



# Genetic study of scores for limb conformation, breed traits, sexual traits, eye pigmentation, and navel size in Hereford and Braford cattle

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**ABSTRACT** - Data from 83,088 Hereford and Braford cattle were used to compare parameters and breeding values obtained using linear and threshold models for visual scores of limb conformation (LCW and LCY), breed traits (BTW and BTY), sexual traits (STW and STY), eye pigmentation (EPW and EPY), and navel size (NSW and NSY) at weaning and yearling, respectively. Additionally, principal component analysis was applied to investigate the relationship among the estimated breeding values. Higher direct heritability were estimated using the threshold model (ranging from 0.134±0.021 to 0.194±0.023) compared with the linear model (ranging from 0.085±0.008 to 0.120±0.009). Rank correlations between breeding values predicted using linear and threshold models ranged from 0.61 to 0.88 (LCW), 0.53 to 0.91 (BTW), 0.66 to 0.87 (STW), 0.80 to 0.96 (EPW), 0.87 to 0.95 (NSW), 0.70 to 0.92 (LCY), 0.49 to 0.93 (BTY), 0.56 to 0.95 (STY), 0.88 to 0.97 (EPY), and 0.80 to 0.95 (NSY). The low genetic variability of the studied traits suggests a small genetic gain in the morphology and adaptation. According to the results obtained in the rank correlation, the percentage of coincident animals and the cross-validation analyses, it is recommended to use the threshold model for limb conformation, breed, and sexual traits. For eye pigmentation and navel size scores, both models can be used. In practical terms, the producer will be able to carry out his own selection, considering other traits that are not currently incorporated in the selection indexes, but that can lead to simultaneous gains in the morphology and adaptation of Hereford and Braford cattle.

**Keywords:** heritability, linear model, morphological traits, principal components, rank correlation, threshold model

## 1. Introduction

The adaptation of animals to a given environment is associated with morphological and functional changes. Thus, selection of Hereford and Braford cattle morphologically adapted to tropical conditions is a way to improve the herd productivity, given the expansion of their use in these environments.

Visual scores have been evaluated in some breeding programs and used to obtain morphologically desirable animals, well adapted to the conditions under which they will be kept. Limb conformation trait is related to the ease of locomotion and comfort, since deficient limbs can compromise not only the pursuit for food and water, but also the mating (Rosa et al., 2003). Breed trait score has been evaluated in beef cattle aiming at identifying the animals that best fit the breed profile, as well as indicating the absence of defects and conferring prepotency. On the other hand, sexual trait score is used in

the selection to identify males with masculine attributes and females with feminine attributes, with particular attention given to the functionality of external genitalia (Cardoso and Lopa, 2017).

In Hereford and Braford breeds, eye pigmentation is relevant due to the predisposition of these animals to ocular carcinoma, besides being a mandatory attribute for the breed standard and registration of Braford cattle. Thus, the selection of animals with higher eye pigmentation is an important tool to decrease ocular carcinoma, allowing a better adaptation to regions of high solar irradiation (Cardoso and Lopa, 2017).

The size and positioning of the navel are used in the identification of more functional animals, especially when kept in extensive production systems. In general, cattle with very long or pendulous navel and foreskin are more susceptible to trauma and injury due to the heterogeneous composition of the pastures, which can lead to reproductive problems, especially in natural mating (Bolognoni et al., 2016).

One relevant aspect of traits related to morphology and functionality in beef cattle is the fact that they are visually obtained, thereby presenting a discrete distribution. While linear models offer ease of application and shorter processing time compared with threshold models (Faria et al., 2008), they may be inadequate for quantifying the discrete nature of categorical data that does not follow a normal distribution. However, comparing the results obtained in analyses using linear and threshold models can help determine the more appropriate model for genetic evaluations of traits measured by scores.

The objective of this research was to compare genetic parameters and breeding values, obtained using linear and threshold animal models, for scores of limb conformation, breed traits, sexual traits, eye pigmentation, and navel size in Hereford and Braford breeds. Additionally, principal component analysis was applied to investigate the relationship among the estimated breeding values (EBV).

## 2. Material and Methods

### 2.1. Animals and traits evaluated

Phenotypic information of 83,088 animals (27,485 of Hereford and 55,603 of Braford), born between 2007 and 2017, belonging to the database of the genetic evaluation program of the Hereford and Braford breeds (PampaPlus) were used. Visual scores of limb conformation, breed traits, sexual traits, eye pigmentation, and navel size obtained at weaning (LCW, BTW, STW, EPW, and NSW, respectively) and at yearling (LCY, BTY, STY, EPY and NSY, respectively) were studied.

Hereford animals are known for their red coats, with the head, extremities, and underbelly being white. The Braford breed originated from the crossbreeding of Hereford and Zebu animals, with a composition of 5/8 Hereford and 3/8 Zebu. It is also permissible to classify animals resulting from intermediate crossings within this breed, which can have compositions of 1/2, 1/4, 3/4, 3/8, or 5/8 Zebu.

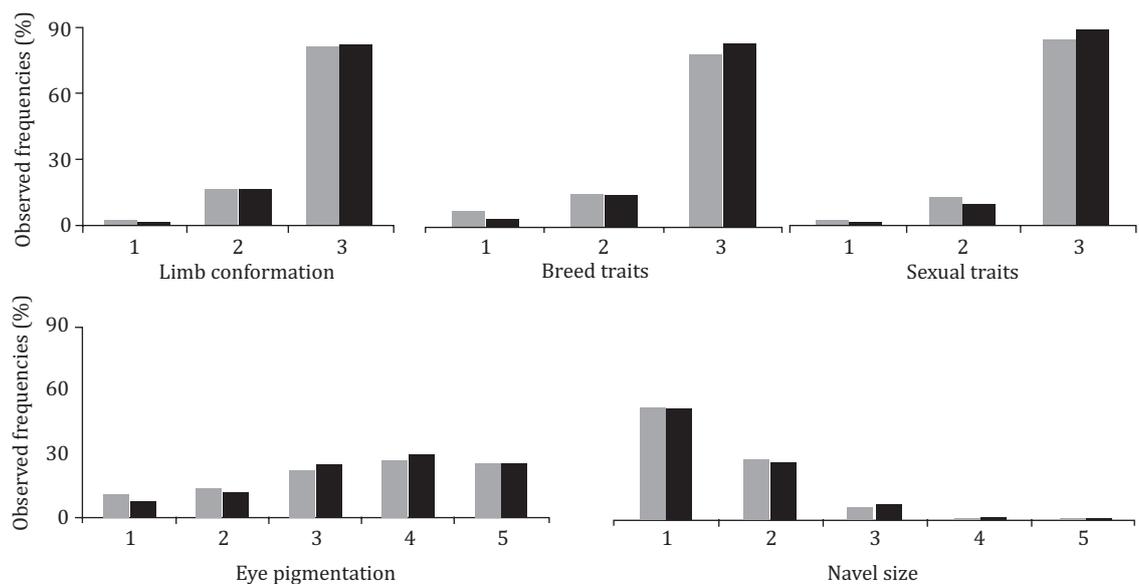
In the studied herds, the animals were raised extensively, with various types of diets, including natural pasture, improved natural pasture, natural pasture with supplementation, grazing, grazing with supplementation, and confinement. Reproductive management was carried out through both controlled natural breeding and artificial insemination. The animals underwent phenotypic evaluation at two stages: weaning and yearling. These evaluations were performed by a certified technician who was qualified and accredited by the breeding program.

