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Fit and genetic parameters of the growth curve of Polled Nellore cattle
Ajuste e parâmetros genéticos da curva de crescimento em bovinos da raça Nelore Mocho

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ABSTRACT

This study was undertaken to compare different non-linear models for fitting growth curves of Polled Nellore animals as well as to estimate genetic parameters for the components of the growth curve. The study involved body weight-age data of 6,717 Polled Nellore cattle from birth to 650 days of age, which belonged to the Brazilian Association of Zebu Breeders (ABCZ), corresponding to the period from 1980 to 2011. Four non-linear models (Brody, Bertalanffy, Logistic, and Gompertz) were fitted and compared by the adjusted coefficient of determination (R^2_{adj}), mean absolute deviation of residuals (MAD), root mean square error (RMSE), Akaike information criterion (AIC), and Bayesian information criterion (BIC). To estimate the genetic parameters and genetic values of asymptotic weight (A), integration constant (B), and maturation rate (K), the Bayesian inference method was adopted. The Brody model showed the lowest values of MAD, RMSE, AIC, and BIC and the highest R^2_{adj}. Heritability estimates for parameters A, B, and K were 0.11, 0.16, and 0.30, respectively, whereas genetic correlations were 0.01 (A-B), -0.91 (A-K), and 0.24 (B-K). The Brody model provided the best fit. The K parameter shows enough genetic variability for selection in the herd. Heavier animals in

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adulthood tend to exhibit lower growth rates. Despite the low heritability estimate of parameter A, there were genetic gains, indicating that selection is being efficient on asymptotic weight.

Keywords: Bayesian approach, beef cattle, goodness of fit, model selection, non-linear model

RESUMO

O objetivo deste estudo foi comparar diferentes modelos não lineares para o ajuste das curvas de crescimento de animais da raça Nelore Mocho e estimar os parâmetros genéticos para os componentes da curva de crescimento. Foram utilizados dados de peso corporal-idade do nascimento aos 650 dias de idades de 6.717 bovinos da raça Nelore Mocho, pertencentes à Associação Brasileira de Criadores de Zebu (ABCZ), referentes ao período de 1980 e 2011. Quatro modelos não lineares (Brody, Bertalanffy, Logístico e Gompertz) foram ajustados e comparados pelo coeficiente de determinação ajustado (R^2_{adj}), desvio médio absoluto dos resíduos (DMA), raiz quadrada do quadrado médio do resíduo (RMSE), critério de informação de Akaike (AIC) e o critério de informação bayesiano (BIC). Para estimativas dos parâmetros genéticos e valores genéticos do peso assintótico (A), constante de integração (B) e taxa de maturação (K), utilizou-se o método de inferência Bayesiana. O modelo Brody apresentou os menores valores de DMA, RMSE, AIC e BIC e o maior R^2_{adj}. As estimativas de herdabilidade foram 0,11; 0,16 e 0,30 para os parâmetros A, B e K, respectivamente, enquanto as correlações genéticas foram de 0,01 (A-B), -0,91 (A-K) e 0,24 (B-K). Constatou-se que o modelo Brody forneceu o melhor ajuste. O parâmetro K apresenta variabilidade genética suficiente para seleção no rebanho. Animais com maior peso na idade adulta tendem a apresentar menores taxas de crescimento. Apesar da baixa estimativa de herdabilidade do parâmetro A, observou-se ganhos genéticos, indicando que a seleção está sendo eficiente sobre o peso assintótico.

Palavras-chaves: Abordagem bayesiana, bovinos de corte, modelo não linear, qualidade de ajuste, seleção de modelo.

INTRODUCTION

Growth is a complex process of cell proliferation that involves interactions between genetics, nutrition, and other environmental influences (POSADA et al., 2014), and understanding this process is important for optimizing management and feeding practices as well as for the genetic improvement of species (DO and MIAR, 2020). In view of this, over the years, several non-linear models have been used to describe the growth curve of beef cattle (DUAN et al., 2021) and other species (ARAÚJO et al., 2020; MENCHETTI et al., 2020; RIBEIRO et al., 2021).

