

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

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17 **Abstract**

18 Growth and carcass traits are essential selection criteria for beef cattle breeding programs. However, it is necessary
19 to combine these measurements with body composition traits to meet the demand of the consumer market. This
20 study aimed to estimate the genetic parameters for visual scores, growth (pre and post-weaning weights), and
21 carcass (rib eye area (REA), back and rump fat thickness) traits in Nellore cattle using Bayesian inference. Data
22 from 12,060 animals belonging to the HoRa Hofig Ramos farm were used. Morphological traits were evaluated
23 by the MERCOS methodology. The heritability estimates obtained ranged from low to high magnitude, from 0.15
24 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
25 between traits of visual scores and growth were generally of moderate to high magnitudes, however, visual scores
26 showed low correlations with carcass traits, except between REA and sacral bone and structure. Selection for
27 visual score traits can lead to favorable responses in body weight and vice versa. Morphological categorical traits
28 can be used as complementary tools that add value to selection.

29

30 **Keywords:** Bayesian methods, genetic association, morphological traits, weight performance, Zebu Cattle.

31

32 **Introduction**

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

39 An ideal biotype within the beef cattle system in tropical environments is individuals with a well-
40 developed bone structure, medium frame, carcass length, conformation, and depth and arch of ribs. Animals must
41 also have evident sexual traits (well-defined femininity or masculinity), sound feet and legs, and moderate sheath.
42 These traits ensure that, in addition to the greater potential for meat production and better body composition,
43 animals have greater adaptability to the rearing system. Most animals in Brazil are reared extensively, which
44 requires functional animals for production and reproduction on pasture (Soares et al., 2022).

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

54 Morphological traits are threshold measures and do not present continuous phenotypic expression,
55 making genetic evaluations difficult. Thus, the estimation of genetic parameters is necessary to maximize the
56 response to selection and design selection strategies with a focus on productivity and carcass quality (Cavani et
57 al., 2015). In Brazil, few studies have been developed for this purpose (Faria et al., 2009a; Araújo et al., 2012;
58 Gordo et al., 2016; Paterno et al., 2017a; Paterno et al., 2017b; Carreño et al., 2019). Considering the economic
59 importance of the Nellore breed and the scarcity of studies involving morphological traits, the aim of this study
60 was to estimate the heritabilities and genetic correlations (residual and phenotypic) between visual scores, growth,
61 and carcass traits in Nellore cattle using Bayesian inference.

62 **Material and Methods**

63

64 *Phenotypic data and evaluated traits*

65 Quantitative traits included live weights at 120 (W120), 210 (W210), 365 (W365), 450 (W450) days of age, rib
66 eye area (REA, cm²), backfat thickness over the 12th-13th ribs (BFT, mm) and at the rump (over the junction of the
67 *Gluteus medius* and *Biceps femoris*; RFT, mm). Categorical measures included the morphological traits of
68 muscularity (M), physical structure (E), racial aspects (R), conformation (C), navel (omphalos; O), and sacrum
69 (SAC) were evaluated according to MERCOS methodology (Lôbo, 1996). Nellore animals (n = 12,060) from a
70 single herd (HoRa Genética Provada, Brasilândia, Mato Grosso do Sul, Brazil) were evaluated, of which 7,804
71 were females and 4,256 were males. The farm participates in the Nellore Brazil Genetic Breeding Program,
72 coordinated by the National Association of Breeders and Researchers (ANCP, Ribeirão Preto, Brazil). Visual
73 scores of 4,175 animals with an average age of 22 months were used.

74

75 *Statistical analysis and genetic parameter estimates*

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

85 CG with fewer than four animals and animals whose phenotypic information was above or below 3.5
86 standard deviations from the mean of the respective CG were excluded from the analysis. In addition, for the
87 muscularity and structure traits, the observations that presented a score equal to 1 were excluded, due to the low
88 frequency observed for these traits. Thus, for genetic analysis, information from 12,060 animals was considered.
89 The distribution of scores for visual assessment traits is shown in Table 1.

