









Estimation of genetic parameters for weaning and yearling weights in a composite population used to form the Purunã breed

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ABSTRACT - We aimed to evaluate the effects of sex and the linear and quadratic components of age of dam at calving, as well as apply a mixed model including maternal effect for the genetic evaluation of weaning (WW) and yearling (YW) weights. The phenotypic database was composed by Charolais, Caracu, Aberdeen Angus, and Canchim purebred and crossbred animals. Single-trait analyses were performed using models that included the maternal effect for WW and YW traits, and a model ignoring this effect on YW (YWNM). The Deviance Information Criterion (DIC), model posterior probabilities (MPP), accuracy of breeding values (ACC), and Spearman's rank correlation were applied to compare the models including and ignoring the maternal effect on YW. Sex and age of dam at calving had significant effects on WW and YW. The direct heritability estimates were 0.21 ± 0.03 and 0.05 ± 0.02 , and the maternal heritabilities were 0.11 ± 0.02 and 0.02 ± 0.01 for WW and YW, respectively. The heritabilities estimated for YW may have been influenced by the several genetic groups in the population and by used conventional animal model, which may not have been the better fit model to evaluate YW in this population. The DIC, MPP, and ACC values indicated that YW outperformed the YWNM model, but the rank correlation and percentages of individuals selected in common suggested that the best animals would be selected independently of the model chosen.

Keywords: body weight, crossbred cattle, growth traits, maternal effect

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1. Introduction

Livestock production is one of the most important activities of Brazilian agribusiness (Silva Neto and Bacchi, 2014). Brazil has the world's second largest commercial cattle herd; it is the largest exporter and the second largest beef producer of the world, according to the United States Department of Agriculture (USDA, 2019). The genetic improvement has an important contribution for the beef industry (Moreira et al., 2019). The estimation of traditional breeding values using phenotypic and

pedigree information to predict breeding values has been very successful in beef cattle, improving the genetic progress of productive and reproductive traits (Miller, 2010).

Growth traits, such as body weight and initial development measures of calves, are important parameters for selection (Baldi et al., 2010). The weight traits are easily measured and present moderate heritabilities, ranging from 0.13 to 0.30 for weaning weight (WW) and from 0.23 to 0.46 for yearling weight (YW), estimated in Angus, Brangus, Caracu, Canchim, Charolais, and Angus × Nellore cattle populations, providing reasonable genetic gain over generations (Crews Jr. et al., 2004; Pereira et al., 2006, 2008; Araújo et al., 2010; Baldi et al., 2010; Costa et al., 2011; Silva et al., 2012; Mello et al., 2013).

The birth and weaning weights of calves are influenced by age of the dam at calving (Santos et al., 2011). According to these authors, the body of the dam undergoes physiological changes throughout its life, which contribute to a better milk production and maternal ability. The maternal effect, defined as any influence on progeny phenotype that can be attributed to dam phenotype, such as gestation and lactation periods, milk production, and colostrum quality, is also an important factor for the development of calves (Corrêa et al., 2006).

The Instituto Agrônomo do Paraná (IAPAR) is working on the constitution of a new beef breed called Purunã, derived from the crossbreeding of Charolais, Caracu, Aberdeen Angus, and Canchim breeds, to improve the use of different breed qualities in crossbreeding programs.

In this context, we aimed to evaluate the effects of sex and the linear and quadratic components of age of dam at calving, as well as apply a mixed model including maternal effect for the genetic evaluation of WW and YW in a composite beef cattle population used to form the Purunã breed. In addition, we aimed to compare the proposed model with a model ignoring the maternal effect on YW using posterior based goodness-of-fit measures.

2. Material and Methods

Analyses were performed using data from IAPAR. The population was composed by Canchim, Aberdeen Angus, Charolais, and Caracu purebred and crossbred animals with different breed compositions, as well as Purunã individuals. The phenotypic database comprised 6,301 and 5,540 records for WW and YW, respectively. Animals were evaluated according to their contemporary group (sex; week, month, and year of weaning and yearling) and breed composition assigned for each individual based on the proportions of Canchim, Aberdeen Angus, Charolais, and Caracu breeds. The pedigree file included 10,287 animals from six generations, with 2,165 sires, 2,321 dams, and 5,801 animals without progeny, including Canchim, Aberdeen Angus, Charolais, and Caracu purebred and crossbred animals.

