

## Fitting of fixed regression curves with different residual variance structures for Nelore cattle growth modeling

### Ajuste da curva fixa da regressão sob estruturas de variância residual para modelagem de crescimento de bovinos Nelore

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#### Highlights:

Fixed function class influences the fitting of Nelore Mocho cattle growth curve.

A class-four function was significantly better for the fitting of Nelore Mocho cattle growth curve.

Residual variance modeling influenced the quality of estimated genetic parameters.

A six-class model had the best fit for the modeling of Nelore Mocho cattle growth.

#### Abstract

Different polynomial functions were tested for mean trajectory modeling with different residual variance structures. A total of 15,148 weight records of 3,115 Nelore Mocho cattle with ages between 1 and 660 days, raised in northern Brazil. First, the mean trajectory of cattle growth curve was fitted by a fixed regression using orthogonal polynomials with orders ranging from two to seven. Analyses were performed using the least-squares method, disregarding animal and/ or maternal random effects. Then, the best model was evaluated using different residual variance structures and homogeneous and heterogeneous classes. We considered as fixed effects those of groups of contemporary and of dam age at birth (as linear and quadratic covariate). The random model part included animal and maternal effects (direct genetic and permanent environments). We concluded that the estimates of variance components and genetic parameters were affected by both fixed regression curve polynomial order and residual variance structure. Moreover, random regression model considering an order-four polynomial function with a fixed curve and six-class residual variance showed better fits.

**Key words:** Mean curve. Genetic parameters. Linear models. Random regression. Residual modeling.

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## Resumo

Diferentes funções polinomiais foram avaliadas para a modelagem da trajetória média de crescimento sob diferentes estruturas de variância residual. Utilizaram-se 15.148 registros de pesos de 3.115 bovinos da raça Nelore Mocho com idade entre 1 e 660 dias, criados na região Norte do Brasil. Inicialmente, a trajetória média da população foi ajustada por uma regressão fixa sob polinômios ortogonais da idade com ordens variando de dois a sete. Estas análises foram executadas por meio do método de quadrados mínimos ordinários, desconsiderando os efeitos aleatórios do animal e materno. Posteriormente, o melhor modelo foi avaliado sob diferentes estruturas de variância residual por meio de classes homogêneas e heterogêneas. Os efeitos fixos considerados foram os de grupos de contemporâneos e a idade da mãe ao parto (como covariável linear e quadrática). Na parte aleatória do modelo incluiu-se os efeitos do animal e materno (genéticos diretos e ambientes permanentes). Concluiu-se que as estimativas de componentes de variância e parâmetros genéticos foram afetados tanto pela ordem polinomial da curva de regressão fixa, como pela estrutura da variância residual, e o modelo de regressão aleatória que considerou uma função polinomial de ordem quatro na curva fixa e seis classes de variâncias residuais apresentou o melhor ajuste.

**Palavras-chave:** Curva média. Modelagem residual. Modelos lineares. Parâmetros genéticos. Regressão aleatória.

### Introduction

Random regression models allow random curve fitting for each individual included in a study. Such curves are expressed as deviations from a mean population curve. According to Bonafé et al. (2011), a mean growth curve is defined by a continuous fixed part function of these random regression models. These models are fitted by a covariance matrix, in which covariance functions are used as an efficient alternative (Sousa, Oliveira, Albuquerque, Boligon, & Martins, 2010). Moreover, the models allow residual variance modeling by means of different structures (Tholon & Queiroz, 2007).

To properly model beef cattle growth curve, some authors have investigated not only the order of the polynomial function fitting to represent the random part but also mean growth curve (Meyer, 2001; Boligon, Mercadante, Baldi, Lôbo, & Albuquerque, 2009; Baldi, Alencar, & Albuquerque, 2010). Concerning the modeling of residual variance in random regression, several studies have shown the need to consider residual variance heterogeneity in a random regression model for dairy cattle (Costa et al., 2008) and for beef cattle (Herrera, El Faro,

Albuquerque, Humberto, & Machado, 2008; J. E. R. Sousa et al., 2010).

Residual variations in growth parameters tend to increase as animals gain weight. Therefore, growth curve modeling considering various residual variance classes as a function of age (heterogeneous) can improve partition of phenotypic variance into variance due to random effect included in the modeling, as observed by Meyer (2001) and Fischer, Van der Werf, Banks and Ball (2004). However, the number of residual variance classes should be increased carefully since a surplus of classes increases the number of parameters to be estimated, which can hinder analysis. When considering the divergences found in the literature regarding fixed curve modeling, as well as residual variation structure in random regression models, studies should be carried out on growth modeling of Nelore Mocho cattle (Barbosa et al., 2017).

Based on the above, this study aimed to compare random regression models to estimate order with the best fit to fixed effects, as well as to determine the most suitable residual variance structure for modeling of Nelore cattle growth in northern Brazil.

