Genetic parameters and trends of growth traits in Nelore cattle raised in the Northern region of Brazil

Parâmetros genéticos e tendências de características de crescimento em gado Nelore criado na região norte do Brasil

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ABSTRACT

The objective of this study was to estimate (co)variances and genetic parameters and to predict genetic trends for weight at 120 (W120), 210 (W210), 365 (W365), and 450 (W450) days of age in Nelore cattle raised in the northern region of Brazil. The database comprised records of 30,387 animals born between 2000 and 2013 in the Brazilian North. Estimates were calculated by the Restricted Maximum Likelihood (REML) method, in single- and multi-trait analyses in an animal model. Heritability as obtained using single- and multi-trait models for W120 (0.22 and 0.31), W210 (0.20 and 0.34), W365 (0.51 and 0.51), and W450 (0.49 and 0.51) indicated moderate to high magnitudes, with the possibility of genetic selection and incorporation into the herd. Genetic correlations between growth traits were favorable, ranging from 0.78 to 0.96. Genetic trends for W120 and W210 varied largely, from -0.31 to 4.68 and -0.53 to 7.62 kg/year, respectively. Smaller fluctuations were observed in genetic trends for W365 and W450, which ranged from -1.08 to 10.90 and -1.29 to 12.51 kg/year, respectively. Selection for W365 and W450 proved to be the criterion of choice for Nelore herds raised in the region; however, it may compromise adult performance because of higher costs and time for production. A thorough analysis of mattings is recommended to allow the selection of earlier-developing animals.
Keywords: Heritability. Performance. Selection. Zebu.

RESUMO

O presente trabalho foi delineado para estimar as (co) variâncias, parâmetros genéticos e de predizer as tendências genéticas para o peso aos 120 (W120), 210 (W210), 365 (W365) e 450 (W450) dias de idade de gado Nelore criado na região norte do Brasil. A base de dados foi constituída por registro de 30387 animais, nascidos entre 2000 e 2013 no norte do Brasil. As estimativas foram calculadas pelo método de máxima restrição de probabilidade (REML) em um modelo animal com análises isoladas e multi variadas. A herdabilidade obtida para os modelos utilizados foi: W120 (0,22 e 0,31); W210 (0,20 e 0,34); W365 (0,51 e 0,51) e W450 (0,49 e 0,51), indicando moderada e alta magnitude com a possibilidade de seleção genética e incorporação no rebanho. As correlações genéticas entre grupos de tendências foram favoráveis variando de 0,78 a 0,96. As tendências genéticas para W120 e W210 apresentaram ampla variação de -0,31 a 4,68 e -0,53 a 7,62 kg/ano, respectivamente. Menores flutuações foram observadas nas tendências genéticas para W365 e W450, as quais variaram de -1,08 a 10,90 e -1,29 a12,51 kg/ano, respectivamente. Foi constatado que a seleção para W365 e W450 deve ser um critério de escolha para os rebanhos Nelore criados na região; contudo ela pode comprometer a performance dos adultos devido aos elevados custos e da duração da produção. Uma completa análise de cruzamentos é recomendada para possibilitar a seleção de animais jovens em desenvolvimento
Palavras-chave: Herdabilidade. Performance. Seleção. Zebu.

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Introduction

Agribusiness represented 26.6% of Brazil's wealth in 2020, with a total turnover of almost two trillion reais and the country has reached records in meat exports, having sold in 2018 about 2.49 million tons of carcass equivalent, generating revenues of US$6.32 billion (Confederação Nacional da Agricultura e Pecuária no Brasil, 2021).

The northern region of Brazil holds approximately 22.5% of the national herd (Instituto Brasileiro de Geografia e Estatística, 2019), and its share in meat production and exports have been growing annually. However, due mainly to the diversity of production systems used, production and reproduction rates of herds raised in the Brazilian North are still below expectations.

Thanks to its vast territory, Brazil is home to a diversity of biomes, which differ in climate, soil, vegetation, sunlight incidence, and rainfall. In addition, cattle farming systems in the country are characterized by climatic, economic, and cultural differences and great availability of natural resources for animal production. Such environmental diversity leads to different opportunities for the expression of the same genotype, which makes it difficult to identify genetically superior individuals for reproduction and to determine herd performance (Ferreira et al., 2017; Lopes et al., 2017).

