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GENETIC TRENDS FOR GROWTH TRAITS IN NELLORE CATTLE RAISED IN THE HUMID TROPICAL REGION OF BRAZIL

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ABSTRACT

(Co)variances, heritability and genetics change were estimated for weight at 120 (W120), 210 (W210), 365 (W365), 450 (W450) and 550 (W550) days of age in Nellore cattle from the Humid Tropical region of Brazil. A total of 65,876 records of animals born between 1993 and 2010 and raised on pasture were used. The (co)variance components were estimated by restricted maximum likelihood, and breeding values were predicted using an individual animal model. The genetic trends were plotted by linear regression of breeding values in the animals' birth year. The heritability coefficients due to direct genetic effect were 0.37±0.019; 0.39±0.019; 0.41±0.013; 0.41±0.015 and 0.41±0.021. The maternal heritability estimates for W120 and W210 were 0.05±0.011 and 0.06±0.011, respectively. The genetic gains were 1.326, 2.014, 2.670, 3.056 and 3.128 kg/year for W120, W210, W365, W450 and W550, respectively. The estimates of genetic parameters and trends indicate the existence of genetic progress in pre- and postweaning traits from herds of Brazil Tropic Humid region.

KEYWORDS: animal breeding program; (co)variances; genetic gain; heritability; postweaning weight; preweaning weight.

TENDÊNCIAS GENÉTICAS PARA CARACTERÍSTICAS DE CRESCIMENTO EM REBANHOS NELORE CRIADOS NA REGIÃO DO TRÓPICO ÚMIDO DO BRASIL

RESUMO

Foram estimados (co)variâncias, coeficientes de herdabilidade e tendências genéticas, bem como preditas mudanças genéticas para peso aos 120 (P120), 210 (P210), 365 (P365), 450 (P450) e 550 (P550) dias de idade em animais da raça Nelore criados na região do Trópico Úmido do Brasil. Foram utilizados 65.876 registros de animais nascidos entre os anos de 1993 a 2010, criados a pasto. Os componentes de (co)variância foram estimados pelo método da máxima verossimilhança restrita e os valores genéticos foram preditos por modelos mistos sob modelo animal. As tendências genéticas foram estimadas pela regressão dos valores genéticos sobre o ano de nascimento dos animais. Os coeficientes de herdabilidade do efeito direto estimados foram de 0,37±0,019; 0,39±0,019; 0,41±0,013; 0,41±0,015 e 0,41±0,021 para P120, P210, P365, P450 e P550, respectivamente. As estimativas de herdabilidades maternais para P120 e P210 foram 0,05±0,011 e 0,06±0,011, respectivamente. Os ganhos genéticos diretos médios foram 1,326, 2,014, 2,670, 3,056 e 3,128 kg/ano para P120, P210, P365, P450 e P550, respectivamente. As estimativas dos parâmetros e tendência genética indicam a existência de progresso genético para pesos pré e pós-desmame, nos rebanhos da região do Trópico Úmido do Brasil.

PALAVRAS-CHAVE: (co)variâncias; ganho genético; herdabilidades; melhoramento genético animal; peso pós-desmama; peso pré-desmama.

INTRODUCTION

The region of the Humid Tropics in Brazil practically merges with the Amazon, represented by the states of Acre, Amapá, Amazonas, Mato Grosso, Pará, Rondônia, Roraima, Tocantins and part of Maranhão (west of meridian 44°), corresponding to approximately 61% of the Brazilian territory (5.2 million km^2). In recent years, the cattle industry in this region has expanded in terms of cattle herds, and much of this growth is related to the migration of farmers from other regions of the country, as well as the adoption of management practices, recovery of pastures, use of technologies and awareness about environmental preservation (DIAS-FILHO, 2011).

According to the Brazilian Institute of Geography and Statistics (IBGE), during the period 1997/2007, there was a 78% increase of cattle herds in the states that compose the Humid Tropics region (IBGE, 2007; 2010). However, the big challenge for animal production on pasture at this Brazilian agricultural border is to increase efficiency through the use of more intensive technologies, both in relation to management and recovery of pastures, as well as the productive and reproductive performance of these herds.