## Material and Methods

Data were gathered from herds from the Ponderal Development Program, Brazilian Association of Zebu Breeders (ABCZ). These herds were being reared in seven states of northern Brazil (Amazonas, Acre, Amapá, Roraima, Rondônia, Pará and Tocantins).

At first, the database had 44,106 weight records; then, this information was edited out, eliminating records of animals with more 660 days of age, animals without sire and/or dam identification, animals with less than 3 weight records, and age-matched groups with less than 3 animals.

Within the age-matched groups, animals were grouped by sex, birth year, calving season, weight measure, weighing month, farm and breeding conditions. The calving seasons were classified into rainy (December to May) and dry (June to November), while the breeding conditions were divided into milk-fed and weaned animals (fed pasture).

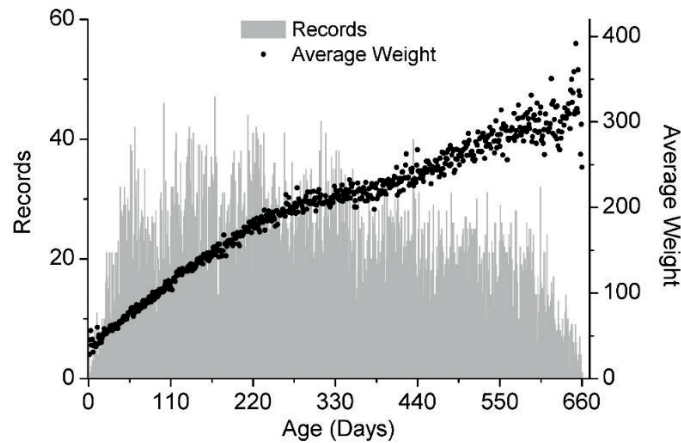
To delete records with measurement errors (outliers), data consistency was analyzed through observations of significant variabilities within each age-matched group. Weight records out of the range given by the mean of the age-matched group ( $\pm 3$  standard deviations) were excluded. As a result, a total of 1,819 age-matched groups with an average of 8.3 records were observed (Table 1).

**Table 1**  
**Summary of the data structure for Nelore Mocho cattle used in the study reared in northern Brazil**

Information	Quantity
Data	15,148
Animals with observation	3,115
With 3 observations	712
With 4 observations	698
With 5 observations	549
With 6 observations	659
With 7 to 10 observations	497
Breeding	282
Matrices	764
Animals in the kinship matrix	5,678
Contemporary groups	1,819

After editing, the database had 15,148 weight records belonging to 3,115 animals, born between 1995 and 2010 and fed pasture, with a mean birth

weight of 28 kg. Figure 1 shows the mean weight and number of records by age.



**Figure 1.** Record number and average body weight by age of Nellore Mocho cattle from northern Brazil

Data were analyzed following two steps: 1) definition of the fit order of the fixed regression curve, and 2) fit of the number of residual variance classes in the random regression models.

First, mean population trajectory was fitted by a fixed regression with orthogonal polynomials of age, with orders ranging from two to seven. For analyses, an ordinary least square method was used disregarding animal and dam random effects. The fixed order effects considered in the analysis were contemporary groups and dam's age at birth, which were taken as linear and quadratic covariates. The fit of the functions of different orders was assessed by the following criteria: 1) residual mean square (RMS) as  $RMS = \frac{1}{n}$ , wherein  $n$  is observation number,  $Y_i$  and  $\hat{Y}_i$  are observed and estimated values, respectively; 2) absolute mean deviation (AMD) as  $AMD = \frac{1}{n} \sum_{i=1}^n Y_i - \hat{Y}_i$  (Sarmiento et al., 2006), which is obtained as the sum of absolute mean deviations; 3) percentage squared bias (PSB) (Ali & Schaeffer, 1987) as  $PSB = \frac{\sum_{i=1}^n (Y_i - \hat{Y}_i)^2}{\sum_{i=1}^n (Y_i)^2} \times 100$ ; and coefficient of determination ( $R^2$ ) by the square of the correlation between observed and estimated weights, as:  $R^2 = 1 - \left(\frac{RMS}{MCSS}\right)^2$ , wherein RMS is residual mean square and MCSS is mean-corrected squared sum.

After defining the best order fit to the fixed regression function modeling and quadratic order functions for random effect modeling, different residual variance class structures were compared. These were considered to model residual variance, considering standard ages that are important for body development evaluation (1, 240, 365, and 550 days of age). For this purpose we first considered age classes (CL $m$ , where  $m$  is the number of classes), grouped as follows: CL1: homogeneous; CL2: 1-240 and 241-660 days; CL3: 1-240, 241-550, and 551-660 days; CL4: 1-240, 241-365, 366-550, and 551-660 days; CL5: 1-240, 241-330, 331-365, 366-550, and 551-660 days; CL6: 1-120, 121-150, 151-240, 241-365, 366-550, and 551-660 days; CL7: 1-120, 121-150, 151-240, 241-365, 366-450, 451-550, and 551-660 days; and CL8: 1-120, 121-150, 151-240, 241-365, 366-410, 411-450, 451-550, and 551 to 660 days of age.