However, there is no consensus on which model is the most suitable for estimating growth curves, since adequacy is particular to each population and each population or breed has a specific growth pattern. Determining the most suitable model in a group of herds is very important for the development of more effective selection strategies and the regulation of management practices (KORKMAZ et al., 2011; ALVES et al., 2020). In addition, it helps technicians and breeders through decisions related to animal production and reproduction (DOMÍNGUEZ-VIVEROS et al., 2020).

In Brazil, studies on the particular growth curves of Polled Nellore cattle are incipient (EVANGELISTA et al., 2020; LOPES et al., 2016). Thus, additional studies are warranted, since the animals' growth rate may vary according to different conditions or farming systems.

Studies that investigated genetic factors related to the coefficients of nonlinear models of growth curve for this breed are scarce. These coefficients have moderate to high heritability, and the selection of these parameters can be effective (SOUSA et al., 2011). Additionally, the development of an efficient breeding program for any animal species requires knowledge of the impact of genetic parameters on economically important characteristics, such as those pertaining to the growth curve (MOHAMMADI et al., 2019; SILVEIRA et al., 2019).

Therefore, the present study was developed to compare different nonlinear models that describe the growth curve of male and female Polled Nellore cattle and to estimate genetic parameters for the coefficients of the nonlinear models of the growth curve.

MATERIAL AND METHODS

The analyses were carried out using body weight-age data from birth to 650 days of age of Polled Nellore herds located in seven states in the northern region of Brazil (Amazonas, Acre, Amapá, Roraima, Rondônia, Pará, and Tocantins), which are part of the Brazilian Association of Zebu Breeders (ABCZ). The database provided by ABCZ contained 43,214 weight records of 10,751 Polled Nellore animals (offspring of 1,200 bulls and 7,500 cows).

Data quality control was initially performed to avoid any possible bias in the analyses. Thus, information from farms with fewer than 10 animals, animals with fewer than three weight records, weight records of ages over 650 days, and animals weighing less than 20 kg at birth or more than 750 kg in adulthood was excluded. Supplementary Table 1 summarizes the descriptive statistics of the phenotypic data of animal body weight at monthly intervals from birth to 650 days of age (21 months).

Table S1. Number of animals, mean, standard deviation, and coefficient of variation of body weight of Polled Nellore at different ages

Age (month)	Number of animals	Mean (kg)	Standard deviation (kg)	Coefficient of variation (%)
1	685	66.91	52.37	78.28
2	1621	73.16	26.35	36.01
3	1889	97.66	40.90	41.87
4	1905	116.02	34.47	29.71
5	2043	136.48	31.46	23.05
6	2018	152.51	35.42	23.22
7	2091	170.31	34.86	20.47
8	2236	187.05	37.77	20.19
9	2251	201.27	40.37	20.06

10	2235	210.55	42.81	20.33
11	2038	225.89	51.19	22.66
12	1750	236.73	61.97	26.18
13	1611	248.56	65.18	26.22
14	1503	258.87	67.99	26.26
15	1413	271.00	68.28	25.20
16	1418	284.64	75.39	26.48
17	1305	296.98	79.18	26.66
18	1325	308.10	82.34	26.73
19	1198	316.21	78.11	24.70
20	997	327.22	89.83	27.45
21	376	332.53	84.94	25.54

After the consistencies were met, 33,831 weight records of 6,717 animals remained. Four non-linear models were used to study the growth curve (Table 1). Each model was fitted separately for body weight records of male (2,672 animals and 13,089 weight records) and female (4,045 animals and 20,742 weight records) Polled Nellore cattle by the Gauss-Newton method, using the NLIN procedure of Statistical Analysis System software (SAS, 2014).

Table 1. Description of nonlinear functions used in modeling the growth curve of Polled Nellore animals

Model	**Function**	**Reference**
Brody	$y_t = A(1-Bexp^{-Kt})+\varepsilon$	Brody (1945)
Bertalanffy	$y_t = A(1-Bexp^{-Kt})^3+\varepsilon$	Von Bertalanffy (1957)
Logistic	$y_t = A/(1+Bexp^{-Kt})+\varepsilon$	Nelder (1961)
Gompertz	$y_t = Aexp(-Bexp^{-Kt})+\varepsilon$	Laird (1965)

In all equations presented, y_t is body weight at age *t*; parameter A refers to the asymptotic weight when *t* tends to plus infinity, that is, this parameter is interpreted as weight in adulthood; *B* is an integration constant, related to the initial weights of the animal and without a well-defined biological interpretation; *K* is interpreted as the maturation rate, which should be understood as the change in weight relative to weight at maturity, i.e., as an indicator of the speed at which the animal approaches its adult size; and ε is the random error (SARMENTO et al., 2006).

