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ANIMAL SCIENCE

Genetic parameters for visual scores, growth and carcass traits in Nellore Cattle

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Abstract: Growth and carcass traits are essential selection criteria for beef cattle breeding programs. However, it is necessary to combine these measurements with body composition traits to meet the demand of the consumer market. This study aimed to estimate the genetic parameters for visual scores, growth (pre and post-weaning weights), and carcass (rib eye area (REA), back and rump fat thickness) traits in Nellore cattle using Bayesian inference. Data from 12,060 animals belonging to the HoRa Hofig Ramos herd were used. Morphological traits were evaluated by the MERCOS methodology. The heritability estimates obtained ranged from low to high magnitude, from 0.15 to 0.28 for visual scores, 0.13 to 0.44 for growth, and from 0.42 to 0.46 for carcass traits. Genetic correlations between visual scores and growth traits were generally of moderate to high magnitudes, however, visual scores showed low correlations with carcass traits, except between sacral bone and structure and REA. Selection for visual score traits can lead to favorable responses in body weight and vice versa, but the same is not true for carcass traits. Morphological categorical traits can be used as complementary tools that add value to selection.

Key words: Bayesian methods, genetic association, morphological traits, weight performance, Zebu Cattle.

INTRODUCTION

For many years, selection indexes for beef cattle have focused on increasing body weight, which has been successful through genetic selection associated with improvements in nutrition, reproduction, and management. However, this strategy combined with the low association with body composition (Paterno 2015) can increase adult weight, and consequently, the maintenance requirements as well as losing sexual precocity and carcass finishing (Silva 2016). Thus, the selection of animals based on weight and carcass traits combined with a better functional biotype is extremely important to meet the demands of the consumer market and the production system.

An ideal biotype within the beef cattle system in tropical environments is an animal with a well-developed bone structure, medium frame, carcass length, conformation, and depth and spring of ribs. Animals must also have evident sexual traits (well-defined femininity or masculinity), sound feet and legs, and moderate sheath or navel. Most animals in Brazil are reared extensively, which requires functional animals for production and reproduction on pasture (Soares et al. 2021).

In this sense, visual or morphological traits can be used for the identification and selection of animals with a suitable biotype for the production system and/or for specific objectives of production systems, such as sexual precocity, finishing, and carcass composition (Regatieri et al. 2011, Gordo et al. 2016). As a result, the use of these traits as selection criteria may assist in obtaining animals with higher live weights, reproductive performance, carcass quality, and better morphological proportions, that meet the demand for carcass quality and yield, and that are also well-adapted to the environment in which they will be raised (Souza 2019, Watanabe et al. 2021). In addition, visual assessment allows the low cost evaluation of a greater number of young animals with less invasive techniques, making the process more agile and less stressful for the animals (Nicholson & Butterworth 1986, Paterno 2015).

Morphological traits are threshold measures and do not present continuous phenotypic expression, making genetic evaluations difficult. Bayesian inference can be a powerful tool to deal with this kind of trait, as it allows the refinement of probability estimates as new data are collected and systematically incorporated into prior knowledge. In this way, the estimation of genetic parameters is the first step to maximize the response to selection and design selection strategies with a focus on productivity and carcass quality (Cavani et al. 2015). Considering the economic importance of the Nellore breed and the scarcity of studies involving morphological traits, this study aimed to estimate the heritabilities and genetic correlations (residual and phenotypic) between visual scores, growth, and carcass traits in Nellore cattle using Bayesian inference.

MATERIALS AND METHODS

Phenotypic data and evaluated traits

The research project was approved by the Ethics and Animal Experimentation Committee/CEUA of the Universidade Federal de Goiás, according to protocol Number 089/20 issued by this institution.

Quantitative traits included live weights at 120 (W120), 210 (W210), 365 (W365), and 450 (W450) days of age. The adjusted weight was calculated using the formula proposed by Garnero et al. (2001), in which the average daily gain (kg/day) of each period is used to adjust weight to a standard age. Carcass traits were obtained by real-time ultrasound (Aloka 500 SSD with transducer 3.5 MHz) as described by BIF (2002), and included rib eye area (REA, cm^2), backfat thickness over the 12^{th}-13^{th} ribs (BFT, mm) and at the rump (between ileum and ischium bones, over the junction of the *Gluteus medius* and *Biceps femoris*; RFT, mm).

Categorical measures included the morphological traits of muscularity (M), physical structure (PS), breed type (T), conformation (C), navel (N), and sacrum (SAC) were evaluated according to MERCOS methodology (Lôbo 1996). Records from 12,060 Nellore animals (7,804 were females and 4,256 were males) created in the semi-intensive system of farm HoRa Genética Provada, located in Brasilândia, Mato Grosso do Sul, Brazil. The region has a tropical climate, latitude 21º31'56.64''S of Ecuador and longitude 52°06'33.88''O of Greenwich Meridian. The farm participates in the Nellore Brazil Genetic Breeding Program, coordinated by the National Association of Breeders and Researchers (ANCP, Ribeirão Preto, Brazil). Visual scores of 4.175 animals with an average age of 22 months were used.

Statistical analysis and genetic parameter estimates

The editing, quality control, and descriptive analysis of the data were performed using R software (R Core Team 2021). The contemporary groups (CG) and the covariates included in the models were defined after analysis of variance, using mixed models to identify the non-genetic factors that influenced the studied traits ($P < 0.05$). Thus, for growth and carcass traits, the CG consisted of animals from the same herd, born in the same year and season, of the same sex and management group at the time of measurement and/or evaluation of each trait. The calving season was grouped into two classes: the dry season (April to September) and the rainy season (October to March). To ensure greater variability within the CG for visual scores (to make sure that the CG had animals with all scores), the CG was composed only of animals from the same herd and birth year, with the other significant effects (sex, season, and management group) included in the model separately as fixed effects.