The above can be expressed in matrix notation as:

$$Y = Xb + Z_1a + Z_2m + Z_3c + Z_4q + e$$

and its respective assumptions can be described as:

$$E \begin{bmatrix} Y \\ a \\ m \\ c \\ q \\ e \end{bmatrix} = \begin{bmatrix} Xb \\ 0 \\ 0 \\ 0 \\ 0 \\ 0 \end{bmatrix}, \text{ and, } \begin{aligned} \text{Var}(a) &= K_a \otimes A, \\ \text{Var}(c) &= K_c \otimes I_{Nd}, \\ \text{Var}(q) &= K_q \otimes I_{Nd}, \\ \text{Var}(e) &= R; \\ \text{Var}(m) &= K_m \otimes A, \end{aligned}$$

Wherein:  $Y$  is the vector of  $N$  observations regarding  $Nd$  animals;  $\beta$  is a vector which contains the fixed effects and the regression coefficients  $bm$  of fixed effects;  $a$  is a vector  $Ka \times ND$  of random regression coefficients of direct additive effects, wherein  $ND > Nd$  denotes the total number of animals analyzed, i.e. in the kinship matrix (5,678);  $Y$  is a vector  $Km \times ND$  of random regression coefficients of maternal genetic effects;  $\delta$  is a vector  $Kc \times Nd$  of random regression coefficients of animal permanent environmental effect;  $\lambda$  is a vector  $Kq \times Nm$  of random regression coefficients of maternal permanent environmental effects, wherein  $Nm$  equals to the number of females with progenies included in the dataset;  $e$  is a vector of random errors;  $X$ ,  $Z1$ ,  $Z2$ ,  $Z3$ , and  $Z4$  are the incidence matrices of fixed effects, direct genetic, maternal genetic, animal permanent environmental, and maternal permanent environmental effects, respectively;  $Ka$ ,  $Kc$ ,  $Km$ , and  $Kq$  are the (co) variance matrices among the regression coefficients of direct genetic, animal permanent environmental, maternal genetic, and maternal permanent environmental effects, respectively;  $A$  is the numerator matrix of the coefficients of relationship among individuals;  $Ind_{Nd}$  is an identity matrix of size  $Nd$ ;  $I_{Nm}$  is an identity matrix of size  $Nm$ ;  $\otimes$  is the Kronecker product; and  $R$  is a diagonal matrix of residual variances, whose size varies with the analysis structure.

Covariance between direct additive genetic effects and breastfeeding was assumed to be zero.

According to the adjusted model, (co) variances among random regression coefficients of direct and maternal additive genetic and permanent environmental and animal feeding were estimated by restricted maximum likelihood (REML), using WOMBAT software (Meyer, 2007).

All models were initially compared by changing maximum likelihood function logarithm (Log L), through likelihood ratio test (LRT), as follows:  $LRT_{ij} = 2 \text{ Log } L_i - 2 \text{ Log } L_j$ ; wherein:  $\text{Log } L_i$  is the likelihood function maximum for a full model  $i$ , and  $\text{Log } L_j$  is the likelihood function maximum for a reduced model  $j$ . The estimate of LRT compared with chi-square table value, with  $d$  degrees of freedom and significance level of 1%, wherein  $d$  is the difference between the number of parameters estimated by the full and reduced models.

Akaike (AIC) and Bayesian Schwarz (BIC) information criteria were used to compare non-nested models and impose penalties according to the number of parameters being estimated.

## Results and Discussion

When comparing function orders fitted by ordinary least squares method, the worst fit was observed for linear order and, as the fit-order is increased, RMS, AMD,  $R^2$ , and PSB improved as well. Moreover, the largest difference was between linear ( $k = 2$ ) and quadratic ( $k = 3$ ) fits (Table 2).

