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ESTIMATES OF GENETIC PARAMETERS FOR WEIGHTS AND MATURING TRAITS DERIVED BY GROWTH FUNCTIONS IN NELLORE CATTLE

(Estimativas de parâmetros genéticos para pesos e características de maturação derivadas de funções de crescimento em bovinos da raça Nelore)

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RESUMO

As funções de Brody e Richards foram utilizadas para ajustar a curva de crescimento de 22.699 animais da raça Nelore, criados na região Nordeste. Após ser verificado que a curva de Brody promoveu melhor ajuste dos dados, esta foi utilizada para derivar características de crescimento e maturação, como os pesos e as taxas de crescimento aos 365 e 550 dias de idade, a idade dos animais quando estes alcançaram 65% do peso adulto, as taxas de crescimento relativo e os graus de maturidade aos 365 e 550 dias de idade, o peso adulto e a taxa de maturação. As variâncias genéticas, direta e materna, as covariâncias genéticas e as variâncias ambientais para estas características e para o peso ao desmame foram estimadas pelo método da Máxima Verossimilhança Restrita (REML), utilizando-se modelos animais com duas características, utilizando sempre o peso ao desmame com cada uma das outras características. Um modelo animal bi-variado, incluindo o peso adulto e a taxa de maturação, também foi avaliado. As estimativas de herdabilidade direta para as taxas de crescimento variaram de 0,23 a 0,47 e para as características de maturação de 0,11 a 0,86. Estimativas de correlações genéticas entre o peso ao desmame e demais características, como pesos preditos e taxas de crescimento, variaram de 0,67 a 0,86. As estimativas de herdabilidade sugerem a possibilidade de alterar a forma da curva de crescimento da população estudada através da seleção massal. Uma correlação genética negativa entre o peso adulto e a taxa de maturação foi verificada.

PALAVRAS CHAVE: bovinos de corte, parâmetros genéticos, crescimento, maturidade

ABSTRACT

Brody and Richards functions were tested to fit the growth curve of 22,699 animals of Nellore breed raised in the Northeast region of Brazil. Both curves were tested and due to the best fit, Brody curves were utilized to derive growth and maturing traits, such as weights and growth rates at 365 and 550 days, the age at which animals reached 65% of mature weight, relative growth rates and degrees of maturity at 365 and 550 days, mature weights and maturation rate index. Direct and maternal genetic and environmental variances and covariances were estimated for these traits and for weaning weight by REML, from a set of two-trait animal models including weaning weight paired with the other traits. A two-trait animal model including mature weight and maturation rate index were performed as well. Direct heritability estimates for growth rates ranged form 0.23 to 0.47, and for maturation traits from 0.11 to 0.86. Estimates of direct genetic correlations of weaning weight with predicted weights and growth rates ranged from 0.67 to 0.86. The estimates of heritability suggest the possibility to alter the shape of the growth curve of the studied population by mass selection. The negative genetic correlation between mature weight and rate of maturing was verified.

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KEY-WORDS: beef cattle, genetic parameters, growth, maturity

INTRODUCTION

Important traits such as relative and absolute growth rates, maturation rate and mature size can be derived by using growth functions. Functions initially described by BRODY (1945) and RICHARDS (1959) have been used to model growth in cattle. The great majority of studies with non-linear equations used to describe the growth curve in animals indicate that presented by RICHARDS (1959) as the best to represent the growth curve of cattle (BROWN et al., 1976; PEROTTO et al, 1992; NESETRILOVA & PULKRABEK, 1995; LÔBO & MARTINS FILHO, 2001). However, the choice of the curve depends on data and problems encountered.

Reports from studies evaluating growth curves are scarce in the literature, especially for zebu cattle in tropical environments, and more so in the Northeast region of Brazil (semi-arid area). The lack of information is greater still for estimates of genetic parameters (heritabilities and genetic correlations).

Thus, the objectives of this paper were to compare Brody and Richards functions to fit the growth curve of Nellore cattle, to compute other traits relative to their growth and to estimate genetic parameters for components of "the best" function and the other growth traits.

MATERIALS AND METHODS

The data involved 28,386 animals of the Nellore breed raised in Northeastern Brazil between 1976 and 1999, and were obtained from the Brazilian Association of Zebu Breeders (ABCZ).

