Breeding Values Accuracy For Growth Traits Using Random Regression And Multi-Trait Models In Nellore Cattle

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Introduction

Usually, in beef cattle, breeding values for growth traits are predicted by finite models using multi-trait analyses (MT). Nowadays, random regression models (RR) have been used for the estimation of genetic parameters of growth traits in beef cattle. More recently, spline functions have been proposed as alternative functions to orthogonal polynomials to model growth trajectories of beef cattle. To assess the risk associated to selection decisions, breeding value estimate (EBV) accuracies have to be computed. For Tier and Meyer (2004), RR models provide higher EBV accuracies than the conventional finite dimensional models since all records available from an animal can be used for genetic evaluation. However, the computation of true accuracies depends on the inversion of large order matrices. To date, it is unclear how much gain in accuracy is possible to obtain, by using RR on Legendre or spline functions compared to MT analysis, using real data. The objective of this study was to quantify the potential increase in accuracy of EBV for weights of Nellore cattle, from birth to mature age, using MT and RR on Legendre polynomials or B-Splines functions.

Material and methods

Data. A total of 87,712 weight records (birth to mature age) from 8,144 female records, belonging to the Nellore Brazil Program, were used. Data set I represented weight records measured at nine standard ages; Data set II consisted of all weight records from birth to eight years of age. Only records of animals that were reared on pasture without supplemental feed and were weaned by their biological mothers were considered. Animals were weaned at 240 days of age. The weight records distribution according to age at recording is presented in Figure 1.

Analyses. The EBVs and correspondent accuracies were obtained considering the following models: MT: multi-trait model using nine weight records; RR-L: random regression models on Legendre polynomials of age and RR-S: random regression models on B-Spline functions

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of age. The MT model included weight records at birth, weaning, 365 and 550 days and 2, 3, 4, 5 and 6 years of age. In the MT, additive direct and maternal plus maternal permanent environmental were considered as random effects for all weights. Contemporary groups (CG-MT: herd, year and season of birth) was included as fixed effect. Linear and quadratic effects of animal age at weighing (except for birth weight), and dam age at calving were included as covariables.

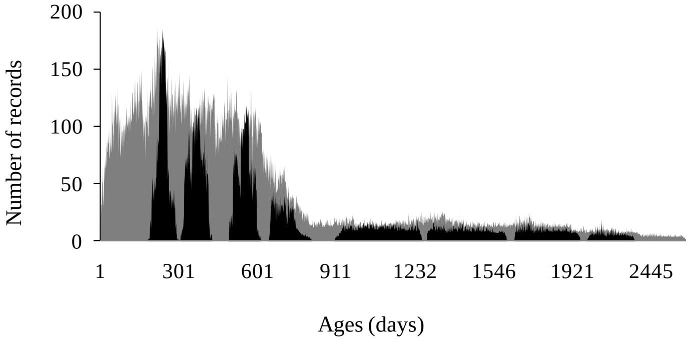

Figure 1: Number of weight records according to age at recording. Data set I (black) and Data set II (grey). Birth weight records not shown.

Fixed effects in the RR models were the same as in MT, adding a quadratic regression on orthogonal Legendre polynomials to model the population mean trends (for RR-L and RR-S). Contemporary groups were defined as GC-MT plus age at recording class (birth and every 45 d of age). For records taken after 3 yr of age CG was defined by farm, year and season of recording. For RR-L, direct genetic and permanent environmental random effects were modeled by polynomials of fourth and sixth order, respectively, while a third order polynomial was used for maternal genetic and permanent environmental effects. For RR-S, all random effects were modeled by quadratic B-splines functions. The additive direct genetic and permanent environmental effects were modeled with 4 knots (2 internal and 2 external), at equidistant intervals of 963 days, corresponding to 3 segments. Maternal genetic and permanent environmental effects were modeled with 2 external knots (only one segment). For more details see Boligon, A.A., Mercadante, M.E.Z., Forni, S. et al. (2010). The covariance components and genetic parameters were estimated using WOMBAT software (Meyer (2006)). In the MT, the EBV accuracy estimates were obtained from standard errors in the diagonal elements of the inverse of MME coefficient matrix. Selected elements of the coefficient matrix inverse, pertaining to sets of random regression coefficients for additive direct effect, were estimated for RR models. Spearman correlation were estimated between sires breeding values obtained in different analyses (MT, RR-L and RR-S)for weights from birth to mature age.