90 The initial values of the (co)variance components were obtained from preliminary analyses using linear
91 models with a restricted maximum likelihood approach, based on the REMLF90 and AIREMLF90 programs
92 (Misztal et al., 2019). These results were used as initial values in two-trait analyses to estimate covariance
93 components, heritabilities, and genetic, residual, and phenotypic correlations using a linear animal model for
94 growth and carcass traits, a threshold model for visual scores, and linear-threshold for the combination of the traits.
95 These analyses were carried out under a Bayesian approach using the THRGIBBS1F90 program (Tsuruta and
96 Misztal, 2006). The numbers of observations and descriptive statistics of the evaluated traits are presented in Table
97 2.

98 In matrix terms, the general model can be described as: $y = X\beta + Z_1a + Z_2m + Z_3c + e$, where: y is
99 a vector of observations; β is the vector of fixed effects; a is the vector of direct additive genetic effects; m is a
100 vector of maternal genetic effects; c is the vector of non-correlated effects (permanent maternal effects); $X, Z_1,$
101 Z_2, Z_3 are incidence matrices that relate β, a, m e c with y , respectively; and e is the vector of residuals
102 associated with each observation.

103 As fixed effects for the growth traits, CG and cow age at calving were included as linear and quadratic
104 covariates (cow's age at calving was only used for P120 and P210). For the other traits, maternal and permanent
105 environment effects were not used, as it was verified through analysis of variance that the contribution of these
106 effects on phenotypic variance was less than 3%. For carcass traits, CG and animal age were considered as fixed
107 effects as linear and quadratic covariate. For the visual scores, the CG was considered as a fixed effect, in addition

108 to sex, calving season, management group, and the animal's age at the time of evaluation as a linear and quadratic
 109 covariate. Age was included as a linear and quadratic covariate, as this model presented the smallest prediction
 110 errors. Considering that only one technician performed the visual evaluation, this effect was not included in the
 111 model.

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

$$115 \begin{bmatrix} \mathbf{a} \\ \mathbf{m} \\ \mathbf{c} \\ \mathbf{e} \end{bmatrix} \sim N(\mathbf{0}, \mathbf{V})$$

$$116 \mathbf{V} = \begin{bmatrix} \mathbf{G} \otimes \mathbf{A} & \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{c} \otimes \mathbf{I}_{Nm} & \mathbf{0} \\ \mathbf{0} & \mathbf{0} & \mathbf{R} \otimes \mathbf{I}_N \end{bmatrix}$$

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

$$121 \mathbf{G} = \begin{bmatrix} \mathbf{Gd} & \mathbf{0} \\ \mathbf{0} & \mathbf{Gm} \end{bmatrix}$$

122 Where: \mathbf{Gd} e \mathbf{Gm} are matrices that represents additive direct effects and maternal effects, respectively.

123 It was assumed that $\mathbf{E}[\mathbf{y}] = \mathbf{X}\boldsymbol{\beta}$, $\mathbf{Var}(\mathbf{a}) = \mathbf{A} \otimes \boldsymbol{\Sigma} \mathbf{a}$, $\mathbf{Var}(\mathbf{m}) = \mathbf{A} \otimes \boldsymbol{\Sigma} \mathbf{m}$, $\mathbf{Var}(\mathbf{c}) = \mathbf{I} \otimes \boldsymbol{\Sigma} \mathbf{c}$, and $\mathbf{Var}(\mathbf{e}) =$
 124 $\mathbf{I} \otimes \boldsymbol{\Sigma} \mathbf{e}$, where $\boldsymbol{\Sigma} \mathbf{a}$ is the direct additive genetic (co)variance matrix, $\boldsymbol{\Sigma} \mathbf{m}$ is the matrix of maternal genetic
 125 variance, $\boldsymbol{\Sigma} \mathbf{c}$ is a matrix of maternal permanent environmental variance, $\boldsymbol{\Sigma} \mathbf{e}$ is a matrix of residual (co)variances,
 126 \mathbf{A} is the numerator relationship matrix, \mathbf{I} is an identity, and \otimes is the Kronecker product.