The animals were from 196 herds (minimum of 5 animals per herd), progeny of 727 sires, born throughout the year, and were broken down into 50.9% males and 49.1% females. General management varied: 65.9% of the animals were raised on pasture (native pasture - "Caatinga", or scrub lands, improved with *Brachiaria* grass), 12.1% managed with supplemental feed (semi-confined) and 22% under confinement. Herds were periodically treated for worms, ticks and flies (endo and ectoparasites) and vaccinated for rabies, FMD and brucellosis. The animals were weighed every three months on average up to two years of age, but many in the database (15%) were weighed up to 2.5 years. There were on average nine weights taken at various ages for each animal.

For a decision on which curve to fit, the observed growth curve of all animals, based on a sequence of paired weight and age observations, was fit with the following form of the Richards function:

$$W_t = A\,(1 - be^{-kt})^{M}$$

and by a Brody growth curve (BRODY, 1945) as formulated by DOREN et al. (1989):

$$W_t = A - (A - W_{t0})e^{-kt}$$

The NLIN procedure from SAS (SAS INSTITUTE INC., 1996) was used to estimate the parameters of the functions, using the Secant method (RALSTON & JENNRICH, 1978). The relative convergence criterion was $[(SSE_{i-1} - SSE_i)/(SSE_i + 10^{-6})]<10^{-8}$, where SSE is the residual sum of squares and *i* denotes the round of iteration. The procedure produces one curve for each animal, but only in 22,699 (80%) of the animals was the convergence criterion attained.

In the equations, the commons parameters are W_t, t, A, *e* and k. W_t represents body weight of the animal at age t. The asymptotic value, A, is interpreted as mature weight. The constant *e* is the base of the natural logarithms. The parameter k is a constant that expresses the rate by which the logarithmic function changes linearly over time and is interpreted biologically as the maturation rate index. It is a measure of the rate of change of weight gain (dW/dt). The parameter b in the Richards function is a constant that is adjusted for situations when W_0 and / or, t_0 are different from zero. The parameter M describes at what proportion of final size (A) the curve's inflection point occurs. This point is undefined for [0 < M £ 1]. In this study, estimates of b and M were restricted to [b £ 0.99] and [1 < M < 10] intervals, respectively. The parameter W_{t0} in the Brody curve is the observed birth weight.

For the choice of the function that best described the data, the criteria used were the coefficient of determination (R2), residual mean square (RMQ) and mean prediction error (MPE) proposed by GOONEWARDENE et al. (1981). R2, RMQ and MPE were 0.7992, 2616.10 and –4.6269, respectively, for the Brody curve, and 0.7955, 2664.60 and –5.9264, respectively, for the Richards curve. According to MPE, weights were overestimated by both functions (negative sign). For the Brody function, A and k were 480.20±2.16kg and 0.001780±0.000013/day, respectively. For the Richards function, A, b, k and M, were 438.60 ± 3.50kg, 0.892 ± 0.005, 0.002290 ± 0.000051/day and 1.18 ± 0.02. Both models presented relatively good fits, with the Brody function being slightly better. Missing data for final weights have a stronger negative effect on the Richards function, thus the Brody function fit the data better and it was chosen to fit the curve of each animal.

Individual curves and their first derivatives were used to compute the following growth traits: maturation rate index (curve parameter k), predicted weight in kilograms at 365 and 550 days of age (365-d and 550-d), growth rates in grams per day at 365-d and 550-d (slopes of the curve at those ages), degrees of maturity at 365-d and 550-d, relative growth rates at 365-d and 550-d measured in grams.day^{-1}.kilogram^{-1} and age in months when an animal reached 65% of mature weight.

The growth rate function (GR_t) was equal to the first derivative of the Brody function:

$$GR_t = k\,(A - W_{t0})e^{-kt}$$

Degree of maturity (DM_t) was defined as follows:

$$DM_t = W_t / A$$

Relative growth rate (RGR_t) was defined as:

$$RGR_t = GR_t / W_t$$

Age when an animal reaches 65% of mature weight (AGE65%) was calculated from the following equation:

$$AGE65\% = 1.(-k^{-1}).ln[(0.35A).(A-W_t)^{-1}]$$

The symbols W_t, e, A and k were previously defined, and *d* and *ln* denote, respectively, the differential and natural logarithms.

Variance and covariance components were estimated using Restricted Maximum Likelihood (REML) for animal models of the following general form:

$$y = Xb + Z_a a + Z_m m + Z_c c + e$$

where *y* is a vector of observations, b is a vector of fixed effects, a is a random vector of additive genetic effects, *m* is a random vector of maternal genetic effects, *c* is a random vector of permanent environmental effects, X, Z_a, Z_m, and Z_c are incidence matrices relating b, a, *m* and *c* to *y*, and *e* is a random error effects vector.