Selection aiming at genetic improvement of the animals is one of the most important decisions of the modern producer who wants to maximize their production. A good indicator of response to selection or to genetic progress to be achieved is the knowledge of the estimates of genetic parameters for weight characteristics of the breeds (GONÇALVES et al., 2011).

Knowledge of phenotypic and genetic performance of a population is important for carrying out the necessary adjustments to the selection process, i.e., in the evaluation of the criteria established in the selection process, as well as for the results of the breeding programs employed. It is possible to follow and establish guidelines to breeding programs through knowledge of genetic parameters and estimates of genetic change, verifying the genetic gains over time in order to use the results as elements guiding future actions (SANTOS et al. 2012).

Some researchers discussed parameters and genetic trends in the Northeast, North, Midwest, South and Southeast regions of Brazil (PIMENTA FILHO et al., 2001; MALHADO et al., 2002; PLASE et al., 2002; GUSMÃO et al., 2009; GONÇALVES et al., 2011; LAUREANO et al., 2011) and, more recently, SANTOS et al., (2012) studied the North region of Brazil. However, effective studies in the Humid Tropics region of Brazil, which also includes states of the Northeast and Midwest regions, assessing the genetic and phenotypic progress of Nellore cattle raised on pasture, are still incipient.

Therefore, the objective of this study was to estimate (co)variances and genetic parameters, as well as to predict the phenotypic and genetic trends for standardized weights at 120, 210, 365, 450 and 550 days of age of Nellore cattle raised on pasture in the Humid Tropics of Brazil.

MATERIAL AND METHODS

We used information regarding Nellore breeding, reared in herds in the States of Maranhão (MA), Mato Grosso (MT), Pará (PA), Rondônia (RO) and Tocantins (TO), participants of the Genetic Improvement Program of Nellore Breed of the National Association of Breeders and Researchers (PMGRN-ANCP).

The characteristics studied were standardized weights at 120, 210, 365, 450 and 550 days of age (W120, W210, W365, W450 and W550), used as selection criteria at the PMGRN (LÔBO et al., 1998). The initial data included 65,876 records of animals born between 1993 and 2010, and raised on pasture. We carried out all descriptive statistics and comparison tests among phenotypical averages, i.e., among the weights adjusted to the standard ages described above, by means of the procedures MEANS and GLM, and compared the means by the multiple comparison test of Tukey (SAS, 2002).

We performed analyses of variance using the GLM procedure (SAS, 2002) to verify the importance of non-genetic sources of variation of the characteristics studied. We considered fixed effects of sex and contemporary group (CG), formed by concatenation (SAS, 2002) of non-genetic factors that affected significantly ($p < 0.001$) the studied characteristics such as herd, year, season of animal birth (January-April = 1; May-August = 2; and September-December = 3). For the characteristics of pre-weaning weights (W120 and W210) we used the age of the cow at calving as a covariate.

The number of animals, bulls, cows, contemporary groups besides means, standard deviations, and coefficients of variation for standardized weights at 120, 210, 365, 450 and 550 days of age are presented in Table 1.

Table 1. Number of animals, mean, standard deviation and coefficient of variation of the characteristics analyzed in Nellore cattle reared in the Humid Tropics of Brazil

Characteristics	No. of animals	No. of bulls	No. of cows	No. of CG	Mean (kg)	SD (kg)	CV (%)
W120	52,726	671	24,569	329	127.51	16.90	13.25
W210	53,518	706	25,118	484	184.76	24.61	13.32
W365	49,305	773	25,388	408	231.37	32.52	14.05
W450	42,561	733	22,276	367	267.05	38.28	14.33
W550	23,646	455	13,441	261	314.79	48.28	15.34

W120 = weight adjusted to 120 days of age; W210 = weight adjusted to 210 days of age; W365 = weight adjusted to 365 days of age; W450 = weight adjusted to 450 days of age; W550 = weight adjusted to 550 days of age; N = number; CG = Contemporary Group; SD = standard deviation; CV = coefficient of variation.