To select the model that best fits the growth curve, the following criteria were used: a) Adjusted coefficient of determination (R^2_{adj}), which was used to compare the goodness of fit of the models by Hojjati & Hossein-Zadeh (2018), given by $R^2_{adj} = 1-[\ (n-1)/\ (n-p\ )] \times (1-R^2)$; b) Mean Absolute Deviation of residuals (MAD), obtained by adding the absolute errors divided by the number of observations, proposed by Sarmento et al. (2006); c) Root Mean Square Error (RMSE): given by $RMSE = \sqrt{RSS}/\ \sqrt{n-p-1}$, where RSS is the residual sum of squares, "n" is the number of observations, and "p" is the number of model parameters; d) Akaike information criterion (AIC), obtained as follows: $AIC = n \ln (RSS) + 2p$, where "ln" is the logarithm; and e) Bayesian information criterion (BIC), given by BIC = n ln (RSS/n)+ p ln(n).

After the best-fitting model was defined, the genetic parameters for the growth curve parameters (A, B, and K) were estimated. The estimates of (co)variance components for the growth curve parameters were obtained by a multivariate animal model, under a Bayesian approach, using the GIBBS2F90 program (MISZTAL et al., 2015), which contained the contemporary group a fixed effect, dam age at birth as a covariate (linear and quadratic effects), and additive and residual genetic effects as random.

The contemporary groups (CG) for the traits (A, B, and K) were formed by the following variables: sex, year of birth, farm, season of birth, rearing condition (suckling and weaning), and diet (pasture, semi-stall, and stall). The birth seasons were classified as rainy (December to May) and dry (June to November). Contemporary groups with fewer than three animals were excluded. The model was as follows:

$$\boldsymbol{y} = \boldsymbol{X}\,\boldsymbol{b} + \boldsymbol{Z}\boldsymbol{a} + \boldsymbol{\varepsilon},$$

where: $\boldsymbol{y}$ = vector of observations of the growth curve traits (A, B, and K of the best-fitting model); $\boldsymbol{b}$ = vector of fixed effects (CG and covariate) associated with y through incidence matrix $\boldsymbol{X}$; a = vector of random effects of direct additive genetic value of the animal, associated with y through incidence matrix $\boldsymbol{Z}$; and $\boldsymbol{\varepsilon}$ = vector of residual effects.

Sample chains (Gibbs sampling) with a length of 700,000 cycles were generated, with an initial burn-in of 200,000 samples and a sampling lag (thin interval) of 20 samples, leaving 25,000 samples that were used for inferences. The convergence of chains was evaluated by the criterion proposed by Geweke (1992), available in the package of the Bayesian Output Analysis (BOA) program of R software (SMITH, 2007).

Genetic trends were estimated by averaging the breeding values (EBV) of parameters A and K in the year of birth and regressing these values on the year of birth. The model used was as follows: $y_a = b_0 + b_1x_a$, where y_a is the mean EBV of year of birth a; x_a is year of birth a; and b_0 and b_1 are the intercept and the linear regression coefficient, respectively.

RESULTS AND DISCUSSION

Table 2 shows the estimates of the parameters and their standard errors for the different non-linear models fitted regarding the weight-age of Polled Nellore males and females. From the animal production standpoint, the asymptotic weight (A) and the maturation rate (K) are considered the two most important parameters, mainly because heavier cows will typically produce faster-growing calves (MARINHO et al., 2013). On the other hand, keeping heavier cows (which consume more) may not be economically advantageous.