For the beef, cattle production system to be efficient and profitable, the knowledge of the population, genetic-phenotypic parameters, and trends in the productive and reproductive characteristics of the herd is extremely crucial, mainly because of the low number of herds evaluated in the northern region of the state. Brazil, which makes selecting genetically superior animals for breeding difficult (Lopes et al., 2017; Souza et al., 2018). Thus, to make an accurate selection, knowing the genetic potential of these animals becomes paramount.

Because of this importance, genetic improvement programs related to growth traits in beef cattle have been developed throughout the country (Santana et al., 2017), aiming at increasing productive and reproductive potential. Estimates of genetic parameters for growth traits in beef cattle are indicators of the response to genetic improvement (Barbosa et al., 2017), allowing classification and selection of the best individuals to be parents in the next generations. One aspect to consider in this context is that several authors have reported on the estimates of genetic parameters in populations of Nelore in different regions of Brazil (Passafaro et al., 2016; Barbosa et al., 2017; Souza et al., 2018; Pereira, 2021) and showed the existence of genetic variability, which allows for genetic progress through selection.

Considering the evolution of the Brazilian herd, in the period from 1994 to 2014, by region and states of the federation, the creation of cattle, mainly beef, migrated over the last 30 years to Northern Brazil. While the herds in Brazil, in the Midwest, South, Southeast, and Northeast regions grew by 34.9%, 3.77%, 2.41%, and 28.59% respectively, the herd in the North region grew by 155.07% (Neiva et al., 2016). Thus, knowledge of trends and genetic and phenotypic parameters for productive, reproductive, meat, and carcass quality traits in herds can be a good indicator of the response to selection or genetic progress to be achieved (Ferreira et al., 2017; Lopes et al., 2017; Souza et al., 2018).

The importance of this knowledge, in a population, is crucial to making the adjustments to the selection process, in which established selection criteria are reorganized, as well as the genetic evaluation of the herd (Lopes et al., 2017). It is possible to monitor and establish guidelines that guide genetic improvement programs, appreciating the genetic gain over time so that the results serve as guiding elements for future actions (Ferreira et al., 2017; Souza et al., 2018).

Traditionally, mixed models based on pedigrees have been used to analyze genetic merit between different environments. Increasingly accurate estimates of the (co) variance components have been required, as it allows for more efficient selection in the desired direction of selection (Boligon et al., 2009; Pedrosa et al., 2014; Pereira, 2021). In addition, methods for estimating covariance components require that all available information be together to reduce bias in the results, especially in traits expressed early in the animal's life, since physiologically many of them are interdependent and have genes in common; therefore, they

should not be considered in isolation (Pedrosa et al., 2014; Lopes et al., 2017; Pereira, 2021).

Therefore, this study had the objective to estimate the genetic parameters and predict the genetic trends for standardized weights at 120, 210, 365, and 450 days of age in Nelore cattle raised in the North region of Brazil and managed in a pasture.

Material and Methods

This study involved information on animals of the Nelore breed, born between the years 2000 and 2013, raised in herds located in the federative units that make up the northern region of Brazil, and which participated in the Nelore Breeding Program (*Nelore Brasil*) of the National Association of Breeders and Researchers (ANCP). The evaluated traits were standardized weights at 120, 210, 365, and 450 days of age (W120, W210, W365, and W450), which are used as selection criteria in the *Nelore Brasil* program.

The initial data included 30,387 records and, for the execution of the analyses, restrictions were applied to the database to ensure its consistency. Editing, consistency checking, and descriptive analysis of the data were carried out using the routines of the lm package of R software (R Core Team, 2013). Measurements that were three standard deviations above or below the mean of the trait and the mean belonging to each contemporary group (CG) were disregarded. In addition, animals belonging to CG with less than five records or that contained progenies from only one bull were excluded.

To construct the kinship matrix, a pedigree file containing 50,634 animals distributed in 14 generations was used. Table 1 describes the descriptive statistics of the data.

The contemporary groups were constituted by sex, year of birth, the season of birth, and management lot at the time of measurement and/or evaluation. The animals' birth seasons were grouped into four classes: January to March (season 1), April to June (season 2), July to September (season 3), and October to December (season 4). Connectivity between contemporary groups was tested

Table 1 – Descriptive statistics of growth traits of Nelore cattle raised in the Brazilian North

Trait	N	Mean (SD)	Maximum	Minimum	CG
W120	27.922	126.9 ±17.7	181	72	702
W210	23.975	186.2 ±25.4	264	108	726
W365	20.465	235.4 ±33.9	340	134	649
W450	17.598	267.8 ±39.5	389	149	598

W120: standardized weight at 120 days, in kg; W210 - standardized weight at 210 days, in kg; W365: standardized weight at 365 days, in kg; W450: standardized weight at 450 days, in kg; N: number of observations per trait; SD: standard deviation; CG: number of contemporary groups per trait.

using AMC software (Roso & Schenkel, 2006), based on the total number of genetic ties and considering the existence of at least 10 genetic ties as a constraint.

