Is there any benefit in the metapopulation for the genetic evaluation of local beef cattle in Spain? The weaning weight, as a case study.

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Summary

Genomic information has been incorporated to the genetic evaluation of the main local beef cattle breeds, Asturiana de los Valles (AST), Avileña Negra Ibérica (ANI), Morucha (MOR), Parda de Montaña (PAR), Pirenaica (PIR), Retinta (RET) y la Rubia Gallega (RUB). The Ministry of Agriculture funded a project to assess the impact of the incorporation of genomic information into their genetic evaluations. Previous studies in these breeds indicated that the degree of genomic relationships and persistence of phase in short-medium distances were high. In addition, simulation studies that mimic the genomic structure of these populations showed a potential benefit of the multibreed approach. Thus, the objective of this work was to evaluate with real data the realize impact of such approach joining together genotypes, pedigree and weaning weights of calves from the breeds mentioned above.

Data consisted of 372.398 weaning weight records. The pedigree file contained 570.836 individuals. Genotypes were obtained with the "Thermofisher Axion Bovine Genotyping" chip. After regular editing of the genotype files in each breed, the final genotypes file had 6.452 animals and 31.754 SNPs in common to all of them. For the analysis of the metapopulation, we used the ssBLUP methodology under a single trait animal model with maternal genetic and permanent effects. To apply this model, we assumed that these breeds have a common based population and that (co)variances were similar and equal to the weighting average of the (co)variance from each breed. The weighting factor was based on the amount of weaning weight records contributed by each of them. In addition, we assumed different means. The model included the effect of the contemporary group (CG) and age at weaning nested within breed. We also fit sex t, cow age and breed effects. CG was taken at random. Results of this model were compared to the result obtained in each breed independently. To do so, we calculated the relative gain in accuracy for the genotype and ungenotyped individuals.

Results were different across breeds. In the genotyped animals, the relative gain in accuracy for the direct component of weaning weight ranged between 0% and 73% for RUB and PAR, respectively. The ungenotyped animals from ANI, MOR, PAR and RET gained also accuracy. For the maternal component the gain in accuracy for the genotyped animals was between 1,3% and 33% for RUB and PAR. The ungenotyped animals from ANI, MOR, PAR and RET gained also accuracy as well. The breeds that benefit most of the metapopulation in this single trait model were those whose breed heritabilities, were smaller than those assumed for the metapopulation and had less amount of information.

This is just a first attempt to evaluate the impact of a multibreed genomic evaluation in these breeds. This approach does not provide any answer to our initial question because the assumptions we made do not exactly fit the data. We are now in the process of applying a multiple trait model making used of the meta-founders theory with a cross-validation strategy to evaluate the predictive ability.