Table 2. Parameter estimates and standard errors for the growth curve parameters of male and female Polled Nellore cattle, as evaluated by different non-linear models

	Model	A	B	K
Males	Brody	650.30±24.54	0.933±0.002	0.00121±0.00007
	Bertalanffy	471.10±7.95	0.506±0.002	0.00285±0.00007

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	Logistic	393.10±3.57	4.431±0.058	0.00597±0.00009
	Gompertz	438.90±5.96	1.962±0.013	0.0037±0.00008
Females	Brody	405.50±6.30	0.903±0.002	0.00200±0.00006
	Bertalanffy	348.20±3.21	0.470±0.002	0.00356±0.00007
	Logistic	312.50±1.77	3.713±0.045	0.00649±0.00009
	Gompertz	334.50±2.62	1.783±0.013	0.00430±0.00007

A: asymptotic weight, B: integration constant, K: maturation rate.

In general, the estimated parameters (A, B, and K) varied between models and between males and females. Parameter “A” is an estimate of the asymptotic weight; in other words, this parameter is interpreted as the adult weight of the animal. The Brody model provided the highest estimates of A (650.30 kg for males and 405.50 kg for females), whereas the Logistic model generated the lowest values (393.10 kg for males and 312.50 kg for females). Adult weight was higher in males than females, as expected. This can be explained by hormonal and physiological differences between the sexes (HOJJATI & HOSSEIN-ZADEH, 2018). Our results corroborate the reports of Carneiro et al. (2014), who studied zebu animals from the northeastern region of Brazil and also found that the females had lower adult weights (376.97 kg) than the males (478.03 kg).

Parameter "B" is related to the initial weight of the animals. The Logistic model indicated the highest values for this parameter (males: 4.431; females: 3.713) and the Bertalanffy model the lowest (males: 0.506; females 0.470), with the females exhibiting lower values than the males. These estimates, for both sexes, were lower than the 0.998 (Logistic) and 0.993 (Bertalanffy) reported by Selvaggi et al. (2017). This fact may be due to several genetics-related factors (maternal ability, genetic value for weight at weaning), besides possible environmental effects impacting the growth curve of the animals.

Lastly, parameter “K”, which indicates the growth speed to reach adult weight, was higher in the females (Table 2), which shows that females reach maturity weight earlier than males. This result corroborates those observed in Nellore animals in Mexico by Domínguez-Viveros et al. (2020), who described that females showed higher K values and that their development was consequently faster than that of males. Furthermore, regardless of sex, the Logistic model provided the highest estimates and the Brody model the lowest, similar to results found in other studies with beef cattle (MOREIRA et al., 2016; HAFIZ et al., 2018).

Thus, the results presented in Table 3 reflect the means of parameters A and K as a function of environmental effects (Supplementary Table 2). Sex had a significant effect on parameter A, which was greater in males than females ($p<0.05$). This result is expected due to hormonal and physiological differences that stimulate the early onset of sexual activity in both sexes (CANAZA-CAYO et al., 2015). However, the females showed higher maturity rates, a behavior related to sexual dimorphism for adult size.

Table S2. Asymptotic weight (A) and maturation rate (K) means estimated by the Brody model in Polled Nellore herds, as a function of environmental effects

