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Selecting the suitable random regression model for genetic evaluations of Brazilian Holstein cattle

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The use of random regression models in genetic evaluations in Brazilian Holstein cattle depends on the identification of the most suitable model to fit lactation curves. The objective of this study was to compare models using different orders of Legendre polynomials to fit test day milk yields and persistency measures. Thus data from 231,923 complete test-day records from the first lactation of Holstein cows were used. All animals had ten records in lactation. The pedigree data included 23,141 cows with records from 245 herds, 2,735 bulls, totaling 51,638 animals. Single-trait random regression models with Legendre polynomials of orders three (LEG3), four (LEG4), five (LEG5) and six (LEG6) were used to fit data. Covariance matrices of random regression coefficients were estimated by the program REMLF90 on the ICE system of CENAPAD. The persistency measures were $PS_1 = (EBV_{280} - EBV_{60})$, $PS_2 = (\sum_{t=106}^{205} EBV_t - \sum_{t=6}^{105} EBV_t)$, $PS_3 = (\sum_{t=206}^{305} EBV_t - \sum_{t=6}^{105} EBV_t)$, $PS_4 = (\sum_{t=61}^{280} EBV_t - EBV_{60})$, $PS_5 = (\sum_{t=60}^{279} EBV_t - EBV_{280})$ and $PS_6 = (EBV_{290} - EBV_{90})$. The models were compared using the Akaike information criterion (AIC) and Bayesian information criterion (BIC) tests. The values for AIC and BIC were 1292089.8 and 1292133.5, 1304620.2 and 1304690.9, 1320646.9 and 1320751.2 and 1183697.9 and 1183842.7 for LEG3, LEG4, LEG5 and LEG6, respectively. The Spearman rank correlations between estimated breeding values (EBV) of models with increasing in the order of Legendre polynomials were 0.97 between LEG3 and other models and 0.98 to 0.99 between LEG4, LEG5 and LEG6. The heritability values were from 0.24 to 0.45, from 0.17 to 0.27, from 0.18 to 0.29 and from 0.07 to 0.29 for LEG3, LEG4, LEG5 and LEG6, respectively. The heritability for persistency measures varied from 0.08 to 0.34, except for LEG3 that was from 0.31 to 0.99. Genetic correlations between PS_i were generally high (-0.41 to 0.99). PS_6 showed medium heritability (0.12) and low genetic correlations with 305-d milk yield (0.08 to 0.12). The trajectories of genetic variances for LEG4, LEG5 and LEG6 were similar, except for LEG3, which showed high variances in the extreme periods of curve and lower in the middle. The trajectory of permanent environmental variances showed the typical U-shaped form for all models, except for LEG3, that presented a W-shaped form. The BIC and AIC values decreased with a decreasing order of Legendre polynomial, except for LEG6 that presented the lowest value. This indicated LEG6 the model that best fitted the lactation curves. On the other hand, there were not significant differences in the trajectories of models with 4 to 6 orders either in the EBVs between them. Besides the not typical U-Shaped for heritability and genetic variance trajectories, model LEG3 super estimated genetic variance and heritability values. Random regression model using Legendre polynomials of sixth-order presented the best quality of adjustment for genetic evaluations of test day milk yield and persistency in Holstein cattle in Brazil.

Keywords: genetic variance, heritability, REMLF90, Legendre polynomial, persistency

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