Indirect predictions for indicine cattle breeds based on a multi-breed genomic evaluation

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Indirect predictions (IP) are used for young genotyped animals that lack phenotypes or are from commercial herds. These animals are often excluded from official evaluations to avoid decreasing accuracy and increasing inflation and bias in genomic breeding values (GEBV). In Brazil, information is scarce for breeds like Brahman, Guzerat, and Tabapua. IP based on a larger reference population could enhance genomic selection accuracy on these breeds and the different genetic bases across breeds can be modeled with Metafounders (MF). This study to compute IP for young genotyped Nellore, Brahman, Guzerat, and Tabapua animals in a multi-breed population in the presence or absence of metafounders to model the genetic differences across breeds. MF are pseudo-individuals acting as proxies for animals in the base population. Records from the four breeding programs of the National Association of Breeders and Researchers (ANCP—Ribeirão Preto, SP, Brazil) were used. Data included pedigree (4.2M), phenotypes (329K), and genotypes (63.5K) across all breeds. The traits analyzed were adjusted weight at 210 (W210) and 450 (W450) days of age and the scrotal circumference at 365 days of age (SC365). Single-breed and multi-breed analyses were performed. Indirect predictions were derived as the sum of the SNP effects weighted by the gene content using four reference populations: single-breed ssGBLUP, multi-breed ssGBLUP with MF and without MF, and for small breeds based on Nellore. The validation was performed using genotyped animals born after 2020 (W450 and SC365) or 2021 (W210), as validation animals. These animals had genotypes and phenotypes for all traits. LR validation method was used to compute the accuracy of IP for these animals and GEBV from the whole data set (GEBVw), when all their information was included. Correlations between SNP effects among all the scenarios were calculated. The results suggest that when young genotyped animals are not included in an official multi-breed evaluation, robust IP can be obtained whether metafounders are used or not, independent of the breed. This helps obtain fast genomic predictions for young animals without overwhelming the evaluation system.

Combining breeds increased the accuracy of IP, mainly when the number of genotyped animals in a single-breed was small. Adding Metafounders helped to decrease bias and avoid under or over-dispersion, with slightly increased accuracy.