

Session 11: Recent developments in genomic evaluations: New traits, new populations. Chairs: Andrew Cromie, María Jesús Carabaño

S11.O-03

INCORPORATING GENOMIC INFORMATION ON THE GENETIC EVALUATION OF SPANISH LOCAL BEEF CATTLE BREEDS.

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Nowadays, genomic selection is a reality for many species and many breeds in many countries. The advantages are very clear in breeds with large population sizes however, we need to understand what value could have for local breeds with limited sizes. Genomic data was first added in genetic evaluations in the Spanish beef local cattle breeds started in 2020. This was done with the support of the Spanish Ministry of Agriculture funding a project with the objective of studying the impact of incorporating genomic information in their genetic evaluation. The project involved the seven most important local breeds in Spain, Asturiana de Valles (AST), Avileña Negra Ibérica (ANI), Morucha (MOR), Parda de Montaña (PAR), Pirenaica (PIR), Retinta (RET) y Rubia Gallega (RUB). The departure situation of their breeding programs was very heterogeneous across breeds. That heterogeneity affects many aspects, their population sizes, their capacity for recording phenotypes, their economic resources to invest in genomics and new phenotypes, the scale of their organizations among others. We also identified that the only phenotype in common to all breeds was weaning weight. Therefore, our first objective was to evaluate the impact of incorporating genomic information for the evaluation of weaning weights. After the end of the project, four breeds (AST, ANI, RET, RUB) out of the seven Breeds Association genotyped more animals, and we also included more traits in the study. In this second round, our objective then was to assess the impact of adding more genomic information in the genetic evaluation of weaning weights as well as the effect in the genetic evaluation of other traits as well, for those four breeds. Those additional traits were calving difficulty for AST and RUB, fertility traits for ANI, RET and RUB, postweaning weight for ANI and carcass traits for ANI and RUB. We applied ssGBLUP methodology using Blupf90+ software (Misztal et al, 2018). Our evaluation criterion was the change in accuracy (defined as a function of the error prediction variances) relative to the accuracy of the model without including genomic data. The amount of phenotypic and genomic data as well as the models of evaluations varied across breeds. In the first round we observed that the increase in accuracy varied among breeds ranging from no gain in AST for direct and maternal weaning weight to an increase of 14% and 16%, respectively for MOR. The impact was higher for the breeds with lowest accuracy. In the second round, we observed that adding more genotypes had a positive impact on the gain in accuracy for all breeds, however that gain again varied among breeds and among groups of individuals per breed. AST was the one with the lowest increased up to 2% and RUB was the one that benefit the most up to 10%. In all cases, candidates to selection and dams without phenotypes were the ones that benefit the most across breeds. In terms of traits, fertility traits and calving difficulty had the most benefit. Each Breed Association is now in a reflection process to make a decision on if and how to go for the next steps.