127 The visual scores were analyzed using the following threshold model:

$$\begin{aligned}
128 \quad f(w_i|y_i) &= \prod_{j=1}^{n_i} 1(l_{ij} < t_1)1(w_{ij} = 1) + 1(t_1 < l_{ij} < t_2)1(w_{ij} = 2) \\
129 \quad &+ 1(t_2 < l_{ij} < t_3)1(w_{ij} = 3) + 1(t_3 < l_{ij} < t_4)1(w_{ij} = 4) \\
130 \quad &+ 1(t_4 < l_{ij} < t_5)1(w_{ij} = 5)
\end{aligned}$$

131 where for each trait i ($i = 1, 2, 3, 4$ ou 5), w_{ij} and l_{ij} are categorical variables and observations of underlying scale
132 j , respectively, t_1 and t_4 are the thresholds that define the categorical response for each trait, and n_i represents the
133 total number of data points for each trait studied. A uniform prior distribution was defined for the thresholds. For
134 traits M and E it was assumed that $t_1 = 0$, so that the vector of estimable thresholds were defined as $t =$
135 $t_2; t_3; t_4 \text{ e } t_5$.

136 A uniform and inverted Wishart distribution was assumed *a priori* for the systematic effects and
137 (co)variance components, respectively. Chains of 200,000 to 400,000 iterations were generated, with a burn-in of
138 100,000 to 300,000 cycles and sampling every 50 and 100 cycles. This variation was used to ensure convergence
139 for each categorical trait or combination of two traits. *A posteriori* estimates were obtained using the
140 POSTGBBSF90 program (Misztal et al., 2019).

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

148 **Results**

149 Table 3 shows the *a posteriori* estimates of the direct (h^2d) and maternal (h^2m) heritability coefficients for growth,
150 carcass, and visual scores traits. Maternal heritability estimates for pre-weaning weights were low and lower than
151 direct heritabilities. Heritability estimates for growth traits were moderate to high, with the highest values observed
152 for W365 and W450 (0.34 ± 0.01 and 0.44 ± 0.01 , respectively). High magnitude heritability estimates were also
153 observed for carcass traits, ranging from 0.42 ± 0.01 to 0.46 ± 0.01 . In contrast, heritability estimates for visual
154 scores ranged from low to moderate magnitude (0.15 ± 0.01 to 0.28 ± 0.01), with the highest values obtained for
155 physical structure score.

156 Tables 4, 5, and 6 show the estimates of genetic, residual, and phenotypic correlations between scores,
157 growth, and carcass traits, respectively. Due to the symmetry and low magnitude of heritability standard deviations
158 (Table 3) and genetic correlations (Tables 4, 5, and 6), the mean was used as a measure of the central tendency of
159 the posterior distributions of the genetic parameters. These parameters demonstrate the low variability between
160 the sample means and adequate precision of the estimates, supporting our previous discussion.

161 Moderate to high genetic correlations were estimated between the visual score traits, ranging from 0.25
162 ± 0.17 to 0.89 ± 0.06 , except between SAC and O (-0.01 ± 0.19). Moderate to high magnitude residual correlations
163 were obtained between M with E, R, C, and SAC (0.41 to 0.65); E with R, C and SAC (0.29 to 0.48); R with C
164 and SAC (0.33 to 0.42); and C with O and SAC (0.24 to 0.37), while the other estimates were low. Estimates of
165 moderate to high magnitude phenotypic correlations were observed between M with E, R, C and SAC (0.33 to
166 0.59); E with R, C and SAC (0.23 to 0.45); R with C and SAC (0.24 to 0.36); and C with SAC (0.35), while the
167 other estimates were low.

