

**Estimação dos parâmetros genéticos de características morfométricas na raça Nelore**

**Estimation of genetic parameters from morphometric measurements in Nelore breed**

**Estimación de parámetros genéticos de características morfométricas en la raza Nelore**

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**RESUMO**

Este estudo teve como objetivo estimar a herdabilidade de características morfométricas e suas correlações fenotípicas e genéticas com características de carcaça de bovinos machos da raça Nelore com o intuito de prever a qualidade da carcaça por um método mais acessível. Informações de peso e medidas morfométricas foram coletadas em cinco idades (335, 391, 448, 504 e 560 dias), e as características da carcaça foram coletadas in vivo aos 560 dias de idade com equipamento de ultrassom de 200 machos da raça Nelore puros. Os animais foram pesados e 11 medidas morfométricas foram coletadas, bem como as características de carcaça área do músculo *longissimus dorsi* (LMA), espessura de gordura na picanha (BF), espessura de gordura na garupa (RF) e cobertura de gordura (FC). As estimativas dos componentes de (co)variância e dos parâmetros genéticos foram obtidas pela metodologia de máxima verossimilhança restrita (REML), utilizando o modelo animal. As estimativas moderadas de herdabilidade ( $h^2$ ) para LMA (0,28) e RF (0,36) indicaram que a seleção para essas características pode trazer bons resultados aumentando a qualidade da carcaça dos animais. As correlações genéticas entre medidas morfométricas e características de carcaça indicaram que o uso dessas características para seleção indireta de carcaça não seria eficiente, sendo mais efetivo a seleção direta, pelo uso das características mensuradas com ultrassonografia. Os resultados demonstraram que o peso pode ser usado para melhorar a LMA dos animais.

**Palavras-chave:** Bovinos de Corte. Carcaça. Componentes de Variância. Correlação Genética. Herdabilidade.

**ABSTRACT**

This study aimed to estimate the heritability of morphometric traits and their phenotypic and genetic correlations with carcass traits of male Nelore beef cattle with the aim of predicting carcass quality using a more accessible method. Information on weight and morphometric measurements was collected at five ages (335, 391, 448, 504, and 560 days), and carcass traits were collected in vivo at 560 days of age with ultrasound equipment from 200 purebred Nelore male animals. The animals were weighed, and 11 morphometric measurements were collected, as well as the carcass traits *longissimus* muscle area (LMA), backfat thickness (BF), rump fat thickness (RF), and fat covering (FC). The estimates of components of (co) variance and genetic parameters were obtained by the restricted maximum likelihood (REML) methodology, using the animal model. Moderate heritability estimates ( $h^2$ ) for LMA (0.28) and RF (0.36) indicated that selection for these traits could bring good results increasing the quality of animal carcasses. Genetic correlations between morphometric measurements

and carcass traits indicated that the use of these traits for indirect carcass selection would not be efficient being more effective, the use of direct selection with characteristics measured by ultrasound. The results showed that weight can be used to improve animals LMA.

**Keywords:** Beef Cattle. Carcass. Variance Components. Genetic Correlation. Heritability.

## RESUMEN

Este estudio tuvo como objetivo estimar la heredabilidad de características morfométricas y sus correlaciones fenotípicas y genéticas con características de la canal en bovinos machos de la raza Nelore, con el fin de predecir la calidad de la canal mediante un método más accesible. Se recolectaron datos de peso y medidas morfométricas en cinco edades (335, 391, 448, 504 y 560 días), y las características de la canal fueron recolectadas in vivo a los 560 días de edad utilizando equipo de ultrasonido en 200 machos de la raza Nelore pura. Los animales fueron pesados y se tomaron 11 medidas morfométricas, así como las características de la canal: área del músculo longissimus dorsi (LMA), espesor de grasa en la picanha (BF), espesor de grasa en la grupa (RF) y cobertura de grasa (FC). Las estimaciones de los componentes de (co)varianza y los parámetros genéticos se obtuvieron mediante la metodología de máxima verosimilitud restringida (REML), utilizando el modelo animal. Las moderadas estimaciones de heredabilidad ( $h^2$ ) para LMA (0,28) y RF (0,36) indicaron que la selección para estas características podría mejorar la calidad de la canal de los animales. Las correlaciones genéticas entre las medidas morfométricas y las características de la canal sugirieron que usar estas medidas para la selección indirecta de la canal no sería eficiente, siendo más efectiva la selección directa basada en las características medidas con ultrasonido. Los resultados mostraron que el peso podría ser utilizado para mejorar el LMA de los animales.