CG with fewer than four animals and animals whose phenotypic information was 3.5 or more standard deviations above or below the mean of the respective CG were excluded from the analysis. In addition, for the muscularity and structure traits, the observations that presented a score equal to 1 were excluded, due to the low frequency observed for these traits. The distributions of scores for visual assessment traits is shown in Table I.

The initial values of the (co)variance components were obtained from preliminary analyses using linear models with a restricted maximum likelihood approach, based on the REMLF90 and AIREMLF90 programs (Misztal et al. 2019). These results were used as initial values in two-trait analyses to estimate covariance components, heritabilities, and genetic, residual, and phenotypic correlations using a linear animal model for growth and carcass traits, a threshold model for visual scores, and a linear-threshold model for the combination of the traits. These analyses were carried out under a Bayesian approach using the THRGIBBS1F90 program (Tsuruta & Misztal 2006). The numbers of observations and descriptive statistics of the evaluated traits are presented in Table II.

In matrix terms, the general model can be described as: $y = \boldsymbol{X}\beta + \boldsymbol{Z}_1 a + \boldsymbol{Z}_2 m + \boldsymbol{Z}_3 c + e$, where: y is a vector of observations; β is the vector of fixed effects; a is the vector of direct additive genetic effects; m is a vector of maternal genetic effects; c is the vector of non-correlated effects (permanent

Table I. Distributions (%) of the MERCOS visual scores in Nellore cattle.

Traits	Visual Scores				
	1	2	3*1	4	5*2
Muscularity (M)	0.00	12.81	40.12	43.55	3.53
Physical structure (PS)	0.00	8.98	55.13	35.00	0.89
Breed type (T)	3.26	31.57	48.77	16.02	0.38
Conformation (C)	0.72	20.17	48.60	29.58	0.93
Navel (N)	1.44	25.65	64.43	7.95	0.53
Sacrum (SAC)	11.71	79.90	8.38	—	—

***1 Ideal score for navel and sacrum. *2 Ideal score for muscularity, physical structure, breed type and conformation.**

Table II. Descriptive statistics for growth traits, carcass and visual scores in Nellore cattle.

Traits	N°	Bulls	Cows	Min.	Max.	Median	Mode	SD	CV (%)	N° CG	Median of CG
W120 (kg)	7131	129	4466	69	199	137	138	19.5	14.2	103	27
W210 (kg)	6879	127	4622	100	279	204	206	26.0	12.7	106	23
W365 (kg)	5287	121	3745	162	408	260	260	34.6	13.3	50	47
W450 (kg)	4220	110	3157	182	476	301	269	47.1	15.7	40	43
REA (cm²)	2177	81	1222	31	88	58.92	60.00	9.31	15.80	45	15
BFT (mm)	2173	81	1222	1	11	3.50	3.00	1.65	47.11	45	15
RFT (mm)	2172	81	1222	1	15	5.16	5.00	2.17	4.14	45	15
M	4170	101	3066	2	5	2.38	4.00	0.75	31.5	23	182
PS	4154	101	3055	2	5	2.28	3.00	0.63	27.7	23	182
T	4175	101	3069	1	5	2.79	3.00	0.76	27.2	23	182
C	4175	101	3069	1	5	3.10	3.00	0.74	24.0	23	182
N	4175	101	3069	1	5	2.80	3.00	0.61	21.9	23	182
SAC	4175	101	3069	1	3	1.97	2.00	0.45	22.7	23	182

No.: number of observations. Min.: minimum values. Max.: maximum values. SD: standard deviation. CV: coefficient of variation. No. CG: number contemporary groups. Average of n° obs. CG: mean of animals per GC. W120: weight at 120 days of age. W210: weight at 210 days of age. W365: weight at 365 days of age. W450: weight at 450 days of age. REA: rib eye area. BFT: backfat thickness. RFT: rump fat thickness. M: muscularity. PS: physical structure. T: breed type. C: conformation. N: navel. SAC: sacrum.

maternal effects); $\boldsymbol{X}, \boldsymbol{Z}_1, \boldsymbol{Z}_2, \boldsymbol{Z}_3$ are incidence matrices that relate β, a, m e c with y, respectively; and e is the vector of residuals associated with each observation.

For the growth traits, CG was used as a fixed effect, and cow age at calving was used as linear and quadratic covariates (cow age at calving was only used for P120 and P210). For the other traits, maternal and permanent environment effects were not used, as it was verified through analysis of variance that the contribution of these effects on phenotypic variance was less than 3%. For carcass traits, CG were considered as a fixed effect and animal age as linear and quadratic covariates. For the visual scores, fixed effects included CG, sex, calving season, and management group, and the animal's age at the time of evaluation was included as linear and quadratic covariates. Age was included as linear and quadratic covariates, as this model presented the smallest prediction errors. Considering that a single technician performed all the visual evaluations, this effect was not included in the model.

For two-trait analyses between categorical and linear measures, according to the Bayesian approach, it was assumed that the distribution of random, uncorrelated, and residual genetic effects follows a multivariate normal distribution, as follows:

$$\begin{bmatrix} \boldsymbol{a} \\ \boldsymbol{m} \\ \boldsymbol{c} \\ \boldsymbol{e} \end{bmatrix} \sim \boldsymbol{N}(0, \boldsymbol{V})$$

$$\boldsymbol{V} = \begin{bmatrix} \boldsymbol{G} \otimes \boldsymbol{A} & 0 & 0 \\ 0 & \boldsymbol{c} \otimes \boldsymbol{I}_{\boldsymbol{Nm}} & 0 \\ 0 & 0 & \boldsymbol{R} \otimes \boldsymbol{I}_{\boldsymbol{N}} \end{bmatrix}$$

where, G represents the (co)variances of the direct genetic effect; A is the numerator relationship matrix; c is a covariance matrix of permanent maternal environmental effects; I is the identity matrix; N_m is the number of dams of animals with phenotypic information; N is the number of animals with phenotypic information; R is the matrix of residual covariances; $\otimes$ is the Haddamard product between two matrices. The **G** matrix was assumed as:

$$\boldsymbol{G} = \begin{bmatrix} \boldsymbol{Gd} & 0 \\ 0 & \boldsymbol{Gm} \end{bmatrix}$$

where: *Gd* e *Gm* are matrices that represent additive direct effects and maternal effects, respectively. It was assumed that $\boldsymbol{E}[\boldsymbol{y}] = \boldsymbol{X}\boldsymbol{\beta}$, $\boldsymbol{Var}(\boldsymbol{a}) = \boldsymbol{A} \bigotimes \Sigma \boldsymbol{a}$, $\boldsymbol{Var}(\boldsymbol{m}) = \boldsymbol{A} \bigotimes \Sigma \boldsymbol{m}$, $\boldsymbol{Var}(\boldsymbol{c}) = \boldsymbol{I} \bigotimes \Sigma \boldsymbol{c}$, and $\boldsymbol{Var}(\boldsymbol{e}) = \boldsymbol{I} \bigotimes \Sigma \boldsymbol{e}$, where $\Sigma \boldsymbol{a}$ is the direct additive genetic (co)variance matrix, $\Sigma \boldsymbol{m}$ is the matrix of maternal genetic variance, $\Sigma \boldsymbol{c}$ is a matrix of maternal permanent environmental variance, $\Sigma \boldsymbol{e}$ is a matrix of residual (co) variances, $\boldsymbol{A}$ is the numerator relationship matrix, $\boldsymbol{I}$ is an identity, and $\bigotimes$ is the Kronecker product.

The visual scores were analyzed using the following threshold model:

$$f(w_i | y_i) = \prod_{j=1}^{n_i} 1\left(l_{ij} < t_1\right) 1\left(w_{ij} = 1\right) + 1\left(t_1 < l_{ij} < t_2\right) 1\left(w_{ij} = 2\right)$$
$$+1\left(t_2 < l_{ij} < t_3\right) 1\left(w_{ij} = 3\right) + 1\left(t_3 < l_{ij} < t_4\right) 1\left(w_{ij} = 4\right)$$
$$+1\left(t_4 < l_{ij} < t_5\right) 1\left(w_{ij} = 5\right)$$

where for each trait i (i = 1, 2, 3, 4 or 5), w_{ij} and l_{ij} are categorical variables and observations of underlying scale j, respectively, t_1 and t_4 are the thresholds that define the categorical response for each trait, and n_i represent the total number of data points for each trait studied. A uniform prior distribution was defined for the thresholds. For traits M and PS it was assumed that $t_1 = 0$, so that the vector of estimable thresholds were defined as $t = t_2; t_3; t_4$ e t_5.

A uniform and inverted Wishart distribution was assumed *a priori* for the systematic effects and (co)variance components, respectively. Chains of 200,000 to 400,000 iterations were generated, with a burn-in of 100,000 to 300,000 cycles and sampling every 50 and 100 cycles. This variation was used to ensure convergence for each categorical trait or combination of two traits. *A posteriori* estimates were obtained using the POSTGBBSF90 program (Misztal et al. 2019).

Convergence was verified through graphical inspection, with trace plots and *a posteriori* density of genetic, residual, maternal, and permanent environment variances (only for W120 and W210) *vs.* the Iterations. Furthermore, the convergence of the chains was evaluated by the criterion proposed by Geweke (1992), and the autocorrelation between the samples was evaluated. These analyses were performed using BOA (Smith 1997) and EasyGEN (Lopes 2019) packages of R (R Core Team 2021). The point estimates of the parameters were calculated as the *a posteriori* means, modes, and medians of their respective variance components, obtained in the two-trait analyses. The credibility intervals of the posterior marginal were obtained with 95% of credibility.

RESULTS

Table III shows the *a posteriori* estimates of the direct (h^2d) and maternal (h^2m) heritability coefficients for growth, carcass, and visual scores traits. Maternal heritability estimates for pre-weaning weights were low and lower than direct heritabilities. Heritability estimates for growth traits were moderate to high, with the highest values observed for W365 and W450 (0.34 ± 0.01 and 0.44 ± 0.01, respectively).

Table III. *Posteriori* estimates of variance components for growth traits, carcass and visual scores in Nellore cattle.

Parameter	Mean ± SD	Mode	Median	CI (95%)
σ^2_a W120	74.03 ± 0.73	63.23	70.62	37.18 - 129.74
σ^2_m W120	43.30 ± 0.36	41.40	42.58	23.98 - 67.14
σ^2_{pe} W120	30.87 ± 6.90	31.66	30.98	16 - 94 - 43.93
σ^2_e W120	122.94 ± 0.29	127.78	124.49	92.85 - 144.30
σ^2_p W120	271.14 ± 0.19	264.08	268.66	170.95 - 385.11
h^2_d W120	0.27 ± 0.01	0.24	0.26	0.22 - 0.34
h^2_m W120	0.16 ± 0.01	0.16	0.16	0.14 - 0.17
σ^2_a W210	120.99 ± 2.46	115.80	118.25	56.59 - 205.54
σ^2_m W210	57.90 ± 1.20	55.54	56.66	29.63 - 93.21
σ^2_{pe} W210	61.32 ± 11.56	61.07	61.22	39.01 - 83.91
σ^2_e W210	190.26 ± 1.09	194.02	191.52	143.22 - 228.86
σ^2_p W210	430.47 ± 1.08	426.43	427.65	268.45 - 611.51
h^2_d W210	0.28 ± 0.01	0.27	0.28	0.21 - 0.34
h^2_m W210	0.13 ± 0.01	0.13	0.13	0.11 - 0.15
σ^2_a W365	163.59 ± 0.32	158.32	162.84	124.90 - 206.25
σ^2_e W365	318.64 ± 0.12	320.98	318.85	286.59 - 349.68
σ^2_p W365	482.23 ± 0.22	479.31	481.69	411.51 - 555.92
h^2_d W365	0.34 ± 0.01	0.33	0.34	0.30 - 0.37
σ^2_a W450	297.50 ± 0.71	295.93	297.06	236.40 - 362.39
σ^2_e W450	378.97 ± 0.40	379.55	378.78	332.76 - 426.62
σ^2_p W450	676.47 ± 0.54	675.47	675.84	569.20 - 789.01
h^2_d W450	0.44 ± 0.01	0.44	0.44	0.42 - 0.46

to be continued

Table III. (continuation)