A set of two-trait animal models was used to estimate (co)variances and heritabilities for growth or maturation traits and their correlations with weaning weight. Weaning weights were preadjusted to a constant age of 205-d, for weaning season, sex of animal and age of dam effects (ABCZ, 2002). A two-trait model was used to estimate correlation between mature weight and maturation rate index. The fixed effect was represented by contemporary groups defined as herd, month and year of birth, sex and management system. For both traits in the model a direct genetic effect was considered; maternal genetic and permanent environmental effects were considered only for weaning weight.

Calculations were carried out using the Multiple Trait Derivative Free Restricted Maximum Likelihood program (MTDFREML; BOLDMAN et al., 1993). Convergence was considered to have been reached when the variance of function values (*-2logL*) in the simplex was less then 10^{-9}. The priors for the two-trait models were the ones calculated in the single-trait analyses.

RESULTS AND DISCUSSION

Descriptive statistics of weaning weight and traits derived from the Brody growth curves are reported in Table 1. The estimate for the A parameter for animals that do not have data points at mature age is a critical point. In Table 1, the standard deviation of A is huge. Similar studies with Nellore cattle are scarce in the literature. However, PEROTTO et al. (1997), utilizing the Richards function, estimated the mean for A to be 441kg for Guzerá cows. The estimate of this parameter was 454.93kg by OLIVEIRA et al. (1994), who utilized the Von Bertalanffy function for Guzerá females.

Table 1. Descriptive statistics for growth and maturing traits predicted from the Brody curve for the Nellore breed (n = 22,699)

Traits	Mean	SD	CV, %[a]
Mature weight, kg	406.95	196.37	48.25
Maturation rate index, day[1]	0.0036	0.0008	22.22
Weaning weight, kg	166.57	34.41	20.66
365 – d weight, Kg	227.50	55.33	24.32
550 – d weight, Kg	275.44	77.50	28.14
365 – d Growth rate, g/d	317.11	156.78	49.44
550 – d Growth rate, g/d	211.60	136.39	64.44
365 – d Degree of maturity	0.64	0.20	31.25
550 – d Degree of maturity	0.75	0.18	23.85
365 – d Relative growth rate, g.d.kg[1]	1.34	0.51	38.25
550 – d Relative growth rate, g.d.kg[1]	0.71	0.36	51.45
Age at 65% of mature weight, day	456.68	211.57	46.32

[a] Coefficient of variation

365-d = 365 days of age

LÔBO et al. (2000a) reported an average mature weight of 408.72kg for cattle in tropical regions (the mean of studies reported in the literature). There is reasonable agreement between these estimates and that from this study. FREITAS et al. (1997) reported estimates of 703kg for A for Holstein heifers under confinement. This greater value for Holsteins is justified for their larger body size when compared with Zebu cattle.

In Table 2, pooled estimates of genetic and environmental parameters for weaning weight are reported. Variance and covariance estimates for weaning weight were consistent across the models. Direct weaning weight heritabilities for Nellore cattle reported in the literature are very diverse, ranging between 0.05 and 0.80 (MERCADANTE et al. 1995). LÔBO et al. (2000a) give a weighted mean for direct heritability estimates for weaning weight of local and Zebu cattle in tropical countries of 0.30. MERCADANTE et al. (1995) found a weighted mean for direct heritability estimates for weaning weight of Zebu cattle of 0.22, which is lower than the value found in the present study. ALBUQUERQUE & MEYER (2001) reported that direct heritability estimates for weights of Nellore cattle decreased from 0.28 at birth, to 0.12-0.13 at about 150 days of age, stayed more or less constant at 0.14-0.16 until 270 days of age and increased with age after that, up to 0.25-0.26.

Estimates of maternal heritability for weaning weight in the present study were similar to those reported in the literature. For Zebu cattle in the tropics, MERCADANTE et al. (1995) found weighted mean of maternal heritability estimates for weaning weight of 0.18. KOOTS et al. (1994) reported a weighted average estimate for maternal weaning weight of 0.13.

Present estimates of the genetic correlation between direct and maternal effects for weaning weight (-0.52) were higher than those reported by

Table 2. Estimates of genetic and environmental parameters for weaning weight in the Nellore breed pooled from the two-trait models utilized in the analysis.