We performed the univariate analysis of the pre-weaning weights (W120 and W210) using the model described in (I), while for W365, W450 and W550 we used the model described in (II).

$$y = X\beta + Z_1a + Z_2m + Z_3p + e \quad \text{(I)}$$

where: y = vector of observations (W120 and W210); β = vector of fixed effects (contemporary group and order of birth); a = vector of direct additive genetic effect; m = vector of maternal additive genetic effect; p = vector of maternal permanent environmental effect; X = incidence matrix which associates β with y; Z_1, Z_2 and Z_3= incidence matrix of direct, maternal, and maternal permanent environmental genetic effects, respectively; and e = vector of residual effects.

$$y = X\beta + Za + e \quad \text{(II)}$$

where: y = vector of observations (W365, W450 and W550);

β= vector of fixed effects (contemporary group and order of birth); a = vector of direct additive genetic effect; X = incidence matrix which associates β com y; Z = incidence matrix of direct effects; and, e = vector of residues.

In full model analysis, distributions and matrix of (co)variances were defined as:

$$E[d] = E[m] = E[p] = E[e] = 0,$$
$$E[y|d,m,p] = X\beta + Z_1d + Z_2m + Z_3p$$

$$Var\begin{bmatrix} d \\ m \\ p \\ e \end{bmatrix} = \begin{bmatrix} A\sigma_d^2 & A\sigma_{dm} & 0 & 0 \\ A\sigma_{dm} & A\sigma_m^2 & 0 & 0 \\ 0 & 0 & I_d\sigma_p^2 & 0 \\ 0 & 0 & 0 & I_N\sigma_e^2 \end{bmatrix}$$

Where:

σ_d^2 = direct additive genetic variance;

σ_m^2 = maternal additive genetic variance;

σ_{dm} = additive genetic covariance between direct and maternal effect;

A = kinship matrix among animals;

σ_p^2 = maternal permanent environmental variance;

σ_e^2 = residual variance;

I_d, I_N = identity matrices of appropriate orders, with d = number of cows (mothers of animals with data) and

N = total number of animals with data.

Estimates of (co) variances were obtained by the method of Derivative-Free Restricted Maximum Likelihood – DFREML, using MTDFREML program (BOLDMAN et al., 1995). We used the regression of annual averages of genetic values (additive and maternal) and of the weights on the year of birth of the animal to evaluate the genetic and phenotypic trends.

To illustrate and to predict the genetic gain based on the variance components and genetic parameters, we simulated the genetic gain by the following formula:

$$\Delta G = \frac{i \times h^2 \times \sigma_a}{L}$$

Where: ΔG is the genetic gain, i is the selection intentisy (1.28, as retaining 10% male and 50% female), h^2 is the herdability due to the direct additive genetic effect, σ_p is the standard deviation (FALCONER, 1996), and L is the mean generation interval (PEREIRA, 1999). For determination of L, we simulated the selection based on the use of bulls for five years (between two and six years) and females for seven years (between three and nine years), resulting in L = 5 years. Therefore, the genetic gain (ΔG) can be given in kg/year.

RESULTS AND DISCUSSION

Averages for standardized weight at 120 days (W120) and weight at 210 days (W210) were 127.51 ± 16.90 kg and 184.76 ± 24.61 kg, respectively. For weight at 205 days of age, HOLANDA et al. (2004), in Brazilian Northeast reagion, found an average of 157.55 (± 22.80) kg, and BOCCHI et al. (2004), who studied Nellore cattle from different regions of Brazil, obtained mean weights, at 205 days of age, of 163.15 (± 27.78) kg

in the Midwest region, 154.23 (± 29.43) kg in the Northeast region, 165.45 (± 28.87) kg in the South region, and 165.45 (± 28.08) kg in the Southeast region. We observed that the weights of the animals at weaning were higher than those reported for other regions of Brazil, which can be justified by different management. purposes and selection criteria, among others.

In general, the average weights in the Brazilian Humid Tropics region are in an intermediate stratum to those described for other regions of the country, being similar to those reported by MERCADANTE et al. (2003), BERTAZZO et al. (2004), MALHADO et al. (2005), BOLLIGON et al. (2008), LAUREANO et al. (2011) and SANTOS et al. (2012)

However, the phenotypic means of the weights among the federal units (Table 2) reveal that for the same standard age, there is a high variability in weight, suggesting that genetic and environmental factors act in different ways among the states that make up the Humid Tropics region. Thus, we can conclude that the design of breeding improvement programs, with their own objectives and criteria, has been conducted differently among the federal units of this region, i.e., a different selection criteria may be used among the States.

