

ESTIMATES OF GENETIC PARAMETERS FOR EARLY GROWTH OF BRAZILIAN NELORE CATTLE

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SUMMARY

Estimates of direct and maternal variances and heritabilities for weights of Zebu cattle at each week (up to 300 days of age) and month of age (up to 630 days of age), are presented. Results from univariate and random regression model analyses are shown. Direct heritability estimates decreased from birth to 150 days of age, stayed almost constant until 270 days of age and increased with age thereafter. Maternal heritability estimates increased from birth to a peak at about 180-210 days and decreased steadily from then onwards. Maternal, permanent environmental effects showed a trend similar to that for maternal genetic effects. Random regression analyses modelled the pattern of variation in the data adequately, with estimates corresponding to those from univariate analyses.

Keywords: Beef cattle, *bos indicus*, maternal effects, random regression models.

INTRODUCTION

There are numerous estimates of genetic parameters for weights of beef cattle at standard ages, e.g. weaning, yearling or 18 month weight, in temperate regions. Reviewing parameter estimates for beef cattle in the tropics, Lôbo *et al.* (2000) presented average heritability estimates for weights at various ages similar to those reported by Koots *et al.* (1994). However, estimates of variances and heritabilities for weights at early ages and of their changes with age are not available.

Random regression (RR) models have been proposed for the analysis of traits such as growth characteristics that are recorded repeatedly for an individual. Applications so far, however, have concentrated on test day production records of dairy cows (e.g. Jamrozik and Schaeffer 1997). In beef cattle, RR analyses have mainly been applied to adult weights. This paper examines changes in variances and genetic parameters of weights of Brazilian Nelore cattle, from birth to 630 days of age. Univariate analyses for narrow ranges of individual ages, and RR model analyses are compared.

MATERIAL AND METHODS

Data. Close to 1.4 million weight records on 247,845 Nelore animals weighed at 90 day intervals from birth to two years of age were obtained from the Brazilian Zebu Breeders Association. For data sets 1 (DS1), records for birth weight (BW) and each week of age at recording, up to 300 days were extracted. This yielded partially overlapping subsets, each (except BW) spanning 15 days, with ages 0, 1-14, 7-21, to 294-308 days. After 300 days, only one age every 4 weeks was chosen, i.e., 323-336 to 603-616 days, resulting in a total of 55 subsets. Due to the narrow range of ages considered in each set, there were few dams with more than one calf weight recorded. To allow genetic and

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environmental maternal effects to be separated, data sets 2 (DS2) were extracted analogously for each month of age considering a much wider range of ages, namely 1-60, 30-90 to 570-630 days. This yielded 21 subsets with an average of 1.8 progeny records per dam. Finally, data set 3 (DS3) comprised a sample of 20,065 weight records on 3,016 animals in a single herd, distributed in 523 contemporary groups (CG). All animals in DS3 had birth weights and at least 3 subsequent records, with 79% of animals having 6 or more records. For all data sets, only records in CG of minimum size 4 (15 for BW) were retained. Pedigree information considering up to three previous generations was obtained for each subset.

Univariate analyses. Univariate REML analyses were carried out for each subset of DS1 and DS2 and DS3, subdivided in the same way as DS2. The model of analysis included CG, defined as herd - sex - weaning status (suckling or weaned) - year and month of recording subclasses, as fixed effects. Age of dam was fitted as a linear and quadratic covariable, and age at recording was taken into account as a linear covariable (except for BW). Two models of analysis differing in the random effects fitted were applied. Model 1, used for analyses of DS1, comprised direct and maternal additive genetic effects. Model 2, invoked for DS2 and DS3, fitted maternal, permanent environmental effects in addition.

Random regression analyses. Fixed effects for RR model analyses of DS3 were as for univariate analysis, with an additional cubic regression on orthogonal polynomials of age to model mean age trends. Furthermore, year and month of birth were added to the previous definition of CG subclasses. To reduce the number of different ages - and thus increase the number of records for each age - ages in four day age intervals were treated as the same age, yielding 159 different age at recording classes. Random effects fitted comprised sets of regression coefficients on Legendre polynomials of age at recording. Model A considered direct, additive genetic effects and direct and maternal permanent environmental effects only, while Model M included additive maternal effects in addition. Orders of polynomial fit were from $k=3$ to $k=6$. Temporary environmental effects were considered independently distributed, with changes in variance over time modelled by a variance function (VF), assuming log variances were described by a quadratic or cubic polynomial function of age. This resulted in up to 77 parameters to be estimated. Covariances among RR coefficients and parameters of the VF were estimated by REML. Results from different models and orders of fit were contrasted using a likelihood ratio test (LRT) with an error probability of 5%, as well as Akaike's (AIC) and Schwarz' Bayesian Information Criterion (BIC).

