

Genetic Analysis Of Growth Traits Considering Genetic Group, Average Numerator Relationship Matrix And A Hierarchical Bayes Model For Nellore Cattle With Uncertain Paternity

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Introduction

Multiple-sire (MS) mating, which consists of simultaneously exposing a group of cows to several bulls, is largely used by beef cattle producers in extensive operations due to its simplicity, and reduced cost and labor demand. However, this mating strategy has considerable disadvantages from the genetic evaluation point of view, as uncertain paternity negatively affect genetic merit prediction accuracy and, consequently, selection response.

The genetic group model is the oldest methodology proposed to predict the genetic merit of animals with uncertain paternity. However, the estimates can be confounded with other effects in the model as, for example, contemporary groups (CG), especially if all MS groups' offspring are exclusively in one CG or if small groups are formed (Quaas, (1988); Cardoso, F.F., Cardellino, R.A. and Campos, L.T. (2004)). Therefore, alternative statistical models have been proposed to predict the genetic merit of animals with uncertain paternity such as the average numerator relationship matrix (Henderson (1988)) and hierarchical Bayes models (Cardoso and Tempelman, (2003)). The objectives of the current study were: (1) to compare genetic group, average numerator relationship matrix and hierarchical Bayes models; (2) to estimate genetic parameters and values for post-weaning gain (PWG) and yearling weight (YW), using genetic groups and uncertain paternity models; and (3) to calculate the Spearman correlation between predicted genetic values from the different statistical procedures.

Material and Methods

Data set: The data refer to Nellore animals born between 1984 and 2006, which were provided by Agropecuária Jacarezinho Ltda, located in São Paulo State, Brazil. The traits considered in the present study were post-weaning gain (PWG) standardized to a 345 day period and yearling weight (YW) (around 550 days of age). After data consistency, performance records of 62,212 Nellore animals were kept, including 519 sires and 27,743 dams. There were 22,758 (36.6%) animals born from multiple sires (MS) mating, and 2,382 animals belonging to a base population with unknown parents. The pedigree file contained a total of 75,088 animals.

Methods: Contemporary groups (combining sex, weaning and yearling rearing farm, birth year and season, weaning and yearling management group information) with less than three animals were deleted. Animals whose measurements for either trait were greater or lower than the mean of their CG, plus or minus 3.5

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standard deviations, respectively, were removed. For all animals with records, at least the dam was known. In the linear mixed models for the PWG and YW, random effects considered were CG and additive genetic effects. For YW, genetic maternal effects and environmental permanent effects were also included as random effects. Effects of age of calf and linear and quadratic effects of age of dam (2-16 years) were included as fixed effects for both traits.

Three different approaches were adopted to deal with uncertain paternity of multiple sire offspring: 1) The genetic group model (GGM), in which "phantom parents" were attributed for animals with uncertain paternity, defining the genetic group as the group of multiple-sires that were jointly mated to their dams within the breeding season (forming 444 genetic groups); 2) The average numerator relationship matrix (ANRM), as proposed by Henderson (1988), which is based on knowledge of true probabilities of each candidate male being the correct sire - equal prior and fixed probabilities were assumed for each sire; 3) A hierarchical Bayes model (HIER), which fully accounts for uncertainty on sire assignments, as proposed by Cardoso and Tempelman (2003). In the HIER model, an equal *prior* probability was specified for each candidate sire of an animal with uncertain paternity using a Dirichlet prior density. These probabilities are changed according to the information contained in the data set to generate *posterior* probabilities.

Univariate analyses were carried out, for all three models, using a Bayesian approach via Markov Chain Monte Carlo (MCMC) methods, with a single chain of 400,000 samples from which the first 10,000 were discarded as burn-in period. The analyses were performed using the Intergen program (Cardoso (2008)). Models were compared using the deviance information criteria (DIC) (Spiegelhalter, D.J., Best, N.G., Carlin, B. P. et al. (2002)) and deviances based on pseudo Bayes factors (PBF) (Gelfand (1996)) computed from the MCMC output. Spearman correlations between predicted genetic values from different models were calculated for both traits. In this work three kinds of files were used. The first included all animals; the second file included only sires and the last one included exclusively multiple sire offspring.

Results and discussion

In the present work, model choice criteria (deviance based on DIC and PFB) were always in favor of the HIER compared to other models, indicating that the HIER model was more appropriate for both traits (Table 1). These results are in agreement with Cardoso, F.F., Cardellino, R.A. and Campos, L.T. (2004), who found that the HIER approach was better when compared to the ANRM model.

Table 1: The average deviance (DEV), penalty for effective number of parameters (PEP, deviance information criterion (DIC) and deviance based on conditional predictive ordinates (CPO) for postweaning gain (PWG) and yearling weight (YW)

Traits	Model	DEV	PEP	DIC	PFB-DEV
PWG	GGM	520,174	11,223	531,396	532,634
	ANRM	520,284	10,895	531,180	522,504
	HIER	519,906	11,133	531,039	522,276
YW	GGM	529,398	20,249	549,648	553,954
	ANRM	527,847	21,084	548,931	532,536
	HIER	525,477	22,305	547,783	531,162

GGM= genetic group model; ANRM= average numerator relationship matrix model; HIER= hierarchical Bayes model.