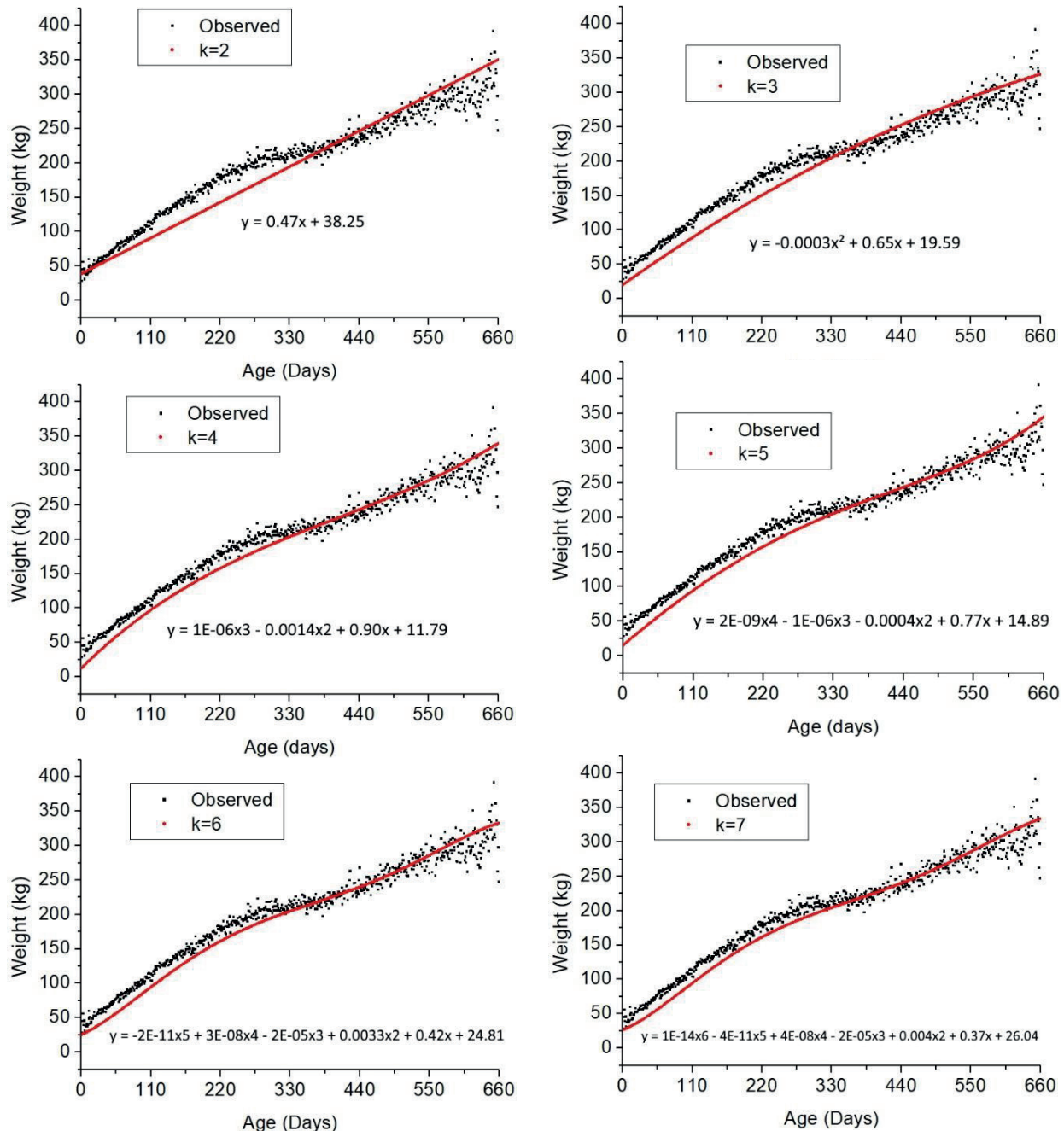
**Table 2**  
**Prediction error residual mean square (RMS), absolute mean deviation (AMD), determination coefficient ( $R^2$ ), percentage square bias (PSB) for the fitting of mean population trajectory by polynomial functions of different orders (k)**

Order	RMS*	ADM*	$R^2$	PSB
K=2	143.94	8.88	0.97	0.33
K=3	138.31 (-5.62)	8.65 (-0.23)	0.98	0.31
K=4	134.21 (-4.10)	8.53 (-0.12)	0.98	0.31
K=5	133.83 (-0.39)	8.51 (-0.01)	0.98	0.30
K=6	132.46 (-1.37)	8.46 (-0.05)	0.98	0.30
K=7	132.43 (-0.03)	8.46 (0.00)	0.98	0.30

\* Data in parentheses represent the difference between the analyzed model and the following model.

A linear fit was the worst among the fitting orders evaluated since it was far from the values observed in the beginning and end of the curve. In the other fit orders, functions differed mainly from the middle to the end of the growth curve, whereas fourth-order functions tended to bring curves closer

to each other (Figure 2). Function orders higher than or equal to four had greater flexibility from the middle to the end of the curve when compared to lower orders. These models have therefore the capacity to represent a mean growth curve that is consistent with cattle body development.



**Figure 2.** Dispersion of observed mean weights according to age and estimated population mean trajectory (fixed regression with orthogonal age polynomials) by least squares according to fit order (K).

