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ABSTRACTS

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cial Palmero cheeses were analyzed. PLINK v. 1.90 software was used to calculate MAF values and the package Adegenet for the R software and fastStructure were used for inferring population structure. The results show that this panel is useful to distinguish the cheeses prepared with a 100% of milk of Palmera, 100% of Tinerfeña and 100% Majorera with assignment coefficients of 0.9962, 0.9999 and 0.9999 respectively. However other proportions of milks are not so clearly differentiated because it is difficult to discriminate mixtures of Tinerfeña and Majorera breeds. Anyway, this panel is highly efficient for identifying variable proportions of Palmera milk in all the experimental cheeses. In conclusion, the panel of 3,385 SNPs designed is a powerful and objective tool to detect milk from other genetically related goat breeds such us Majorera and Tinerfeña. The systematic analysis of milk or cheese with this set of markers can be used by the Palmero Cheese Denomination of Origin Regulating Council to ensure the quality and the authenticity of this product. This study was funded by the RTA2014–00047–00–00 Project (INIA).

Key Words: Palmera goat, quality, Majorera

P410 Extended haplotype homozygosity analysis reveals positive selection patters in 6 Spanish goat breeds. T. E. Ziegler[1,2], A. Molina[3], G. Anaya[3], and S. Demyda-Peyrás*[2,4], [1]*IGEVET, Instituto de Genética Veterinaria, La Plata, Buenos Aires, Argentina,* [2]*FCV-UNLP, Facultad de Ciencias Veterinarias, Universidad Nacional de La Plata, La Plata, Buenos Aires, Argentina,* [3]*Departamento de Genética, Universidad de Córdoba, Córdoba, Spain,* [4]*CONICET, Consejo Superior de Investigaciones Científicas y Tecnológicas, La Plata, Buenos Aires, Argentina.*

Goats are a major livestock resource in Spain. Their adaptability and resilience in adverse environments and their increased productivity even in intensive schemes make them valuable livestock resources. For this reason, several local breeds were developed, focused on meat or dairy production during the last decades. In this study, we determined the presence of selection fingerprints in dairy (n = 2) and meat (n = 3) Spanish goat breeds, by estimating the integrated haplotype score (iHS) of the extended haplotype homozygosity (EHH) analysis using SNP array information. Samples from178 Spanish individuals including 46 Malagueña (MLG), 43 Florida (FLO) and 25 Murciano-Granadina (MUR) dairy goats, and 24 Bermeya (BER), 20 Mallorquina (MLL) y 20 Blanca de la Rasquera (RAS) were genotyped using the Illumina GoatSNP50 BeadChip (55,000 markers). Data were pruned by LD and MAF using PLINK and analyzed (per breed) using the *REHH* package of the statistical environment R. Finally, candidate regions (selection sweeps, SS) were selected based on the iHS P-value with a minimum length of 1Mb. Results showed a clear and distinctive iHS peak in the CHI12, despite their productive ability. This selective signature, located in a chromosome previously associated with adaptability, could be related to a genetic ability to cope with the Spanish environment, in which all these breeds were bred during the last 50 years, characterized as harsh and with low levels of forage lands. In addition, meat breeds showed an increased number of selective sweeps but more diffuses than dairy breeds (19 vs 11 on average). In particular, the less selected breeds (RAS and MLL) showed more than 20 small selective sweeps located in 15 different chromosomes, whereas the most selected breed (FLO) showed only 8 candidate regions located in 5 different chromosomes, including a clear peak in CHI6. Overall, we demonstrated that iHS could be an interesting tool to analyze differences in adaptability and selection process in Spanish goats. Further research, including functional analysis of the regions detected, is necessary to obtain more precise conclusions.