**Palabras clave:** Ganado de Carne. Canal. Componentes de Varianza. Correlación Genética. Heredabilidad.

## 1 INTRODUCTION

Morphological evaluation, which consists of evaluating a set of visual characteristics to identify the body structure of animals for conformation, muscularity, structure, and precocity, among other characteristics, has long been used in selection and genetic improvement programs (Faria et al., 2007; Ferriani et al., 2013; Koury Filho, 2001; 2005; 2010). However, this evaluation can be carried out by different methods and subjectively, which can affect its potential to predict and correlate with other productive traits.

An alternative to evaluate the body structure of animals less subjectively is through the use of morphometric measurements of individuals. Although studies with morphometric measurements are still scarce, the results have indicated that this information can be used to develop statistical models capable of predicting productive and carcass traits, thus making it possible to anticipate the moment of selection, reducing the interval between generations and increasing genetic progress (Cominotti et al., 2020; De Paula et al., 2013; Fernandes et al., 2010; Fonseca et al., 2016; Fonseca et al., 2017; Martins et al., 2020; Wang et al., 2021; Weber et al., 2020).

Using morphometric measurements in the selection process is essential to estimate genetic parameters. Studies with cattle have demonstrated that some morphometric measurements present moderate to high positive correlations with each other, as well as moderate to high heritabilities, especially when taken in animals aged two to three years (Cyrillo et al., 2001; Lima et al., 1989; Yokoo et al., 2007).

Considering the importance of beef cattle and the expressive representation of the Nellore breed in this production chain in Brazil, it is important to conduct studies aiming for better ways (more accurate) of selecting animals with superior genetic quality, thus contributing to the genetic progress of the breed.

In this context, this study aimed to estimate the heritability of morphometric traits measured at different ages and their phenotypic and genetic correlations with carcass traits of male Nellore beef cattle.

## 2 METHODOLOGY

### 2.1 EXPERIMENTAL GROUP

Records on weight and body and carcass morphometric measurements of 200 purebred male Nellore animals at five different ages (335, 391, 448, 504, and 560 days) were collected (Table 1).

Table 1. Estimates of variance components for adjusted weight and morphometric and carcass measurements in male Nellore beef cattle analyzed by a single-trait model.

| Trait                  | $\sigma^2_a$ | $\sigma^2_e$ | $\sigma^2_p$ | $h^2$ |
|------------------------|--------------|--------------|--------------|-------|
| Adjusted weight        | 312.15       | 456.7        | 768.85       | 0.41  |
| Hindlimb height        | 1.32         | 2.04         | 3.36         | 0.39  |
| Forelimb height        | 0.92         | 1.43         | 2.35         | 0.39  |
| Body length            | 0.29         | 0.91         | 1.20         | 0.24  |
| Forelimb width         | 0.57         | 1.45         | 2.02         | 0.28  |
| Thoracic depth         | 0.15         | 0.31         | 0.46         | 0.33  |
| Thoracic perimeter     | 0.18         | 0.29         | 0.47         | 0.38  |
| Rump length            | 0.54         | 1.36         | 1.90         | 0.28  |
| Ischium width          | 1.05         | 3.02         | 4.07         | 0.26  |
| Ilium width            | 1.17         | 3.72         | 4.89         | 0.24  |
| Hind limb width        | 1.18         | 2.12         | 3.30         | 0.36  |
| Scrotal perimeter      | 1.14         | 2.88         | 4.52         | 0.25  |
| LMA (cm <sup>2</sup> ) | 13.12        | 37.3         | 48.96        | 0.27  |
| BF (mm)                | 0.07         | 0.86         | 1.09         | 0.06  |
| RF (mm)                | 0.68         | 1.12         | 1.90         | 0.36  |
| FC (mm)                | 0.09         | 0.94         | 1.02         | 0.09  |

$\sigma^2_a$ : additive genetic variance;  $\sigma^2_e$ : residual variance;  $\sigma^2_p$ : phenotypic variance;  $h^2$ : heritability; LMA: *longissimus* muscle area; BF: backfat thickness; RF: rump fat thickness; FC: fat covering (65% RF + 35% BF).