Sakaguti et al. (2002) asserted that the lower flexibility of cubic functions compared to higher-order functions has no effect on the fit of growth models to cattle body weight data. According to the authors, this is because cubic order functions provide a growth curve highly consistent with animal body development, which was thus chosen to represent a fixed function in random models. Additionally, higher-order functions over-parameterize models and hence hinder data convergence in genetic parameter analyses.

In this study, the second stage, which aimed to fit model residue, considered a cubic-order model for fixed regression fitting and quadratic functions to the model random part with different residual variance structures. Table 3 shows a model fit improvement as the number of residual variation class increases. LRT indicates a larger difference in Log L between CL6 and CL5 models. Such improvement is noticeable when comparing models by AIC and BIC.

**Table 3**  
**Number of parameters (NP), maximum likelihood function logarithm (Log L), Akaike information criterion (AIC), Bayesian information criterion (BIC), and likelihood ratio test (LRT) estimated by the different tested models**

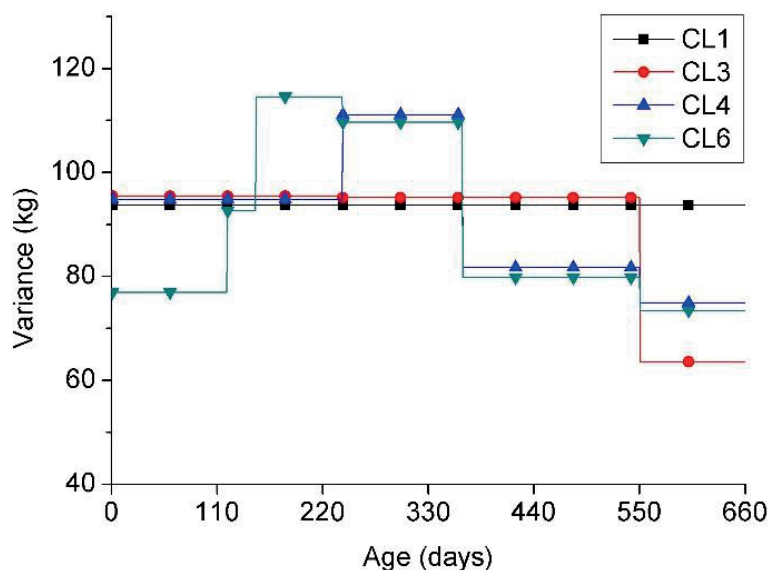
Model	NP	Log L	AIC	BIC	
CL1	25	-43848.1	87746.2	87933.6	
CL2	26	-43847.6	87747.3	87942.2	(CL2-CL1) = 0.9 <sup>ns</sup>
CL3	27	-43842.7	87739.4	87941.8	(CL3-CL2) = 9.9 **
CL4	28	-43829.7	87715.3	87925.2	(CL4-CL3) = 26.0 **
CL5	29	-43828.5	87715.0	87932.4	(CL5-CL4) = 2.3 <sup>ns</sup>
CL6	30	-43808.4	87676.9	87901.8	(CL6-CL5) = 40.1 **
CL7	31	-43807.9	87677.9	87910.3	(CL7-CL6) = 1.0 <sup>ns</sup>
CL8	32	-43807.9	87679.9	87919.8	(CL8-CL7) = 0 <sup>ns</sup>

CL: Model name added by the number of residual classes; <sup>ns</sup> Non-Significant; \*\*Significant (P<0.01).

The fulfillment of AIC and BIC criteria is important to ascertain fit quality since both criteria consider the number of estimated parameters in a model. Also, their formulas downgrade more parameterized models, which can make it difficult to calculate genetic parameters due to variance decomposition. After analyzing different fitting models, these criteria were the most promising for the model selection process. As shown in Table 3, model CL6 had better fits regarding AIC and BIC guidelines and a more significant Log L improvement when compared to the previous one (CL5). Still according to Log L, AIC, and

BIC standards, CL1 was the least suitable model, thereby, models considering a homogeneous residual variation are charged as less suitable for analysis of genetic parameters.

If compared to the significantly different heterogeneous classes (CL3, CL4, and CL6), the homogeneous class (CL1) showed residual variations at the beginning and the end of the curve smaller than that in the middle thereof (Figure 3). This way, a fit model that considers a single variation class is unsuitable since it disregards changes in residual variation.