168 Overall, estimates of positive and moderate to high genetic correlations between visual scores and growth
169 traits were obtained, ranging from 0.20 ± 0.23 to 0.57 ± 0.13 . However, negative and moderate estimates were
170 observed between R with W120 and W210 (0.35 ± 0.18 and 0.34 ± 0.21 , respectively), and low between O with

171 W210 and between SAC with W210 and W450, ranging from -0.13 ± 0.22 to -0.04 ± 0.14 . In addition, the genetic
172 correlations of racial aspects with post-weaning weights, conformation with W210 and W450, omphalos with
173 W120, W210 and W450, and between SAC with W210, W365, and W450 were low. Phenotypic correlations of
174 moderate magnitude were obtained between M with post-weaning weights (0.27 to 0.29) and between the score of
175 E with W365 and W450 (0.30 and 0.23, respectively) and C with W450 (0.22).

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

181

182 **Discussion**

183 The low estimates of maternal heritability are within the values reported for Nellore cattle by Kamei et al. (2017)
184 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
185 these results, as maternal influence originates in the mother's genotype and environmental action, genetic
186 variability for the maternal effect in different environments is an important source of variation for performance.
187 Therefore, it is valid to test and consider the maternal influence on pre-weaning weights, to avoid overestimation
188 of the direct additive genetic value, and to assess the female's ability to raise her progeny until weaning (Kluska et
189 al., 2018). Even so, the response to selection for the maternal effect may be slower than for the direct one for pre-
190 weaning weights. On the other hand, heritability estimates of moderate to high magnitude for the direct effect of
191 growth traits indicate the viability of selection and obtaining genetic gains, especially for post-weaning weights.

192 Higher heritability estimates for W365 and W450 indicate that they may have greater genetic gains
193 compared to pre-weaning weights. This result may be associated with greater proportions of additive genetic effect

194 relative to environmental variance. That is, post-weaning traits are less influenced by the environment than pre-
195 weaning traits. Considering that the animals are subjected to the same management conditions, there should be
196 little variation in the environment (Brunes, 2017). The estimates of heritabilities for direct additive effects obtained
197 are within the range presented in the literature for Nellore cattle, whose values range from 0.14 to 0.28 for W120,
198 0.17 to 0.32 for W210, 0.14 to 0.44 for W365, and 0.36 to 0.44 for W450 (Garnero et al., 2010; Araújo et al.,
199 2014; Moreira et al., 2015; Barbosa et al., 2017; Kamei et al., 2017; Lopes et al., 2017). Intensifying selection for
200 yearling weight can influence the adult weight and maintenance requirement of animals (Miranda et al., 2006 and
201 Silva, 2016). To address his problem, selection indexes composed of traits associated with weight and body
202 composition such as carcass and visual scores, leading to precocious animals, are recommended (Brunes, 2017).

203 The high heritability estimates for REA, BFT, and RFT suggest that genes with additive effects have a
204 considerable influence on carcass yield and finish. These results demonstrate that these traits can respond similarly
205 to selection, due to the proportion of phenotypic variance attributed to genetics (Brunes, 2017). The results
206 obtained in this study are in line with other studies that evaluated Nellore cattle, whose values are, in general, from
207 moderate to high magnitude, ranging from 0.30 to 0.66 for REA; 0.17 to 0.74 for BFT and 0.25 to 0.68 for RFT
208 (Faria et al., 2015; Paula et al., 2015; Ceacero et al., 2016; Moraes et al., 2019). The variation in heritability
209 estimates for carcass-related traits can be attributed to several factors such as the number of animals evaluated,
210 effects included in the statistical model, environmental differences, and herd management. In this sense, the results
211 found in this study demonstrate the existing genetic variability for these traits, which can be included as selection
212 criteria to obtain genetic progress in the herd.