Genetic analyses were performed by fitting a model that included the following effects: cow age as a covariate (linear and quadratic effect), animal sex, the season of birth, and farm. To define the fixed effects included in the contemporary groups, the GLM (General Linear Model) procedure was used, and genetic analysis was performed by fitting the animal model. In matrix notation, the mixed linear models for pre-weaning (W120 and W210) and post-weaning (W365 and W450) traits were established according to models (1) and (2), respectively, considering the single-trait model. For the multi-trait models, the matrix form followed Equation 1:

$$y = X\beta + Z_{1a} + Z_{2m} + Z_{3pe} + e \text{ ,}$$

where

$$Cov(a, m) = A\sigma_{am} \quad\quad (1)$$

$$y = X\beta + Z_a + e \quad\quad (2)$$

where y corresponds to the phenotype vector; **X** is the incidence matrix for the fixed effects; β represents the vector of fixed effects (group of contemporaries and age of cow at calving considering the linear and quadratic effects); **a**, **m**, and **pe** are the vectors of random effect (additive direct, maternal direct, and maternal permanent environmental effects) associated with incidence matrices $\mathbf{Z_1}$, $\mathbf{Z_2}$, and $\mathbf{Z_3}$, respectively; and e is the vector of residual effects.

Heritability coefficients and genetic correlations were calculated based on the estimated variance components.

Genetic trends were calculated using breeding values estimated for each individual, with BLUPF90 software (Misztal et al., 2002). The breeding values of the animals were then grouped by year of birth to calculate the average annual breeding values, which were evaluated by the number of observations for the period from 2002 to 2013.

Subsequently, from the means of breeding values, the regression was calculated relative to the year of birth of the animals using the routines of the *lm* package of R software, following a linear trend. The breeding values for the analyzed traits represented the dependent variable, whereas the year of birth of the animals constituted the independent variable. The following regression equation was used:

$$Y_i = b_o + b_1 x_i + e \text{ ,}$$

where $\mathbf{Y_i}$ = breeding value for the evaluated traits in birth year i; $\mathbf{b_o}$ = intercept; $\mathbf{b_1}$ = slope of the line; $\mathbf{x_i}$ = birth year i; and $\mathbf{e_i}$ = random error.

To illustrate and predict genetic gain based on variance components and genetic parameters, a simulation of genetic gain was performed by the following formula:

$$\Delta G = \left(i \times \sigma_p \times h^2\right)/L ,$$

where ΔG is the genetic gain; i is the selection intensity (1.28, with 10% retention of males and 50% retention of females); h^2 is heritability because of the direct additive genetic effect; σ_p is the phenotypic standard deviation (Falconer & Mackay, 1996), and L is the average generation interval.

To determine L, the selection was simulated based on the use of bulls for five years (between two and six years) and females for seven years (between three and nine years), which resulted in L = 5 years. Thus, genetic gain (ΔG) can be given in kg/year.

The inbreeding coefficient (F) was calculated using the recursive algorithm that assumes non-zero inbreeding for animals with unknown parents, implemented in the INBUPGF90 computer program (Aguilar & Misztal, 2008).

The formula for calculating F was developed by Wright (1923) and corresponds to the probability that both alleles in a zygote are descendants of the same allele, originating from an ancestor common to both parents, according to the equation below:

$$F_x = \frac{1}{2}\Sigma\left(\frac{1}{2}\right)^n \left(1 + F_A\right) ,$$

where F_x = inbreeding coefficient of individual x; n = number of in-between generations that link both parents to the common ancestor; and F_A = inbreeding coefficient of each common ancestor.

Results and Discussion

Table 1 shows the descriptive statistics of standardized weights (W120, W210, W365, and W450 days of age) of Nelore cattle raised in the northern region of Brazil. Compared with data from other regions of the country, the pre-weaning weights found in this study (W120 and W210) were average and similar to those of some regions (Lira et al., 2013 (Northern region); Araújo et al., 2014 (Central West region); Guimarães, 2016 (São Paulo, Goiás and Mato Grosso country); Lopes et al., 2017 (Northern region)) and lower than those reported by Brunes (2017) in the central western region of Brazil. However, post-weaning data (W365 and W450) lie in an intermediate stratum when compared with data from studies conducted in other regions of the country (Lira et al., 2013 (Northern region); Araújo et al., 2014 (Central West region); Guimarães, 2016 (São Paulo, Goiás and Mato Grosso country); Lopes et al., 2017 (Northern region)).