Parameter	Mean ± SD	Mode	Median	CI (95%)
σ^2_a REA	13.77 ± 0.03	13.65	13.68	9.57 - 18.6
σ^2_e REA	19.36 ± 0.01	19.33	19.37	16.20 - 22.40
σ^2_p REA	33.13 ± 0.02	32.98	33.05	25.7 - 37.80
h^2_d REA	0.42 ± 0.01	0.41	0.41	0.37 - 0.53
σ^2_a BFT	0.65 ± 0.01	0.64	0.64	0.44 - 0.86
σ^2_e BFT	0.76 ± 0.01	0.76	0.76	0.62 - 0.89
σ^2_p BFT	1.41 ± 0.01	1.39	1.40	1.07 - 1.76
h^2_d BFT	0.46 ± 0.01	0.46	0.46	0.42 - 0.49
σ^2_a RFT	1.05 ± 0.01	1.04	1.05	0.78 - 1.33
σ^2_e RFT	1.26 ± 0.01	1.26	1.26	1.06 - 1.44
σ^2_p RFT	2.31 ± 0.01	2.30	2.30	1.85 - 2.78
h^2_d RFT	0.46 ± 0.01	0.45	0.45	0.42 - 0.48
σ^2_a M	0.06 ± 0.01	0.06	0.06	0.03 - 0.09
σ^2_e M	0.23 ± 0.01	0.20	0.22	0.15 - 0.35
σ^2_p M	0.29 ± 0.02	0.26	0.28	0.19 - 0.45
h^2_d M	0.21 ± 0.01	0.23	0.22	0.19 - 0.20
σ^2_a PS	0.05 ± 0.01	0.05	0.05	0.03 - 0.07
σ^2_e PS	0.14 ± 0.01	0.13	0.13	0.10 - 0.18
σ^2_p PS	0.19 ± 0.02	0.18	0.19	0.13 - 0.26
h^2_d PS	0.28 ± 0.01	0.28	0.28	0.24 - 0.27
σ^2_a T	0.02 ± 0.01	0.02	0.02	0.01 - 0.03
σ^2_e T	0.06 ± 0.01	0.05	0.06	0.04 - 0.12
σ^2_p T	0.08 ± 0.02	0.08	0.08	0.06 - 0.16
h^2_d T	0.25 ± 0.01	0.29	0.27	0.25 - 0.21
σ^2_aC	0.02 ± 0.01	0.02	0.02	0.00 - 0.02
σ^2_e C	0.06 ± 0.01	0.06	0.06	0.05 - 0.08
σ^2_p C	0.08 ± 0.02	0.01	0.02	0.01 - 0.03
h^2_d C	0.25 ± 0.01	0.29	0.27	0.27 - 0.24
σ^2_a N	0.004 ± 0.01	0.004	0.004	0.00 - 0.05
σ^2_e N	0.02 ± 0.01	0.02	0.02	0.01 - 0.03
σ^2_p N	0.03 ± 0.02	0.02	0.02	0.01 - 0.04
h^2_d N	0.15 ± 0.01	0.16	0.16	0.12 - 0.14
σ^2_a SAC	0.03 ± 0.01	0.02	0.03	0.01 - 0.04
σ^2_e SAC	0.12 ± 0.01	0.12	0.12	0.10 - 0.13
σ^2_p SAC	0.15 ± 0.02	0.15	0.15	0.12 - 0.18
h^2_d SAC	0.18 ± 0.01	0.17	0.18	0.11 - 0.24

CI: confidence interval the 95%. σ^2a: direct additive genetic variance. σ^2m: maternal variance. σ^2pe: permanent environmental genetic variance. σ^2e: residual variance. σ^2p: phenotypic variance. h^2d: direct heritability. W120: weight at 120 days of age. W210: weight at 210 days of age. W365: weight at 365 days of age. W450: weight at 450 days of age. REA: rib eye area. BFT: backfat thickness. RFT: rump fat thickness. M: muscularity. PS: physical structure. T: breed type. C: conformation. N: navel. SAC: sacrum.

High magnitude heritability estimates were also observed for carcass traits, ranging from 0.42 ± 0.01 to 0.46 ± 0.01. In contrast, heritability estimates for visual scores ranged from low to moderate magnitude (0.15 ± 0.01 to 0.28 ± 0.01), with the highest values obtained for physical structure score.

Tables IV, V, and VI show the estimates of genetic, residual, and phenotypic correlations between scores, growth, and carcass traits, respectively. Due to the symmetry and low magnitude of heritability standard deviations (Table III) and genetic correlations (Tables IV, V, and VI), the mean was used as a measure of the central tendency of the posterior distributions of the genetic parameters. These parameters demonstrate the low variability between the sample means and adequate precision of the estimates, supporting our previous discussion.

Moderate to high genetic correlations were estimated between the visual score traits, ranging from 0.25 ± 0.17 to 0.89 ± 0.06, except between SAC and N (-0.01 ± 0.19). Moderate to high magnitude residual correlations were obtained between M with PS, T, C, and SAC (0.41 to 0.65); PS with T, C and SAC (0.29 to 0.48); T with C and SAC (0.33 to 0.42); and C with N and SAC (0.24 to 0.37), while the other estimates were low. Moderate to high magnitude phenotypic correlations were observed between M with PS, T, C and SAC (0.33 to 0.59); PS with T, C and SAC (0.23 to 0.45); T with C and SAC (0.24 to 0.36); and C with SAC (0.35), while the other estimates were low.