Analyses of variance were conducted using the GLM procedure of SAS software (Statistical Analysis System, version 9.0) to evaluate the effects of sex and the linear and quadratic components of age of dam on WW and YW, considering the contemporary group and breed composition effects. Afterwards, single-trait analyses were performed by Bayesian inference using models including the maternal effect for WW and YW traits and a model ignoring the maternal effect on YW (YWNM). A multitrait analysis (2×2) was also performed to evaluate the genetic correlation between the traits. The Bayesian methodology provides a better description of the genetic parameters through *a posteriori* marginal distributions (Madureira et al., 2009).

The general single-trait animal model, in matrix notation, can be written as:

$$y = Xb + Za + Wm + e, \quad (1)$$

in which y is the vector of WW and YW observations; b is the vector of fixed effects (contemporary group and breed composition) and covariates (age of dam at calving, with the linear and quadratic components, birth weight for WW and weaning weight for YW); a is the vector of random direct additive genetic effects, assuming $a \sim N(0, A\sigma_a^2)$, in which A is the numerator relationship matrix and σ_a^2 is the additive genetic (co)variance matrix; m is the vector of random maternal additive genetic

effects, assuming $m \sim N(0, A\sigma_m^2)$, in which σ_m^2 is the maternal additive genetic (co)variance matrix; and e is the vector of residual effects, assuming $e \sim N(0, I\sigma_r^2)$, in which I is the identity matrix and σ_r^2 is the residual (co)variance matrix; X , Z , and W are the incidence matrices of fixed, direct additive genetic, and maternal additive genetic effects, respectively.

The bivariate model, in matrix notation, can be written as:

$$\begin{bmatrix} y_1 \\ y_2 \end{bmatrix} = \begin{bmatrix} X_1 & 0 \\ 0 & X_2 \end{bmatrix} \begin{bmatrix} b_1 \\ b_2 \end{bmatrix} + \begin{bmatrix} Z_1 & 0 \\ 0 & Z_2 \end{bmatrix} \begin{bmatrix} a_1 \\ a_2 \end{bmatrix} + \begin{bmatrix} W_1 & 0 \\ 0 & W_2 \end{bmatrix} \begin{bmatrix} m_1 \\ m_2 \end{bmatrix} + \begin{bmatrix} e_1 \\ e_2 \end{bmatrix}, \quad (2)$$

in which y_1 is the phenotypic observation vector for the WW trait; y_2 is the phenotypic observation vector for the YW trait; b_1 is the vector of fixed effects (contemporary group and breed composition) and covariates (age of dam at calving, with the linear and quadratic components, and birth weight) for WW; b_2 is the vector of fixed effects (contemporary group and breed composition) and covariates (age of dam at calving, with the linear and quadratic components, and weaning weight) for YW; a_i is the vector of random direct additive genetic effects for the i ($i = 1, 2$); m_i is the vector of random maternal additive genetic effects for i ; e_i is the vector of residual effects for the i , assuming $a_i \sim N(0, G_0 \otimes A)$, $m_i \sim N(0, M_0 \otimes A)$, and $e_i \sim N(0, R_0 \otimes I)$, in which G_0 , M_0 , and R_0 are the direct additive genetic, maternal additive, and residual (co)variance matrices, respectively; A is the numerator relationship matrix; and I is the identity matrix; X_i , Z_i , and W_i are the incidence matrices of fixed, direct additive genetic, and maternal additive genetic effects for the i , respectively.

The GIBBS1F90 software from the BLUPF90 family of programs (<http://nce.ads.uga.edu/>) was used for the genetic analyses, considering a total of 800,000 iterations, with burn-in of 150,000 and thin of 50, resulting in a total of 13,000 samples. The size of the chain was defined according to the Raftery and Lewis (1992) method, available in the BOA package of R software (R Core Team, 2018). Gibbs post-sampling analyses were conducted in POSTGIBBSF90 software from the BLUPF90 family of programs (<http://nce.ads.uga.edu/>). The variance components and genetic parameters convergence analyses were assessed by the criteria proposed by Geweke (1992) and by verification of the sampled values.

The Deviance Information Criterion (DIC) (Spiegelhalter et al., 2002) was applied to compare the models including and ignoring the maternal effect on the YW trait. Considering θ as a vector containing the model parameters, the DIC was computed as follows:

$$DIC = D(\bar{\theta}) + 2p_D, \quad (3)$$

in which $D(\bar{\theta})$ is a point estimate of the deviance obtained by substituting the parameters by their posterior means estimates in the likelihood function and p_D is the effective number of parameters in the model.