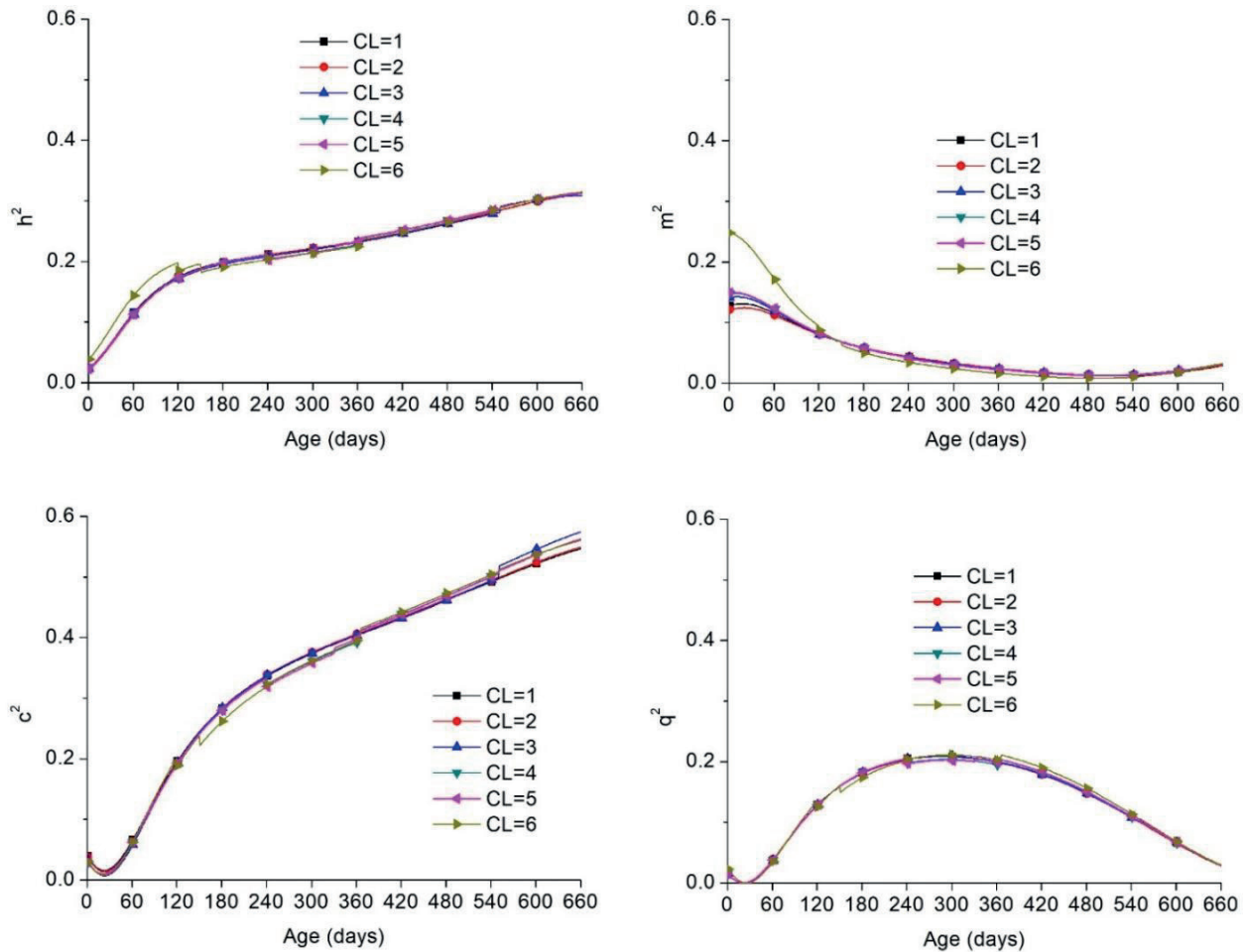
**Figure 3.** Estimates of homogeneous (CL1) and heterogeneous (CL3, CL4, and CL6) residual variance

Figure 3 also shows that residual variation estimates at the beginning of the growth curve were high for all models except for CL6, which had low variation (76.9 kg). Toral, Alencar and Freitas (2009) assessed residual variations in beef cattle growth curves by different structures and reported similar results. They observed that residual variation starts low and increases sharply right at the beginning of the curve but tends to decrease in the end.

Once residual variation is assumed homogeneous, considerable distortions are created in total variance partitioning (Sousa, Silva, Sarmento,

Sousa, & Souza, 2010). We observed implications in the estimated residual variations, unlike those considering heterogeneity. Figure 4 shows the effect of different residual classes on various sources of variation such as direct and maternal heritabilities, the ratio of permanent and maternal environmental variations, and phenotypic variation. Thus, unsuitable residual variance modeling entails uneven total variance decomposition, what has serious implications mainly on the direct heritability estimates of a given trait.





**Figure 4.** Direct heritability ( $h^2$  - upper left) and maternal ( $m^2$  - upper right) and variance components for animal permanent environment ( $C^2$  - lower left) and maternal ( $q^2$  - lower right) as a proportion of the phenotypic variance.

When estimated by a homogeneous model, maternal heritability was about 0.12 near parturition, and by the heterogeneous model CL6, it was 0.25. Maternal heritability different from zero at parturition is biologically consistent, as dams have an influence on offspring since pregnancy, i.e., maternal effects contribute since before animal birth (Sarmiento et al., 2006).