Visual assignments are performed through a scale determined by pre-established standards and defined by a technical board. Thus, the scores vary from 1 to 3 or from 1 to 5, depending on the trait (Figure 1). For LCW and LCY, the animals are evaluated in the frontal, lateral, and posterior positions and, in general, the more vertical form the better. For these visual scores, grades could be 1 (bad), 2 (acceptable), and 3 (ideal). For BTW and BTY, the animals are evaluated according to the standard of each breed, defined by the Associação Brasileira de Hereford e Braford (ABHB, 2017), with scores of 1 (animals outside the breed standard), 2 (admissible animals), and 3 (animals within the breed standards). For STW and STY, sexual and secondary attributes are evaluated. In males, it is important to exhibit a masculine head, a robust neck, well-developed muscles, and testicles of suitable size for

their breeding and age. Females, on the other hand, should possess a refined head, a slender and clean neck, an angular body shape, and a gentle front end combined with a strong hind end, indicating a favorable pelvic opening. For this score, values of 1 (disabled animals), 2 (acceptable condition), and 3 (ideal) are assigned.

The measurement of EPW and EPY is based on a reference for each breed. For Hereford cattle, the percentage of pigmentation in the upper and lower eyelids of each eye is observed separately. The following scores were considered: 1 (absence of pigmentation), 2 (one eye partially pigmented), 3 (one eye fully pigmented), 4 (both eyes partially pigmented), and 5 (both eyes fully pigmented). On the other hand, for Braford cattle, pigmentation around the entire mucosa in both eyes is required. The amount of red pigmentation around the eyes is observed, and the following scores were considered: 1 (absence of pigmentation), 2 (one or both eyes partially pigmented), 3 (all mucosa around the eyes pigmented), 4 (presence of glasses, indicating good pigmentation around both eyes), and 5 (masked or covered glasses).

For NSW and NSY, evaluations are made based on a reference for size and position (navel, sheath, and foreskin) for each breed. The animals should have a healthy-looking navel, with an angle of less than 45 degrees, the preputial ostium facing forward, no excess folds, or too pendulous, and no preputial prolapse. The assigned values for this score are 1 (very small navels, almost glued to the belly), 2 (small), 3 (medium), 4 (large and acceptable), and 5 (very large and unacceptable).



**Figure 1** - Distribution of visual scores for limb conformation, breed traits, sexual traits, eye pigmentation, and navel size at weaning (■) and yearling (■) in Hereford and Braford cattle.

## 2.2. Contemporary groups

Contemporary groups (CG) were formed by herd and year of birth, sex, animal and dam breed composition (zebu percentage of 3/8z, 1/4z or 1/2z), nutritional management, and date of measurement. Once formed, the CG was subdivided until the range of animals' age within each group was 90 days or less.

For all traits, the CG were formed by at least three animals, and CG formed only by animals with the same score (i.e., groups without variability) were eliminated. The pedigree file used to assemble the relationship matrix contained identification of the animal, sire, and dam, totalizing 149,542 animals. The information used in the analyses, after edition, is presented in Table 1.

**Table 1** - Descriptive statistics of visual scores at weaning and yearling measured in the Hereford and Braford cattle

| Trait             | Number of animals | Median | Number of sires | Number of dams | Number of contemporary groups | Means±SD age at measurement (days) | Means±SD cow age at calving (years) |
|-------------------|-------------------|--------|-----------------|----------------|-------------------------------|------------------------------------|-------------------------------------|
| Limb conformation |                   |        |                 |                |                               |                                    |                                     |
| Weaning           | 82,433            | 3      | 7,509           | 39,758         | 3,317                         | 193.82±39.28                       | 8.73±5.03                           |
| Yearling          | 42,015            | 3      | 4,004           | 25,753         | 2,642                         | 535.58±51.33                       | 9.73±4.86                           |
| Breed traits      |                   |        |                 |                |                               |                                    |                                     |
| Weaning           | 83,088            | 3      | 7,546           | 40,031         | 3,365                         | 193.86±39.29                       | 8.72±5.03                           |
| Yearling          | 42,063            | 3      | 4,006           | 25,769         | 2,649                         | 535.58±51.31                       | 9.72±4.86                           |
| Sexual traits     |                   |        |                 |                |                               |                                    |                                     |
| Weaning           | 82,405            | 3      | 7,505           | 39,746         | 3,318                         | 193.82±39.29                       | 8.73±5.03                           |
| Yearling          | 42,062            | 3      | 4,006           | 25,770         | 2,649                         | 535.59±51.31                       | 9.72±4.86                           |
| Eye pigmentation  |                   |        |                 |                |                               |                                    |                                     |
| Weaning           | 75,308            | 4      | 6,504           | 36,452         | 3,104                         | 193.11±39.76                       | 8.75±5.02                           |
| Yearling          | 37,649            | 4      | 3,454           | 23,390         | 2,473                         | 534.88±50.60                       | 9.78±4.87                           |
| Navel size        |                   |        |                 |                |                               |                                    |                                     |
| Weaning           | 75,221            | 1      | 7,370           | 36,040         | 2,995                         | 192.24±39.38                       | 8.71±5.02                           |
| Yearling          | 37,840            | 1      | 3,841           | 23,506         | 2,649                         | 535.59±51.31                       | 9.72±4.86                           |

SD - standard deviation.

### 2.3. Genetic analyses

Visual scores were analyzed using linear and threshold animal models, and the results were compared. In the threshold model, it is assumed that the traits have a continuous normally distributed underlying scale, limited by thresholds that divide it into scores.

To obtain (co)variances components and genetic parameters, single-trait analyzes were performed by Bayesian method, with GIBBSF90 and THRGIBBS1F90 programs (Misztal et al., 2014). The systematic effects of CG and the covariates of animal age at measurement and dam age at calving (linear and quadratic effects) were considered. Direct additive genetic, maternal genetic, and maternal permanent environmental effects were included as random. Maternal effects were included only for the traits measured at weaning.

The general model used in the analyses can be represented as:

$$y = X\beta + Z_1a + Z_2m + Wc + e,$$

in which  $y$  is the vector of observations;  $\beta$  is the vector of systematic effects;  $a$  is the vector of random direct additive genetic effects;  $m$  is the vector of random maternal genetic effects;  $c$  is the vector of random maternal permanent environmental effects;  $e$  is the vector of random residual effect; and  $X$ ,  $Z_1$ ,  $Z_2$ , and  $W$  are the incidence matrices for systematic, direct additive genetic, maternal genetic, and maternal permanent environmental effects, respectively.

The models assumptions were:

$$E(y) = X\beta$$

$$\begin{bmatrix} a \\ m \\ c \\ e \end{bmatrix} \sim N \left( \begin{bmatrix} 0 \\ 0 \\ 0 \\ 0 \end{bmatrix}, \begin{bmatrix} A\sigma_a^2 & A\sigma_{am} & 0 & 0 \\ A\sigma_{am} & A\sigma_m^2 & 0 & 0 \\ 0 & 0 & I_p\sigma_c^2 & 0 \\ 0 & 0 & 0 & I_n\sigma_e^2 \end{bmatrix} \right)$$

in which  $\sigma_a^2$  is the direct additive genetic variance,  $\sigma_m^2$  is the maternal additive genetic variance,  $\sigma_{am}$  is the covariance between direct and maternal genetic additive effects,  $\sigma_c^2$  is the maternal permanent

environment variance,  $\sigma_e^2$  is the residual variance,  $A$  is the relationship matrix of the animals,  $I$  is the identity matrix,  $p$  is the number of dams of animals with measures, and  $n$  is the number of animals with measures.