Source: Authors.

The animals were from two distinct groups, the first one consisting of 100 animals participating in the 68th Pasture performance test promoted by Embrapa Cerrados in partnership with the Association of Zebu Breeders of Goiás (AGCZ), and the second group, was composed of 100 animals, of which 50 individuals came from the 74th Pasture performance test and the other 50 individuals participated in the 75th Pasture performance test, promoted by the Association of Nellore Breeders of Mato Grosso (ACNMT).

## 2.2 COLLECTION OF MORPHOMETRIC MEASUREMENTS

The animals were weighed on an electronic scale, and, subsequently, the morphometric measurements were collected (Table 2). The morphometric evaluation was performed following the methodology adapted from Cyrillo et al. (2012). The standard deviation for mean age in days on the date of collections was  $\pm 22.50$  days and the mean interval between collections was 56.30 days.

In addition to the morphometric evaluations described above, carcass evaluations were also carried out in the fifth evaluation in animals with an average age of

560 days, using ultrasound equipment. The following traits were measured by ultrasonography by a certified company: a) *longissimus* muscle area (LMA) (cm<sup>2</sup>); b) backfat thickness (BF) (mm), measured between the 12th and 13th ribs, the last site of fat deposition; c) rump fat thickness (RF); and d) fat covering (FC) (mm), obtained from the following formula (BF × 0.35 + RF × 0.65).

Animal genealogy data were collected for the relationship matrix, with information up to the third generation of ancestors of the participating animals, totaling 1,337 kinship relationships in a total of 928 individuals in the relationship matrix.

### 2.3 STATISTICAL ANALYSES

Restrictions were applied to the database for the execution of the genetic analyses to guarantee the consistency of the information. Data editing, consistency, and descriptive analysis were performed using the R software, version 4.1.0 (R Core Team, 2021). Phenotypes that were ±3.50 standard deviations from the mean of the respective contemporary group (CG) were excluded from the analyses. Descriptive statistics of the collected data are presented in Table 3.

The data were previously evaluated with mixed models and analysis of variance to identify whether the different performance tests, considered as non-genetic factors, would be influencing the evaluated traits ( $P < 0.05$ ). The CG was constituted by the combination performance test x collection age. Thus, 10 CG were considered for the genetic analysis. Weights were adjusted for 335, 391, 448, 504, and 560 days of age.

Table 2. Additive genetic correlations (top) and phenotypic correlations (bottom) between adjusted weight and morphometric measurements.

|              | Wadj. | HH   | FH   | BL   | FW   | TD   | TP   | RL   | IsW  | IiW  | HW   | SP    |
|--------------|-------|------|------|------|------|------|------|------|------|------|------|-------|
| <b>Wadj.</b> | 1     | 0.15 | 0.13 | 0.18 | 0.16 | 0.26 | 0.28 | 0.28 | 0.23 | 0.24 | 0.11 | 0.34  |
| <b>LMA</b>   | 0.31  | 0.17 | 0.14 | 0.12 | 0.14 | 0.09 | 0.11 | 0.25 | 0.27 | 0.26 | 0.22 | 0.11  |
| <b>BF</b>    | 0.11  | 0.10 | 0.16 | 0.08 | 0.02 | 0.12 | 0.18 | 0.08 | 0.04 | 0.11 | 0.09 | 0.05  |
| <b>RF</b>    | 0.13  | 0.10 | 0.10 | 0.06 | 0.03 | 0.04 | 0.05 | 0.07 | 0.09 | 0.08 | 0.10 | 0.08  |
| <b>FC</b>    | 0.09  | 0.13 | 0.14 | 0.10 | 0.03 | 0.18 | 0.21 | 0.10 | 0.03 | 0.06 | 0.10 | -0.05 |
| <b>Wadj.</b> | 1     | 0.75 | 0.57 | 0.84 | 0.74 | 0.76 | 0.84 | 0.79 | 0.68 | 0.78 | 0.76 | 0.74  |
| <b>LMA</b>   | 0.22  | 0.17 | 0.25 | 0.21 | 0.07 | 0.20 | 0.27 | 0.23 | 0    | 0.24 | 0.22 | 0.10  |