213 According to Forni et al. (2007), traits evaluated visually tend to be influenced by environment,
214 consequently, responses of small magnitude to direct selection can be expected, in agreement with the low to
215 moderate magnitude heritabilities estimated in the present study. There are few studies using the MERCOS
216 methodology (Lôbo, 1996). Still, Faria et al. (2009a) using this same evaluation method found estimates similar

217 to those found in this study, whose values were 0.21; 0.27; 0.20, and 0.29 for M, E, R, and C, respectively, in
218 Nellore cattle evaluated at 22 months of age. Using different methodologies to obtain visual scores in Nellore
219 cattle, Paterno et al. (2017a,b) and Silveira et al. (2019) found different results, whose values were 0.33 to 0.40 for
220 E; 0.40 to 0.44 for P and 0.35 to 0.37 for M. These estimates, compared with those found in the present study,
221 show that visual scores can respond to individual selection and promote genetic gains, especially structure scores,
222 racial aspects, and conformation.

223 Muscularity showed a higher genetic association with conformation (0.89), showing that both traits are
224 largely influenced by the same sets of genes. These were expected since animals with better conformation tend to
225 be more precocious and have more developed musculature (Sima, 2015). Similarly, muscularity was shown to be
226 highly correlated with physical structure (0.79), indicating that muscle development and distribution may be highly
227 correlated with animal support. The genetic correlation between these traits is explained by the association of
228 musculature and conformation with animals with a better structure to support the limbs, greater sexual precocity,
229 and finishing. Although Nellore animals commonly present greater size, body length, and short rib length
230 compared to taurine breed, that is, higher classifications for E and lower classifications for C (Sima, 2015), the
231 evaluated herd was submitted to simultaneous genetic selection for both traits. That is, were identified animals
232 with longer ribs, maintaining an adequate structure, changing the body biotype of the animals in response to
233 selection, and the additive (co)variances.

234 Araújo et al. (2010) report that the M, E, and P scores describe the whole animal meat production
235 potential, that is, they are direct components of the animal's body weight, thus the one that is easier to measure,
236 with the highest heritability and less influenced by the evaluator would be recommended as selection criteria. The
237 genetic correlations obtained in the present study between M, E, and C scores corroborate the data found by (Koury
238 Filho et al. (2009), Araújo et al. (2010), Regatieri et al. (2011), Toral et al. (2011), Santana Júnior et al. (2013),

239 Duitama et al. (2015), Paterno et al. (2017a), Silveira et al. (2019), Souza et al. (2020), whose reported values
240 ranged from 0.49 to 0.98, in Nellore animals evaluated under different methodologies.

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

245 The high genetic correlation between structure and conformation can be attributed to the fact that better-
246 conforming animals are those with better physical structures. The high coefficients of genetic correlations between
247 E scores with R, C, and O scores corroborate the results found by Lima et al. (2013) in Nellore cattle, whose
248 estimates were of high magnitude, confirming that the selection of animals with greater structure can lead to direct
249 selection of earlier animals, with better conformation and better breed standard. However, it can result in the
250 selection of animals with pendulous navels, as they are animals of larger body size, so it is recommended that the
251 selection consider both traits as selection criteria and seeking animals with moderate navels.

252 The moderate genetic correlation between E and SAC demonstrates that these traits are also influenced
253 by the same group of genes, and that selection for structure can lead to animals with desirable sacral bone (Faria
254 et al., 2009a). That is, it can lead to obtaining females with greater calving ease, as the flatter the sacrum, the more
255 mobile its joint connections will be, consequently, the female will have greater ease at the time of birth (Roberts,
256 1971; Oliveira, 2008).