Table 2. Average weights and standard deviation of the characteristics W120, W210, W365, W450 and W550 days of age, according to the distribution by the most representative States in the Humid Tropics of Brazil

State	W120	W210	W365	W450	W550
MA	121.63^{b} ±15.34	179.30^{b} ±23.17	211.21^{d} ±29.15	240.67^{d} ±32.09	282.65^{d} ±38.84
MT	129.17^{a} ±17.41	186.85^{a} ±25.19	231.48^{b} ±32.42	269.88^{b} ±37.79	319.88^{b} ±45.87
PA	128.56^{a} ±15.28	187.62^{a} ±21.93	239.79^{a} ±29.95	274.00^{a} ±36.21	328.08^{a} ±45.34
RO	119.46^{c} ±15.10	169.31^{c} ±20.67	217.35^{c} ±28.61	242.19^{d} ±31.90	277.79^{e} ±38.45
TO	114.65^{d} ±15.79	164.49^{d} ±23.19	217.54^{c} ±36.71	252.64^{c} ±41.92	297.87^{c} ±51.98

MA=Maranhão; MT= Mato Grosso; PA= Pará; RO= Rondônia; TO= Tocantins; W120 = weight adjusted to 120 days of age; W210 = weight adjusted to 210 days of age; W365 = weight adjusted to 365 days of age; W450 = weight adjusted to 450 days of age; W550 = weight adjusted to 550 days of age; different letters in the same column differ significantly ($p < 0.05$) by Tukey test.

We compared the phenotypic means for the different weights calculated (W120, W210, W365, W450 and W550 days) and observed statistically significant differences ($p < 0.01$) for these weightings among States (Table 2). The results showed that, in the federal units, the phenotypic means of the weights can be influenced by the environmental conditions of each region, since the weights of each characteristic studied (W120, W210, W365, W450 and W550) varied among States.

Estimates of direct heritability and their standard errors for the Humid Tropics region of Brazil, obtained in univariate analysis, were 0.37 (± 0.019), 0.39 (± 0.019), 0.41 (± 0.013) , 0.41 (± 0.015) and 0.41 (± 0.021) for W120, W210, W365, W450 and W550 days of age, respectively. The coefficients of heritability for the maternal characteristics W120 and W210 were 0.05 (± 0.011) and 0.06 (± 0.011), respectively.

Direct heritability estimates for pre-weaning weights showed moderate magnitude, being similar to the values described by CÂMPELO et al. (2004) and SANTOS et al. (2012), and higher than those found by MERCADANTE et al. (2004), BOLIGNON et al. (2007) BOLIGON et al. (2008). LIRA et al. (2008) reported average estimates of direct heritability of 0.08 and 0.64 for weight at 120 days and weight at 205 days of age, respectively. However, these results are lower than those described by CYRILLO et al. (2004), who reported heritability of 0.44 to 0.68 for weights at 120 days and 210 days of age, respectively.

By assessing the estimated direct heritabilities for pre-weaning weights (W120 and W210) in the states of Maranhão, Mato Grosso, Pará, Rondônia and Tocantins, we observed (Table 3) that the variability among states is large, ranging from 0.22 to 0.61 for W120 and from 0.30 to 0.57 for W210. The state with the lowest heritability for W120 and W210 was Rondônia (0.22 and 0.30 in the same order) and the one with the highest heritability for the same weights was the state of Tocantins. The high variability found in the states of Maranhão and Tocantins may be related to increased selection pressure of females (mothers) for maternal ability, since the herds in these states have relatively new breeding programs and are still being formed. Another related factor may be the repeatability of cows (c^2), indicated by the permanent common environmental effect among these animals, which was 65% and 25% in the states of Tocantins and Maranhão, respectively.