The inbreeding coefficient of the studied animals ranged from 0 to 44%, averaging 1.87% (Figure 1). In total, 98% of the animals showed an F lower than 6.25%, while only 0.08% had an F higher than 25% (Table 2).

Table 2 – The number of animals per inbreeding coefficient (F) class and respective percentages for Nelore animals raised in the Brazilian North.

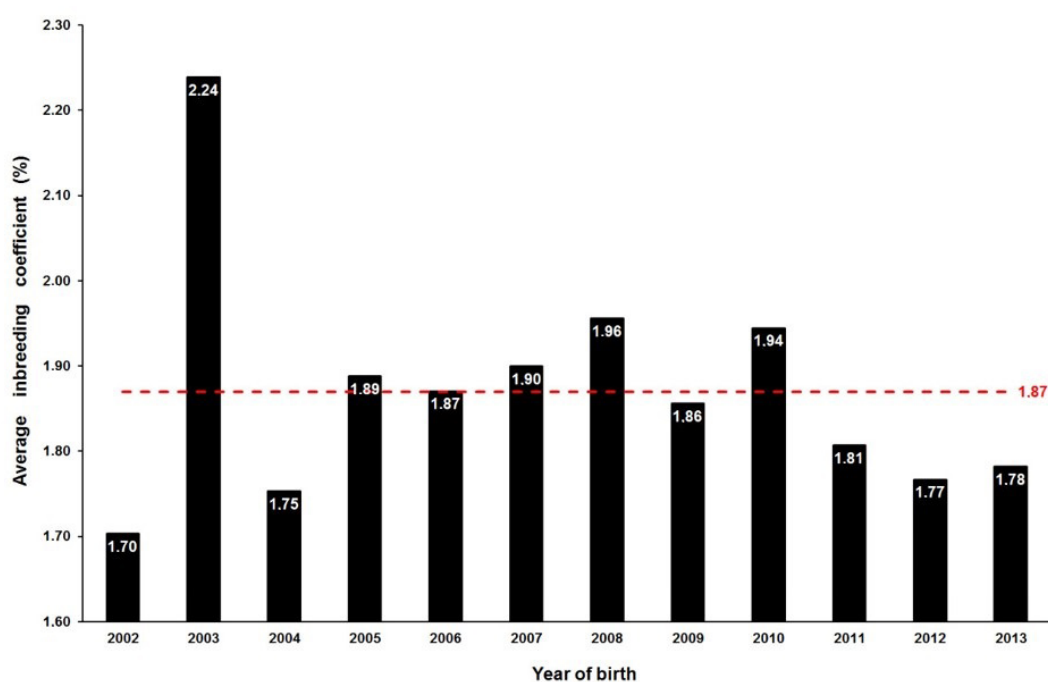| F class	Animals per class	Percentage
0.00	25,280	49.92
0.00 to 6.25	24,126	47.65
6.25 to 12.50	878	1.73
12.50 to 18.75	236	0.47
18.75 to 25.00	75	0.15
Greater than 25.00	42	0.08

Figure 1 – Average inbreeding coefficients are classified according to the year of birth of the studied animals.

A low degree of inbreeding was observed in the herd of the farms in the northern region of Brazil.

The low degree of inbreeding observed in the herd of farms belonging to the northern region of Brazil was expected since numerous generations (approximately 14) were detected, which allowed greater genetic variability of the herd, a large number of founders, and ancestors. Thus, it is understood that those responsible for the formation of the herds sought to avoid consanguineous mating, and introduced new genotypes in the population and ancestors, since the degree of kinship between individuals is not, on average, high.

These results disagree with those reported by Dotta et al. (2019), who found an average inbreeding coefficient of 8.74% in Nelore herds raised in the Amazon biome. In this study, the authors reported low pedigree integrity and a large number of founders and/or ancestors. A possible explanation could be the studied database and the established period since there are differences between the studies. Table 3 shows the estimates of (co)variance and heritability components, as obtained by single- and multi-trait analyses, for growth traits.