The lower DIC estimate represents better fit (Corrêa et al., 2009). However, this criterion only expresses which evaluated model presented the best goodness of fit, being the magnitude of this difference subjective. Thus, the model posterior probabilities (MPP) were calculated from DIC (Silva et al., 2011), which is given by:

$$p(M_t | \theta) = \frac{\exp\left(-\frac{\Delta_t}{2}\right)}{\sum_{t=1}^4 \exp\left(-\frac{\Delta_t}{2}\right)}, \quad (4)$$

t is the different evaluated models (1 = YW and 2 = YWNM)

in which $p(M_t | \theta)$ is the posterior probability of model t and Δ_t is the DIC difference between model t and the best model (that presents smaller DIC value). The Δ_t value for the best model is equal to zero.

Moreover, after prediction of breeding values, individual accuracies were estimated as follows (Mrode, 2014):

$$ACC_i = \sqrt{1 - \left(\frac{PSD_i^2}{\sigma_a^2} \right)}, \quad (5)$$

in which ACC_i is the accuracy of breeding value for animal i , PSD is the posterior standard deviation from BLUP equations, and σ_a^2 is the additive genetic variance of the evaluated trait.

Spearman's rank correlation coefficients between the breeding values predicted with the YW and YWNM models were obtained. Furthermore, the percentage of individuals in common selected at 1, 10, and 20% based on both evaluated models was compared.

3. Results

Means of 166.00 and 209.16 kg were observed for WW and YW, respectively (Table 1). Sex had a significant effect on both evaluated traits ($P < 0.01$). Females were lighter at WW (162 kg) and YW (195 kg) than males (170 and 224 kg, respectively) (Table 2). Age of dam at calving showed significant linear and quadratic effects on WW and a significant linear effect on YW ($P < 0.01$).

Table 1 - Descriptive statistics of weaning weight (WW) and yearling weight (YW) traits (kg) from a beef cattle composite population used to form the Purunã breed

Trait	Parameter					
	Total number	Mean	SD	CV%	Minimum	Maximum
WW	6,301	166.00	41.31	24.90	80	313
YW	5,339	209.16	50.53	24.20	120	424

SD - standard deviation; CV - coefficient of variation.

Table 2 - Fixed effects estimates and standard error in parentheses for weaning weight (WW) and yearling weight (YW) traits from a beef cattle composite population used to form the Purunã breed

Effect	Level	WW (kg)	YW (kg)
Sex	Female	162.05 (0.75)b	194.948 (1.06)b
	Male	169.91 (0.72)a	223.886 (0.80)a
Genetic groups	CH	161.212 (2.20)ab	192.59 (2.54)abc
	CA	163.203 (1.76)ab	210.623 (2.21)abc
	1/2CH 1/2CA	168.05 (1.80)a	212.256 (2.40)abc
	1/4CH 3/4CA	164.7 (3.34)a	199.274 (3.54)abc
	3/4CH 1/4CA	169.43 (3.65)a	207.459 (3.95)abc
	3/8CH 5/8CA	160.039 (4.37)ab	200.589 (5.28)abc
	5/8CH 3/8CA	175.689 (5.25)a	209.658 (5.48)abc
	1/3CH 2/3CA	140.364 (8.39)b	187.182 (8.95)c
	2/3CH 1/3CA	176.16 (8.00)a	219.696 (9.90)a
	AB	154.682 (1.85)ab	184.603 (2.54)c
	CN	167.983 (1.66)a	204.871 (2.13)abc
	1/2AB 1/2CN	165.653 (1.74)a	207.763 (2.40)abc
	1/4AB 3/4CN	170.331 (3.11)a	200.171 (3.44)abc
	3/4AB 1/4CN	168.784 (3.66)a	201.181 (4.55)abc
	3/8AB 5/8CN	162.424 (3.63)ab	188.071 (3.78)bc
	5/8AB 3/8CN	169.8 (4.54)a	197.216 (4.73)abc
	1/3AB 2/3CN	173.161 (5.94)a	213.034 (7.91)abc
2/3AB 1/3CN	157.355 (6.40)ab	187.111 (6.59)c	
1/4CH 1/4CA 1/4AB 1/4CN	167.421 (0.85)a	217.761 (1.17)ab	

CH - Charolais; CA - Caracu; AB - Aberdeen Angus; CN - Canchim.