Visual scores assigned from 1 to 5 were analyzed using the following threshold model:

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

in which for each trait  $i$  ( $i = 1, 2, 3, 4$  or  $5$ ),  $w_{ij}$  and  $l_{ij}$  are categorical variables and underlying scale of observation  $j$ , respectively;  $t_1$  to  $t_4$  are the thresholds that define the categorical response for each trait; and  $n_i$  represents the total number of data for each trait studied. Uniform initial distribution for the thresholds was defined. For scores ranging from 1 to 3, the model is similar, but considering only two thresholds.

The prior distribution of systematic effects was considered uniform. For the variance matrices of residual random effects, an inverted chi-squared distribution was considered. The analyses consisted of chains with 800,000 cycles, with a conservative burn-in period of 200,000 cycles and a thinning interval of 50 cycles, totaling 12,000 samples to obtain the subsequent (co)variance distributions. To confirm the convergence of parameters estimated, graphical inspections and statistical tests of Heidelberger and Welch (Heidelberger and Welch, 1983) were performed using the Coda package (Plummer et al., 2006) from the R program (R Core Team, 2015).

#### 2.4. Rank correlations of breeding values

Breeding values for visual scores were used to calculate the rank correlations (Spearman) between the predictions obtained using linear and threshold models, for 50, 20, 10, and 2% of the best animals with phenotypic measurements, sires with progeny having phenotypic measurements, and sires with progeny having phenotypic measurements and accuracy above 0.40. These animals were selected based on breeding values predicted using the linear model.

#### 2.5. Cross-validation of linear and threshold models

Cross-validation of the models was carried out using R software (R Core Team, 2019). For this purpose, five groups of animals with phenotypic information for each trait were randomly selected as clusters. In each analysis, one group of data was excluded, while the remaining four groups were used as the reference population to EBV for animals with missing data (validation set). As a result, all animals had their EBV predicted at some point without using their own phenotypic information. The cross-validation analyses were conducted following the method described by McHugh et al. (2014).

#### 2.6. Principal component analyses

Breeding values predicted for visual scores of LCW, BTW, STW, EPW, NSW, LCY, BTY, STY, EPY, and NSY were standardized and used in principal component analysis. The principal components are linear combinations of the original variables and, in this study, they were obtained from eigenvalues of the covariance matrix. The principal component eigenvalue is associated with the variance of all the traits included. Therefore, each eigenvalue is associated with a unit vector, called an eigenvector. The eigenvectors represent the strength and direction of the variance of each trait within the principal component.

In this study, it was assumed that the principal components that explain most of the original genetic variations were those with eigenvalues above 1, as suggested by the Kaiser test (Kaiser, 1958). The analysis was performed using the R software (R Core Team, 2015).

### 3. Results

Visual scores obtained at weaning and yearling did not show a phenotypic normal distribution in this study (Figure 1). For LCW, BTW, STW, LCY, BTY, and STY, the largest proportion of animals received score 3 and few received score 1. On the other hand, for EPW and EPY, the most frequent scores were 3, 4, and 5. In the visual assessment of NSW and NSY, the least frequent scores observed were 3, 4, and 5.

For all evaluated scores, higher values of direct and maternal heritability were estimated with threshold compared with linear models (Table 2). Low direct heritability values were estimated for LCW and LCY using linear ( $0.086 \pm 0.010$  and  $0.042 \pm 0.008$ , respectively) and threshold models ( $0.134 \pm 0.021$  and  $0.084 \pm 0.019$ , respectively). Direct heritability values estimated for BTW and BTY were of  $0.111 \pm 0.012$  and  $0.038 \pm 0.008$ , respectively (using linear model), and  $0.194 \pm 0.023$  and  $0.099 \pm 0.002$ , respectively (using threshold model). Similarly, higher direct heritability was obtained for STW rather than STY, for the linear model ( $0.089 \pm 0.011$  and  $0.011 \pm 0.005$ , respectively) and for the threshold model ( $0.141 \pm 0.025$  and  $0.039 \pm 0.015$ , respectively). On the other hand, lower direct heritability was estimated for EPW and NSW compared with EPY and NSY, using one model or another. Using both models, null maternal heritability were obtained for all weaning visual scores studied.

Rank correlations obtained between breeding values predicted with linear and threshold models for visual scores (Table 3) indicate that different animals would be selected for LCW, LCY, BTW, BTY, STW, and STY, especially when greater selection intensity is applied. These scores showed a lower

**Table 2** - Means ( $\pm$  standard deviations) of variances components and heritability and highest posterior density of heritability estimated using linear and threshold models for visual scores measured at weaning and yearling in Hereford and Braford cattle