Item	Estimate
Direct additive genetic variance	419.73
Maternal additive genetic variance	133.43
Direct – maternal covariance	- 122.27
Permanent environmental variance	29.65
Environmental variance	468.56
Direct heritability	0.45
Maternal hereditability	0.14
Direct – maternal correlation	- 0.52

KOOTS et al. (1994) and MERCADANTE et al. (1995), who reported weighted direct-maternal genetic correlations of –0.16 and –0.23, respectively. LÔBO et al (2000b) reported an estimate of –0.50 for this direct-maternal genetic correlation in Guzerá cattle.

Estimates of variance components and heritabilities for growth and maturity traits are presented in Table 3. Heritability estimates for predicted weights and growth rates in the present study ranged from 0.23 to 0.47. LÔBO et al. (2000a) reported weighted means of direct heritability estimates for weights at 365-d and 550-d, and weight gains from weaning to 12 months of age and from 12 to 18 months of age of 0.37, 0.31, 0.31 and 0.13, respectively. KOOTS et al. (1994) reported an average heritability across cattle breeds for direct genetic effects on yearling weight of 0.35. KAPS et al. (2000) reported heritability estimates for 365-d and 550-d weights, 365-d and 550-d growth rates of 0.46, 0.49, 0.52 and 0.47, respectively, in Angus cattle. For Nellore, LÔBO & MARTINS FILHO (2001) reported heritability estimates of 0.20 and 0.28 for predicted weights at 365 and 550-d, respectively, utilizing the Brody function.

In the present study, estimates of heritability for maturation traits (i.e., for curve parameter *k*, degrees of maturity, relative growth rates, age to reach 65% of mature weight and mature weight) ranged from 0.11 for age at 65% of mature weight to 0.86 for maturation rate index. Estimates of heritability for these characteristics are scarce in the literature. For mature weight, higher estimates of heritability were cited by JENKINS et al. (1991), who utilized the Brody function (0.61, within-breed and 0.91, between-breed). MACNEIL et al. (2000), also utilizing the Brody curve, reported a heritability of 0.32 for this trait in Hereford cattle. MEYER (1995), utilizing the Gompertz curve, reported heritability values of 0.47 and 0.73 for mature weight for Hereford and Wokalups (multi-breed synthetic cows), respectively. FREITAS et al. (1997), utilizing the Richards curve, reported a heritability of 0.21 for mature weight in Holstein cattle. For Angus cattle, KAPS et al. (1999) reported an estimate of heritability for mature weight of 0.53. LÔBO et al. (2000a) reported weighted average heritability of 0.28 to mature weight.

The estimate of heritability for curve parameter k (maturation rate index) in the present study was high, probably due to the isolation between herds and the absence of selection for maturation rate. Generally, the selection practiced in these herds basically considers corporal weights in detriment to other traits. MACNEIL et al. (2000) presented an estimate of 0.10 for the k parameter in Hereford cattle. JENKINS et al. (1991) also reported high estimates for the maturation rate index (0.27, within-breed and 0.54, between-breed). Similarly, MEYER (1995) reported an estimate of 0.32 for Hereford and 0.33 for Wokalups for the same trait.

Covariances and genetic and environmental correlations of predicted growth traits with weaning weight are presented in Table 4. As expected, estimates of direct genetic correlations of weaning weight with predicted weights and growth rates were high, ranging from 0.67 to 0.86. LÔBO et al. (2000a) reported weighted average direct genetic correlations between weaning weight with 365-d weight, 550-d weight, weight gains from weaning to 12 and 18 months of age of 0.75, 0.74, 0.22 and 0.11, respectively.

Table 3. Estimates of additive and environmental variances and heritabilities for growth and maturing traits for the Nellore breed

	Variance estimate		
Trait	Additive	Environmental	Heritability
Mature weight	5401.49	29415.88	29415.88
Maturation rate index	0.8 x 10-4	0.1 x 10-4	0.1 x 10-4
365 – d weight, Kg	355.56	1192.08	1192.08
550 – d weight, Kg	1445.12	3520.19	3520.19
365 – d Growth rate	6536.17	15565.04	15565.04
550 – d Growth rate	8482.68	9691.43	9691.43
365 – d Degree of maturity	0.01	0.03	0.03
550 – d Degree of maturity	0.00	0.02	0.02
365 – d Relative growth rate	0.05	0.18	0.18
550 – d Relative growth rate	0.13	0.05	0.05
Age at 65% of mature weight, day	17418.47	146393.62	146393.62

365-d = 365 days of age

Similarly to what was observed by KAPS et al. (2000) for Angus cattle, correlations of maternal genetic weaning weight with direct genetic weights at 365-d and 550-d in the present study were positive, but those with growth rates were negative. In that study, correlations of maternal genetic weaning weight with direct genetic weights at 365-d and 550-d, and growth rates at 365-d and 550d were 0.25, 0.15, -0.12 and –0.36, respectively.

