Estimates of genetic covariance functions for growth from birth to 550 days of age in Tabapuã cattle

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OBJECTIVES

The objective of the present paper was to estimate genetic parameters for weights from birth to 550 days of age in Tabapuã cattle, using random regression models.

MATERIAL AND METHODS

➢Data were provided by Brazilian Zebu Association (ABCZ)

➢21,762 weighting records from 4,221Tabapuã animals, born from 1975 to 2000, were used.

➢Tabapuã is a Brazilian Polled Zebu breed➢Animals were weighed, on average, every 90 days from birth to 550 days of age. ➢Only records of animals raised on pasture, with at least five weights and in contemporary groups (CG) with at least 8 animals were kept.

➢CG definition included: herd, year and month of birth, sex, weaning state (suckling or weaned), and year and month of record.➢ Pedigree information considering up to three previous generations were obtained.

➢All animals had birth weight. A higher number of weight records occurred around 240 days of age (weaning age).

Table 1. Summary of data structure

Number	
Records	21,762
Animals with records	4,221
Sires	347
Dams	2,821
Animals in analysis	10,112
Contemporary groups	1,546

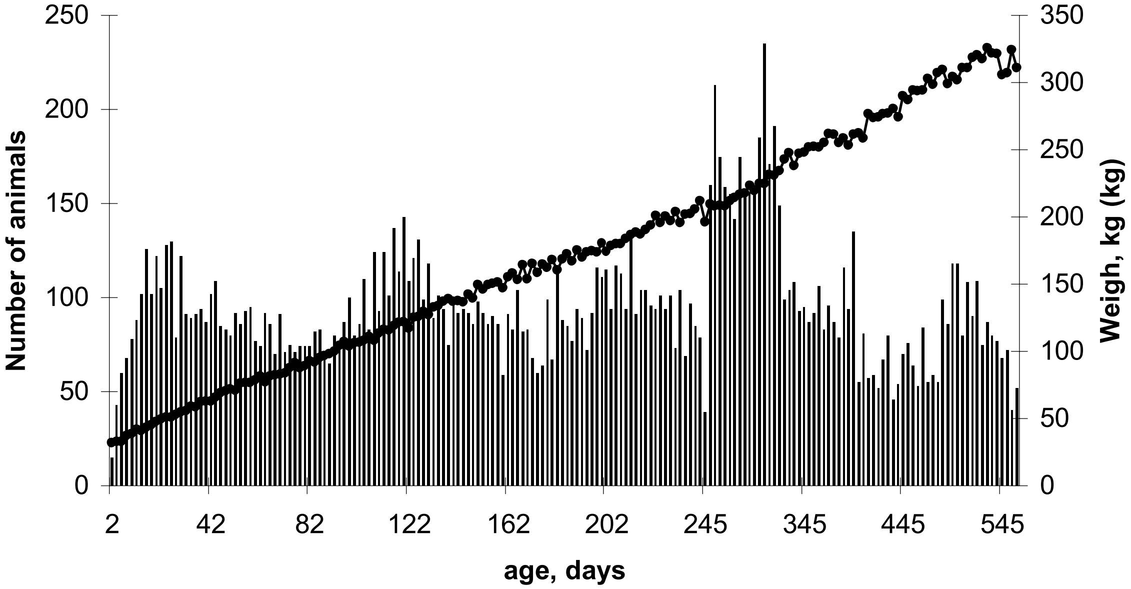

Figura 1 – Weight means (•) and number of observation (bars). Number of animals with birth weigh (4,221) not plotted

- Fixed effects:
    - contemporary groups,
    - age of dam as a quadratic covariable
    - cubic regression on orthogonal polynomials of animal age.
- Random Effects
    - genetic direct (A) and maternal (M)
    - direct (Q) and maternal (C) permanent environmental effects
    - modelled by random regression on Legendre polynomials of age at recording
- Changes in residual variances with age were considered through a variance function.
- Orders of polynomial fit were from 2 to 5, resulting in up to 51 parameters to be estimated.
- Covariances between random regression coefficients were estimated by REML using the program DXMRR (Meyer, 1998). Models were compared by Aikake´s (AIC) and Schwarz´ Bayesian Information Criterion (BIC).

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RESULTS

➢Considering heterogeneity of residual variances, significantly increased the log likelihood function (log L) and decreased AIC and BIC (Table 2).

