

Leptin receptor LEPR gene is associated with reproductive seasonality in Rasa Aragonesa sheep breedK. Lakhssassi¹, M. Serrano², B. Lahoz¹, P. Sarto¹, L. Iguacel¹, J. Folch¹, J.L. Alabart¹ and J.H. Calvo^{1,3}¹Centro de Investigación y Tecnología Agroalimentaria de Aragón – IA2, Zaragoza, 50059, Spain, ²INIA, Madrid, 28040, Spain, ³ARAID, Zaragoza, 50018, Spain; klakhssassi@cita-aragon.es

Leptin gene and its receptor have been strongly associated with production and reproduction traits. The aim of this research was to perform an association study among some polymorphisms detected in the *LEPR* gene and three reproductive seasonality traits: the total days of anoestrus (TDA), based on weekly individual plasma progesterone levels and defined as the sum of days in anoestrus; the progesterone cycling months (P4CM), defined for each ewe as the rate of cycling months between January and August, and also based on progesterone determinations; and the oestrus cycling months (OCM) defined for each ewe as the rate of months cycling between January and August, and based on oestrus records. A total of 239 Rasa Aragonesa ewes from one flock were controlled from January to August 2012. We sequenced the exons 4 and 20 of the *LEPR* of 20 ewes with extreme phenotype values for TDA and OMC to search polymorphism. Four non-synonymous SNPs were selected for genotyping the whole population (n=203): one in exon 4 (rs411478947), and 3 in exon 20 (rs412929474, rs428867159, and rs405459906). Only, the interaction between the SNP and age affected the TDA, P4CM and OMC traits for SNP rs412929474 in exon 20, showing different effects between mature and young ewes. After Bonferroni correction, the TDA phenotype differed among genotypes in young ewes, finding significant differences between the GG and AG genotypes. The haplotype and the interaction haplotype × age, affected also the TDA and OMC traits. Two haplotypes were associated with OMC variability considering the whole population. Thus, ewes with 0 copies of these haplotypes showed more (h2) or less (h4) oestrous cycling months (depending on the haplotype) that those with 1 copy. Also, other haplotype was associated with TDA phenotype in both young and adult ewes, finding significant differences between animals carrying 0 or 1 copies. This genetic information address for the first time the role of the *LEPR* gene in ruminant's reproductive seasonality.

Sequence-based GWAS on carcass traits and organ proportions in Charolais cowsP. Martin¹, S. Taussat^{1,2}, D. Krauss³, D. Maupetit³, A. Vinet¹ and G. Renand¹¹Institut National de la Recherche Agronomique, UMR1313 Génétique Animale et Biologie Intégrative, Domaine de Vilvert, 78352 Jouy en Josas, France, ²Alice, 149 rue de Bercy, 75012 Paris, France, ³Institut National de la Recherche Agronomique, UE332 Unité expérimentale de Bourges, Domaine de la Sapinière, 18390 Osmoy, France; pauline.martin@inra.fr

Slaughter traits have a main economic value in beef cattle. They are also an important information source on the physiological variability among animals. To investigate the genomic control of some of these traits, a sequence-based GWAS was performed on 578 adult Charolais cows. Animals were slaughtered at seven years of age, after a fattening period. They were phenotyped for 18 traits: empty body weight (EBW), carcass yield, percentage of muscle, percentage of fat, 5th quarter, 5th quarter's fat, leather, rumen, omasum, abomasum, intestines, total digestive tract, total reproductive tract, liver, lungs, heart, kidneys and spleen. The carcass yield and all 5th quarter and organ traits were expressed relative to the EBW. Cows were genotyped with the BovineSNP50 SNPchip (Illumina Inc., San Diego), and their genotypes were imputed up to the sequence level based on the run6 of the 1000 bull genomes project (2,333 animals including 128 Charolais bulls), using successively the FImpute and Minimac software. GWAS analyses were performed using the GCTA software. All traits together, we identified 19 significant QTL at the stringent sequence based Bonferroni threshold (-logP>8.19). The carcass yield, the percentages of muscle and fat, the 5th quarter and the 5th quarter's fat were all found highly associated with the same region of the BTA2. These QTL reflect the well-known effect of the myostatin major gene on the carcass composition. Even though the relative weight of the 5th quarter shows a strong association with this gene, no QTL was observed at this position for the organs taken individually. Other QTL were detected in association with the kidneys (several QTL on BTA 18 and 24), with the lungs (two QTL on BTA 19), with the rumen (BTA 2 and 28), with the heart (BTA5) and with the abomasum (BTA 28). Further investigation will be made in parallel with other phenotypes such as feed efficiency.