Estimates with the same letter within trait and effect did not differ significantly ($P < 0.01$).

The direct and maternal genetic variances were 268.10 and 136.21 for WW, and 31.72 and 11.50 for YW (Table 3). The direct heritability estimates were 0.21 ± 0.03 and 0.05 ± 0.02 , and the maternal genetic heritabilities were 0.11 ± 0.02 and 0.02 ± 0.01 for WW and YW, respectively. The direct heritability estimate for YWNM was 0.06 ± 0.01 . The direct additive genetic correlation between WW and YW was 0.85 ± 0.06 .

The smaller DIC value was found using the YW model, being the difference in relation to YWNM model value equal to 16.61 (Table 4). The higher ACC value was observed using the YW model, in which the estimated ACC_{YW} and ACC_{YWNM} were 39 and 30%, respectively. Comparing both models, the smallest DIC value and the highest probability and accuracy values indicate that the YW model is the most appropriate to estimate the genetic parameters and breeding values for YW.

Spearman's (rank) correlation between the breeding values predicted with the YW and YWNM models was 0.99. Many animals in common would be selected using both models. Considering percentage thresholds of 1, 10, and 20%, the percentage of individuals selected in common were 94, 96, and 97%, respectively.

Table 3 - (Co)variance components and genetic parameters for weaning weight (WW) and yearling weight (YW) traits from a beef cattle composite population used to form the Purunã breed

Trait	(Co)variance component and genetic parameter				
	σ_a^2	σ_m^2	σ_{am}	h_a^2	h_m^2
WW	268.10	136.21	-108.79	0.21 ± 0.03	0.11 ± 0.02
YW	31.72	11.50	0.22	0.05 ± 0.02	0.02 ± 0.01
YWNM	40.13	-	-	0.06 ± 0.01	-

YWNM - yearling weight without maternal effect; σ_a^2 - direct additive genetic variance; σ_m^2 - maternal additive genetic variance; σ_{am} - genetic (co)variance between direct and maternal additive genetic effects; h_a^2 - heritability for the direct additive genetic effect; h_m^2 - heritability for the maternal genetic effect.

Table 4 - Deviance information criteria (DIC), model posterior probabilities (MPP), and average accuracy of breeding values (ACC) for models including (YW) and ignoring (YWNM) the maternal effect on yearling weight from a beef cattle composite population used to form the Purunã breed

Model	DIC	MPP	ACC (%)
YW	50,310.84	1.0	39
YWNM	50,327.45	0.0	30

4. Discussion

In the current study, sex had a significant effect on WW and YW traits ($P < 0.01$). Schiermiester et al. (2015) also reported a significant sex effect on these traits in a composite population represented by purebred Angus, Hereford, Red Angus, Charolais, Gelbvieh, Simmental, Limousin, and Composite MARC III (1/4 Angus, 1/4 Hereford, 1/4 Pinzgauer, 1/4 Red Poll), corroborating the results found by Alencar et al. (2009) and Fialho et al. (2015), who evaluated crossbred animals created by crossing Angus \times Nelore and Simmental \times Nelore cows and Angus, Bonsmara, and Canchim bulls; and purebred and crossbred calves derived from Nellore, Brangus, Wagyu, and $\frac{1}{2}$ Brangus \times $\frac{1}{2}$ Nellore cows, crossed with bulls of the Aberdeen Angus, Red Angus, Brangus, Nellore, and Wagyu breeds, respectively.

According to Sushma et al. (2006), the weight differences between sexes may be attributed to production of different hormones and their effects on growth. Souza et al. (2000) reported that, under the same environmental conditions, males are 10% heavier than females due to the greater weight gain capacity presented by male calves and their more developed structure. In the current research, males were 8 kg heavier than females for WW and 29 kg heavier for YW. Males' and females' average weights found were lower than reference standard for ponderal development for Purunã animals in pasture systems

(175 and 165 kg for WW and 235 and 197 kg for YW, for males and females, respectively), but they were higher than average weights found in the genetic evaluation of Purunã breed in 2019 (167.30 kg at weaning for males and 158.39 kg for females) (Santos and Perotto, 2019).