As part of phenotypic variation, permanent animal environment estimated considering residual variation homogeneity and heterogeneity differed only from the third part of the curve to the end, showing very low magnitude (Figure 4), as did the

maternal permanent environment. Different results were observed by Sarmiento et al. (2011) and by S. C. D. Sousa et al. (2010), who observed variations in estimates between models that were much more expressive.

Differences between homogeneous (CL1) and heterogeneous (CL6) models were evaluated using predicted genetic values for the five best animals at birth, 240 and 660 days of age (Table 4). When homogeneity was assumed, predicted genetic values were almost all underestimated if compared to those considering a heterogeneous residual variation.

**Table 4**  
**Predicted genetic values of the five best animals for birth weight at 240 and 660 days of age, considering residual variation homogeneity and heterogeneity (CL6)**

Age (days)	Animal	Predicted Genetic Value (kg)			
		Homogeneous	CL6	Deviation (%) <sup>1</sup>	Correlation ( $\rho$ )
	12032	3.12	4.61	-32.48	
	10755	3.29	4.60	-28.40	
	18367	2.61	3.42	-23.80	
	1291	2.35	3.22	-27.01	
	18358	2.26	3.08	-26.61	
	11374	2.40	3.07	-21.64	
	16075	2.18	3.06	-28.91	
	8337	2.18	2.95	-25.97	
	18345	1.82	2.80	-35.06	
	13904	2.34	2.78	-15.89	
	15445	2.16	2.77	-21.91	
	10637	2.11	2.72	-22.17	
	10749	1.96	2.66	-26.37	
	578	2.30	2.65	-13.27	
	11947	1.98	2.60	-23.72	
Birth	18237	1.79	2.56	-30.09	0.97
	12251	1.77	2.54	-30.16	
	18343	1.65	2.54	-34.96	
	17641	1.73	2.53	-31.81	
	18355	1.76	2.53	-30.57	
	7932	2.11	2.52	-16.20	
	18338	1.80	2.52	-28.50	
	14569	1.95	2.48	-21.24	
	10810	1.44	2.42	-40.31	
	17916	1.67	2.42	-30.76	
	57	1.90	2.41	-21.46	
	18357	1.70	2.39	-29.07	
	7821	1.71	2.32	-26.48	
	17686	1.78	2.29	-22.04	
	11817	1.72	2.26	-23.93	
	18341	1.63	2.25	-27.38	
	15426	1.52	2.24	-32.45	
	11170	1.59	2.24	-28.87	
	15279	1.87	2.23	-16.23	
	10819	1.36	2.22	-38.86	
	16016	1.52	2.21	-31.34	
	17036	1.77	2.21	-19.57	
	101	1.63	2.19	-25.48	
	10796	1.60	2.18	-26.80	
	18389	1.68	2.17	-22.68	

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	17615	23.23	23.13	0.44	
	17917	22.35	21.70	2.98	
	1045	21.26	21.18	0.36	
	10755	20.54	21.16	-2.91	
	17206	20.47	20.92	-2.17	
	17537	20.11	20.10	0.04	
	18345	19.41	19.71	-1.52	
	16664	19.29	19.49	-1.03	
	17557	19.77	19.37	2.04	
	16075	19.23	18.96	1.43	
	17536	18.66	18.51	0.79	
	16945	18.43	18.19	1.33	
	18237	18.54	18.12	2.32	
	18343	17.24	17.39	-0.88	
	16029	17.23	17.16	0.39	
	16033	16.98	17.11	-0.78	
	5910	17.98	17.07	5.32	
	8517	16.77	16.90	-0.80	
	15973	17.04	16.89	0.93	
240 days	16036	16.60	16.46	0.84	0.99
	8700	16.47	16.38	0.53	
	17503	15.98	16.14	-0.99	
	18303	16.32	16.11	1.28	
	16007	15.87	16.05	-1.11	
	16038	16.30	16.02	1.79	
	17659	17.35	16.00	8.42	
	18358	15.91	15.99	-0.47	
	8693	16.12	15.97	0.93	
	8680	15.76	15.84	-0.56	
	8725	15.76	15.83	-0.39	
	18352	15.86	15.81	0.32	
	15426	16.10	15.81	1.86	
	13617	16.06	15.72	2.16	
	16133	15.34	15.59	-1.62	
	18305	15.66	15.58	0.49	
	17825	15.62	15.55	0.43	
	18119	15.68	15.42	1.68	
	17275	16.52	15.41	7.19	
	16790	15.63	15.37	1.70	
	17920	15.47	15.32	1.03	