Overall, estimates of positive and moderate to high genetic correlations between visual scores with growth traits were obtained, ranging from 0.20 ± 0.23 to 0.57 ± 0.13. However, negative and moderate estimates were observed between T with W120 and W210 (0.35 ± 0.18 and 0.34 ± 0.21, respectively), and low between N with W210 and between SAC with W210 and W450, ranging from - 0.13 ± 0.22 to -0.04 ± 0.14. In addition, the genetic correlations of bred type with post-weaning weights, conformation with W210 and W450, navel with W120, W210 and W450, and between SAC with W210,

Table IV. ***Posteriori*** **estimates of genetic, residual, and phenotypic correlations between visual scores traits in Nellore cattle.**

Parameters	Genetic Correlations				Residual Correlations	Phenotypic Correlations
	Mean ± SD	Mode	Median	CI (95%)		
M x PS	0.79 ± 0.08	0.80	0.80	0.62 - 0.92	0.65	0.51
M x T	0.37 ± 0.14	0.36	0.37	0.08 - 0.62	0.41	0.36
M x C	0.89 ± 0.06	0.94	0.90	0.74 - 0.98	0.60	0.59
M x N	0.50 ± 0.13	0.54	0.51	0.23 - 0.73	0.18	0.20
M x SAC	0.44 ± 0.15	0.49	0.45	0.12 - 0.68	0.44	0.33
PS x T	0.63 ± 0.10	0.65	0.64	0.41 - 0.81	0.29	0.32
PS x C	0.64 ± 0.11	0.67	0.64	0.4 - 0.82	0.48	0.45
PS x N	0.63 ± 0.11	0.68	0.64	0.37 - 0.81	0.12	0.18
PS x SAC	0.25 ± 0.17	0.29	0.26	0.00 - 0.56	0.34	0.23
T x C	0.54 ± 0.12	0.56	0.55	0.27 - 0.75	0.42	0.36
T x N	0.51 ± 0.14	0.52	0.51	0.21 - 0.75	0.11	0.17
T x SAC	0.36 ± 0.15	0.38	0.37	0.05 - 0.63	0.33	0.24
C x N	0.65 ± 0.12	0.69	0.67	0.38 - 0.85	0.24	0.18
C x SAC	0.57 ± 0.14	0.63	0.58	0.24 - 0.80	0.37	0.35
N x SAC	-0.01 ± 0.19	-0.07	-0.01	-0.30 - 0.35	0.19	0.09

CI: confidence interval the 95%. M: muscularity. PS: physical structure. T: breed type. C: conformation. N: navel. SAC: sacrum.

Table V. ***Posteriori*** **estimates of genetic, residual, and phenotypic correlations between visual score and growth traits in Nellore cattle.**

Parameters	Genetic Correlations				Residual Correlations	Phenotypic Correlations
	Mean ± SD	Mode	Median	CI (95%)		
M x W120	0.37 ± 0.24	0.39	0.36	(-0.09) - 0.85	0.09	0.04
M x W210	0.44 ± 0.18	0.47	0.45	0.05 - 0.76	0.11	0.08
M x W365	0.57 ± 0.13	0.58	0.57	0.33 - 0.80	0.19	0.29
M x W450	0.39 ± 0.11	0.40	0.40	0.17 - 0.59	0.21	0.27
PS x W120	0.35 ± 0.20	0.41	0.37	(-0.06) - 0.72	0.13	0.08
PS x W210	0.41 ± 0.19	0.44	0.42	0.04 - 0.76	0.15	0.14
PS x W365	0.46 ± 0.11	0.47	0.46	0.22 - 0.67	0.21	0.30
PS x W450	0.43 ± 0.10	0.45	0.43	0.23 - 0.63	0.29	0.23
T x W120	-0.35 ± 0.18	-0.38	-0.36	(-0.65) - 0.05	0.14	0.02
T x W210	-0.34 ± 0.21	-0.25	-0.32	(-0.69) - 0.05	0.12	0.06
T x W365	0.05 ± 0.12	0.06	0.06	(-0.19) - 0.28	0.08	0.15
T x W450	0.10 ± 0.13	0.13	0.10	(-0.17) - 0.35	0.22	0.14
C x W120	0.24 ± 0.23	0.18	0.24	(-0.21) - 0.65	-0.04	0.13
C x W210	0.05 ± 0.21	0.03	0.05	(-0.40) - 0.44	0.03	0.12
C x W365	0.31 ± 0.25	0.34	0.32	0.01 - 0.60	0.13	0.21
C x W450	0.10 ± 0.13	0.13	0.10	(-0.17) - 0.35	0.22	0.22
N x W120	0.08 ± 0.21	0.07	0.08	(-0.36) - 0.47	0.09	0.08
N x W210	-0.13 ± 0.22	-0.13	-0.13	(-0.60) - 0.31	0.14	0.12
N x W365	0.26 ± 0.13	0.26	0.27	(-0.01) - 0.50	0.01	0.20
N x W450	0.13 ± 0.12	0.16	0.14	(-0.12) - 0.36	0.07	0.21
SAC x W120	0.20 ± 0.23	0.25	0.21	(-0.26) - 0.62	-0.12	-0.08
SAC x W210	-0.08 ± 0.20	-0.06	-0.07	(-0.47) - 0.28	0.00	-0.07
SAC x W365	0.08 ± 0.16	0.13	0.08	(-0.26) - 0.39	0.03	0.00
SAC x W450	-0.04 ± 0.14	-0.04	-0.04	(-0.31) - 0.22	0.07	0.00

CI: confidence interval the 95%. W120: weight at 120 days of age. W210: weight at 210 days of age. W365: weight at 365 days of age. W450: weight at 450 days of age. M: muscularity. PS: physical structure. T: breed type. C: conformation. N: navel. SAC: sacrum.