257 Considering the genetic correlations obtained between R and O (0.51), animals with better navel
258 placement are those with the best racial pattern, corroborating the high estimates between these scores found by
259 Lima et al. (2013) evaluating Nellore cattle. Accordingly, selection for animals with a better racial pattern may
260 also result in obtaining animals with better conformation and sacrum bone structure, considering the genetic
261 correlation estimates obtained. Considering that it is recommended that animals of the Nellore breed should not

262 have protruding sacral bone, but at the same level as the hips, the selection of animals with a better racial pattern
263 may result in the selection of animals with better rump, supporting the moderate genetic correlations obtained.

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

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

282 In addition, for many combinations of traits or score pairs, genetic correlations have higher estimates than
283 phenotypic ones, which can optimize the selection process and genetic gain, justifying the use of morphological
284 traits as selection criteria. Genetic correlations of moderate to high magnitude between M, E, and growth traits

285 indicate that animals with greater accumulation of muscle mass and well-developed structure to support the body
286 can result in the selection higher body weights animals (Paterno et al., 2017a; Silveira et al., 2019). Heavier
287 animals are generally those with greater muscle mass. In addition, the score for structure indicates the area that the
288 animal covers and the body length, and is, consequently, associated with animals with greater body weight (Abreu,
289 2014). Thus, muscle and physical structure proved to be important traits used as complementary selection criteria
290 along with growth measures (Koury Filho et al., 2009).

291 Faria et al. (2008), Paterno et al. (2017a) and Silveira et al. (2019) reported high magnitude genetic
292 correlations between M and E scores with pre-and post-weaning weights, ranging from 0.58 to 0.88 for M and
293 0.89 to 0.99 for E in Nellore cattle. This information corroborates the results obtained, that cattle with better
294 morphological measures, such as greater muscle mass and a well-developed structure to support the body can
295 result in the selection of animals with greater body weights.

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

304 The low genetic association between racial aspects and performance traits (except for pre-weaning
305 weights) was expected, as the heavier animals are not necessarily those with breed characteristics closer to the
306 ideal standard. The racial pattern in Nellore cattle takes into account criteria like coat, skin pigmentation, and
307 mucous membranes, also, the vulva and anus, teats and perineum, the shape of the head, which have a low

308 connection with body weight. This process helps to identify animals that better fit the breed standard, as these are
309 considered to be more balanced, harmonious, and functional animals (Lôbo, 1996). The results obtained in this
310 study corroborate those presented by Lima et al. (2013), who showed low magnitude genetic correlations between
311 racial pattern and post-weaning weight.

312 Similar results to the present study were found by Taveira et al. (2016) evaluating Nellore cattle, who
313 reported a moderate correlation (0.35) between conformation and yearling weight. On the other hand, superior
314 results were found by Faria et al. (2008), between C and W210, W365 and W450 of 0.89, 0.92 and 0.99,
315 respectively. Araújo et al. (2010) and Souza et al. (2020) reported genetic correlations of 0.52 and 0.66 between
316 C and weaning weight and between C and yearling weight, respectively, in Nellore cattle. Although the estimates
317 of C with W120 and W365 were moderate, W210 and W450 were low, showing that the animal's weight is not
318 always related to its conformation. In this case, the animal may have a lot of muscling but deposited in places that
319 do not lead to an adequate conformation. These results can be attributed to the fact that heavier animals are
320 commonly late-maturing animals, while C is a trait that is linked to precocity. Thus, weight traits that are evaluated
321 in advance, such as W365, can be a better indicator of conformation.

322 The low genetic correlations obtained between navel size and body weights show that animals with better
323 performance are not necessarily those with better navel positioning, since the animal is still in the growth and limb
324 formation phase, mainly for pre-weaning weights. However, for W365 moderate genetic correlations were
325 observed, as the animals already passed a culling criterion at weaning and at 365 days of age, so that animals
326 remaining on the farm had good performance and adequate sheath and navel. Araújo et al. (2012), Campos et al.
327 (2019), Gordo et al. (2012) and Taveira et al. (2016) reported correlations of low magnitudes between navel (O)
328 score and weaning and yearling weights, ranging from 0.08 to 0.22 in Nellore, Brangus, Hereford, and Braford
329 breeds. These results corroborate those obtained in the present study.