RESULTS

Univariate analyses. Estimates of genetic parameters from analyses of DS1 and DS2 are shown in Figure 1. Direct heritability (h^2) estimates decreased from 0.28 at birth to 0.12-0.13 at about 150 days of age. They then remained almost constant until about 270 days of age, with estimates around 0.13-0.16 for both data sets. Thereafter, h^2 increased with age to 0.24-0.26 for DS1 and 0.21-0.25 for DS2 at 570-600 days of age. Maternal heritability estimates (m^2), for DS2, increased from birth (0.01) to 180-210 days of age (0.07-0.08) decreasing with age after that. Estimates for DS1 were slightly higher than for DS2, but exhibited the same pattern of changes with age. Nelore calves are generally weaned around 240 days of age. Hence results show that maternal genetic effects started to

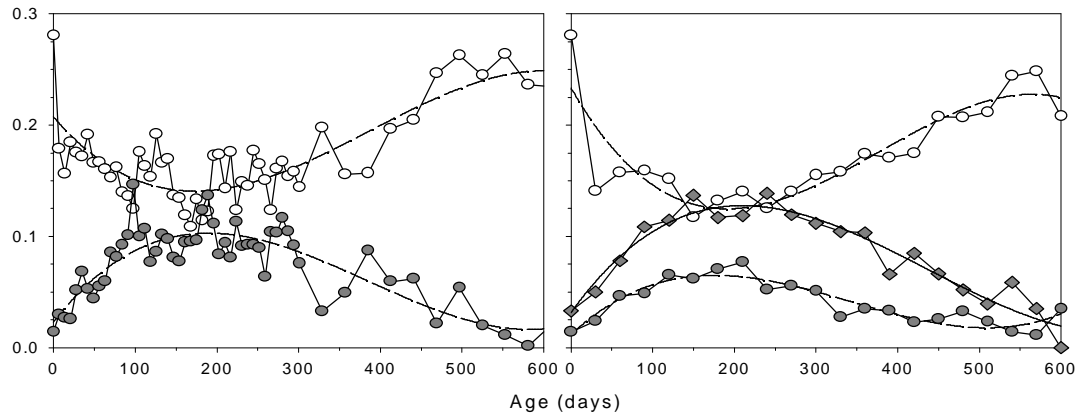


Figure 1. Estimates of direct (○) and maternal (●) heritabilities and maternal, permanent environmental effects (◆) from univariate analyses (Left: data sets 1, right: data sets 2).

decrease before weaning. Estimates of permanent environmental variances, expressed as a proportion of phenotypic variances (c^2), were 1.5 to 4 times larger than m^2 , but again showed a similar trend.

Random regression analyses. Initially, Model A with orders of fit of 6, 0, 6 and 6 ($k=6066$), for genetic direct and maternal effects, animal and maternal environmental permanent effects, respectively, was applied. Measurement error variances were modelled by a quadratic VF, resulting in a total of 66 parameters to be estimated. Estimates of covariances between RR coefficients indicated that there was little variation for the fifth (quartic) and sixth (quintic) regression coefficients due to maternal permanent environmental effects. Fitting a reduced model with $k=6064$ (55 parameters) thus did not increase the likelihood (log L) significantly, and AIC and BIC were smaller for this model than for $k=6066$. Modelling measurement error variances through a cubic rather than a quadratic VF, however, yielded a significant increase in log L. Adding maternal genetic effects to the model of analysis (model M) significantly increased log L and reduced the corresponding AIC. However, with 61 or more parameters for model M, BIC selected a model without maternal genetic effects ($k=6064$) as best. Further analyses in turn reduced the order of fit for direct genetic and permanent environmental effects to 4. In the end, both, LRT and AIC indicated that a model with $k=6664$ and a cubic VF for residual variances, with a total of 77 parameters, was necessary to model the variances in the data. A more parsimonious model with $k=4463$ and 51 parameters was chosen as best on the basis of BIC.