Fixed effect	A	K
Sex		
Males	641.35^{a}	0.00127^{b}
Females	433.74^{b}	0.00199^{a}
Birth season		
Rainy	641.35^{a}	0.00197^{a}
Dry	433.74^{a}	0.00165^{b}
Reading condition		
Suckling	597.68^{a}	0.00310^{a}
Weaning	582.56^{a}	0.00521^{a}
Feeding regime		
Pasture	502.05^{b}	0.00128^{a}
Semi-stall	568.67^{a}	0.00138^{a}
Stall	601.60^{a}	0.00106^{a}
Year of birth		
1980	513.03^{hij}	0.00210^{defg}
1981	366.02^{n}	0.00102^{fgh}
1982	-	0.00559^{a}
1983	477.01^{l}	0.00386^{bc}
1984	599.25^{bc}	0.00097^{fgh}
1985	506.63^{j}	0.00174^{defgh}
1986	537.11^{fgh}	0.00291^{bcd}
1987	551.99^{ef}	0.00219^{defg}
1988	510.87^{j}	0.00239^{cdef}
1989	537.63^{fg}	0.00070^{gh}
1990	-	0.00236_{cdef}
1991	-	0.00236_{cdef}
1992	-	0.00130_{efgh}
1993	503.45^{j}	0.00099_{fgh}
1994	505.17^{j}	0.00137_{defgh}
1995	573.02^{de}	0.00193_{defgh}
1996	527.84^{fghi}	$0.00195_{def}gh$
1997	506.00^{j}	0.00223_{def}
1998	534.76^{fghi}	0.00224_{def}
1999	509.10^{j}	0.00408_{b}
2000	$480.31k^{l}$	0.00052^{h}
2001	689.09^{a}	0.00146^{defgh}
2002	513.41^{ghi}	0.00177^{defgh}
2003	427.58^{m}	0.00094^{fgh}
2004	470.96^{l}	0.00268^{bcde}
2005	532.76^{fghi}	0.00200^{defgh}
2006	533.08^{fghi}	0.00178^{defgh}
2007	586.72^{cd}	0.00149^{defgh}
2008	531.27^{fghi}	0.00190^{defgh}
2009	467.13^{l}	0.00259^{bcde}
2010	694.96^{a}	0.00179^{defgh}
2011	-	0.00175^{defgh}

Means followed by different letters in the column (within each effect) are significantly different by Tukey's test ($p<0.05$).

The feeding regime had an influence on parameter A ($p<0.05$). The stall and semi-stall regimes provided higher asymptotic weights, indicating that these systems allow for greater weight development than pasture. There was no effect of diet on growth rate, which indicates that Polled Nellore cattle are growth-efficient regardless of the diet used in the season (Supplementary Table 2). On the other hand, Polled Nellore cattle are earlier-developing when born in the rainy season (statistically, they showed a higher K value), which is usually a period associated with the growth of highly nutritious forages. This may have contributed to the growth of the animals during this time of year.

Year of birth also influenced parameters A and K ($p<0.05$). However, it is noteworthy that the lowest value of parameter A occurred in 1981, whereas the highest value was seen in 2010. This effect can be attributed to changes in management conditions and greater investment in the use of technologies and genetic material over the years (Supplementary Table 2).

Table 3 describes the results of the comparison of non-linear models for the growth curve of male and female Polled Nellore cattle, considering the goodness of fit of the R^2_{adj}, RMSE, MAD, AIC, and BIC measures.

Table 3. Comparison of the goodness of fit for growth curves of male and female Polled Nellore cattle, for different nonlinear models

	Model	R^2_{adj}	RMSE	MAD	AIC	BIC
Males	**Brody**	**0.95**	**53.99**	**35.22**	**228498.96**	**104443.86**
	Bertalanffy	0.95	54.21	35.63	228604.36	104549.27
	Logistic	0.95	54.74	36.59	228860.54	104805.44
	Gompertz	0.95	54.34	35.87	228666.24	104611.15
Females	**Brody**	**0.95**	**48.66**	**31.33**	**367332.97**	**161183.05**
	Bertalanffy	0.95	48.83	31.67	367483.02	161333.11
	Logistic	0.95	49.28	32.46	367861.29	161711.38
	Gompertz	0.95	48.94	31.87	367573.16	161423.24

R^2_{adj} = adjusted coefficient of determination; RMSE = root mean square error; MAD = mean absolute deviation of residuals; AIC = Akaike information criterion; BIC = Bayesian information criterion.

Overall, the R^2_{adj} were equivalent and showed considerably high and similar values between the four models evaluated, in both sexes. The models had a satisfactory performance in estimating the growth curve parameters, agreeing with results presented by other authors in beef cattle (GONÇALVES et al., 2011; ARRUDA et al., 2018).

Considering the RMSE, MAD, AIC, and BIC, the Brody model obtained the lowest values, which indicates that, among the models used in this study, this was the best and most suitable to explain the growth pattern of Polled Nellore males and females. Silva et al. (2011) evaluated 12 non-linear models for Nellore cattle in the state of Minas Gerais and cited Brody as the recommended model to describe the growth curve of Nellore cattle, due to the good evaluators of goodness of fit and high percentage of convergence.