|   | Linear model             |                          |                          |                          |                          | Threshold model          |                          |                          |                          |                          |
|---|--------------------------|--------------------------|--------------------------|--------------------------|--------------------------|--------------------------|--------------------------|--------------------------|--------------------------|--------------------------|
|   | LC                       | BT                       | ST                       | EP                       | NS                       | LC                       | BT                       | ST                       | EP                       | NS                       |
| Weaning visual score                      |                          |                          |                          |                          |                          |                          |                          |                          |                          |                          |
| Direct additive genetic variance          | 0.013<br>( $\pm 0.001$ ) | 0.031<br>( $\pm 0.003$ ) | 0.012<br>( $\pm 0.001$ ) | 0.138<br>( $\pm 0.013$ ) | 0.025<br>( $\pm 0.002$ ) | 0.075<br>( $\pm 0.011$ ) | 0.340<br>( $\pm 0.038$ ) | 0.092<br>( $\pm 0.015$ ) | 0.407<br>( $\pm 0.053$ ) | 0.068<br>( $\pm 0.008$ ) |
| Maternal genetic variance                 | 0.002<br>( $\pm 0.001$ ) | 0.005<br>( $\pm 0.002$ ) | 0.002<br>( $\pm 0.001$ ) | 0.008<br>( $\pm 0.005$ ) | 0.002<br>( $\pm 0.001$ ) | 0.014<br>( $\pm 0.008$ ) | 0.087<br>( $\pm 0.032$ ) | 0.033<br>( $\pm 0.013$ ) | 0.028<br>( $\pm 0.014$ ) | 0.009<br>( $\pm 0.004$ ) |
| Maternal permanent environmental variance | 0.006<br>( $\pm 0.001$ ) | 0.003<br>( $\pm 0.002$ ) | 0.003<br>( $\pm 0.001$ ) | 0.008<br>( $\pm 0.005$ ) | 0.009<br>( $\pm 0.002$ ) | 0.031<br>( $\pm 0.008$ ) | 0.058<br>( $\pm 0.021$ ) | 0.032<br>( $\pm 0.009$ ) | 0.030<br>( $\pm 0.018$ ) | 0.009<br>( $\pm 0.005$ ) |
| Residual variance                         | 0.135<br>( $\pm 0.001$ ) | 0.245<br>( $\pm 0.002$ ) | 0.127<br>( $\pm 0.001$ ) | 0.825<br>( $\pm 0.009$ ) | 0.256<br>( $\pm 0.002$ ) | 0.458<br>( $\pm 0.011$ ) | 1.423<br>( $\pm 0.035$ ) | 0.579<br>( $\pm 0.015$ ) | 1.835<br>( $\pm 0.167$ ) | 0.355<br>( $\pm 0.007$ ) |
| Direct heritability                       | 0.086<br>( $\pm 0.010$ ) | 0.111<br>( $\pm 0.012$ ) | 0.089<br>( $\pm 0.011$ ) | 0.120<br>( $\pm 0.009$ ) | 0.085<br>( $\pm 0.008$ ) | 0.134<br>( $\pm 0.021$ ) | 0.194<br>( $\pm 0.023$ ) | 0.141<br>( $\pm 0.025$ ) | 0.171<br>( $\pm 0.017$ ) | 0.150<br>( $\pm 0.017$ ) |
| Highest posterior density (95%)           | 0.086 to 0.087           | 0.111 to 0.112           | 0.089 to 0.090           | 0.120 to 0.121           | 0.085 to 0.086           | 0.134 to 0.135           | 0.194 to 0.195           | 0.141 to 0.142           | 0.171 to 0.172           | 0.150 to 0.151           |
| Maternal heritability                     | 0.001<br>( $\pm 0.001$ ) | 0.018<br>( $\pm 0.009$ ) | 0.017<br>( $\pm 0.008$ ) | 0.007<br>( $\pm 0.004$ ) | 0.009<br>( $\pm 0.003$ ) | 0.025<br>( $\pm 0.015$ ) | 0.050<br>(0.019)         | 0.051<br>( $\pm 0.021$ ) | 0.012<br>( $\pm 0.007$ ) | 0.020<br>( $\pm 0.009$ ) |
| Highest posterior density (95%)           | 0.001 to 0.002           | 0.018 to 0.019           | 0.017 to 0.018           | 0.007 to 0.008           | 0.009 to 0.010           | 0.025 to 0.026           | 0.050 to 0.051           | 0.051 to 0.052           | 0.012 to 0.013           | 0.020 to 0.021           |
| Yearling visual score                     |                          |                          |                          |                          |                          |                          |                          |                          |                          |                          |
| Direct additive genetic variance          | 0.005<br>( $\pm 0.001$ ) | 0.007<br>( $\pm 0.001$ ) | 0.001<br>( $\pm 0.001$ ) | 0.163<br>( $\pm 0.015$ ) | 0.029<br>( $\pm 0.003$ ) | 0.039<br>( $\pm 0.009$ ) | 0.110<br>( $\pm 0.023$ ) | 0.027<br>( $\pm 0.010$ ) | 0.584<br>( $\pm 0.106$ ) | 0.097<br>( $\pm 0.011$ ) |
| Residual variance                         | 0.124<br>( $\pm 0.001$ ) | 0.172<br>( $\pm 0.002$ ) | 0.094<br>( $\pm 0.001$ ) | 0.738<br>( $\pm 0.012$ ) | 0.264<br>( $\pm 0.003$ ) | 0.431<br>( $\pm 0.013$ ) | 0.998<br>(0.032)         | 0.669<br>( $\pm 0.023$ ) | 2.402<br>( $\pm 0.381$ ) | 0.398<br>( $\pm 0.011$ ) |
| Direct heritability                       | 0.042<br>( $\pm 0.008$ ) | 0.038<br>( $\pm 0.008$ ) | 0.011<br>( $\pm 0.005$ ) | 0.181<br>( $\pm 0.015$ ) | 0.101<br>( $\pm 0.010$ ) | 0.084<br>( $\pm 0.019$ ) | 0.099<br>( $\pm 0.002$ ) | 0.039<br>( $\pm 0.015$ ) | 0.195<br>( $\pm 0.018$ ) | 0.196<br>( $\pm 0.021$ ) |
| Highest posterior density (95%)           | 0.042 to 0.043           | 0.038 to 0.039           | 0.011 to 0.012           | 0.181 to 0.182           | 0.100 to 0.101           | 0.084 to 0.085           | 0.099 to 0.100           | 0.039 to 0.040           | 0.195 to 0.196           | 0.196 to 0.197           |

LC - limb conformation; BT - breed traits; ST - sexual traits; EP - eye pigmentation; NS - navel size.

percentage of animals coinciding with the use of these two different models. However, for EPW, EPY, NSW, and NSY, few changes would occur in the rank, as the correlations and the percentage of coincident animals showed high values.

Considering sires which are parents of animals with phenotypic measures and sires that were parents of animals with phenotypic measures and with accuracy above 0.40, the ranking differences found with the use of the evaluated models (linear and threshold) were more evident for LCW, LCY, BTW, BTY, and STW, which are obtained with scores varying between 1 and 3 (Table 3). These scores showed a lower percentage of coincident animals and lower correlation values, in accordance with the selection intensity applied. This indicates that the choice of model would cause changes in the classification of sires. On the other hand, few changes are expected in the classification of sires for STY, EPW, EPY, NSW, and NSY traits (Table 3).

**Table 3** - Spearman correlations (and respective percentage of coincident animals) of predicted breeding values for visual scores using linear and threshold models, considering different proportions of animals selected in Hereford and Braford cattle

| Proportion of selected | Weaning score   |               |               |               |               | Yearling score |               |                |               |               |
|------------------------|---|---------------|---------------|---------------|---------------|----------------|---------------|----------------|---------------|---------------|
|                        | LC  | BT            | ST            | EP            | NS            | LC             | BT            | ST             | EP            | NS            |
|                        | Animals with phenotypic measures  |               |               |               |               |                |               |                |               |               |
| 50%                    | 0.81<br>(90%)   | 0.84<br>(92%) | 0.79<br>(90%) | 0.96<br>(96%) | 0.93<br>(92%) | 0.90<br>(93%)  | 0.90<br>(94%) | 0.91<br>(92%)  | 0.97<br>(96%) | 0.94<br>(91%) |
| 20%                    | 0.67<br>(76%)   | 0.79<br>(81%) | 0.70<br>(76%) | 0.90<br>(91%) | 0.91<br>(91%) | 0.74<br>(86%)  | 0.74<br>(86%) | 0.82<br>(87%)  | 0.91<br>(92%) | 0.88<br>(89%) |
| 10%                    | 0.61<br>(68%)   | 0.74<br>(78%) | 0.69<br>(68%) | 0.87<br>(87%) | 0.90<br>(88%) | 0.84<br>(75%)  | 0.65<br>(78%) | 0.84<br>(76%)  | 0.88<br>(89%) | 0.85<br>(86%) |
| 2%                     | 0.73<br>(48%)   | 0.53<br>(63%) | 0.66<br>(57%) | 0.80<br>(82%) | 0.91<br>(90%) | 0.83<br>(79%)  | 0.50<br>(64%) | 0.56<br>(80%)  | 0.91<br>(88%) | 0.80<br>(80%) |
|                        | Sires, parents of animals with phenotypic measures                              |               |               |               |               |                |               |                |               |               |
| 50%                    | 0.88<br>(86%)   | 0.91<br>(93%) | 0.87<br>(86%) | 0.95<br>(96%) | 0.88<br>(80%) | 0.92<br>(84%)  | 0.93<br>(89%) | 0.88<br>(80%)  | 0.97<br>(96%) | 0.82<br>(77%) |
| 20%                    | 0.87<br>(85%)   | 0.88<br>(91%) | 0.85<br>(88%) | 0.93<br>(92%) | 0.93<br>(93%) | 0.91<br>(91%)  | 0.92<br>(90%) | 0.91<br>(90%)  | 0.94<br>(93%) | 0.92<br>(96%) |
| 10%                    | 0.79<br>(88%)   | 0.82<br>(88%) | 0.82<br>(85%) | 0.93<br>(91%) | 0.91<br>(90%) | 0.85<br>(88%)  | 0.87<br>(90%) | 0.86<br>(89%)  | 0.91<br>(92%) | 0.91<br>(88%) |
| 2%                     | 0.67<br>(72%)   | 0.74<br>(71%) | 0.76<br>(76%) | 0.82<br>(83%) | 0.89<br>(85%) | 0.83<br>(76%)  | 0.66<br>(75%) | 0.79<br>(86%)  | 0.91<br>(82%) | 0.89<br>(86%) |
|                        | Sires, parents of animals with phenotypic measures and with accuracy above 0.40 |               |               |               |               |                |               |                |               |               |
| 50%                    | 0.80<br>(90%)   | 0.84<br>(93%) | 0.84<br>(89%) | 0.96<br>(95%) | 0.93<br>(92%) | 0.87<br>(95%)  | 0.90<br>(95%) | 0.83<br>(89%)  | 0.97<br>(96%) | 0.95<br>(94%) |
| 20%                    | 0.66<br>(79%)   | 0.77<br>(81%) | 0.81<br>(78%) | 0.91<br>(91%) | 0.88<br>(90%) | 0.80<br>(85%)  | 0.71<br>(83%) | 0.87<br>(87%)  | 0.91<br>(94%) | 0.91<br>(87%) |
| 10%                    | 0.68<br>(67%)   | 0.69<br>(76%) | 0.75<br>(75%) | 0.83<br>(88%) | 0.87<br>(86%) | 0.78<br>(79%)  | 0.68<br>(75%) | 0.95<br>(82%)  | 0.88<br>(88%) | 0.90<br>(89%) |
| 2%                     | 0.65<br>(52%)   | 0.58<br>(71%) | 0.68<br>(72%) | 0.90<br>(82%) | 0.95<br>(87%) | 0.70<br>(70%)  | 0.49<br>(73%) | 0.80<br>(100%) | 0.93<br>(92%) | 0.83<br>(87%) |