|           |      |      |      |      |       |      |      |      |       |      |      |       |
|-----------|------|------|------|------|-------|------|------|------|-------|------|------|-------|
| <b>BF</b> | 0.11 | 0.10 | 0.16 | 0.08 | 0.02  | 0.12 | 0.18 | 0.08 | 0     | 0.11 | 0.09 | 0.09  |
| <b>RF</b> | 0.20 | 0.15 | 0.21 | 0.13 | -0.06 | 0.16 | 0.22 | 0.15 | -0.09 | 0.21 | 0.15 | -0.03 |
| <b>FC</b> | 0.19 | 0.16 | 0.22 | 0.13 | -0.04 | 0.16 | 0.23 | 0.15 | -0.07 | 0.20 | 0.15 | -0.01 |

Wadj.: adjusted weight; HH: hindlimb height; FH: forelimb height; BL: body length; FW: forelimb width; TD: thoracic depth; TP: thoracic perimeter; RL: rump length; IsW: ischium width; IIW: ilium width; HW: hindlimb width; SP: scrotal perimeter; LMA: *longissimus* muscle area; BF: backfat thickness; RF: rump fat thickness; FC: fat covering (65% RF + 35% BF).

Source: Authors.

## 2.4 ESTIMATION OF (CO) VARIANCE COMPONENTS AND GENETIC PARAMETERS

The estimates of (co) variance components and genetic parameters were obtained by the restricted maximum likelihood (REML) methodology, using the animal model, in which direct additive and residual genetic effects were considered random for all traits, while CG groups were considered as fixed effects, in single-and bi-trait analyses, with the BLUPF90 program (Misztal et al., 2018). The methodology is described in detail in Supplementary Material 1.

Table 3. Additive genetic correlations (top) and phenotypic correlations (bottom) between adjusted weight and carcass traits were collected by ultrasound.

|              | <b>LMA<br/>(cm<sup>2</sup>)</b> | <b>BF<br/>(mm)</b> | <b>RF<br/>(mm)</b> | <b>FC<br/>(mm)</b> |
|--------------|---------------------------------|--------------------|--------------------|--------------------|
| <b>Wadj.</b> | 0.31                            | 0.11               | 0.13               | 0.09               |
| <b>LMA</b>   | 1.00                            | 0.03               | 0.05               | 0.07               |
| <b>BF</b>    | 0.03                            | 1.00               | 0.32               | 0.36               |
| <b>RF</b>    | 0.05                            | 0.32               | 1.00               | 0.34               |
| <b>FC</b>    | 0.07                            | 0.36               | 0.34               | 1.00               |
| <b>Wadj.</b> | 0.22                            | 0.11               | 0.20               | 0.19               |
| <b>LMA</b>   | 1.00                            | 0.27               | 0.47               | 0.46               |
| <b>BF</b>    | 0.27                            | 1.00               | 0.56               | 0.71               |
| <b>RF</b>    | 0.47                            | 0.56               | 1.00               | 0.98               |
| <b>FC</b>    | 0.46                            | 0.71               | 0.98               | 1.00               |

Wadj.: adjusted weight; LMA: *longissimus* muscle area; BF: backfat thickness; RF: rump fat thickness; FC: fat covering (65% RF + 35% BF).

Source: Authors.

## 3 RESULTS AND DISCUSSION

The estimate of variance components of carcass traits were presented in Table 1. The heritability ( $h^2$ ) for the adjusted weight (0.41) and LMA (0.27) is similar to those obtained by Lima Neto (2009) when working with Guzurat

animals.

