the frequency of unfavorable homozygous (<1.2%) among the selected group compared with the corresponding original genotypic frequencies of 22.7% and 28.1%, respectively. Thus, the predicted genotypes could be used for selection decisions to increase the frequency of favorable alleles for the desired monogenic trait. Furthermore, animals that are likely to have the favorable homozygous genotype could be identified and genotyped before breeding to confirm their genotype status. Therefore, an animal linear model could provide additional information that could be used in a breeding program to select for monogenic traits.

Key Words: monogenic trait, animal linear model, genetic improvement, selection

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P60 Abstract withdrawn

P61 Association studies for the age at first lambing in Rasa Aragonesa ewes. L. P. Iguacel*[1], K. Lakhssassi[1], M. P. Sarto[1], B. Lahoz[1], J. Folch[1], M. A. Jiménez[2], M. Serrano[2], J. L. Alabart[1], and J. H. Calvo[3], [1]*CITA-IA2, Zaragoza, Spain, [2]Department of Animal Breeding and Genetics, INIA, Madrid, Spain, [3]CITA-ARAID-IA2, Zaragoza, Spain.*

In sheep, delays in the age at first lambing (AFL) give rise to unproductive periods and a decrease in productive life. Despite its proven influence on economic profitability, in the Rasa Aragonesa sheep breed the efforts in the last years to improve it have been scarce. The aim of this study was to identify new SNPs/genes associated with the AFL trait in sheep by using a SNP panel for parentage assigment that also include functional SNPs. For this purpose 191,114 fist lambing records (ewes mated without hormonal treatments) from 327 farms were analyzed using the GLM procedure (SAS), and were corrected for environmental

effects. The model included $FecX^R$ genotype, farm, month and year of birth as fixed effects. Model residuals were used in the association studies. A total of 351 ewes from one farm were genotyped using KASP technology with a panel of 172 SNPs that included 153 SNPs for parentage assignment and 19 functional SNPs. The association analysis was performed with the GCTA software (Yang et al., 2011). Sixteen SNPs were found associated with AFL trait at $p_{nominal} < 0.05$. These SNPs were located in *BMP15*, *KISS1R*, *MTNR1A*, *SPTAN1*, *FA2H*, *TMEM154* and *MTUS1* genes. However, associations at the genome level ($p_{Bonferroni} < 0.05$) were only found for SNP rs421419167 (*BMP15/FecX^R* allele). Associations at genome-wise suggestive significance ($p_{suggestive} \leq 1/n$) were found for SNPs rs421419167, rs398938610 and rs412567923 located in *BMP15* (*FecX^R* allele), *KISS1R* and *SPTAN1* genes, respectively. The *FecX^R* allele causes increased prolificacy in heterozygous and sterility in homozygous ewes. The SNP rs398938610 is a non-conservative mutation (p. C309F) located in *KISS1R* gene. This mutation was predicted as tolerated but with a low SIFT value (0.06) by VEP software. Kisspeptin (KISS1) and its receptor (KISS1R) form a system that regulate the release of GnRH that modulates the release of gonadotropins from the pituitary. KISS1/KISS1R system appear to be important for aspects of reproductive physiology, ranging from the initiation of puberty to the induction of ovulation. These results have to be validated in a bigger population before undertaking decisions about its management in the selection program of this breed.

Key Words: sheep, age at first lambing, SNP panel, KASP technology

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P62 Genome-wide association study (GWAS) identifies the FecX^Gr allele in BMP15 segregating in Rasa Aragonesa sheep breed. L. Chantepie[1], M. Serrano[2], M. P. Sarto[3], L. P. Iguacel[3], M. A. Jiménez[2], J. L. Alabart[3], J. Folch[3], B. Lahoz[3], S. Fabre[1], and J. H. Calvo*[4], [1]*Université de Toulouse, INRA, Toulouse, France, [2]INRA, Madrid, Spain, [3]CITA-IA2, Zaragoza, Spain, [4]CITA-ARAID-IA2, Zaragoza, Spain.*

Rasa Aragonesa is an autochthonous Mediterranean sheep breed, mainly reared in extensive or semiextensive farming systems and oriented to meat production. The Cooperative Oviaragon-Grupo Pastores carries out since 1994 a selection program for prolificacy in this breed, with 490,337 controlled ewes at present. A *FecX*-mutated allele called *FecX^R* in *BMP15* gene was described in Rasa Aragonesa sheep breed. This polymorphism causes increased prolificacy in heterozygous and sterility in homozygous ewes. However, highly prolific ewes without the *FecX^R* allele have been found in the population. A genome-wide association study (GWAS) was performed to identify other hyperprolific genetic variants in the Rasa Aragonesa sheep breed. The GWAS was performed with the GCTA software (Yang et al., 2011) using 158 ewes (73 high prolific *vs*. 85 low prolific ewes) with the Illumina AgResearch Sheep HD (680K) microarray. Ewes having at least 3 lambing records, and without the *FecX^R* allele were selected from the whole Cooperative Oviaragon-Grupo Pastores database. These ewes came from 33 and 36 different farms for high prolific and low prolific ewes, respectively, and were selected as unrelated as possible based on their pedigree information. A significant association at the genome level ($p_{Bonferroni} < 0.05$) was found for SNP oar3_OAR27_50971170_dup located in *BMP15* gene (Oar3.1 X: g. 50971170C > T). This is the *FecX^Gr* mutation (NM_001114767.1: c.950C > T) associated with increased prolificacy in other sheep breeds. Only 14 heterozygous animals were found (MAF = 0.04), all of them associated with high prolific ewes. These animals were sequenced for *BMP15*, finding only the *FecX^Gr* allele. No homozygous animals were found for this allele. This allele was first described in Grivette (Demars et al., 2013), and recently in Mouton Vendeen (Chantepie et al., 2018), Romanov, Dorper and Ovella Galega (Vera et al., 2018) sheep breeds. These results could indicate the ancestry of this variant in sheep. The selection program should implement the genotyping of reproducers for the *FecX^Gr* allele, to know its frequency and the size of its effects to be able to undertake decisions about its management.

Key Words: *FecX^Gr*, *FecX^R*, *BMP15*, Rasa Aragonesa, prolificacy