LC - limb conformation; BT - breed traits; ST - sexual traits; EP - eye pigmentation; NS - navel size.

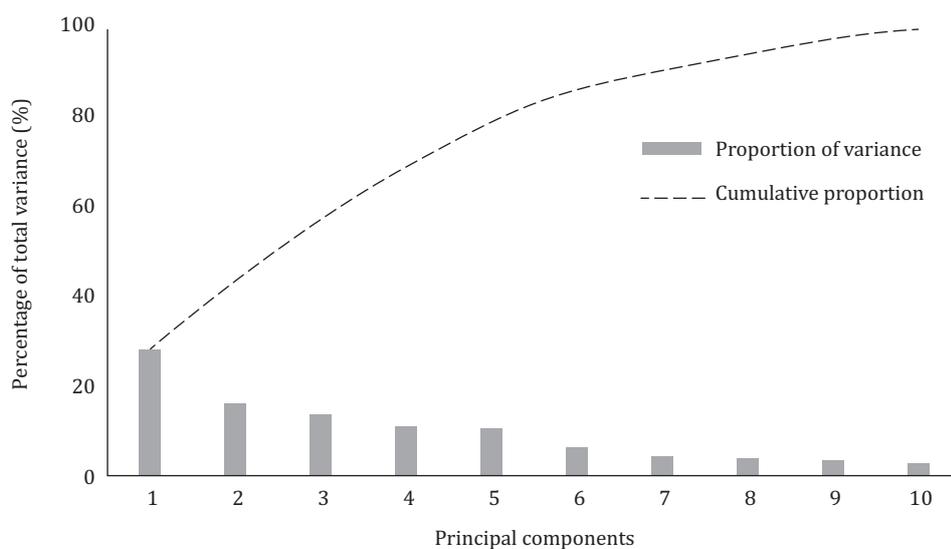
Similarly, the cross-validation showed that the criteria used to compare the goodness of fit of the models indicated that the threshold model best fits the data for limb conformation, breed traits, and sexual traits. There was only a small difference among these criteria for eye pigmentation and navel size, suggesting that the genetic evaluation of these traits could be performed with both linear and threshold models (Table 4).

**Table 4** - Cross-validation with random animals including regression coefficients ( $\beta$ ) on the logit scale (log of the odds) of phenotypic performance (scores) on the breeding values for each trait in relation to the reference score, pseudo McFadden determination coefficient ( $R^2$ ), and Akaike's criterion (AIC) for each model

| Trait | Score | Linear model |        |            | Threshold model |        |            |
|-------|-------|--------------|--------|------------|-----------------|--------|------------|
|       |       | $\beta$      | $R^2$  | AIC        | $\beta$         | $R^2$  | AIC        |
| LCW   | 1     | 37.8500      | 0.6414 | 13183.1981 | 36.7433         | 0.7243 | 11285.4322 |
|       | 2     | 95.3766      |        |            | 94.0984         |        |            |
| LCY   | 1     | 80.8786      | 0.5986 | 6628.6482  | 54.1883         | 0.6522 | 6151.7508  |
|       | 2     | 171.6434     |        |            | 116.8844        |        |            |
| BTW   | 1     | 25.0839      | 0.5629 | 17183.9675 | 22.4090         | 0.6567 | 14565.5300 |
|       | 2     | 58.6915      |        |            | 57.6876         |        |            |
| BTY   | 1     | 44.7137      | 0.4879 | 8171.4525  | 25.8461         | 0.5699 | 7354.5209  |
|       | 2     | 119.6410     |        |            | 73.8047         |        |            |
| STW   | 1     | 46.9900      | 0.6556 | 12267.4521 | 41.3299         | 0.7056 | 11208.0771 |
|       | 2     | 104.5344     |        |            | 94.2097         |        |            |
| STY   | 1     | 120.2734     | 0.5600 | 6443.2820  | 68.3476         | 0.6435 | 5803.4583  |
|       | 2     | 318.6265     |        |            | 176.8270        |        |            |
| EPW   | 1     | 13.8785      | 0.5374 | 42702.1062 | 13.7692         | 0.5382 | 42684.3839 |
|       | 2     | 25.3333      |        |            | 25.0685         |        |            |
|       | 3     | 37.3390      |        |            | 37.2126         |        |            |
|       | 4     | 49.5344      |        |            | 49.4444         |        |            |
| EPY   | 1     | 6.3018       | 0.5120 | 18314.7107 | 6.1688          | 0.5140 | 18299.1047 |
|       | 2     | 13.7844      |        |            | 13.5542         |        |            |
|       | 3     | 25.7001      |        |            | 25.6168         |        |            |
|       | 4     | 37.8306      |        |            | 37.7114         |        |            |
| NSW   | 1     | 23.3872      | 0.6188 | 25536.0257 | 23.3012         | 0.6197 | 25532.9625 |
|       | 2     | 34.4748      |        |            | 34.3056         |        |            |
|       | 3     | 45.9213      |        |            | 45.7254         |        |            |
|       | 4     | 56.2391      |        |            | 56.0187         |        |            |
| NSY   | 1     | 18.8594      | 0.5946 | 12861.8468 | 18.7953         | 0.5969 | 12858.7174 |
|       | 2     | 31.8844      |        |            | 31.3435         |        |            |
|       | 3     | 39.1432      |        |            | 39.0174         |        |            |
|       | 4     | 46.6823      |        |            | 46.2975         |        |            |

LCW - limb conformation at weaning; LCY - limb conformation at yearling; BTW - breed traits at weaning; BTY - breed traits at yearling; STW - sexual traits at weaning; STY - sexual traits at yearling; EPW - eye pigmentation at weaning; EPY - eye pigmentation at yearling; NSW - navel size at weaning; NSY - navel size at yearling.

The first five components explained 79.91% of the total variance of breeding values for the studied visual scores, which is considered sufficient to capture most of its variation (Figure 2). Breeding values for all traits studied showed a negative association with the first principal component (Table 5), with higher magnitudes observed for scores obtained at weaning (LCW, BTW, STW, and NSW), with values ranging from  $-0.61$  to  $-0.71$ . Relating to the second principal component, LCW, BTW, STW, LCY, BTY, and STY were negatively correlated. On the other hand, EPW and EPY showed greater discrimination power, with a correlation of  $0.87$ . Both NSW and NSY were negatively correlated to the third principal component, with a linear correlation of  $-0.66$  and  $-0.71$ , respectively. For the fourth principal component, positive and high linear associations were estimated with LCY and STY, with correlation of  $0.74$  and  $0.51$ , respectively. The fifth principal component was more closely associated with breeding values of LCW, with a higher discriminatory power of  $0.62$ .



