to identify profiles that are indicative of chromosome abnormalities, including additional X-linked markers in usual panels for pedigree and parentage. Abnormal profiles of genetic markers located on sex chromosomes can help identify animals with chromosomal defects. Markers panel used for sheep DNA testing by Laboratorio Central de Veterinaria (Madrid) consisting of 17 autosomal microsatellite markers (CD5, CSRD247, ETH152, HSC, ILSTS005, ILSTS011, INRA005, INRA006, INRA023, INRA049, INRA063, INRA172, MAF65, McM42, McM527, OarFCB20 and SPS115), 2 microsatellite markers linked to sex chromosomes (ILSTS017 and OarAE133) and the Amelogenin marker, a gene with distinct X and Y alleles, has been proved as a very useful tool for genealogical control and detection of chromosomal abnormalities in sheep. A new markers panel with additional sex-linked markers (OarAE25, OarCP131, INRA030 and SRYM18) was imple-