Table VI. ***Posteriori*** **estimates of genetic, residual, and phenotypic correlations between visual score and carcass traits in Nellore cattle.**

Parameters	Genetic Correlations				Residual Correlations	Phenotypic Correlations
	Mean ± SD	Mode	Median	CI (95%)		
M x REA	0.03 ± 0.17	0.03	0.03	(-0.29) - 0.34	0.26	0.32
M x BFT	0.14 ± 0.17	0.15	0.14	(-0.19) - 0.49	0.10	0.25
M x RFT	0.05 ± 0.15	0.06	0.05	(-0.24) - 0.34	0.13	0.24
PS x REA	0.22 ± 0.17	0.24	0.22	(-0.11) - 0.53	0.14	0.13
PS x BFT	-0.02 ± 0.18	0.01	-0.02	(-0.35) - 0.33	0.12	0.01
PS x RFT	-0.02 ± 0.16	-0.01	-0.02	(-0.31) - 0.31	0.14	0.05
T x REA	0.10 ± 0.15	0.06	0.10	(-0.19) - 0.39	-0.01	0.00
T x BFT	0.14 ± 0.17	0.14	0.14	(-0.21) - 0.46	-0.10	-0.04
T x RFT	0.02 ± 0.15	0.05	0.02	(-0.25) - 0.31	0.00	-0.01
C x REA	0.09 ± 0.17	0.06	0.08	(-0.24) - 0.41	0.04	0.25
C x BFT	0.14 ± 0.19	0.15	0.14	(-0.22) - 0.50	0.08	0.25
C x RFT	0.16 ± 0.17	0.20	0.17	(-0.15) - 0.47	0.05	0.29
N x REA	0.18 ± 0.18	0.15	0.18	(-0.16) - 0.52	0.04	0.24
N x BFT	0.17 ± 0.20	0.18	0.18	(-0.22) - 0.53	-0.07	-0.04
N x RFT	0.28 ± 0.19	0.28	0.28	(-0.07) - 0.66	-0.06	-0.08
SAC x REA	-0.37 ± 0.20	-0.39	-0.37	(-0.78) - 0.02	0.14	0.00
SAC x BFT	0.10 ± 0.21	0.12	0.10	(-0.31) - 0.49	0.04	0.00
SAC x RFT	0.14 ± 0.18	0.16	0.14	(-0.22) - 0.47	0.00	0.01

CI: confidence interval the 95%. REA: rib eye area. BFT: backfat thickness. RFT: rump fat thickness. M: muscularity. PS: physical structure. T: breed type. C: conformation. N: navel. SAC: sacrum.

W365, and W450 were low. Phenotypic correlations of moderate magnitude were obtained between M with post-weaning weights (0.27 to 0.29) and between of PS and W365 and W450 (0.30 and 0.23, respectively) and C with W450 (0.22).

Genetic correlations between visual and carcass score traits were low, except between REA with PS and SAC (0.22 and -0.37, respectively) and between N and RFT (0.28). The muscle score showed a moderate residual correlation (0.26) with REA. Phenotypic correlations of moderate magnitude were observed between visual scores of muscularity and conformation with carcass traits (REA, BFT, and RFT). However, M showed a greater phenotypic correlation with REA (0.32).

DISCUSSION

The low estimates of maternal heritability are within the values reported for Nellore cattle by Kamei et al. (2017) and Lopes et al. (2017), whose estimates range from 0.03 to 0.32 for W120 and 0.09 to 0.29 for W210. Despite these results, as maternal influence originates in the mother's genotype and environmental action, genetic variability for the maternal effect in different environments is an important source of variation for performance. Therefore, it is valid to test and consider the maternal influence on pre-weaning weights, to avoid overestimation of the direct additive genetic value, and to assess the female's ability to raise her progeny until weaning (Kluska et al. 2018).

Higher heritability estimates for W365 and W450 indicate that they may have greater genetic gains compared to pre-weaning weights. This result may be associated with greater proportions of additive genetic effect relative to environmental variance. That is, post-weaning traits are less influenced by the environment than pre-weaning traits. Considering that the animals are subjected to the same management conditions, there should be little variation in the environment (Brunes et al. 2022). Intensifying selection for yearling weight can influence the adult weight and maintenance requirement of animals (Miranda et al. 2006, Silva 2016). To address this problem, selection indexes composed of traits associated with weight and body composition such as carcass and visual scores, leading to precocious animals, are recommended (Brunes et al. 2022).

The high heritability estimates for REA (0.42), BFT (0.46), and RFT (0.46) suggest that genes with additive effects have a considerable influence on carcass yield and finish. These results demonstrate that these traits can respond similarly to selection, due to the proportion of phenotypic variance attributed to genetics (Brunes et al. 2022). The results of this study demonstrate the existing genetic variability for these traits, which can be included as selection criteria to obtain genetic progress in the herd.

According to Forni et al. (2007), traits evaluated visually tend to be influenced by environment, consequently, responses of small magnitude to direct selection can be expected, in agreement with the low to moderate magnitude heritabilities estimated in the present study. There are few studies using the MERCOS methodology (Lôbo 1996) and these estimates show that visual scores can respond to individual selection and promote genetic gains, especially structure scores, breed type, and conformation.

Muscularity showed a high genetic association with conformation (0.89), showing that both traits are largely influenced by the same sets of genes. These were expected since animals with better conformation tend to be more precocious and have more developed musculature (Sima 2015). Similarly, muscularity was shown to be highly correlated with physical structure (0.79), indicating that muscle development and distribution may be highly correlated with animal support structures. The genetic correlation between these traits is explained by the association of musculature and conformation with animals with a better structure to support the limbs, greater sexual precocity, and finishing. Although Nellore animals commonly present greater size, body length, and less depth and spring of rib compared to taurine breeds, that is, highest classifications for PS and lowest classifications for C (Sima 2015), the evaluated herd was submitted to simultaneous genetic selection for both traits. That is, animals were identified with greater depth and spring of ribs, and an adequate structure, and along with the additive (co)variances this evaluation can assist in changing the body biotype of the animals in response to selection.