**Figure 2** - Percentage of the total variation associated with each of the 10 principal components.

**Table 5** - Correlation coefficients between breeding values of visual scores with the five principal components in Hereford and Braford cattle

| Trait | Principal component |        |        |        |        |
|-------|---------------------|--------|--------|--------|--------|
|       | First               | Second | Third  | Fourth | Fifth  |
| LCW   | -0.617              | -0.089 | 0.180  | -0.107 | 0.628  |
| BTW   | -0.612              | -0.044 | 0.362  | -0.476 | -0.224 |
| STW   | -0.712              | -0.112 | 0.175  | -0.188 | 0.383  |
| EPW   | -0.165              | 0.874  | 0.132  | -0.029 | -0.004 |
| NSW   | -0.633              | 0.081  | -0.666 | -0.018 | -0.060 |
| LCY   | -0.378              | -0.015 | 0.236  | 0.749  | 0.171  |
| BTY   | -0.555              | -0.181 | 0.344  | -0.104 | -0.283 |
| STY   | -0.566              | -0.129 | 0.100  | 0.516  | -0.306 |
| EPY   | -0.099              | 0.875  | 0.162  | 0.043  | -0.040 |
| NSY   | -0.577              | 0.102  | -0.712 | -0.024 | -0.081 |

LCW - limb conformation at weaning; BTW - breed traits at weaning; STW - sexual traits at weaning; EPW - eye pigmentation at weaning; NSW - navel size at weaning; LCY - limb conformation at yearling; BTY - breed traits at yearling; STY - sexual traits at yearling; EPY - eye pigmentation at yearling; NSY - navel size at yearling.

## 4. Discussion

The phenotypic distribution observed for the studied visual scores, both at weaning and yearling, possibly occurred because the attribution was made considering pre-established standards for each trait in both breeds. Most of the animals in this population did not show problems of limb conformation and presented traits specific to their sex. For EPW and EPY, the most frequent scores indicate that most of the cattle showed reasonable to excellent pigmentation. On the other hand, most animals had ideal NSW and NSY for the Hereford breed (scores 1 and 2), but not so much for the Braford breed, since scores 2 and 3 were its ideal.

Higher values of direct and maternal heritability were obtained with the threshold model, suggesting that the model was able to better capture the genetic variability of studied traits. The fact that the scores did not present a normal distribution (Figure 1), possibly because they were measured considering pre-established standards and not in relation to the average of the CG to which the animal belongs, could explain the differences observed in the genetic parameters estimated with the use of both models.

Similar to the results obtained in the present study, Campos et al. (2019) reported higher heritability for navel score at yearling using threshold model ( $0.42 \pm 0.02$ ) compared with linear model ( $0.22 \pm 0.02$ ) and recommended its use in genetic evaluation for the trait. On the other hand, in Nelore breed, no differences were reported between linear and threshold models in obtaining genetic parameters for scores of limb conformation, breed characterization, sexual traits, and navel (Passafaro et al., 2013; Boligon et al., 2016).

The heritability estimated for LCW and LCY suggests limited genetic progress with selection for these traits due to reduced variation attributed to additive genetic effects. It is worth noting that good limb conformation is relevant especially in extensive production systems, due to the need for animals to have good mobility skills, which can be obtained by selecting based on that score or by discarding animals with defects. Similar to that obtained in the present study, Lima et al. (2013) reported low heritability ( $0.05 \pm 0.01$ ) for score of posture in Nelore cattle, with visual attribution ranging from 1 to 4 and using a linear model. On the other hand, higher heritability was obtained in other studies. Koury Filho et al. (2002) estimated heritability of 0.35 for limb conformation at weaning in Nelore breed, with visual assignments ranging from 1 to 5 and using a linear model. A similar result was reported by Gutiérrez and Goyache (2002) for Asturiana de Los Valles breed, with heritability of  $0.33 \pm 0.02$  for legs line score ranging from 1 to 9 and using a linear model. Using linear and threshold models, Passafaro et al. (2013) reported heritability of 0.20 and 0.30, respectively, for limb conformation attributed to sires kept in pasture-based weight gain trials and ranging from 1 to 4. Santana Jr. et al. (2013) estimated moderate heritability (0.26) for bone structure score (legs and hocks) at yearling in Nelore animals, ranging from 1 to 3 and evaluated with a threshold model. For Guzerá breed, Abreu et al. (2018) reported higher heritability ( $0.39 \pm 0.04$ ) for limb score (solidity of legs and feet), with scores ranging from 1 to 4 and using a threshold model.

Evaluating the yearling leg and feet score considering values of 1 (animal with defects) or 0 (animal without defects) in Nelore cattle, Vargas et al. (2017) reported higher heritability ( $0.18 \pm 0.04$ ) in relation to that obtained for LCY in the present study. Subsequently, for score of legs and feet, however ranging from 1 (less desirable) to 5 (more desirable) and attributed to the 20% higher animals according to the selection index adopted by the program, the authors estimated a higher heritability ( $0.39 \pm 0.07$ ). It should be noted that those animals that had a defect at yearling were not candidates and, consequently, were not evaluated in the second phase. According to the authors, the strategy of discarding animals based on score of legs and feet, aiming to reduce disturbances of locomotion that can lead to productive and reproductive losses, contributed to the genetic progress of the trait in the Nelore breed. In general, it is common to use different methodologies to obtain scores related to support and locomotion in beef cattle, with few studies conducted using the same attribution for the score of limb conformation considered in the evaluated population, which may explain the differences in the heritability estimated.

Low genetic variability was estimated for breed traits in the studied population, especially when evaluated at yearling. Similarly, low heritability was reported for scores related to breed standard in Nelore cattle, ranging from 0.18 to 0.24 (Faria et al., 2009; Lima et al., 2013; Passafaro et al., 2013; Boligon et al., 2016). In the studied herds, animals that do not conform to the breed standards do not receive certification from breed organizations, leading to a decrease in their commercial value. Therefore, selection for this trait, especially at weaning, is expected to gradually increase the proportion of animals that meet the standards of the Hereford and Braford breeds.

Higher heritability (0.34) in relation to those obtained in the present study was reported by Koury Filho et al. (2002) for breed aspects measured at weaning, using a linear model and score ranging from 1 to 5. For breed traits score in Guzerá cattle, assigned from 1 to 4 and evaluated with a threshold model, Abreu et al. (2018) also estimated heritability of 0.34. For breed standard of Hereford and Braford animals, evaluated by scores ranging from 1 to 5, Reimann et al. (2018) reported heritability of  $0.33 \pm 0.02$ , using threshold model. In general, BTW and BTY in the studied population showed low variability in its phenotypic expression, which may justify, in part, the reduced genetic variability estimated for the trait and, consequently, the low heritability.

Limited genetic gains are expected for STW and STY traits when used as selection criteria in Hereford and Braford population. No studies evaluating sexual traits were found for those breeds or even crossbreeds. Different heritability magnitudes were reported in the literature for sexual traits score in Zebu cattle. For Nelore cattle, values ranging from 0.18 to 0.34 were obtained (Koury Filho et al., 2002; Lima et al., 2013; Passafaro et al., 2013). For sexual traits score in Brahman animals, that were obtained with scores from 1 to 10 and using a linear animal model, Fair et al. (2014) estimated heritability close to zero (0.06). On the other hand, higher genetic variability was estimated with a threshold model for sexual traits score in Guzerá breed, with a value of  $0.46 \pm 0.04$  (Abreu et al., 2018). In general, different heritability values may be due to methodologies applied in obtaining phenotypic traits related to sexual aspects in beef cattle, in addition to the common variations expected between the different populations studied.

