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ACCEPTED MANUSCRIPT

Genomic selection for meat quality traits in Nelore cattle

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Abstract. The objective of this study was to present heritability estimates and accuracy of genomic prediction using different methods for meat quality traits in Nelore cattle. Approximately 5,000 animals with phenotypes and genotypes of 412,000 SNPs, were divided into two groups: (1) training population: animals born from 2008 to 2013 and (2) validation population: animals born in 2014. A single-trait animal model was used to estimate heritability and to adjust the phenotype. The methods of GBLUP, Improved Bayesian Lasso and BayesCπ were performed to estimate the SNP effects. Accuracy of genomic prediction was calculated using Pearson's correlations between direct genomic values and adjusted phenotypes, divided by the square root of heritability of each trait (0.03 - 0.19). The accuracies varied from 0.23 to 0.73, with the lowest accuracies estimated for traits associated with fat content and the greatest

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