➢Based on AIC and BIC, a quintic variance function modeled the residual variances best.

➢Adding maternal genetic effects to the model of analysis decreased both criteria.➢Variance component estimates, in general, were similar to those obtained with correspondent standard univariate analysis (Figure 2).

➢Likewiase, heritability estimates obtained by the random regression model and by standard univariate analysis were similar. However, for direct effects RR heritability estimates were always larger than those from univariate analysis (Figure 3).

➢Direct heritability estimates decreased after birth (0.31) until animals were about 140 days of age (0.19) and, after that increased slightly with age reaching 0.23 at 550 days of age.

➢Estimates of maternal heritability estimates were very low, increasing from birth (0,05) to around 130 days of age (0,10), remained almost constant until 170 days of age, decreasing with age thereafter.

➢Direct genetic correlation estimates (not shown) between weights at standard ages (birth, weaning, yearling and final weights) were moderate to high while maternal genetic correlations, in general, were high but those with birth weight.

IMPLICATIONS

➢Changes in covariances with age were modelled adequately by a RR model, with estimates similar to those obtained by univariate analysis.

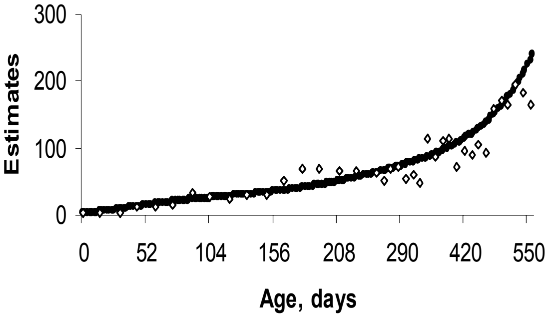
➢A higher response to selection for maternal ability could be achieved if selection were based on preweaning weights.

References

MEYER, K. “DXMRR”- a program to estimate covariance functions for longitudinal data by restricted maximum likelihood. In: WORLD CONGRESS ON GENETICS APPLIED TO LIVESTOCK PRODUCTION, 6. 1998, Armidale, **Proceedings**.. Armidale, 1998, v.27, p. 465-466.

Table 2. Order of fit for animal direct (k_A) and maternal (k_M) genetic effects, animal (k_Q) and maternal (k_C) permanent environmental effects, and residual (h= homogeneus and VF_x = variance function of x order), number of parameters (np) Akaike´s Information Criterion (AIC), Bayesian Information Criterion (BIC) (all – 100,000) and log likelihood function (log L -50,000).