Similarly, Lopes et al. (2016) evaluated growth curves of Polled Nellore cattle from herds of the Brazilian Agricultural Research Corporation (EMBRAPA) and reported that the Brody model was the most suitable to represent the average growth curve and can be used in studies on the growth of Polled Nellore cattle, due to the lower MAD and RMS and higher R^2, compared with the other models. These results confirm the effectiveness of the Brody model to describe the growth curve of male and female Polled Nellore, a breed that has been little studied in Brazil.

On the other hand, the Logistic model provided the highest values of MAD, RMSE, AIC, and BIC for both sexes (males and females), followed by the models by Gompertz and Bertalanffy. These findings are in line with the results obtained by Domínguez-Viveros et al. (2013) in Tropicarne cattle in Mexico. However, they differ from those reported by Hafiz et al. (2018), who evaluated mathematical models to fit the growth curve of beef cattle in Malaysia and found that the Logistic model showed the best fit, given the higher R^2 and lower MAD and RMSE. Our results also disagree with those published by Selvaggi et al. (2017), who described that the Logistic and Richards models provided the best overall fit, thus being useful for studying the growth of Podolica bulls located in the region of Basilicata, southern Italy.

Figure 1 shows the estimated growth curves according to the Bertalanffy, Brody, Gompertz, and Logistic models, together with the average weights observed for male and female Polled Nellore cattle.

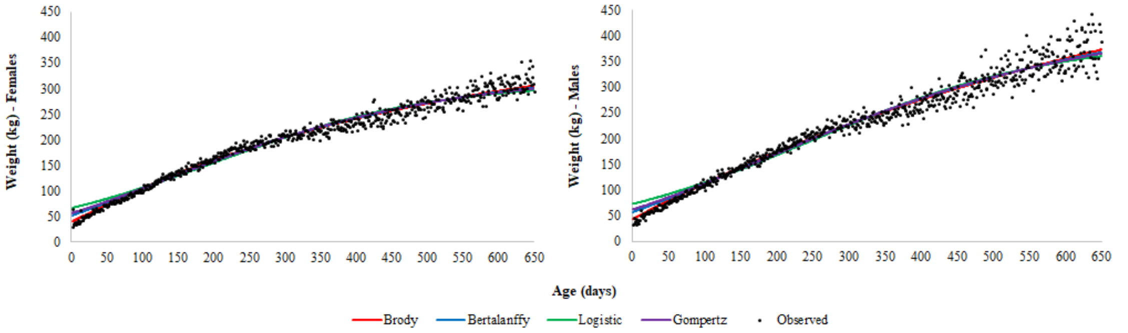

Figure 1. Growth curves estimated by the Brody, Bertalanffy, Gompertz, and Logistic models for Polled Nellore cattle.

Although all models showed similarity, the Bertalanffy, Gompertz, and Logistic models overestimated the initial weight of the growth curve, whereas the Brody model estimated results closer to those observed. These results support the theory that Brody is the model that most closely corresponds to the initial weights of beef cattle (MARINHO et al., 2013; MOREIRA et al., 2016), i.e., it indicates a greater association between observed and estimated weights.

With advancing age, the weight difference between males and females increased, especially after weaning (205 days) (Figure 2). Silveira et al. (2019) observed a similar behavior in Nellore cattle raised in the state of Mato Grosso do Sul. The researchers mentioned that the difference between male and female growth increases with age, with a small magnitude in the pre-weaning phase that reaches its maximum at around two years of age.