Results and discussion

Using Data set I, in general, heritability estimates for weights from weaning to 2 years of age, obtained by MT, RR-L and RR-S models, were similar. However, heritability estimates for birth weight and weights after 3 years of age, obtained by MT were slightly lower than those from RR models. With the Data set II, the heritability estimates obtained by both RR models were very similar. For all weights, the heritability estimates obtained in the Data set II were slightly higher than those estimated with the Data set I (results not shown). In the Data set I, the rank correlations of sires EBVs obtained from MT and RR varied from 0.53 to 0.76. Nevertheless, rank correlations above 0.87 were observed between EBVs obtained by RR-L and RR-S. In the data set considering all weights available (Data set II) the estimates of sires rank correlations between EBVs from both RR were slightly higher (ranging from 0.90 to 0.98) than those obtained with the same models in Data set I (ranging from 0.87 to 0.94). These results indicate that practically the same sires will be selected independent of the RR model applied for genetic evaluation. In the data set considering weight records measured at standard ages (Data set I) the accuracies of EBV obtained by RR were a little higher than those obtained by MT model (Table 1). This could be attributed to more appropriate modeling of variances and genetic parameters in the RR analysis (Boligon, A.A., Mercadante, M.E.Z., Forni, S. et al. (2010)). When all weight records available were included (Data set II), considerably higher values of accuracy were obtained with RR than with MT models, and these differences were even higher for ages with small number of records (up to 67%), such as birth and weights measured at later ages (Table 1). Thus, RR models resulted in more accurate EBVs due to allowing the inclusion of all data available and better modeling the covariance structure in the data. These results agree with those from Meyer (2004) using simulated data and considering four weight records. But, comparing RR and MT models, the author, reported only slightly higher breeding value accuracy estimates (up to 8.3%) with RR. However, Bohmanova, J., Misztal, I., and Bertrand, J.K. (2005), also with simulated data, showed that EBV accuracy estimates were similar between MT and RR (using LP or spline functions), using a set of data with weight records measured at standard ages (birth, 205 and 365 days of age). However, considering weight records measured at different ages, randomly distributed along ages, RR shown slightly higher EBV accuracy estimates than MT model.

In the present study, for both data sets, the breeding value accuracies obtained with RR-S were equal or higher than RR-L (Table 1), particularly, at extreme ages where RR-S accuracies were from 5 to 15% higher, suggesting that RR-S fits the data better than RR-L for ages with small number of records. For Meyer (2005) B-spline functions are less susceptible to estimation problems at the end of the trajectory, due to the lower degree of polynomials in the individual segments. Our results differ from those reported by Bohmanova, J., Misztal, I., and Bertrand, J.K. (2005), that using simulated weights, from birth to 410 days of age, reported slightly more accurate EBVs with RR-L than with RR-S. Real data studies, comparing breeding value accuracy estimates with RR using different basis functions (Legendre polynomials and B-Spline functions), were not found in the literature. Nevertheless, simulated data results are highly dependent on assumptions considered for both, genetic parameters and variance estimates, as for the data and pedigree structure. The genetic gain is dependent, among other factors, of the availability of accurate EBVs for young candidates to selection. Usually, EBVs for growth traits of young sires (with no or just a few offspring) have shown low accuracies. In the current study, accuracy estimates for young sires EBVs, without progeny records, varied from 0.61 to 0.66 when considering MT model (Data set I) and from 0.76 to 0.79 with RR (Data set II).

Table 1: Mean, minimum (Min.) and maximum (Max.) sires' breeding value accuracy estimates obtained by multi-trait (MT) and random regression models on Legendre polynomials (RR-L) or B-Spline functions (RR-S).

Traits[1]	Data set I (530 sires)								
	MT			RR-L			RR-S		
	Mean	Min.	Max.	Mean	Min.	Max.	Mean	Min.	Max.
BW	0.51	0.30	0.71	0.57	0.44	0.70	0.61	0.50	0.78
W240	0.59	0.37	0.81	0.64	0.54	0.81	0.67	0.56	0.79
W365	0.58	0.35	0.76	0.62	0.53	0.76	0.64	0.56	0.78
W550	0.54	0.38	0.78	0.58	0.48	0.77	0.59	0.48	0.79
W2Y	0.49	0.27	0.76	0.53	0.46	0.72	0.54	0.47	0.75
W3Y	0.47	0.24	0.74	0.52	0.44	0.71	0.53	0.49	0.70
W4Y	0.54	0.22	0.76	0.60	0.51	0.77	0.62	0.53	0.78
W5Y	0.52	0.27	0.79	0.60	0.50	0.79	0.62	0.53	0.81
W6Y	0.48	0.25	0.75	0.59	0.46	0.74	0.62	0.46	0.76

Traits[1]	Data set II (530 sires)					
	RR-L			RR-S		
	Mean	Min.	Max.	Mean	Min.	Max.
BW	0.75	0.67	0.89	0.79	0.68	0.89
W240	0.82	0.72	0.96	0.84	0.74	0.94
W365	0.80	0.69	0.91	0.82	0.71	0.93
W550	0.76	0.65	0.93	0.78	0.67	0.92
W2Y	0.72	0.67	0.92	0.73	0.66	0.94
W3Y	0.71	0.64	0.94	0.72	0.67	0.95
W4Y	0.80	0.73	0.95	0.82	0.72	0.94
W5Y	0.80	0.68	0.92	0.83	0.70	0.99
W6Y	0.78	0.64	0.90	0.81	0.68	0.96

BW: birth weight; W240: weaning weight; W365: weight at 365 days; W550: weight at 550 days; W2Y, W3Y, W4Y, W5Y and W6Y: weight at two, three, four, five and six years of age, respectively

Conclusion

The results indicate that random regression models provide more accurate EBVs over the traditionally finite multi-traits models. Thus, higher genetic gains are expected for beef cattle growth traits by replacing a multi-trait model with random genetic models for genetic evaluation. B-Splines functions could be applied as alternative to Legendre polynomials to model covariance functions for weights from birth to mature age.

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