However, in the Humid Tropics of Brazil, the maternal heritability (h^2) for the characteristics

W120 and W210 were of low magnitude (0.05 ± 0.011 and 0.06 ± 0.011, respectively), showing little genetic and environmental influence of the cow on the performance of individuals in pre-weaning. This result was expected since the effect of the common environment of the cows (c^2), for W120 and W210, was similar (10.5%).

For the postweaning characteristics (W365, W450 and W550), the direct estimated heritabilities showed high and similar magnitude among federal units (Table 3). Although there is the possibility of selecting for the traits analyzed, this shows that the selection pressure exerted for the characteristics (P365, P450 and P550) is equivalent in the region. In general, heritability estimates for weights at different ages in this study indicated that a substantial part of the variation of these traits among animals is due to differences in the genetic merit of the animals; therefore, there appears to be agreement among the federal units for greater selection pressure for postweaning weights.

Table 3. (Co)variances estimates and genetic parameters for pre- and postweaning characteristics, according to the federal unit

Characteristic	State	σ^2_a	σ^2_m	σ^2_p	h^2_a	h^2_m
W120	MA	81.08	27.91	187	0.43	0.15
	MT	76.62	4.65	203	0.38	0.02
	PA	64.12	18.88	197.3	0.32	0.10
	RO	35.58	30.41	158.7	0.22	0.19
	TO	143.1	-	233.4	0.61	-
W210	MA	219.5	58.37	457.1	0.48	0.13
	MT	179.4	14.90	426.6	0.42	0.03
	PA	132	45.79	415.1	0.32	0.11
	RO	101.2	28.13	335.1	0.30	0.08
	TO	230.1	-	401.5	0.57	-
W365	MA	327.0	-	628.5	0.52	-
	MT	314.2	-	701.5	0.45	-
	PA	330.9	-	665.8	0.50	-
	RO	205.3	-	568.5	0.36	-
	TO	447.7	-	672	0.67	-
W450	MA	308.4	-	674.6	0.46	-
	MT	361.2	-	866.7	0.42	-
	PA	421.4	-	888.9	0.47	-
	RO	285.0	-	660	0.43	-
	TO	712.2	-	1121	0.64	-
W550	MA	325.0	-	442.0	0.74	-
	MT	539.0	-	1208	0.45	-
	PA	365.7	-	1116	0.33	-
	RO	291.6	-	785.7	0.37	-
	TO	-	-	-	-	

σ^2_a = direct genetic variance; σ^2_p = phenotypic variance; σ^2_m = maternal variance; h^2_a = direct heritability; and, h^2_m = maternal heritability.

The estimates for the (co)variances and genetic parameters were similar to those described by TORAL et al. (2004) and SANTOS et al. (2012). The similarity among the values of the estimated heritability for W365, W450 and W550 implies that genes that control these weights contributed equally to phenotypic variance and direct variance. Thus, these values are due to the existence of genetic variability in the herd and not only to the influence of the environment on these characteristics.

In general, the heritabilities for postweaning traits (W365, W450 and W550) in different Brazilian states showed high magnitude, demonstrating the possibility of selection. Similar results were reported by SANTOS et al. (2012), who analyzed data from the Northern region of Brazil and obtained estimates

of heritability for weight at 365 and 550 days of age, ranging from 0.41 to 0.51, respectively.

Genetic trends of pre-weaning weights (Figures 1, A and B) in the Humid Tropics of Brazil revealed selection of animals with higher genotypic performance over the years. Figure 1 (A and B) shows that the selection for weight, not for maternal ability, has been carried out.