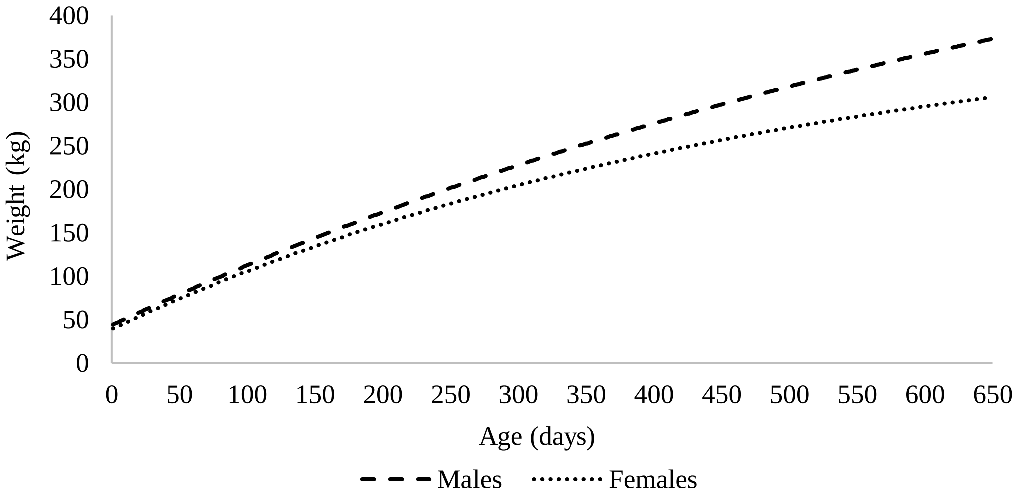

Figure 2. Estimation of weight as a function of age for each sex, as estimated by the Brody model in Polled Nellore herds

The observed difference in body weight between males and females (Figure 2) can be explained by sexual dimorphism, which warrants the adoption of different management systems for males and females to achieve greater economic efficiency (SOUSA et al., 2021). Therefore, it would be interesting to categorize the animals by sex (males and females) to adequately define the feeding management strategy and slaughter age for each category (PAZ et al., 2018).

Because of the better fit of the Brody model, it was used to estimate the genetic parameters of the growth curve parameters (A, B, and K). Table 4 shows the heritability estimates and genetic correlations between the growth curve parameters.

Heritability estimates for parameters A (0.11±0.01) and B (0.15±0.01) were of low magnitude, meaning there is a great influence of non-genetic factors in the expression of these traits and, consequently, the possibility of genetic gain through selection will be small. Possible factors for the estimation of low heritability may be related to the use of data only from young animals (up to 650 days of age), in which case the environmental influence becomes great. Therefore, improvements in environmental factors (herd management, rearing system, feeding system) can lead to more significant improvements in these traits, rather than genetic selection.

Table 4. Estimates of heritability (diagonal) and genetic correlations (above the diagonal) between the growth curve parameters of Polled Nellore cattle, based on the Brody model

	A	B	K
A	**0.11±0.01**	0.01±0.03	-0.91±0.03
B		**0.16±0.01**	0.24±0.04
K			**0.30±0.02**

A: asymptotic weight, B: integration constant, K: maturation rate

Rios et al. (2019) observed similar results in a population of Brangus cattle. The authors argued that the low heritability may be related to the early maturity of these animals, with greater variations occurring in environmental variance than in additive genetic variance. However, their findings differ from those observed in Nellore cattle by Lopes et al. (2012), who found a heritability of 0.21±0.013 and concluded that parameter A shows favorable genetic variability, which can allow genetic gains when used as a selection criterion.

The heritability estimate for parameter K was of moderate magnitude (Table 4), suggesting that an improvement in this parameter (K) can be achieved through direct selection and, therefore, it can be used as an instrument to change the growth curve to a desirable shape. Domínguez-Viveros et al. (2017) described a similar result reported in Tropicarne cattle in Mexico. The authors estimated a heritability value of 0.30 for parameter K, which indicates that the growth rate parameter (K) has enough genetic variability to be incorporated into breeding programs for Polled Nellore.

Table 4 displays the genetic correlations between the growth curve parameters. The genetic correlation between A × B was weak and close to zero (0.01). These results differ from those reported by Mohammadi et al. (2019), who estimated a positive genetic correlation between parameters A and B (0.48). The authors explained that animals born heavier tend to be heavier at maturity, and concluded that genetic and physiological mechanisms control both traits. The disagreement between our results and those of other researchers can be explained by differences in the methods for estimating genetic parameters, sample size used, genetic differences between individuals, etc.