In both models, the estimates of direct genetic variances and direct heritability for pre-weaning traits (W120 and W210) varied according to the model, as the heritability coefficients ranged from low to moderately high (single- and multi-trait models, respectively). A likely explanation could be the fact that multi-trait models better represent the results of selection, as they consider several traits together in the estimation analyses (Boligon et al., 2009; Pedrosa et al., 2014).

This increase in the difference in additive genetic variance reflects the reduction of the existing bias in the analyses that consider only the performance of an individual trait or that consider only two traits as the evaluation criteria (Meyer, 1992; Boligon et al., 2009). According to Meyer (1992), Kaps et al. (1999), and Boligon et al. (2009), in herds in which a pre-selection is performed at weaning

and the actual selection takes place at one year of age or later because of economic reasons, these data should be included in the analysis of adult weight to consider the effect of selection.

Maternal heritability values for W120 and W210 were low (h^2_mW120 = 0.14 and h^2_mW210 = 0.15), possibly because of the low selection pressure for maternal effect applied to the herd and the high number of bulls used, which provided a large number of different generations. This explanation is supported by the estimates obtained in the multi-trait model, which the effects of selection into account (Boligon et al., 2009; Baldi et al., 2010) .

Variance estimates of maternal genetic effects were low and explained the little contribution of the maternal effect to the expression of the pre-weaning phenotype for growth traits in the Nelore cattle. The maternal permanent environmental effect contributed 13% to W120 and 15.62% to W210, also having a little effect on the post-weaning phenotype of the individuals.

Heritability estimates for the maternal effect were of low magnitude. Higher estimates were obtained in single-trait analysis, whereas in multi-trait analysis lower maternal heritability values were associated with higher direct heritability coefficients. This could be because of differences in the partition of direct and maternal genetic variances for the weights from birth to 12 months of age.

Maternal heritability estimates in single- and multi-trait analysis were low and similar to those reported by Baldi et al. (2010): 0.06 for birth weight, 0.09 for weaning weight, and 0.05 for weight at 12 months. Souza et al. (2018) found values close to those observed in this study for weaning weight (h^2_m = 0.06). These values suggest a smaller selection focus for this trait in the northern region of Brazil since the obtained heritability value was of low magnitude.

It is noteworthy that the high frequency of use of bulls in the region did not affect the frequency of replacement of females in the herd, which may have contributed to the

Table 3 – Estimates of genetic parameters for growth traits of Nelore cattle raised in the Brazilian North, as obtained by single-trait and multi-trait analysis

Model	Trait	σ^2_a	σ^2_m	σ^2_{pe}	σ^2_e	$h^2_d \pm$ SD	$h^2_m \pm$ SD
UNI	W120	51.49	32.40	31.99	114.60	0.22±0.02	0.14±0.01
	W210	83.92	64.22	64.72	201.50	0.20±0.02	0.15±0.01
	W365	254.66	-	-	244.92	0.51±0.01	-
	W450	272.86	-	-	278.57	0.49±0.02	-
MULTI	W120	65.18	6.92	6.70	126.05	0.31 ±0.01	0.07± 0.08
	W210	134.73	27.37	7.82	232.54	0.34 ±0.01	0.06± 0.06
	W365	287.47	-	-	278.02	0.51 ±0.01	-
	W450	326.46	-	-	313.67	0.51 ±0.01	-

UNI: single-trait model; MULTI: multi-trait model; W120: standardized weight at 120 days, in kg; W210: standardized weight at 210 days, in kg; W365: standardized weight at 365 days, in kg; W450: standardized weight at 450 days, in kg; SD: standard deviation; σ^2_a: animal direct genetic variance; σ^2_m: maternal genetic variance; σ^2_{pe}: permanent environmental genetic variance; and σ^2_e: residual genetic variance; h^2_d: direct heritability; and h^2_m: maternal heritability.

low maternal heritability estimates. In general, many studies (Santos et al., 2012; Lira et al., 2013; Nepomuceno et al., 2013; Ferreira et al., 2014, 2017) with Nelore herds in the same Brazilian region reported results similar to those found in the present study for maternal heritability estimates.

The multi-trait analysis provided higher estimates of the additive genetic variance than the single-trait analysis, especially for W365 and W450. This difference reflects the elimination of selection bias in multi-trait models (Meyer, 1992). As for the post-weaning traits (W365 and W450), there was no significant variation for heritability in neither the single- nor multi-trait analyses. This finding reinforces the hypothesis that in the studied herds, the greatest selection pressure is applied to the post-weaning traits. In this study, because the animal selection for breeding was based on post-weaning weights, the use of weights obtained before selection in multi-trait analysis allowed the elimination of selection bias from additive genetic variance.