Eye pigmentation is one of the phenotypic traits of great relevance for the adaptation of Hereford and Braford breeds, being generally assessed visually by score. For this score, low heritability was obtained, thus moderate genetic gains for the trait are expected, even if in the long term, once the selection of animals with better genetic potential for eye pigmentation is a simple and viable alternative to reduce the incidence of ocular carcinoma in cattle, especially those intended for reproduction, as they remain for a longer period in herds. Similar to that obtained in the present study, Teixeira et al. (2015) and Piccoli et al. (2017) reported heritability of 0.18 and 0.20, respectively, for eye pigmentation score at yearling in Hereford and Braford cattle, ranging from 1 to 5 and assessed using a linear model. On the other hand, for the same breeds, Reimann et al. (2018) estimated a higher heritability ( $0.46 \pm 0.02$ ) for eye pigmentation score at yearling, however attributed by scores ranging from 1 to 3 and using the threshold model.

Despite the low genetic variability, selection based on NSW and NSY can lead to genetic gains in the long term, providing satisfactory correction of the trait in the studied population and, consequently, reducing the risks of injuries that can compromise the reproductive performance of animals used in reproduction. For Angus and Angus  $\times$  Nelore crossbred cattle, Viu et al. (2002) reported similar heritability to that obtained in the present study, with values of 0.09 and 0.10 at weaning and 0.06 and 0.20 at yearling, for foreskin and navel scores, respectively, with visual assignments ranging from 0 to 5. Higher heritability for navel score, compared with that obtained in the present study, was also reported in the literature. Using linear models, Gordo et al. (2012) and Neves et al. (2014) estimated heritability of  $0.38 \pm 0.06$  and  $0.45 \pm 0.15$ , respectively, for yearling navel size score in Nelore breed. For the same breed, Boligon et al. (2016) reported heritability of  $0.16 \pm 0.01$  and  $0.29 \pm 0.01$  for navel score at weaning and yearling, respectively, using a linear model; and  $0.22 \pm 0.03$  and  $0.42 \pm 0.03$  for the same score and measurement ages using the threshold model. Recently, evaluating the navel score at yearling for Hereford and Braford animals, Campos et al. (2019) reported heritability of  $0.22 \pm 0.02$  and  $0.42 \pm 0.02$  using linear and threshold models, respectively.

Similar to that obtained in the present study, Boligon et al. (2016) reported changes in the classification of sires using linear and threshold models for breed characterization score in Nelore cattle. Differences in the classification of sires using linear and threshold models were also observed for navel size score in Nelore (Boligon et al., 2016) and Hereford and Braford (Campos et al., 2019) breeds, differing from that found in the present research.

In general, the use of the threshold model is recommended in genetic evaluations of LCW, BTW, STW, LCY, BTY, and STY in the population studied, even with the need to explain to producers a new interpretation of the breeding values with the application of this model. On the other hand, for EPW, NSW, EPY, and NSY, both models evaluated can be used, once the choice of the model should have little influence on the ranking of sires and cross-validation analyses.

In the studied population, the first five components are sufficient to explain most of the variation between the breeding values predicted for visual scores at weaning and yearling. Using breeding values predicted for growth and reproductive traits in Nelore cattle, Boligon et al. (2016) reported that the first three principal components were sufficient to explain 79.06% of the total variation. On the

other hand, evaluating traits of growth, reproductive, and visual scores of body structure, precocity of finishing, and musculature in Nelore cattle, Viana et al. (2020) reported that the first two principal components were sufficient to explain more than 96% of the cumulative proportion of the total variation.

In the present study, negative correlations obtained between the first principal component and all visual scores indicate a common association among the evaluated traits. Thus, most of the genetic variability found in this population is related to average performance of animals for morphological traits, except for EPW and EPY due the low association with this component. On the other hand, the second principal component was more associated with EPW and EPY, suggesting that this component could be used in the selection for ocular pigmentation. The third principal component contrasted mainly lower breeding values for NSW and NSY with higher breeding values for BTW and BTY. The fourth principal component showed higher association with LCY and STY, and the fifth principal component with breeding values for LCW and STW. Therefore, the results of the principal component analysis allow breeders to construct selection indices considering the correlations among variables (breeding values), aiming to simultaneously improve morphological traits in the studied population. In practical terms, these indices would be used as selection criteria to achieve a particular breeding objective.

## 5. Conclusions

Visual scores of limb conformation, breed traits, sexual traits, eye pigmentation and navel size showed low genetic variability in Hereford and Braford population, with higher heritability values estimated using threshold rather than linear models. The threshold model is recommended in the genetic evaluations for limb conformation, breed traits, and sexual traits. For eye pigmentation and navel size scores, both models (linear and threshold) can be used. The traits studied can be genetically analyzed with the first five main components. Furthermore, it is possible to construct selection indices that simultaneously improve the morphology and adaptation of Hereford and Braford animals.

## Conflict of Interest

The authors declare no conflict of interest.

## Author Contributions

**Conceptualization:** Souza, J. S.; Silveira, D. D.; Teixeira, B. B. M. and Boligon, A. A. **Data curation:** Souza, J. S.; Silveira, D. D. and Teixeira, B. B. M. **Formal analysis:** Souza, J. S.; Silveira, D. D.; Teixeira, B. B. M. and Boligon, A. A. **Funding acquisition:** Boligon, A. A. **Investigation:** Souza, J. S. **Methodology:** Souza, J. S.; Silveira, D. D. and Teixeira, B. B. M. **Project administration:** Boligon, A. A. **Resources:** Teixeira, B. B. M. and Boligon, A. A. **Software:** Souza, J. S. and Silveira, D. D. **Supervision:** Boligon, A. A. **Visualization:** Souza, J. S. **Writing – original draft:** Souza, J. S. **Writing – review & editing:** Souza, J. S. and Boligon, A. A.

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## References

ABHB - Associação Brasileira de Hereford e Braford. 2017. História da raça Hereford. Available at: <<http://www.abhb.com.br/herford/herford/>>. Accessed on: Oct. 25, 2017.