Considering all the population, the average WW (166 kg) was lower than the weights reported by Barichello et al. (2010) and Moura et al. (2014), similar to that found by Fialho et al. (2015), and higher than those presented by Fernandes et al. (2002) and Gomes et al. (2013), who reported a WW (kg) of 208.9 (Canchim), 205.0 (Purunã), 177.7 (crossbred), 154.8 (Charolais), and 155.9 (Caracu crossbred), respectively. The average YW (209.16 kg) was greater than the average YW found by Leite et al. (2010) and similar to the result found by Baldi et al. (2010), who reported YW for Purunã and Canchim cattle of 196.23 and 219.9 kg, respectively. The variation of the analyzed data may be a result of differences in herd management and breed compositions in the evaluated population.

Regarding age of dams at calving, previous studies have reported its significant linear and quadratic effects on WW (Santos et al., 2011; Szabó et al., 2012; Chud et al., 2014; Goldberg and Ravagnolo, 2015), corroborating the results found in the current study ($P < 0.01$). In addition, Queiroz et al. (2013) found significant linear and quadratic effects of age of dam on YW gain in a Brangus cattle population, showing the influence of this parameter on the performance of calves after the weaning period. Similarly, in the current study, significant linear effect of age of dam at calving was found for YW ($P < 0.01$), which can be interpreted as a residual effect of this source of variation, since the animal performance after weaning may be connected to the expression of its own genetic potential for growth.

The maternal genetic variance also decreased when age of calves increased, and its influence represented 11 and 2.5% of the total phenotypic variation for WW and YW, respectively. In a study performed by Sarmiento et al. (2003) with Nellore cattle, the maternal effect contribution for the total phenotypic variation until weaning was approximately 45%, decreasing to a maternal effect contribution of 12 and 0.6% for YW and 18-month weight, respectively. Costa et al. (2011) observed a decrease in the maternal effect on WW compared with YW in Angus cattle, with an estimated maternal effect contribution for the phenotypic variation of 23.2 and 11.6% for WW and YW, respectively.

The direct genetic and maternal heritability estimates for WW and YW were of low and medium magnitude (Table 3). Different heritability estimates for body weights in Charolais, Caracu, Aberdeen Angus, and Canchim breeds and crossbred animals were found in literature (Crews Jr. et al., 2004; El-Saied et al., 2006; Pereira et al., 2006, 2008; Utrera et al., 2007; Orengo et al., 2009; Weber et al., 2009; Baldi et al., 2010; Costa et al., 2011; Mello et al., 2013). Although several researchers have been studying body weights in purebred and crossbred beef cattle, as mentioned above, the genetic evaluation for WW and YW traits in a population including several genetic groups, which is derived from crosses between Charolais, Caracu, Aberdeen Angus, and Canchim breeds (Table 2), has not been yet reported.

The direct (0.21) and maternal (0.11) heritabilities estimated for WW were consistent with specialized literature. According to literature reports, direct and maternal heritabilities for WW ranged from 0.13 to 0.43 and from 0.01 to 0.25, respectively, in purebred and crossbred cattle populations (Pereira et al., 2006, 2008; Costa et al., 2011; Haile et al., 2011; Lukaszewicz et al., 2015; Schiermiester et al., 2015; Torres-Vázquez and Spangler, 2016). Previous studies with purebreds, used to form the Purunã breed, have reported heritability estimates close to those of the current study. In studies with a Canchim, Charolais, and Angus cattle populations, direct and maternal heritabilities estimated for WW were 0.23 and 0.09, 0.23 and 0.17, and 0.24 and 0.07, respectively (Orengo et al., 2009; Weber et al., 2009; Baldi et al., 2010).

The YW and YWNM models resulted in genetic parameter estimates inconsistent with specialized literature. The direct heritability estimates for YW and YWNM (0.05 and 0.06, respectively) were lower than the results found in Canchim (0.23 and 0.46), Angus (0.43), and Caracu (0.36) breeds (Pereira et al., 2008; Baldi et al., 2010; Costa et al., 2011; Mello et al., 2014). The maternal heritability estimated (0.02) for YW was close to heritability described in studies with purebred and crossbred cattle populations (0.03 and 0.05) (Baldi et al., 2010; Haile et al., 2011; Schiermiester et al., 2015). However, there are

no reports in literature of studies evaluating a cattle population with several genetic groups derived from crosses between Charolais, Caracu, Aberdeen Angus, and Canchim breeds as the current study (Table 2). According to Canaza-Cayo et al. (2018), different factors can influence the genetic parameter estimates such as population size, analysis model, evaluated traits, and others. Previous studies found heritability estimates higher in a smaller population than the current study (Pereira et al., 2008; Mello et al., 2013). Thus, we could assume that the population size was appropriate to estimate the genetic parameters for YW. The heritabilities in the current study may have been influenced by the different estimates of direct and maternal genetic variances, which may be affected by the heterogeneity of the population, composed by several genetic groups used in crossbreedings with different heterosis levels.