In a multi-trait analysis from 12 months of age onwards, the phenotypic variance was higher than that obtained in single-trait analysis, which is likely because of the increase in additive genetic variance from that age. In the case of residual variances, there were no differences in the magnitude of variances obtained from single- and multi-trait analysis. Nevertheless, Boligon et al. (2009) found lower phenotypic and residual variances in multi-trait analysis for weights from one year of age onwards.

Residual variance values for W120, W210, W365, and W450 increased with animal age (Table 3). This was an expected result since these animals were predominantly raised on pasture and thus subject to various environmental effects, besides less control and the management to which older cattle are subjected, compared with younger animals. These values suggest a need for improving the environment and greater control of environmental conditions to provide uniformity to the environment where the individuals are raised.

The estimates of direct heritability suggest that the studied population has enough genetic variability to achieve considerable genetic gains from the selection. This is especially true from the weaning age since estimates in the post-weaning period remained practically constant and high in both the single- and multi-trait models. Estimates of direct heritability for pre-weaning weights differed between single- and multi-trait analyses, which may be because the multi-trait model considers weights before selection in the analysis (Meyer, 1992), thus reducing estimation bias.

Estimates of genetic correlations between all traits were high and positive, indicating a strong genetic association between the growth traits. Yokoo et al. (2009) and Araújo et al.

(2011) described similar estimates in Nelore cattle. The genetic correlations between pre- and post-weaning weights were high and positive, suggesting that many of the genetic factors that influence body weight at weaning are the same as those that influence it at adult age.

Table 4 displays genetic correlations between production traits (W120, W210, W365, and W450). The correlation values were considered high and significant for all traits under study. These results suggest genetic improvement in these traits, provided by selection at an appropriate age.

Because the genetic correlations between all traits in this study were high and positive, selection based on weaning weight (W210) may be a good option, as there are two important effects at this age (direct and maternal genetic effects). Thus, weight at 210 days of age should be preferred when aiming to improve the maternal capacity of the cows (mothers). In addition, selection for post-weaning weight can be used if the animals have a higher weaning weight and a high post-weaning growth rate, as it is possible to shorten the time between weaning and slaughter based on this trait.

However, a drawback of selecting animals at weaning is that the maternal effect persists at this stage. Therefore, despite having a positive genetic association with other traits (W365 and W450), these selection criteria cannot be suggested as the only criteria for increasing slaughter weight.

It is worth stressing that, over the years, selection for post-weaning weights can generate an increase in production costs, from age to slaughter and finishing of the animals. Therefore, greater attention is warranted along with the selection of animals with greater potential for pre-weaning weights since this is the life period in which the animal has the highest speed of growth and development. In this way, the selection of animals for greater weaning weights would allow a reduction in the time for the animal to reach the ideal weight to be slaughtered, thereby reducing production costs and slaughter age.

Moreover, the correlation coefficients decreased as the difference between the weight measurement ages increased, which is attributed to a greater temporal distance between

Table 4 – Genetic correlations (above the diagonal) and standard deviation (below the diagonal) between growth traits in Nelore cattle raised in the Brazilian North, as obtained by multi-trait analysis

Trait	W120	W210	W365	W450
W120	-	0.94	0.84	0.78
W210	0.0086	-	0.94	0.89
W365	0.0196	0.0097	-	0.96
W450	0.0244	0.0143	0.0037	-

W120: standardized weight at 120 days, in kg; W210: standardized weight at 210 days, in kg; W365: standardized weight at 365 days, in kg; W450: standardized weight at 450 days, in kg.

measurements. This can also be attributed to the non-additive or environmental genetic association between weight traits, which are largely affected by the same environmental conditions.

Figure 2 shows the genetic trends for W120 and P210 (A and B). The analysis of genetic trends showed a linear and considerable increase for these traits, with genetic gains ranging from -0.31 to 4.68 kg/year and -0.53 to 7.62 kg/year for W120 and W210, respectively. The non-establishment of these traits as a selection criterion can explain this variation. Furthermore, genetic trends for W120 and W210 (Figures 2A and 2B) revealed a selection of animals with superior genotype performance over the years.

