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Poster 12

A SNP-BLUP genomic evaluation with breed-specific SNP effects for three-way dairy crossbreds

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Crossbreeding is a growing strategy among dairy farmers, usually chosen to compensate for weaknesses of a breed, in order to obtain robust cows, to facilitate the transition to a different farming system (organic farming, specifications of a PDO, etc.) or to combine various breed strengths. However, in many countries, genetic evaluation is only available for purebred cattle and farmers who choose to implement a crossbreeding scheme lose access to genetic evaluation information. This study proposed to investigate the prediction accuracy of a SNP-BLUP genomic evaluation with breed-specific SNP effects, in the case of a three-(or n-) breed rotational crossbreeding scheme, in the frame of the GenTORE European project. This approach requires the breed of origin of alleles to be known. A first software was developed to determine the breed of origin of alleles, based on haplotype identification, and tested on simulated data, in a three-breed rotational crossbreeding scheme. Estimated breeds of origin were compared to the true breeds of origin and the error rate was 1.5%. Hence, this approach was accurate enough to be used for the purpose of crossbred genomic evaluation. A second software developed for genomic evaluation was validated through simulation. Data were simulated based on 50K SNP, for different reference population sizes and trait architectures. Prediction accuracy and bias were estimated using a validation study. They were compared to the ones obtained using a classical multiracial SNP-BLUP, in which all animals were evaluated as part of a single population, with no distinction between breeds. Attention was paid to computing time and memory requirements. This approach will be used to analyse real datasets including purebred and crossbred animals. To this end, more than 8,500 genotyped crossbred animals from different types of crosses (2 or 3-way crosses) have been collected in the EVAGENOC project funded by Apis-Gen.



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OPTIBOV-PT: genomic characterisation of Portuguese native cattle for optimal performance

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Iberian native cattle retain high genetic diversity relative to that of their European counterparts, including: taurine Y1 and Y2 unique patriline; distinct Q-maternal lineages and a strong influence of T1-matrilines of African origin; as well as African taurine cattle ancestry in their autosomal genomes. This renders Iberian breeds a great model to study the genomic impact of cattle diversification. The OPTIBOV international project aims to study bovine populations from 6 biogeographic regions, from north to south, in Europe and Africa. Here, the genomic variability of the Barrosã, Mirandesa and Mertolenga Portuguese native breeds will be investigated to identify markers for (positive) adaptation traits and for (negative) traits to be improved. Recommendations of The Food and Agriculture Organization of The United Nations were followed for phenotyping 30 animals of each of these breeds. Whole-genome resequencing data was generated to carry out association studies of well-defined phenotypes under local conditions. We will study inbreeding in detail and genomic regions which have been under natural (environmental adaptation) as well as artificial (human-mediated) selection. An important deliverable of OPTIBOV is a genotyping assay specific for more diverse traditional cattle to include markers associated with specific traits. OPTIBOV results will be used to improve breeding programs. Also, some unique adaptive features of local cattle to harsh environments can be useful for adjusting mainstream breeds to climate change.