As shown in Figure 2, variance component estimates from both RR models were similar, and agreed with those from corresponding univariate analyses. Decreasing the order of fit for direct, genetic effects from 6 to 4 slightly changed the partition of animal effect variances. Direct and maternal heritability estimates from both models ($k=6664$ and $k=4463$) agreed closely with those obtained from univariate analyses of DS3. Estimates of h^2 decreased from 0.32 at birth until animals were about 120-180 days old (0.14), increased slowly until 270 days of age (0.17), and increased faster after that. Estimates of m^2 increased from birth (0.02) to about 110-120 days of age (0.25), and decreased with age thereafter. At 240 days, the mean weaning age, the estimate of m^2 was 0.20.

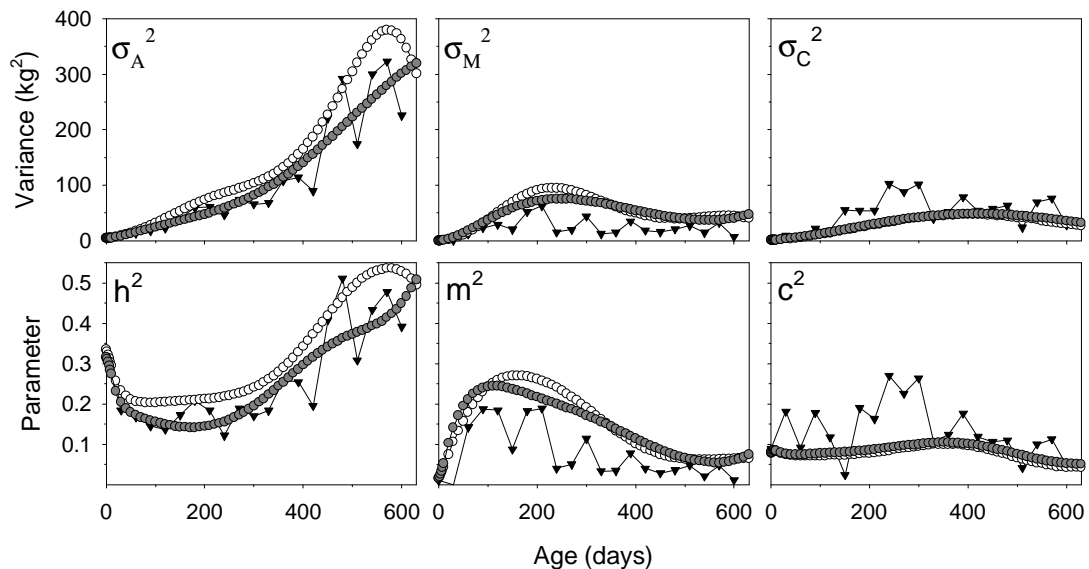


Figure 2. Estimates of variance components and genetic parameters from univariate (\blacktriangledown) and random regression (\bullet : $k=4463$, \circ : $k=6664$) analyses; direct genetic : σ_A^2 and h^2 , maternal genetic : σ_M^2 and m^2 , and maternal, permanent environmental : σ_C^2 and c^2 .

Direct, permanent environmental effects (not shown), expressed as a proportion of the phenotypic variance, increased fast from 0.28 at birth to 0.42 at about 50 days of age, remained almost the same, with a slightly trend to decrease until 580 days, and, after that, decreased fast with age. Estimates for c^2 (Figure 2), were virtually the same for both RR models ($k=4463$ and $k=6664$), were essentially unaffected by age, and were lower than m^2 . Estimates of c^2 from univariate analyses were somewhat larger than those obtained with RR models, differences presumably reflecting sampling variation in partitioning of the total variation. Additive genetic direct correlation estimates between weights at standard ages (birth, weaning, yearling and final weight) were moderate to high and maternal genetic and environmental correlations were consistently high.

CONCLUSIONS

Direct heritability estimates changed with age and were largest when maternal heritability estimates were lowest. The importance of maternal genetic effects for weights started to decrease close to weaning, indicating that a higher response to selection for maternal ability could be expected if selection were based on pre-weaning weights, around 180-200 days of age, rather than weaning weights. A model with RR modelled the pattern of variation in the data adequately, with estimates similar to those obtained with univariate analyses.

REFERENCES

- Jamrosik, J. and Schaeffer, L.R. (1997). *J. Dairy Sci.* **80** : 762.
 Koots, K.R., Gibson, J.P., Smith, C. and Wilton, J.W. (1994) *Anim. Breed. Abstr.* 62: 309.
 Lôbo, R.N.B., Madalena, F.E., and Vieira, A.R. (2000). *Anim. Breed. Abstr.* **68**: 433.