The same behavior was observed for genetic trends for post-weaning traits (W365 and W450), where genotype performance and/or genetic gains increased throughout the generations. Genetic trends for these traits ranged from -1.08 to 10.90 kg/year for W365 and from -1.29 to 12.51 kg/year for W450 (Figures 3A and 3B).

Souza et al. (2011) also observed highly significant genetic trends for direct additive effects and reported annual increases of 0.16% and 0.20% in direct genetic gain for W240 and W420, respectively, relative to the average of the adjusted weights (0.2744 kg for W240 and 0.5062 kg for W420). Likewise, Ferraz et al. (2002) found genetic trends of direct effects in the studied period of 0.134, 0.207, and 0.276 kg/year for W205, W365, and W550, respectively, and also reported greater gains in older animals, which were nonetheless lower than those described in this study.

In other studies, with Nelore cattle in the Brazilian North, Santos et al. (2012) found smaller gains for traits measured before weaning vs. after weaning. This suggests that selection in the northern region of Brazil has been mainly aimed at the post-weaning weight. Similarly, in herds from the
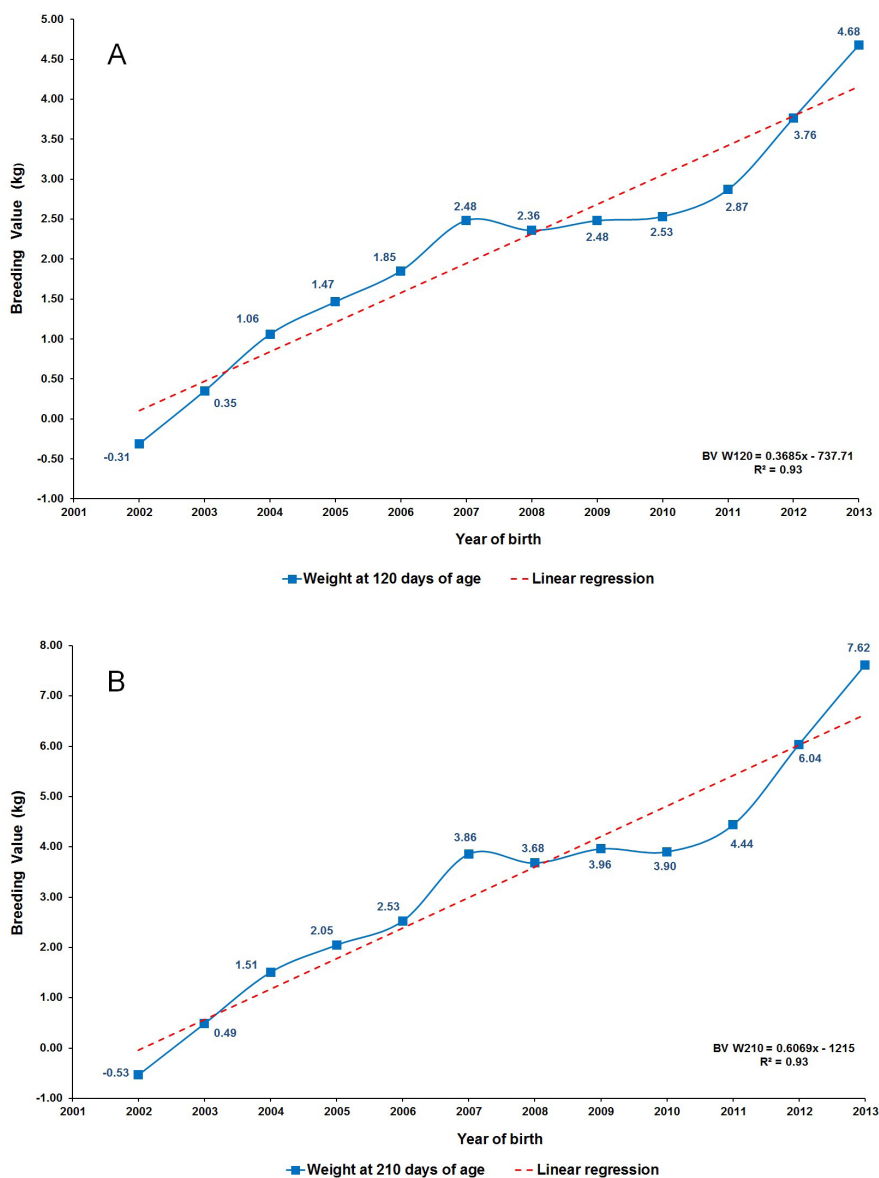