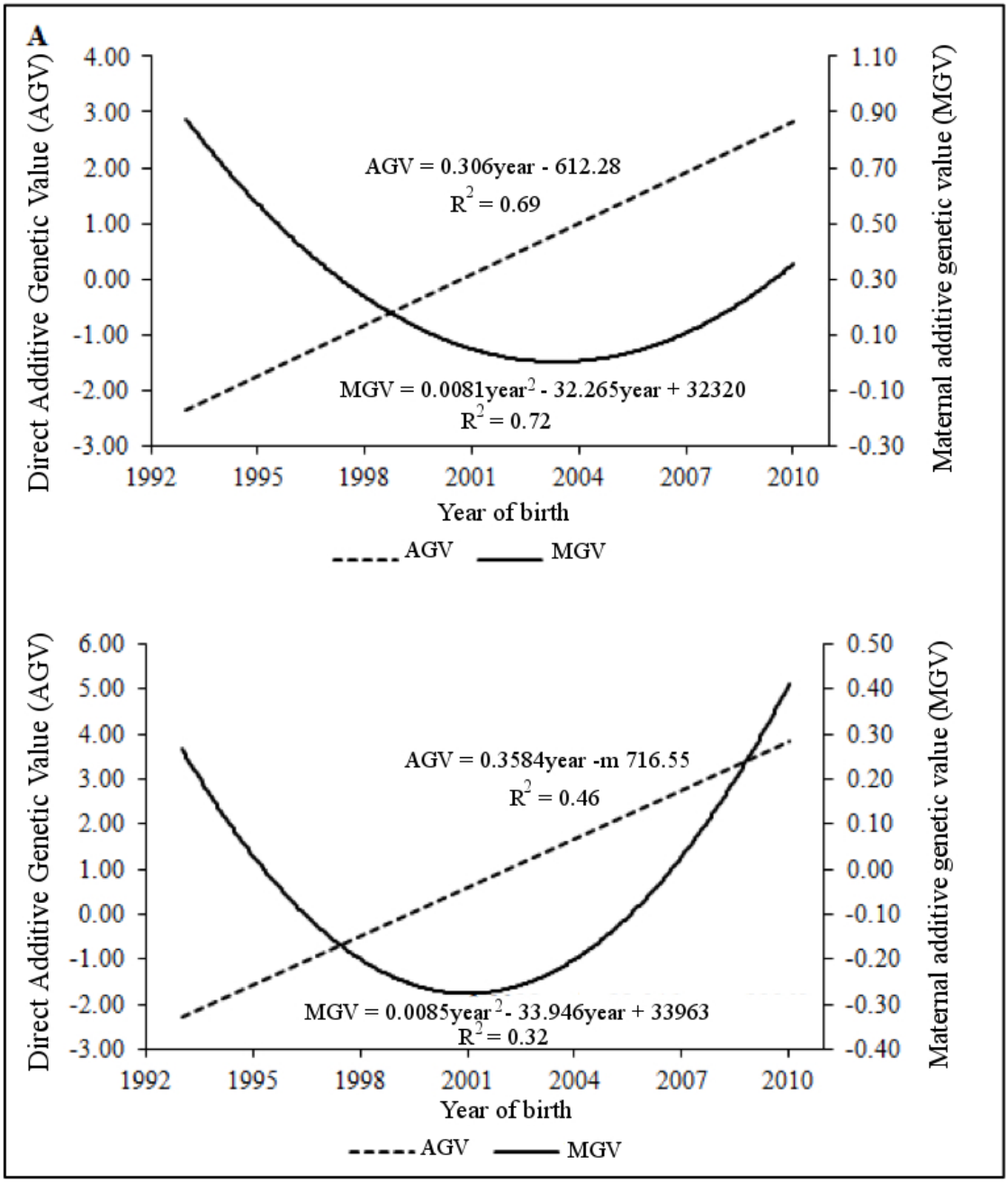

Figure 1. Genetic trends for standardized weight at 120 days of age (A) and standardized weight at 210 days of age (B), in bovines raised in the Humid Tropics of Brazil.

For W120 and W210, we observed mean genetic value of 0.242 and 0.784 kg/year, respectively. Based on these genetic values, direct heritability estimates and phenotypic standard deviation (FALCONER, 1960; PEREIRA, 1999), we performed a simulation, considering retention of 50% of females and 10% of males (selection intensity of 1.28) and a mean generation interval of five years. Thus, it was possible to predict genetic gains of 1.33 and 2.01 kg/year, representing increases of 1.04% and 1.09% in the weights calculated at 120 and 210 days of age,

respectively. As for W365, W450 and W550, the mean additive genetic value was 3.136; 3.190 and 3.351 kg/year, respectively. Considering the information of the previous simulation, it was possible to predict genetic gains of 2.67, 3.05 and 3.13 kg/year, representing increases of 1.15%, 1.14% and 0.99% in the calculated weights at 365, 450 and 550 days, respectively.