The most important correlation for a growth curve is between parameters A and K (HOSSEIN-ZADEH, 2015). The correlation between these parameters in the present study was negative and high (-0.91). An interpretation for this correlation would be that the selection of animals with higher maturation rates (K) should lead to a decrease in adult weight. Lopes et al. (2016) described a similar behavior in herds of Polled Nellore cattle, mentioning that this antagonism can be explained by the relationship that exists between the weight and body size of the animals, with larger animals having higher nutritional requirements for their maintenance, thus being later-developing, and having a lower growth rate, and consequently, later maturity. From the selection standpoint, the antagonism between both parameters is favorable, since animals with high mature-weight values will take less time to reach their inflection point, causing individuals with high mature weight to be identified earlier (CANAZA-CAYO et al., 2015).

In contrast, the genetic correlation between B × K was positive and of moderate magnitude (0.24), showing that, in this data set, heavier-weaned cattle tend to have higher maturation rates. This demonstrates that the growth curve parameters related to the integration constant and the maturation rate may be genetically connected, and selection in favor of one trait would improve the other. Figure 3 illustrates the average estimated breeding values (EBV) per year of birth for parameters A and K in Polled Nellore cattle.

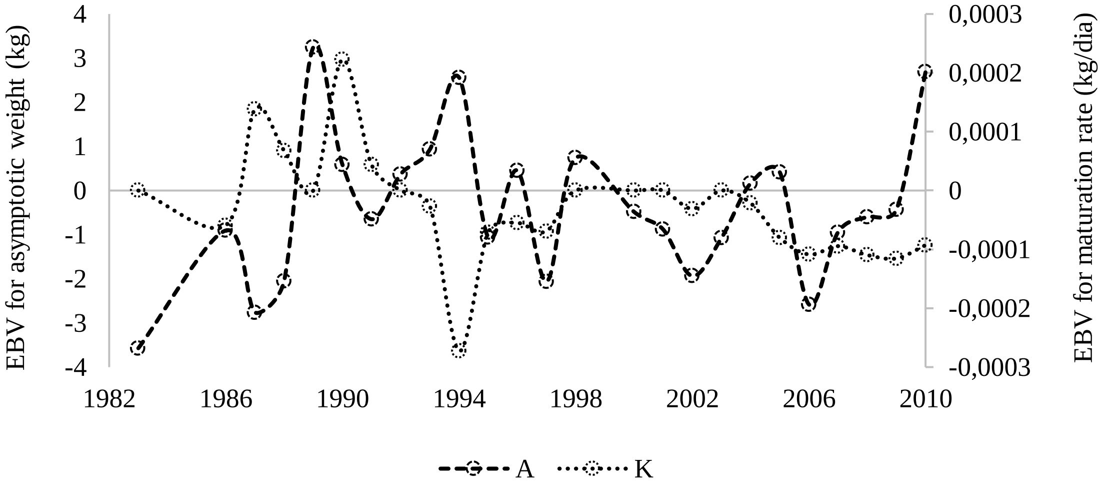

Figure 3. Mean estimated breeding values (EBV) for the Brody model of asymptotic weight (A) and maturation rate (K) per year of birth in Polled Nellore cattle.

The EBV for the asymptotic weight (A) showed a significant growth between the years 1989 and 1994. After this period, these values became negative and close to zero, only becoming positive again from 2010 onwards. The EBV for the maturation rate (K) increased until 1990, decreasing thereafter until 1994, when they became negative and close to zero. The negative or close to zero genetic trends for asymptotic weight and maturation rate over the 28 years evaluated may be indicating an absence of direct selection on these traits in Nellore herds (GARNERO et al., 2006). This trend confirms that the selective breeding program adopted on these farms under study has been efficient for parameter A, which is probably related to direct selection for other related traits, such as weight gain or weight evaluated at different ages. However, results for parameter K indicate that there is no selection for this trait and that direct selection for other traits of economic interest is not affecting genetic progress for this parameter.

CONCLUSION

The Brody model showed the best fit to describe the growth curve of male and female Polled Nellore cattle. The heritability estimate for parameter K of the growth curve of Polled Nellore herds from northern Brazil showed enough genetic variability to provide genetic gains when this parameter is used for herd selection. The negative correlation between parameters A and K showed that animals that are heavier in adulthood tend to have lower growth rates. In addition, the predicted breeding values for parameter A showed a slight genetic gain, suggesting greater selection pressure for asymptotic weight.

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