Figure 2 – Genetic trends for W120 (A) and W210 (B) in Nelore cattle raised in the Brazilian North.
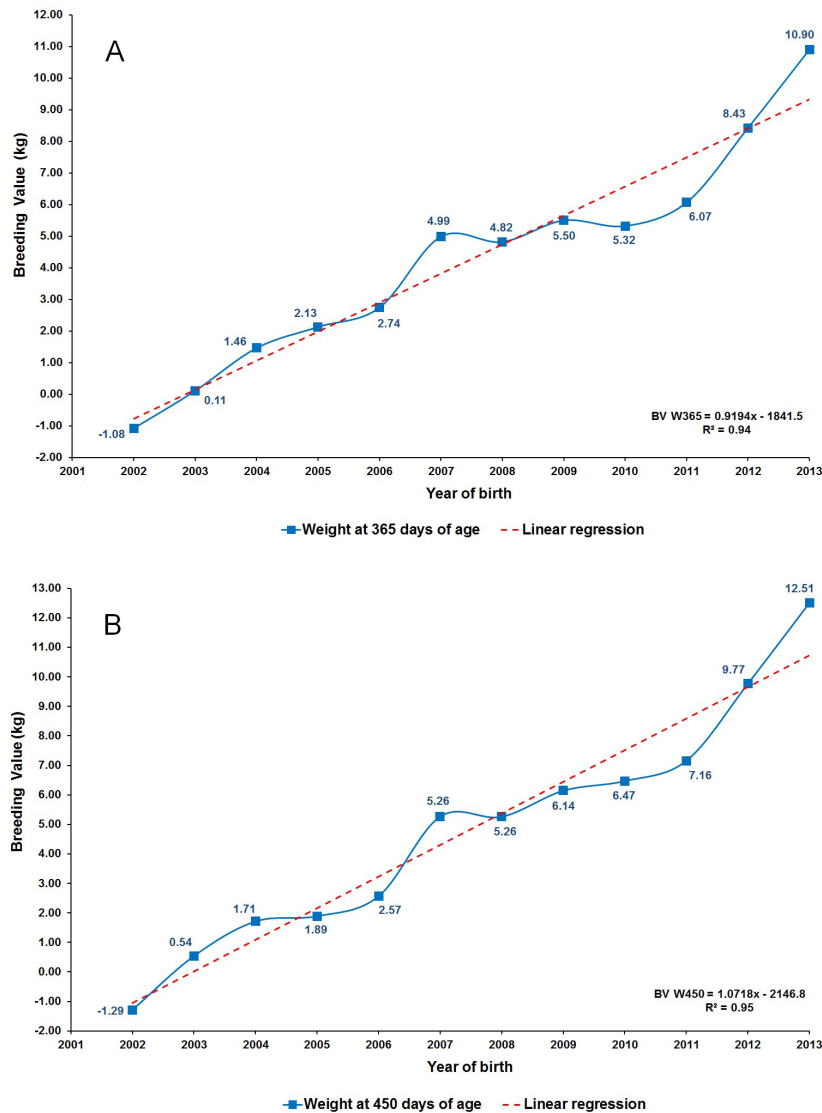
Figure 3 – Genetic trends for W365 (A) and W450 (B) in Nelore cattle raised in the Brazilian North.

humid tropical region of Brazil, Lira et al. (2013) observed average direct genetic gains of 1,326, 2,014, 2,670, 3,056, and 3,128 kg/year for W120, W210, W365, W450, and W550, respectively, indicating the existence of genetic progress for pre- and post-weaning weights in herds of that region.

Conclusion

The obtained estimates of direct heritability for the weights were of medium to high magnitude, indicating that there is an additive genetic variance for selection in the Nelore herd in the northern region of Brazil. In other words, there is an opportunity for genetic gain through selection for weight in this breed.

Considering our results, greater selection pressure should be applied for the maternal effect and a higher herd replacement rate (dams) should be adopted so that animals with higher maternal effects are selected.

Despite fluctuations, the present results for direct genetic trends for W120, W210, W365, and W450 are characterized as positive progress that must be considered, since gains were stable, cumulative, and permanent throughout the studied period.

Conflict of Interest

The authors declare no conflicts of interest.

Ethics Statement

This study was perfomed with a dataset provided by the Nellore Breeding Program (*Nelore Brasil*) of the National Association of Breeders and Researchers (ANCP), thus there is no relevance for approval of the work by the ethics committee from Federal University of Tocantins Northern.

Acknowledgements

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