Araújo et al. (2010) report that the M, PS, and P scores describe the meat production potential of the whole animal, that is, they are direct components of the animal's body weight, however weight is easier to measure, has a higher heritability and is less influenced by the evaluator, therefore would be recommended as a selection criterion.

Genetic correlation estimations of moderate to high magnitude between M scores with T, N, and SAC indicate that the selection of animals with better muscle development can result in the selection of animals with a better breed type, medium-sized navels, and animals with level sacrum and *vice versa*. These results may be associated with the selection by which the herd was submitted, which includes simultaneously M, T, N, and SAC.

The high genetic correlation between structure with conformation can be attributed to the fact that better-conforming animals are those with better physical structures. Lima et al. (2013) confirm that the selection of Nellore cattle with greater structure can lead to direct selection of earlier-maturing animals, with better conformation and better breed type. However, it can result in the selection of animals with pendulous navels, as they are animals of larger body size, so it is recommended that selection consider both traits as selection criteria and seeking animals with moderate navels.

The moderate genetic correlation between PS and SAC demonstrates that these traits are also influenced by the same group of genes, and that selection for structure can lead to animals with desirable sacral bones. That is, it can lead to obtaining females with greater calving ease, as the flatter the sacrum, the more mobile its joint connections will be, consequently, the female will have greater ease of calving (Roberts 1971, Oliveira 2008).

Considering the genetic correlations obtained between T and N (0.51), animals with better navel placement are those with the best breed type. Accordingly, selection for animals with a better breed type may also result in obtaining animals with better conformation and sacrum bone structure, considering the genetic correlation estimates obtained. Considering that it is recommended that animals of the Nellore breed should not have a protruding sacral bone, but rather at the same level as the hips, the selection of animals with a better breed type may result in the selection of animals with better rump, supporting the moderate genetic correlations obtained.

A high genetic correlation between sacral bone structure and conformation was expected, since the skeleton is observed, with the opening of the ischium, dorsal line, and ribs, which should be parallel or open in the same direction as the rump. Thus, the search for animals with better carcass conformation may lead to the selection of those with better rump and *vice versa*. The same behavior can be observed between conformation and navel scores, indicating that part of the same genes affects these traits in the same direction, so that selection for better-conforming animals leads to a correlated response in the same direction for animals with medium navels, which is desirable for the breed.

It is noteworthy that the evaluation of morphological traits presents a degree of subjectivity attributed to the evaluator, in addition to being influenced by the environment, especially feeding, management, and non-additive genetic effects. Therefore, visual assessment methodologies must follow a consistent standard at the time of data collection, such as carrying out assessments within groups of contemporaries. That is, with animals of similar age, same-sex and management group, to control environmental factors that may influence the animals' performance. Furthermore, it is important to use information from developmental data, as well as weights, carcass measurements, and reproductive data, giving greater reliability to the scores obtained. Due attention to these items significantly contributes to the better assessment of an individual morphological type, making the attribution of grades less biased. Even so, considering the estimates of phenotypic correlation obtained, environmental changes that favor better performance for muscularity may lead to better structure, conformation, in addition to desirable breed type and sacral bone, and vice versa.

In addition, for many combinations of traits or score pairs, genetic correlations have higher estimates than phenotypic ones, which can optimize the selection process and genetic gain, justifying the use of morphological traits as selection criteria. Genetic correlations of moderate to high magnitude between M, PS, and growth traits indicate that animals with greater accumulation of muscle mass and well-developed structure to support the body can result in the selection for greater body weight (Paterno et al. 2017, Silveira et al. 2019). Heavier animals are generally those with greater muscle mass. In addition, the score for structure indicates the area that the animal covers and the body length, and is, consequently, associated with greater body weight (Abreu 2014). Thus, muscle and physical structure proved to be important traits used as complementary selection criteria along with growth measures (Koury Filho et al. 2009).

Despite the high correlation between these traits, selection for a single group of traits (i.e., just visual scores or just growth traits) may bring undesirable results to the production system. The inclusion of visual score traits associated with performance as selection criteria allows the increase of body weight, maintaining morphological types that are more economically efficient, and avoiding the multiplication of extreme biotypes in the herd (Koury Filho et al. 2010). The moderate phenotypic correlations between M and W365 and W450 and between E and W365 and W450 indicate that environmental changes that promote an increase in yearling weight lead to improvements in the morphological type for muscularity and structure of the animals. Furthermore, these traits can be used as phenotypic indicators of animals with greater post-weaning weight.

The low genetic association between breed type and performance traits (except for pre-weaning weights) was expected, as the heavier animals are not necessarily those with breed characteristics closer to the ideal standard. The breed type in Nellore cattle takes into account criteria like the pigmentation of coat, skin, and mucous membranes, also, the vulva and anus, teats and perineum; and the shape of the head, all of which have little to no connection with body weight. This process helps to identify animals that better fit the breed standard, as these are considered to be more balanced, harmonious, and functional animals (Lôbo 1996).

Although the genetic correlation estimates of C with W120 and W365 were moderate, and with W210 and W450 were low, showing that the animal's weight is not always related to its conformation. For example, the animal may have a lot of muscling but distributed in anatomical locations that do not lead to an adequate conformation. These results can be attributed to the fact that heavier animals are commonly late-maturing animals, while C is a trait that is linked to precocity. Thus, weight traits that are evaluated in advance, such as W365, can be a better indicator of conformation.

The low genetic correlations obtained between navel size and body weights show that animals with better performance are not necessarily those with better navel positioning, since the animal is still in the growth and limb formation phase, mainly for pre-weaning weights. However, for W365 moderate genetic correlations were observed, as the animals already passed a culling criterion at weaning and at 365 days of age, so that animals remaining on the farm had good performance and adequate sheath and navel.