Key Words: goat and related species, population genomics, breed diversity, homozygosity

P411 Unveiling genomic regions that underlie footrot resistance in Portuguese sheep Merino. D. Gaspar*[1,2], A. Usié[1,3], C. Leão[3,4], C. Matos[5], L. Padre[3], C. Dias[3], C. Ginja[2], and A. M. Ramos[1,3], [1]*CEBAL – Centro de Biotecnologia Agrícola e Agro-Alimentar do Alentejo, Beja, Portugal,* [2]*CIBIO/InBIO – Research Centre in Biodiversity and Genetic Resources, University of Porto, Vairão, Porto, Portugal,* [3]*MED-Mediterranean Institute for Agriculture, Environment and Development, University of Évora, Évora, Portugal,* [4]*INIAV – Instituto Nacional de Investigação Agrária e Veterinária, Santarém, Portugal,* [5]*ACOS – Agricultores do Sul, Beja, Portugal.*

Footrot is an acute necrotic and highly contagious disease, caused by a co-infection of 2 g-negative anaerobic bacteria, *Dichelobacter nodosus* and *Fusobacterium necrophorum*. It affects the interdigital skin and hooves of sheep, being the main cause of lameness and a major animal welfare and economical concern for the wool, milk and meat sheep industries worldwide. Current effective strategies to control footrot are costly and rely on the use of antibiotics, which could result in the development of parasite resistance mechanisms in the long term. The development of genomic markers associated with footrot resistance can provide a more reliable strategy for classifying and selecting sheep with increased resistance, besides enhancing our understanding of the biology of this disease. We aimed to identify genomic regions and molecular mechanisms associated with resistance to footrot in Portuguese native Merino breeds. For this, a set of 50k single nucleotide polymorphisms (SNPs) was specifically designed based on whole-genome data obtained for 39 sheep (depth of coverage >22X). A total of 1,466 Portuguese Merino sheep were genotyped using this SNP array. Genome-wide association analysis was performed using a quantitative trait approach based on the modified Egerton system (scores from 0 to 5) for foot integrity and footrot lesions. Genome-wide significance was determined using corrected P-values for multiple testing and SNPs significantly associated with footrot resistance were filtered at a genome-wise false discovery rate of 5%. Our results revealed a set of promising SNPs associated with resistance to footrot that overlaps candidate genes related to immune response and wound healing. These findings contribute to better understanding the architecture of footrot resistance in Merino sheep and to enhance the development of genomic tools to control infections. Also, the whole-genome data were used to investigate the underlying population structure of these native Iberian Merino breeds in the context of worldwide sheep, which is useful to define conservation and management programs.

Key Words: sheep, Merino, footrot, GWAS

P412 Comparative transcriptome analysis between suckling lambs with different levels of perirenal adipose tissue in the carcass. M. Alonso-García[1], A. Suárez-Vega[1], J. Mateo[2], H. Marina[1], R. Pelayo[1], C. Esteban-Blanco[1], J. J. Arranz[1], and B. Gutiérrez-Gil*[1], [1]*Departamento de Producción Animal, Facultad de Veterinaria, Universidad de León, León, León, Spain,* [2]*Departamento de Higiene y Tecnología de los Alimentos, Facultad de Veterinaria, Universidad de León, León, León, Spain.*

Suckling lamb meat is very appreciated in the European-Mediterranean region. This meat is tender, juicy and shows a smooth texture. Suckling lamb carcass quality is positively related to the amount of perirenal adipose tissue, which is the predominant carcass internal fat depot. Quality traits of interest in this production show a strong influence of maternal effects as the lambs are fed exclusively of milk and slaughtered between 21 and 30 d of age. RNA sequencing (RNA-seq) has proven to help expand our understanding of the relationships between the transcriptome and the phenotype across different physiological, treatment, or disease conditions. The objective of the present study was to compare the perirenal fat transcriptome between lambs with high and low percentages of perirenal fat in the carcass. For that, 18 male Spanish Assaf lambs born in the same flock and lambing season from primiparous ewes were initially considered. After birth the lambs had colostrum access for 4 to 8 h, and they were then fed ad libitum with reconstituted milk replacer powder. The animals were slaughtered when they reached the market live-weight (9–12 kg). At slaughter, perirenal adipose tissue samples were collected from each lamb for RNA extraction. After a phenotypic characterization of the carcass composition, RNA samples from the 4 lambs with the high-