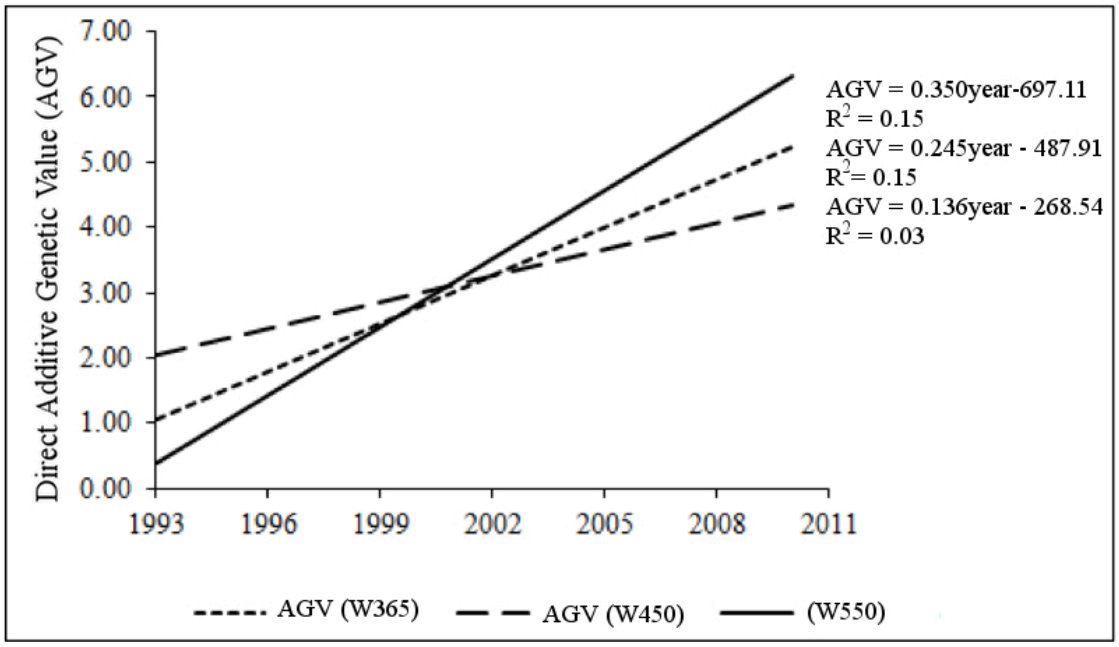

Figure 2. Genetic trends for standardized weight at 365, 450 and 550 days of Nellore breeds raised in the Humid Tropics of Brazil.

The analyses of the trends for the direct additive genetic effects for W120, W210, W365, W450 and W550 allowed us to infer that the selection of the herd in the Humid Tropics region of Brazil has emphasized mainly the postweaning weights, which is supported by the relationship between genetic values and phenotypic values, whose genotypic values showed percentages of 0.19%, 0.42%, 1.36%, 1.19% and 1.06% in relation to their respective standard weights for weights at 120, 210, 365, 450 and 550 days, respectively. In other words, for the postweaning weight, the genetic effects have contributed with over 1% of the phenotype of the animals, while for pre-weaning weights, this effect did not exceed 0.5%.

It is noteworthy that the selection for postweaning weights can generate, over the years, an increase in costs of production, and age at slaughter and finishing of animals. Accordingly, we suggest that greater attention and selection of animals with greater potential for pre-weaning weights, because it is the period of life in which the animal presents faster growth and development. Therefore, with the selection of animals for heavier weight at weaning, it would be possible to reduce the time for the animal to reach the ideal weight at slaughter, reducing production costs and age at slaughter.

CONCLUSIONS

The heritability estimates, for presenting moderate to high magnitudes, indicated the existence of enough additive genetic variability to allow genetic gains by means of selection for the studied traits. Over the years, positive increments were observed for all traits. Given the quadratic trend for the maternal effect, we suggest more attention and selection of females with better maternal ability. In general, the predicted genetic gains showed the possibility of improvement of production traits, especially standardized weights at 365, 450 and 550 days of age.

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