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Accuracy of genomic predictions for navel length in Dairy Gir cattle

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Validating genomic prediction equations is essential for sustainable breeding programs, as it allows for assessment of model reliability through parameters such as prediction accuracy. In Zebu cattle, navel length, particularly in males, is a relevant trait due to its association with increased risks of injuries and infections. Therefore, the objective of this study was to validate genomic predictions for navel length in Gir dairy bulls. For this purpose, data from the National Gir Dairy Cattle Breeding Program (PNMGL), a technical cooperation between Embrapa Dairy Cattle and ABCGIL, were used. The dataset included 10,975 phenotypic records and 198,503 pedigree records, along with genotypes for 56,092 animals obtained using SNP chips of varying densities. The Illumina BovineHD (777K) chip was used as the reference, and genotypes from other chips were imputed to a common set of approximately 420,000 SNPs. A cross-validation methodology was applied to calculate the correlation between genomic estimated breeding values (GEBVs) of the validation groups and the traditional estimated breeding values (EBVs) and GEBVs from the training population. Genetic and genomic evaluations were performed using an animal model. The contemporary group was defined as the combination of evaluator, year of evaluation, and herd. Season, age, and age squared were included as fixed effects, while permanent environmental and direct additive genetic effects were included as random effects. The estimated heritability for navel length was 0.33. The validation population consisted of 36 bulls, each with more than 20 phenotyped daughters, randomly distributed to three groups. To conduct the validation, all descendant information (phenotypes and pedigree) was removed for each group of bulls. Subsequently, evaluations were conducted to estimate EBVs and GEBVs for both the training and validation populations using the BLUPF90 software suite. Prediction accuracy was assessed using Pearson correlation: $GEBV_{TR} \times GEBV_{VAL}$, and $EBV_{TR} \times GEBV_{VAL}$. The results indicate a promising outlook for the early selection, supported by the strong correlation between the GEBVs of the training and validation populations ($r = 0.79$). Additionally, the correlation between EBV and GEBV ($r = 0.73$) highlights the model's strong ability to predict genomic breeding values for navel length. These results suggest that incorporating genomic information enhances the model's ability to capture additive genetic variability, particularly in populations where only phenotypic and pedigree data are available, conditions that often reduce the precision of traditional analyses. These findings reinforce the value of genomic selection as a tool for early decision-making in breeding programs. However, they also suggest that prediction accuracy could be further improved by increasing the number of phenotyped and genotyped animals in the population.

Keywords: *Bos indicus*, prepuce, validation.

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