Matarim (2015) worked with information from 13,256 male and female Nellore animals and found values of  $\sigma^2a$ ,  $\sigma^2e$ ,  $\sigma^2p$ , and  $h^2$  of 13.99, 30.44, 44.43, and 0.31 for LMA, 0.36, 1.39, 1.75, and 0.21 for BF, and 0.67, 1.55, 2.23, and 0.30 for RF, respectively. The estimated values for these parameters in the present study were 13.12, 37.30, 48.96, and 0.27 for LMA, 0.07, 0.86, 1.09, and 0.06 for BF, and 0.68, 1.12, 1.90, and 0.36 for RF, respectively. Except for BF estimates, the others were very similar, even considering the higher number of data, which demonstrates that the amount of information used to estimate these parameters in the present study was not a limitation. The difference in the BF estimates between the studies could be due to the use of males and females and the greater variation of this trait between individuals of different sexes.

The  $h^2$  estimate obtained in the present study for RF (0.36) was similar to that obtained by Yokoo et al. (2008) (0.39) and higher than that obtained by Caetano et al. (2013) (0.23), both for Nellore animals. The estimates obtained for RF indicate that the selection for this trait would be successful, thus allowing the selection of precocious animals since the fat deposition in this region occurs before the deposition of subcutaneous fat in the *Longissimus thoracis* muscle.

The  $h^2$  of body length, forelimb width, rump length, ischium width, ilium width, scrotal perimeter, hindlimb height, forelimb height, thoracic depth, thoracic perimeter, and hindlimb were moderate to high which indicates that selection for these traits based exclusively on phenotypic information can be efficient.

The  $h^2$  value of 0.39 estimated in the present study for the hindlimb height was similar to those obtained by Cirylo et al. (2001) (0.38), Koury Filho et al. (2009) (0.37), and Ferriani et al. (2013) (0.36), and lower than that obtained by Lima et al. (1989) (0.47). This difference occurred because Lima et al. (1989) used animals between 24 and 36 months old, and consequently, they had already reached their total bone development and, therefore, the estimate can capture less non-genetic influence on the variance of the trait.

The  $h^2$  obtained for forelimb height was 0.39 and, therefore, lower than the estimate of 0.54 obtained by Filho et al. (2010) and 0.56 obtained by Magnabosco et al. (2002), the latter using Brahman animals. The estimate of  $h^2$  of 0.24 for



body length in the present study was lower than the estimates of 0.40 obtained by Cirylo et al. (2001) and closer to the value of 0.32 found by Magnabosco et al. (2002) but in a study with Brahman animals.

No other studies that estimated  $h^2$  of forelimb width and thoracic depth were found in the literature, but the values estimated in the present study identified estimates of 0.28 and 0.33, respectively. The thoracic perimeter, after the forelimb height and hindlimb height traits, presented the highest estimate for  $h^2$  (0.38), which was the same estimate observed by Filho et al. (2010), who worked with Nellore animals aged 8 to 16 months.

Rump length had an  $h^2$  estimate of 0.28, similar to the estimate of 0.33 found by Cirylo et al. (2001). The same authors also obtained  $h^2$  estimates of 0.23 and 0.08 for ilium width and ischium width, respectively. In the present study, the  $h^2$  estimates for these traits were 0.24 and 0.26, respectively, that is, very close for ilium width and higher for ischium width.

The  $h^2$  estimate for the trait scrotal perimeter in the present study was 0.25, which is a lower value than those obtained by Lima et al. (1989) and Cirylo et al. (2001), who obtained estimates of 0.57, 0.57, and 0.52, respectively. This variation may have occurred because  $h^2$  was estimated at different ages and the estimation captured higher interference from non-genetic factors in the variances observed in this trait, as the animals are still under body development at this stage of life.

Variations in  $h^2$  found in the present study compared to the various studies mentioned above reinforce that this parameter is characteristic of a given population and may change over time, as a result of selection and management decisions. Additionally, the estimation of this parameter is affected by the population and trait structure, the number of information, and the statistical models used, among other factors.