- Abreu, L. R. A.; Mota, L. F. M.; Ferreira, T. A.; Pereira, I. G.; Pires, A. V.; Villela, S. D. J.; Merlo, F. A. and Martins, P. G. M. A. 2018. Genetic evaluation of bodyweight, scrotal circumference, and visual appraisal scores in *Bos indicus* cattle. *Animal Production Science* 58:1584-1594. <https://doi.org/10.1071/AN16548>
- Boligon, A. A.; De Vargas, L.; Silveira, D. D.; Roso, V. M.; Campos, G. S.; Vaz, R. Z. and Souza, F. R. P. 2016. Genetic models for breed quality and navel development scores and its associations with growth traits in beef cattle. *Tropical Animal Health and Production* 48:1679-1684. <https://doi.org/10.1007/s11250-016-1143-1>
- Campos, G. S.; Reimann, F. A.; Schimdt, P. I.; Cardoso, L. L.; Sollero, B. P.; Braccini, J.; Yokoo, M. J.; Boligon, A. A. and Cardoso, F. F. 2019. Threshold and linear models for genetic evaluation of visual scores in Hereford and Braford cattle. *Animal Production Science* 59:619-627. <https://doi.org/10.1071/AN17436>
- Cardoso, F. F. and Lopa, T. M. B. P. 2017. Pampa Plus: avaliação genética Hereford e Braford. Embrapa Pecuária Sul, Bagé.
- Fair, M. D.; Naser, F. W. C. and van Wyk, J. B. 2014. Estimation of genetic parameters of type traits for Namibian Brahman beef cattle. In: *Proceedings of the 10th World Congress of Genetics Applied to Livestock Production, Canada*.
- Faria, C. U.; Magnabosco, C. U.; Albuquerque, L. G.; de los Reyes, A.; Bezerra, L. A. F. and Lobo, R. B. 2008. Análise genética de escores de avaliação visual de bovinos com modelos bayesianos de limiar e linear. *Pesquisa Agropecuária Brasileira* 43:835-841. <https://doi.org/10.1590/S0100-204X2008000700007>
- Faria, C. U.; Magnabosco, C. U.; Albuquerque, L. G.; Bezerra, L. A. F. and Lôbo, R. B. 2009. Estimativas de correlações genéticas entre escores visuais e características de carcaça medidas por ultrassonografia em bovinos Nelore utilizando modelos bayesianos linear-limiar. *Revista Brasileira de Zootecnia* 38:2144-2151. <https://doi.org/10.1590/S1516-35982009001100011>
- Gordo, D. G. M.; Baldi, F.; Lôbo, R. B.; Koury Filho, W.; Sainz, R. D. and Albuquerque, L. G. 2012. Genetic association between body composition measured by ultrasound and visual scores in Brazilian Nelore cattle. *Journal of Animal Science* 90:4223-4229. <https://doi.org/10.2527/jas.2011-3935>
- Gutiérrez, J. P. and Goyache, F. 2002. Estimation of genetic parameters of type traits in Asturiana de los Valles beef cattle breed. *Journal of Animal Breeding and Genetics* 119:93-100. <https://doi.org/10.1046/j.1439-0388.2002.00324.x>
- Heidelberger, P. and Welch, P. D. 1983. Simulation run length control in the presence of an initial transient. *Operations Research* 31:1109-1144. <https://doi.org/10.1287/opre.31.6.1109>
- Kaiser, H. F. 1958. The varimax criterion for analytic rotation in factor analysis. *Psychometrika* 23:187-200. <https://doi.org/10.1007/BF02289233>
- Koury Filho, W.; Ferraz, J. B. S.; Eler, J. P.; Meister, N. C. and Pineda, N. 2002. Estimativas de herdabilidades e correlações genéticas entre escores de avaliações visuais e características de desenvolvimento ponderal em uma população da raça Nelore. In: *Anais do 4º Simpósio Nacional de Melhoramento Animal*. Sociedade Brasileira de Melhoramento Animal, Campo Grande.
- Lima, P. R. M.; Paiva, S. R.; Cobuci, J. A.; Braccini Neto, J.; Machado, C. H. C. and McManus, C. 2013. Genetic parameters for type classification of Nelore cattle on central performance tests at pasture in Brazil. *Tropical Animal Health and Production* 45:1627-1634. <https://doi.org/10.1007/s11250-013-0408-1>
- McHugh, N.; Cromie, A. R.; Evans, R. D. and Berry, D. P. 2014. Validation of national genetic evaluations for maternal beef cattle traits using Irish field data. *Journal of Animal Science* 92:1423-1432. <https://doi.org/10.2527/jas.2013-6658>
- Misztal, I.; Tsuruta, S.; Lourenco, D.; Masuda, Y.; Aguilar, I.; Legarra, A. and Vitezica, Z. 2014. Manual for BLUPF90 family of programs. University of Georgia, Athens, USA.
- Neves, H. H. R.; Reis, F. P.; Paterno, F. M.; Guarini, A. R.; Carvalheiro R.; Silva L. R.; Oliveira, J. A. and Queiroz, S. A. 2014. Herd-of-origin effect on the post-weaning performance of centrally tested Nelore beef cattle. *Tropical Animal Health and Production* 46:1235-1241. <https://doi.org/10.1007/s11250-014-0633-2>
- Passafaro, T. L.; Raidan, F. S. S.; Aquino, M. P.; Escarce, T. C.; Josahkian, L. A. and Toral, F. L. B. 2013. Parâmetros genéticos para escores visuais de tourinhos Nelore com modelos lineares e de limiar. In: *Anais do 10º Simpósio Brasileiro de Melhoramento Animal*. Sociedade Brasileira de Melhoramento Animal, Uberaba.
- Piccoli, M. L.; Brito, L. F.; Braccini, J.; Cardoso, F. F.; Sargolzaei, M. and Schenkel, F. S. 2017. Genomic predictions for economically important traits in Brazilian Braford and Hereford beef cattle using true and imputed genotypes. *BMC Genetics* 18:2. <https://doi.org/10.1186/s12863-017-0475-9>
- Plummer, M.; Best, N.; Cowles, K. and Vines, K. 2006. CODA: convergence diagnosis and output analysis for MCMC. *R News* 6:7-11.
- R Core Team. 2015. *The R: a language and environment for statistical computing*. R Foundation for Statistical Computing, Vienna, Austria.
- R Core Team. 2019. *R: a language and environment for statistical computing*. R Foundation for Statistical Computing, Vienna, Austria.
- Reimann, F. A.; Boligon, A. A.; Campos, G. S.; Cardoso, L. L.; Junqueira, V. S. and Cardoso, F. F. 2018. Genetic parameters and accuracy of traditional and genomic breeding values for eye pigmentation, hair coat and breed standard in Hereford and Braford cattle. *Livestock Science* 213:44-50. <https://doi.org/10.1016/j.livsci.2018.04.007>

Rosa, A. N.; Silva, L. O. C. and Amaral, T. B. 2003. Avaliação zootécnica e funcional de touros na fazenda. Embrapa Gado de Corte, Campo Grande.

Santana Jr., M. L.; Eler, J. P.; Cucco, D. C.; Bignardi, A. B. and Ferraz, J. B. S. 2013. Genetic associations between hip height, body conformation scores, and pregnancy probability at 14 months in Nelore cattle. *Livestock Science* 154:13-18. <https://doi.org/10.1016/j.livsci.2013.02.018>

Teixeira, B. B. M.; Costa, R. F.; Sollero, B. P.; Yokoo, M. J. and Cardoso, F. F. 2015. Herdabilidades e correlações genéticas para critérios de seleção das raças Hereford e Braford. In: Anais do 11<sup>o</sup> Simpósio Brasileiro de Melhoramento Animal. Sociedade Brasileira de Melhoramento Animal, Santa Maria.

Vargas, G.; Neves, H. H. R.; Cardoso, V.; Munari, D. P. and Carvalheiro, R. 2017. Genetic analysis of feet and leg conformation traits in Nelore cattle. *Journal of Animal Science* 95:2379-2384. <https://doi.org/10.2527/jas.2016.1327>

Viana, A. F. P.; Rorato, P. R. N.; Mello, F. C. B.; Machado, D. S.; Figueiredo, A. M.; Bravo, A. P. and Feltes, G. L. 2020. Principal component analysis of breeding values for growth, reproductive and visual score traits of Nelore cattle. *Livestock Science* 241:104262. <https://doi.org/10.1016/j.livsci.2020.104262>

Viu, M. A. O.; Tonhati, H.; Cerón-Munõz, M. F.; Friez, L. A. and Teixeira, R. A. 2002. Parâmetros genéticos do peso e escores visuais de prepúcio e umbigo em gado de corte. *Ars Veterinária* 18:179-184.