

Comparison on genomic predictions for milk, fat and protein yield in Guzerat breed using GBLUP and BayesC π methods.

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Abstract:

Genetic evaluations using SNP markers information have received attention in many dairy cattle breeding programs of the world, because it provides benefits such as increased genetic gain through increasing the prediction accuracy and decreasing the generation interval. Thus, the aim of this study was to obtain the reliabilities of genomic predictions for milk (MY), fat (FY) and protein yield (PY) in Guzerat breeds comparing GBLUP and BayesC π models. The criteria assumed for quality markers were call rate greater than 0.98, MAF greater than 2% and HWE up to 10⁻⁶. For quality control of samples were adopted call rate of 0.90 and heterozygosity rate of ± 3 SDs from the mean. After the quality control of the data, were obtained a set of 45 bulls and 856 cows with 25024 SNPs. The phenotypes used for prediction of genomic breeding values (GEBV) were deregressed estimated breeding values (dEBV) according to Garrick et al., (2009). The methods used for genomic prediction were GBLUP and BayesC π through using GS3 software (Legarra et al., 2013). The prediction model was given by markers, polygenes and residual effects. In order to validate the results, were used the cross-validation methodology using Perl scripts to randomly partition the data into training and validation sets and, at the same time, enable the processing of GS3. Thus, 100 validation and 100 training populations with 701 and 200 individuals, respectively, were generated for each trait. The predictive ability of the models used for each sample population was obtained by the correlation between the dEBV and GEBVm, which was obtained only by the marker effects (rm), and also the correlation between dEBV and GEBVt, obtained by marker effects + polygenes (rt) of the animals from validation population. The averages of prediction ability obtained by GBLUP and BayesC π models were compared by t test ($P < 0.01$). Considering the GBLUP, the amplitudes (means) of for MY, FY and PY were 0.71-0.85 (0.78), 0.68-0.81 (0.75) and 0.65-0.78 (0.73) and the amplitudes of the for MY, FY and PY were 0.21-0.54 (0.33), 0.34-0.57 (0.44) and 0.12-0.43 (0.26). Considering the BayesC π , the amplitudes (means) of for MY, FY and PY were 0.73-0.84 (0.79), 0.68-0.82 (0.76) and 0.68-0.81 (0.77) and the amplitudes of the for MY, FY and PY were 0.20-0.54 (0.35) 0.28-0.54 (0.41), and 0.18-0.64 (0.36). The averages of for GBLUP and BayesC π were statistically different only for PY. All comparisons for averages were significant. The model BayesC π obtained the best results for all the studied traits using GEBVt and GEBVm. The predictive ability obtained using GEBVt demonstrates that genomic selection can be applied in the Guzerat breed. These predictions can be used as pre-selection criteria of bulls to be used in the progeny test.