Table 2 shows the estimates of additive genetic correlations and phenotypic correlations between weight and morphometric measurements. Phenotypic correlations were identified between weight and morphometric measurements, with values higher than 0.70, standing out phenotypic correlations between body length and thoracic perimeter of 0.84 and 0.79

between weight and rump length.

Among the morphometric measurements and carcass traits, the highest correlations were observed between LMA and ischium width, ilium width, rump length, and hindlimb width, with estimated correlations of 0.27, 0.26, 0.25, and 0.22, respectively. The other genetic correlations between morphometric measurements and carcass traits were lower than 0.20. The low correlation between LMA and heights (forelimb and hindlimb) may indicate that larger animals tend to have lower carcass yields. In addition, the results of the genetic correlations between morphometric traits and RF, BF, and FC corroborate the fact that larger animals deposit fat later. In general, morphometric traits are directly associated with growth traits, which partially explains the genetic correlations found between them and LMA and weight.

The genetic correlation between SP and LMA (0.11), indicates that bulls with larger scrotal perimeter contribute at a small proportion to the selection for bigger LMA, while the results of the correlation between SP and BF, RF and FC suggest null influence in the selection of these traits. These considerations are important for the producer to choose and define criteria to be applied in the selection of animals. To select animals with good carcass quality and sexual precocity, producers would have to perform direct selection for these traits.

Carcass traits collected by ultrasound showed genetic correlations (Table 3) for BF with RF and FC of 0.32 and 0.36, respectively, and between RF and FC of 0.34. No other higher genetic correlation was identified between these traits, not even with FC, which is a trait obtained from proportions of BF and RF (35 and 65%, respectively).

LMA and weight showed a genetic correlation of 0.31, indicating moderate genetic correlation between the traits. The genetic correlations of other carcass traits with weight were low. Lima Neto et al. (2009) observed a correlation between weight and LMA of 0.79, while Zuin et al. (2012) found a value of 0.69. The estimates in these studies were higher than those obtained in the present study.

Lima Neto et al. (2009) estimated a genetic correlation of 0.20 for weight and RF, the closest value to that obtained in the present study (0.13). The authors

also stated that the high correlations between weight and carcass traits would allow the use of indirect selection for carcass traits based on selection by weight, but the correlations found in the present study do not make it possible to agree with this statement. Matarim (2015) also identified low correlations between weight and carcass fat measurements, indicating that selection for weight does not promote improvement in carcass quality, except for LMA, which correlated 0.45 with weight, results similar to those obtained in the present study.

According to Marques et al. (2013), these low genetic correlations are justified by the fact that the diet of animals participating in pasture performance tests aims at the production of young bulls and not finishing. Thus, a higher increase for growth traits, such as weight, is expected than fat covering.

The results of this study demonstrate that the direct selection performed for carcass traits does not increase the animal size, with a moderately positive impact only on weight, which is relevant since larger animals have higher maintenance requirements, negatively affecting the resources of the property.

In contrast, the analysis of phenotypic correlations showed higher correlations between carcass traits, with FC presenting correlations of 0.98 and 0.71 with RF and BF, as it originates from these two measurements. LMA showed estimated phenotypic correlations of 0.47 and 0.46 with RF and FC, respectively, but the value with BF was 0.27, and, therefore, irrelevant. Finally, the phenotypic correlation found between RF and BF was 0.56.

#### 4 CONCLUSIONS

The study enables the estimation of previously unestimated genetic parameters for several morphometric traits that can be used in carcass quality prediction models, making selection for these traits faster and more cost-effective. Heritability estimates for LMA and RF indicate that selection for these traits could bring results to selection programs. Heritability estimates for weight, forelimb height, hindlimb height, thoracic perimeter, and hindlimb width showed the highest potential for inclusion in breeding programs among the morphometric measures analyzed in the present study, but the other traits can also be used

together. Genetic correlations between morphometric measurements and carcass traits indicate that indirect selection would not be efficient to obtain animals with better carcasses. Moreover, the weight could be used to improve the *longissimus* muscle area in animals. Considering that the number of animals used was small, studies conducted on larger populations could confirm the results found.

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