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Session 54 Poster 16

Whole genome association study for reproductive seasonality trait in the Rasa Aragonesa sheep breed

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Many sheep breeds from the Mediterranean area have seasonal patterns of oestrous behaviour and ovulation. Maximal reproductive activities occur from August to March. This reproductive seasonality induces great variation in lamb production and, therefore, in the market price of lamb meat. This spring ovulatory activity is under genetic control, yet to date only a small proportion of the total variation has been explained by genes identified through linkage analysis and candidate gene association studies. To address the lack of information at the genomic level we present a results from a preliminary whole genome association study that was performed using data on reproductive seasonality for 141 ewes of the Rasa Aragonesa Spanish sheep breed that were genotyped using the OvineSNP50K BeadChip platform of Illumina®. Biannual registration data of seasonality was measured in an experimental flock as total days of anestrus (TDA) based on weekly blood progesterone levels from January to August, and corrected for age and body condition score. TDA was defined as the sum of periods in which three or more consecutive samplings having plasmatic progesterone levels lower than 0.5 ng/ml. Results have pointed to new regions across the genome not previously described that are potentially associated with natural cyclicity in this breed. Use of a greater number of samples and next generation high density BeadChips could help to accurately identify loci that are involved in controling the seasonality of sheep. Financed by Ministerio de Economía y Competitividad and FEDER (INNPACT Project IPT-010000-2010-33) and INIA (B. Lahoz grant).

Session 54 Poster 17

Towards a genomic monitoring of intra-breed sheep variability

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Limiting the number of breeding stock used can result in the loss of genetic variability in most breeds, and may restrict the capacity to improve and adapt breeds to future needs. The objective of the VARUME project (genetic Variability of RUMinants and Equine species) was to quantify the genetic variability in French ruminant and equine species, based both on pedigree and molecular data. The selection program of the four main dairy sheep breeds in France (Lacaune, Manech Tête rousse, Manech Tête noire and Basco-Béarnaise) is based on the selection of a few elite breeding animals. To assess the variability in genomic information, males were genotyped using the SNP50 chip. The genetic variability in these four breeds will be determined by calculating the effective population size based on linkage disequilibrium over multiple generations. As the effective population size may depend on parameters, data source and methods used, a comparison will be made with the effective population size based on pedigree information, the differences will be interpreted considering the size of the sample and structure of the population. This information can be used to observe the evolution of genetic variability in the breeds and in turn improve the breed's capability for adaptation.

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