The PWG variance components and genetic parameters estimates were very similar across the different models (Table 2). The posterior means of heritability for PWG were similar to other research results with field data in Brazil (Cardoso, F.F., Cardellino, R.A. and Campos, L.T. (2004); Malhado, C.H.M., Martins Filho R., Lobo, R.N.B. et al. (2005); Paneto, J.C.D.C., Lemos, D.C., Bezerra, L.A.F. et al. (2002)). These results corroborate reports that weight gains from weaning to 365 days of age for Nellore animals are subject to large environmental influence (Paneto, J.C.D.C., Lemos, D.C., Bezerra, L.A.F. et al. (2002)).

Table 2: Posterior means of genetic parameters for postweaning gain (PWG) and yearling weight (YW) obtained by genetic groups (GGM), average numerator relationship matrix (ANRM) and hierarchical Bayes model (HIER)

Traits	Model	σ_a^2	σ_e^2	σ_m^2	σ_{am}	h_d^2	h_m^2	rg_{dm}
PWG	GGM	53.75	520.51	-	-	0.18	-	-
	ANMP	61.35	250.69	-	-	0.19	-	-
	HIER	63.04	249.35	-	-	0.20	-	-
YW	GGM	134.74	290.55	9.77	2.26	0.29	0.02	0.07
	ANMP	160.16	283.46	47.42	-23.59	0.33	0.10	-0.27
	HIER	188.63	273.39	10.67	-7.52	0.39	0.02	-0.16

σ_a^2 = additive genetic variance; σ_e^2 = residual variance; σ_m^2 = maternal effect; σ_{am} = covariance between maternal and direct effects; h_d^2 = direct heritability; h_m^2 = maternal heritability; rg_{dm} = correlation between direct and maternal genetic effects.

However, for YW, the HIER model tended to produce larger direct heritability estimates compared to the other models (Table 2). Estimates of direct heritabilities (Table 2) were similar to those described for Zebu cattle (Bittencourt, T.C.C., Rocha, J.C.M.C., Lôbo, R.B. et al. (2002); Giannotti, J. D. G., Packer, I. U., Mercadante, M. E. Z., et al. (2005); Boligon, A. A., Albuquerque, L. G. and Rorato, P. R. N. (2008)) The results indicate that a larger genetic gain would be expected by individual selection for YW relative to PWG, agreeing with the work of Gunsky, R. J., Garneiro, A. D. V., Borjas, A. R. L. et al. (2001).

Estimated maternal heritabilities were low (Table 2) and similar to those described in the literature for Nellore cattle (Gunsky, R. J., Garneiro, A. D. V., Borjas, A. R. L. et al. (2001); Ribeiro, M.N., Pimenta Filho, E.C., Martins, G.A. et al. (2001)). These results support the statement that the total phenotypic variation for weight at 550 days of age depends in great proportion on direct additive genetic effects compared to other genetic effects (Ribeiro, M.N., Pimenta Filho, E.C., Martins, G.A. et al. (2001)). The covariance and correlation between direct and maternal genetic effects, estimated by GGM model, were positive (Table 2). Moreover, the small magnitude of the correlation between direct and maternal effects suggests that this is not a very important effect from a biological point of view (Eler, J.P., Van Vleck, L.D., Ferraz, J.B. et al. (1995)).

For both PWG and YW, the Spearman correlation between genetic values obtained by HIER and ANMP models were consistently high in all subsets (Table 3). These high correlations suggest that regardless of the model chosen between these two, selection decision will be pragmatically the same. However, we observed that the correlations between the predicted breeding values obtained by GGM and the other models were smaller, mainly in multiple sire offspring file. Therefore, the choice between GGM and these models could generate changes in animal ranking.

Table 3: Correlation between genetic values predicted by genetic groups (GGM), average numerator relationship matrix (ANRM) , and hierarchical mixed effects model (HIER) for postweaning gain (PWG) and yearling weight (YW)

Traits	Correlation	Files		
		All animals	Sires	multiple sire offspring
PWG	HIER x ANMP	0.984	0.995	0.952
	HIER x GGM	0.569	0.795	0.469
	GGM x ANMP	0.564	0.796	0.470
YW	HIER x ANMP	0.964	0.984	0.971
	HIER x GGM	0.599	0.784	0.566
	GGM x ANMP	0.576	0.790	0.551

Conclusion

Results from different model selection criteria indicated the hierarchical mixed effects model as the best methodology for both the PWG and the YW. However, the rank correlations indicated that the choice of model can interfere with the classification of animals for selection, especially for multiple sire offspring. Lastly, results indicate that yearling weight will respond to selection more effectively than postweaning gain.

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