In the present study, correlations between weaning weight and mature weight was moderate and positive for maternal-direct genetic (0.21) and direct-direct genetic correlations (0.31). For Angus, KAPS et al. (1999) reported genetic correlations between maternal and direct weaning weight with mature weight of –0.34 and 0.63, respectively. Direct genetic correlations for weaning weight with relative growth rates were small and assumed to be unimportant, similar to that observed by KAPS et al. (2000). However, in the present study, the direct genetic correlations between weaning weight and degrees of maturity were moderate and positive (0.27 and 0.35). Direct genetic correlation between weaning weight and age at 65% of mature weight was –0.30. High weaning weights reflect low age when animals reach 65% of mature weights. Maternal-direct genetic correlation estimates between weaning weight and degrees of maturity were negative.

KAPS et al. (2000) discussed the possibility that the improved maternal ability increased the rate of maturation. However, the results from the present study contrast with the literature. MEYER (1997) found that large negative estimates of direct and maternal genetic covariances are associated with overestimates of additive direct and maternal genetic variances. For Zebu cattle in Brazil, there are difficulties in obtaining reliable estimates of the correlation between direct and maternal genetic effects (LÔBO et al., 2000b; ALBUQUERQUE & MEYER, 2001).

The direct genetic correlation between mature weight and maturation rate index of -0.32±0.08 agrees with literature (JENKINS et al., 1991; MEYER, 1995; AHUNU & OSEIAMPONSAH, 1996; FREITAS et al., 1997). MEYER (1995)

Table 4. Estimates of covariances and correlations between weaning weight and other growth and maturation traits

	Covariance estimates			Correlation estimate	
Trait	Direct genetic	Environmental	Maternal direct genetic	Direct genetic	Environmental
Mature weight	461.11	914.08	239.35	0.31 ± 0.02	0.24 ± 0.01
Maturation rate index	0.08	- 0.07	- 0.11	0.43 ± 0.01	-0.89 ± 0.04
365 – d weight, Kg	211.94	551.79	3.06	0.86 ± 0.02	0.80 ± 0.02
550 – d weight, Kg	517.30	1161.30	124.99	0.76 ± 0.02	0.76 ± 0.02
365 – d Growth rate	1334.37	1001.68	- 266.46	0.67 ± 0.04	0.39 ± 0.01
550 – d Growth rate	1780.39	- 407.16	- 67.93	0.78 ± 0.04	-0.21 ± 0.01
365 – d Degree of maturity	0.68	0.00	- 0.22	0.35 ± 0.04	0.00 ± 0.01
550 – d Degree of maturity	0.33	0.46	- 0.15	0.27 ± 0.05	0.12 ± 0.01
365 – d Relative growth rate	-0.06	- 0.06	0.10	-0.01 ± 0.03	-0.01 ± 0.01
550 – d Relative growth rate	-0.07	- 0.16	- 0.86	-0.01 ± 0.01	-0.03 ± 0.01
Age at 65% of mature weight, day	-827.95	- 1099.39	354.14	-0.03 ± 0.02	-0.13 ± 0.01

365-d Weight = 365 days of age weight

reported correlations of –0.5 and –0.7 between maturation rate index and mature weight for Hereford and Wokalups, respectively. Similarly, FREITAS et al. (1997) reported a correlation of –0.53 between mature weight and maturation rate index. These results suggest that early-maturing animals are less likely to attain heavy mature weights than later maturing animals. This result implies that animals with higher mature weights require more energy for maintenance and reach puberty later in life. Thus, a larger mature mass is not desirable for the breeding herd (OWENS et al., 1993).

CONCLUSION

Non-linear functions, such as the Brody curve, provide an appropriate description of the growth curve of animals, and supply parameters that allow selection for characteristics of economic interest such as growth and maturation traits. This additional information could be considered for use in genetic evaluation programs instead of evaluations performed only for points along the growth curve.

The heritabilities estimated suggest the possibility of changing the shape of the growth curve of the studied population by mass selection. On the other hand, an effort should be made to reduce the effects of the negative correlation between mature weight and weight gains at young ages.

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