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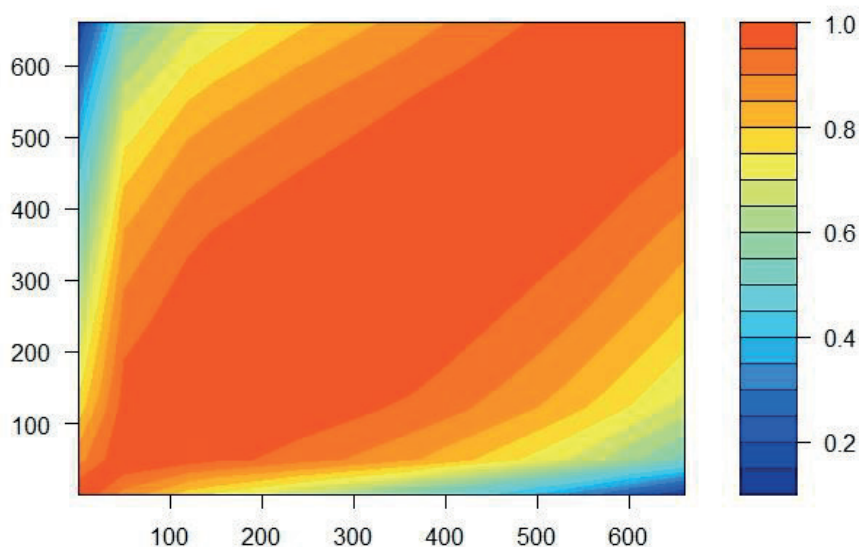
	1045	66.50	67.35	-1.26	
	17615	64.19	64.90	-1.10	
	17536	63.51	64.38	-1.37	
	17206	55.77	57.23	-2.56	
	13617	51.34	52.62	-2.42	
	16945	49.12	49.47	-0.70	
	16939	47.49	47.84	-0.72	
	16038	47.01	47.53	-1.08	
	16664	45.38	46.36	-2.10	
	16286	45.49	46.09	-1.30	
	18305	45.02	45.38	-0.78	
	17557	44.11	44.87	-1.71	
	17537	44.60	44.86	-0.58	
	8693	44.10	44.82	-1.60	
	8725	43.71	44.42	-1.60	
	16033	43.42	44.14	-1.63	
	17743	43.69	43.74	-0.12	
	17917	42.70	43.12	-0.99	
	17540	41.45	42.12	-1.58	
660 days	15980	41.77	41.96	-0.45	0.99
	17547	41.57	41.91	-0.82	
	15591	41.48	41.82	-0.82	
	16009	41.46	41.67	-0.52	
	16573	40.94	41.21	-0.66	
	17545	40.38	40.93	-1.34	
	16790	40.34	40.91	-1.38	
	18303	40.35	40.76	-1.00	
	17843	40.09	40.63	-1.33	
	16665	39.66	40.43	-1.91	
	16996	40.09	40.42	-0.83	
	16186	39.99	40.42	-1.06	
	17750	39.77	40.36	-1.45	
	8680	39.58	40.14	-1.39	
	17503	39.35	39.97	-1.54	
	17920	39.48	39.95	-1.17	
	17203	38.25	39.71	-3.66	
	16960	39.50	39.69	-0.48	
	17275	41.35	39.55	4.56	
	15870	38.73	39.16	-1.10	
	17140	38.76	39.14	-0.98	

<sup>1</sup>Deviations of the genetic values predicted by the homogeneous and CL6 models (expressed as a percentage).

In analyzing the deviations of predicted genetic values (in percentage), the largest values were found for birth weight, ranging from 23.80 to 32.48%, for the five best animals within the population. At 240 and 660 days of age, the relative variation accounted for between 1 and 3% of the genetic value. We also found that the Spearman correlation between the models for age at birth was 0.97.

Our findings confirm that improper residual modeling results in erroneous estimates of animal

genetic value, which, in turn, lead to the selection of less productive animals, and in the long term, large production losses for wasting herd genetic potential. Predicting the genetic value of early-stage animals is an important decision-making tool in terms of genetic improvement. It allows to increase genetic gain and reduce intergenerational interval. Thus, the correlation between genetic values tends to increase when they are predicted at closer ages, as shown in Figure 5.



**Figure 5.** Spearman correlation of direct additive genetic value obtained at different ages by a 6-class residual variance model (CL6).

The correlation of genetic values had moderate to high magnitude between animals with 660 days of age and at weaning (240 days). Therefore, selecting the best animals by weight at 240 days of age presupposes selecting the best animals at 660 days of age.

## Conclusion

An order-four (cubic) polynomial function is the best suited to describe the mean growth curve of Nellore Mocho cattle by random regression models.

A heterogeneous residual variation structure is more suitable for correctly modeling variations in

the growth curve of Nellore Mocho cattle.

A six-class model was superior for growth modeling of Nellore Mocho cattle, reared in northern Brazil and with birth age of 660 days.

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