k_A	k_M	k_Q	k_C	residual	np	BIC	AIC	Log L
4		4	4	h	31	14,735	14,488	-7213
4		4	4	VF_1	32	12,472	12,216	-6077
4		4	4	VF_2	33	11,413	11,149	-5542
4		4	4	VF_3	34	11,237	10,965	-5449
4		4	4	VF_4	35	11,242	10,962	-5446
4		4	4	VF_5	36	11,185	10,897	-5413
4	4	5	4	VF_5	51	11,049	10,642	-5270
4	4	5	3	VF_5	47	11,010	10,634	-5271
4	3	5	3	VF_5	43	10,978	10,633	-5275
4	3	5	2	VF_5	40	**10,950**	**10,631**	-5276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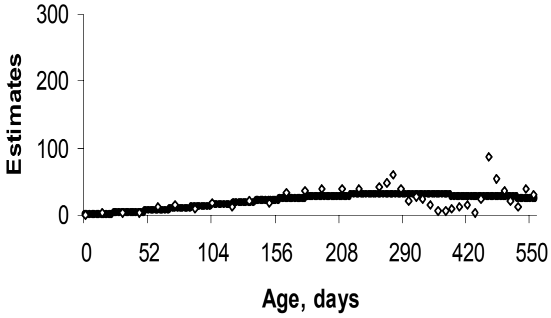
Age, days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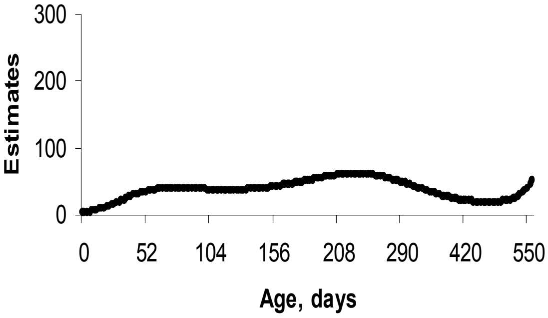
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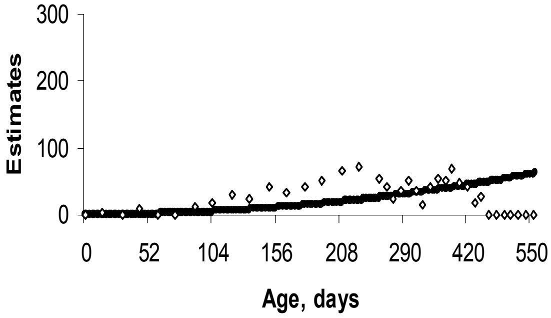
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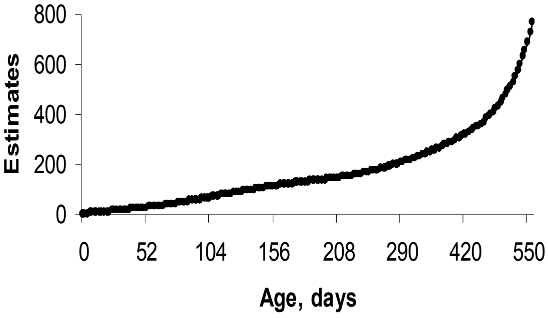
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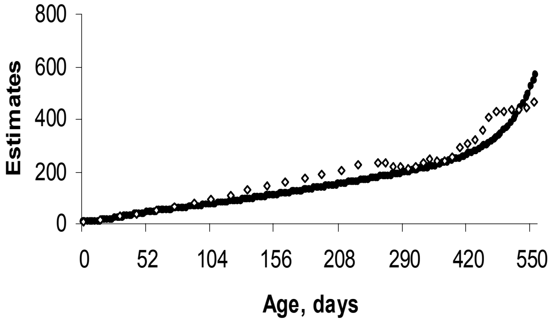
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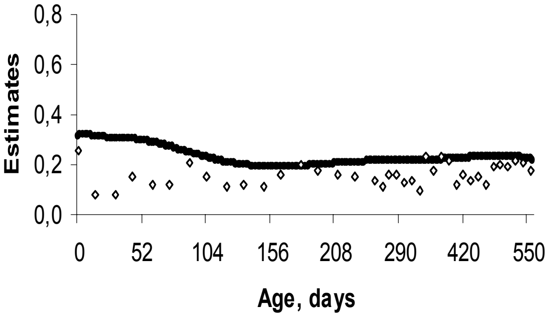
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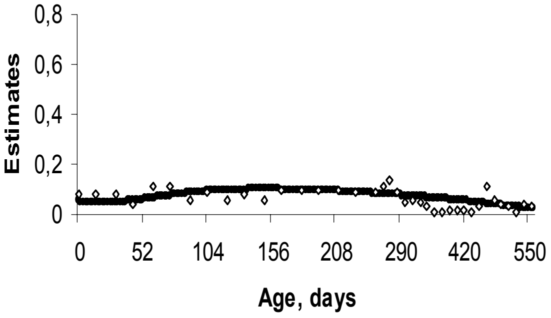
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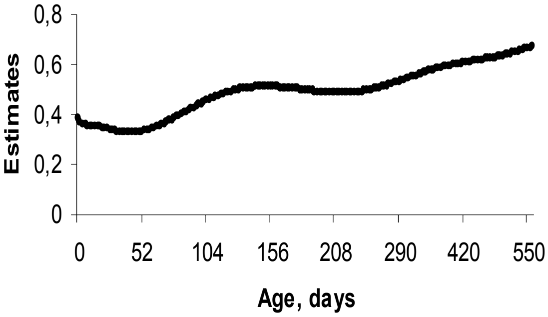
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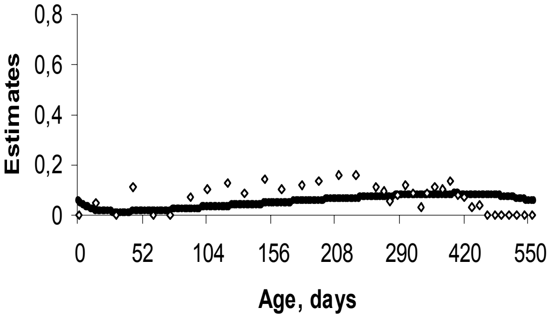
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