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

338 The genetic correlations found between visual scores and carcass traits suggest that selection for SAC
339 will lead to greater and unfavorable changes in REA than in BFT and RFT, than the use of other morphological
340 traits as selection criteria. Thus, REA and SAC should be included as criteria for obtaining more harmonious
341 animals. To best our knowledge, no studies were found evaluating the association between REA and SAC. In this
342 sense, further studies are needed to better understand the relationship between these traits.

343 Genetic correlations similar to those found in the present study were reported by Marques et al. (2013)
344 between E and REA (0.24) in Nellore cattle. In contrast with our results, studies evaluating visual scores such as
345 muscularity, structure, and precocity/conformation with carcass traits in Nellore cattle reported estimates of
346 moderate to high genetic correlations (0.24 to 0.91) (Faria et al., 2009b; Yokoo et al., 2009; Marques et al., 2013).

347 The moderate residual correlation between the muscle score and REA indicates that some environmental
348 conditions simultaneously influence these traits so that environmental improvements that lead to an increase in
349 REA can positively result in the selection of animals with larger muscles. An estimate lower than that of this work
350 (0.16) was reported by Yokoo et al. (2009), between REA and M in Nellore animals.

351 Although the phenotypic correlations between muscle and conformation scores with carcass traits were
352 moderate, M showed a greater phenotypic correlation with REA. Our results were similar to Yokoo et al. (2009),

353 showing that the distribution of muscle mass throughout the animal's body favors a larger area of the *Longissimus*
354 *dorsi* muscle, which is used for measuring REA and thus, a greater yield of meat cuts. In this sense, M and C can
355 be used as phenotypic indicators of animals with higher yields and carcass finishing, which are currently
356 requirements demanded by the consumer market, in addition to being associated with better quality carcasses and
357 slaughterhouse yield. So, the producer can be better paid for the quality of their final product (Yokoo et al., 2009
358 Lima Neto et al., 2009; Vaz et al., 2012; Cancian et al., 2014; Faria et al., 2015; Gordo et al., 2016). On the other
359 hand, the morphological traits of E, R, O, and SAC are poor phenotypic indicators of carcass yield and finishing.

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

369 Another factor that may have influenced these estimates is that only 17% of the animals evaluated in the
370 analyses presented a phenotype for both groups of traits, which could lead to low estimates being obtained. Thus,
371 the performance of visual and ultrasound evaluation of carcass at similar ages and the inclusion of both groups of
372 traits as phenotypic evaluations might influence the estimated variance components and the selection responses.
373 Furthermore, the visual scores, although they are a result of the assessment of the animals as a whole, are subject
374 to variation as a result of the technician performing the assessment. The traits obtained by ultrasound are more

375 objective, but take into account a maximum of three points on the carcass, while the evaluation of visual scores
376 evaluates the animal as a whole, which may account for the low associations obtained (Toral et al., 2011).

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

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

395 Growth, carcass, and morphological composition traits present genetic variability and would respond to
396 direct selection. However, muscularity, structure, racial aspects, and conformation may present a greater response
397 to selection when compared to omphalos (navel) and sacrum bone structure. Selection for visual scores can lead

398 to favorable changes among themselves and in growth traits, especially between M and E with body weights. On
399 the other hand, genetic selection for visual scores can lead to a limited genetic gains in carcass traits. Thus, greater
400 genetic gains can be expected if carcass and morphological traits are included simultaneously as selection criteria,
401 aiming to meet the demands of the consumer market and the industry. Morphological categorical traits can be used
402 as complementary tools that add value to objective selection. However, if the animals are not evaluated with
403 objective measurements and visual scores are used as the only selection criteria, genetic gains in weight,
404 composition, and carcass quality will occur, but more slowly.

405

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417

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425

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428

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430

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