In the same sense, the low genetic correlation estimates between sacral bone structure and growth traits demonstrate that better-performing animals are not necessarily those with ideal rump or sacral bone, both in size and inclination. These results show that selection for performance alone will not contribute to harmonic animals in the posterior region, with long, flat, and wide sacral bones. Therefore, these scores should be included as an additional selection criterion, as it may lead to the selection of females with greater calving ease (Roberts 1971, Oliveira 2008). In addition, the sacrum bone is the basis of prime meat cuts such as the round, which can be subdivided into the top round, bottom round, bottom round rump, and eye of round roast cuts, which are high- value cuts, adhered to the sacral bone and ileum (Feijó 2021), so selection for this trait can also lead to greater meat production.

The low genetic correlations found between visual scores and carcass traits suggest that use of morphological traits as selection criteria would largely have no effect on carcass traits. An exception is the selection for SAC, which would lead to unfavorable changes in REA. Thus, REA and SAC should both be included as criteria for obtaining more harmonious animals. To the best of our knowledge, no studies were found evaluating the association between REA with SAC. In this sense, further studies are needed to better understand the relationship between these traits. The moderate residual correlation between the muscle score with REA indicates that some environmental conditions simultaneously influence these traits so that environmental improvements that lead to an increase in REA can positively result in the selection of animals with larger muscles.

Although the phenotypic correlations between muscle and conformation scores with carcass traits were moderate, M showed a greater phenotypic correlation with REA. On the other hand, the morphological traits of PS, T, N, and SAC are poor phenotypic indicators of carcass yield and finishing. Our results were similar to Yokoo et al. (2009), showing that the distribution of muscle mass throughout the animal's body favors a larger area of the *Longissimus dorsi* muscle, which is used for measuring REA and thus, a greater yield of meat cuts. In this sense, M and C can be used as phenotypic indicators of animals with higher yields and carcass finish, which are currently requirements demanded by the consumer market, in addition to being associated with better quality carcasses and slaughterhouse yield. So, by improving carcass traits the producer can be better paid for the quality of their final product (Yokoo et al. 2009, Faria et al. 2015, Gordo et al. 2016). The present results suggest that genetic selection for carcass traits must include direct measurements of carcass traits rather than visual scores.

Although visual scores and carcass traits obtained by ultrasound can be used to improve carcass quality, some possible explanations led to low estimates of genetic correlations between these traits, which are: different observations for both assessments; variation in the measurement age, as the animals were first submitted to visual evaluation and later to carcass evaluations (Oliveira & Cardoso 2008), among others. These measurements are influenced by the time of assessment, as they follow the allometric growth curve of the animals. Cattle show bone growth, followed by muscle and later by adipose tissue, so tissue deposition changes with growth and weight, in addition to sex, genotype, and management (Sainz & Araujo 2001). Thus, the association between carcass traits and visual scores might be influenced by the age of assessment. The results may have been different had the evaluations been conducted at similar ages.

Another factor that may have influenced these estimates is that only 17% of the animals evaluated in the analyses presented a phenotype for both groups of traits, which could lead to low estimates being obtained. Thus, the performance of visual and ultrasound evaluation of carcasses at similar ages and the inclusion of both groups of traits as phenotypic evaluations might influence the estimated variance components and the selection responses. Furthermore, the visual scores, although they represent the assessment of the animals as a whole, are subjective and subject to variation due to the technician performing the assessment. The traits obtained by ultrasound are more objective, but take into account a maximum of three points on the carcass, while the evaluation of visual scores evaluates the animal as a whole, which may account for the low associations obtained (Toral et al. 2011).

One of the biggest limitations in the Brazilian beef industry is the lack of standardized carcass grading (Castro et al. 2014). In this sense, the international market requires better meat and carcass quality, offering better remuneration for better quality animal products (Lima Neto et al. 2009). Thus, the use of ultrasound measurements, which are well-established techniques for improving carcass and meat traits, and visual scores as auxiliary measures to select better conformed/balanced individuals, can be important tools to increase the quality and added value of the Zebu meat.

Visual scores of muscularity, structure, breed type, and conformation must respond to individual selection and show greater genetic progress and their inclusion as selection criteria in Zebu herds is indicated. This will make it possible to obtain more harmonious animals, with adequate muscle distribution, adequate physical structure to support the limbs, and well conformed, that is, animals with greater potential for meat production. Thus, these traits must be used mainly as criteria for culling animals that do not fit the herd profile and that do not meet the requirements of the breed and production system. This is because the selection and culling based on visual scores can eliminate traits that lead to reduced performance or health and reproductive problems, as when it is performed based on animals that have physical structure problems, protruding sacral bone, lack of musculature, and poor conformation. Consequently, responses can also be observed in the increase in performance and growth traits. Even so, given the low genetic association between visual scores and carcass traits, simultaneous selection for both groups of traits is recommended to obtain animals with a more harmonious and functional biotype, as well as better conformation and carcass quality.

Growth, carcass, and morphological composition traits present genetic variability and thus respond to direct selection. However, muscularity, structure, breed type, and conformation may present a greater response to selection when compared to navel and sacrum bone structure. Selection for visual scores can lead to favorable changes among themselves and in growth traits, especially between M and PS with body weight. On the other hand, genetic selection for visual scores would lead to limited genetic gains in carcass traits. Thus, greater genetic gains can be expected if carcass and morphological traits are included simultaneously as selection criteria, aiming to meet the demands of the consumer market and the beef industry. Morphological categorical traits can be used as complementary tools that add value to objective selection. However, if the animals are not evaluated with objective measurements and visual scores are used as the only selection criteria, genetic gains in weight and composition will occur, but more slowly.

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Sores BB performed the statistical analysis, wrote the paper, and contributed to the collection of morphological traits. Brunes LC and Magnabosco CU contributed to the statistical analysis and assisted in the writing and revision of the paper. Baldi FS and Carmo AS supported the statistical analysis and interpretation of the results. Pereira LS and Carvalho RA contributed to the collection of morphological traits. Narciso MG contributed to the statistical analysis. Amorim ST and Sainz RD were responsible for article translation.