Heterosis effects has immense importance in the performance of crossbreeds in many production systems (Schiermiester et al., 2015; Otto et al., 2018; Prastowo et al., 2021). Although the genetic basis of heterosis is still a subject of investigation, its effect is difficult to quantify. Thus, heterozygosity, which represents the proportion of heterozygote genotypes in the population, may be a useful indicator and has been often used to evaluate the degree of heterosis (Akanno et al., 2018; Iversen et al., 2019; Prastowo et al., 2021). According to Queiroz et al. (2013), heterozygosity has a significant effect on performance traits in Brangus animals and its inclusion in the model may improve prediction accuracy (Raidan et al., 2018). Therefore, heterozygosity should be included in models for estimation of genetic parameters and breeding values of crossbred animals (Schiermiester et al., 2015; Raidan et al., 2018; Iversen et al., 2019). Although the benefits of using the heterozygosity effect on growth traits have been well documented, given the limitations of our data, we were not able to include it in the model to evaluate WW and YW in the current population.

The genetic groups in the evaluated population can be a problem to fit the analysis to a conventional animal model. Thus, the used model may not have been the better fit model to evaluate YW in this population, influencing the heritability estimates. Besides the inclusion of heterozygosity effect on the model, the multiple-breed evaluation can be an option to improve the estimation of genetic parameters and breeding values in a composite population. To evaluate crossbred and purebred individuals in one analysis, differences in breed composition, as additive and nonadditive effects and heterogeneous variances, should be included in the genetic evaluation to allow a better estimate of animals with two or more breeds in their pedigree (Cardoso and Tempelman, 2004; VanRaden et al., 2007, 2011). Ribeiro et al. (2019) described that in a multiple-breed population, the breed composition of the evaluated progeny can influence the parameters and breeding values of the sires. According to Cardoso and Tempelman (2004), a multiple-breed animal model represents a viable alternative to conventional animal model for multiple-breed genetic evaluations. These authors found superior fit for multiple-breed animal model evaluating simulated data and inferences for additive heritabilities substantially different in a Nellore-Hereford population. Moreover, a meta-analysis showed that direct and maternal breed and heterosis effect estimated using crossbreeding study data can supplement the direct prediction in a multibreed evaluation (Williams et al., 2013). Although the multiple-breed evaluation can be an alternative to evaluate YW, to better understand their genetic architecture in the evaluated composite population, this analysis requires a much larger number of variance components to be estimated and it is computationally more complex, besides presenting multicollinearity problems, and thus may be cumbersome for practical applications (Cardoso and Tempelman, 2004; Bueno et al., 2012; Prestes et al., 2019).

Direct additive genetic correlation between WW and YW (0.85 ± 0.07) was lower than the 0.90 estimate described by Baldi et al. (2010) and Costa et al. (2011) in Canchim and Caracu animals, respectively, and higher than the 0.84 estimate reported in an Angus cattle population (Pereira et al., 2008). The estimated genetic correlation suggests that genetically superior animals for body weight at weaning will also be superior at a later age. In this context, the selection for higher weight at young ages may result in increased YW.

Regarding the YW and YWNM model comparison, according to Corrêa et al. (2009), the lower DIC estimate represents better fit. The DIC values (Table 4) indicate that the YW model presented better

fit. Moreover, Spiegelhalter et al. (2002) stated that to be considered as different the evaluated models must have differences in DIC ranging from 3 to 7. The DIC difference value found in the current study (16.61) was higher than these reference values, indicating the superiority of YW over YWNM. The MPP and average ACC of breeding values of each model was also calculated. The accuracy increased in 9% using the YW model, showing that this model allowed predicting breeding values more accurately than YWNM. Furthermore, the highest MMP was observed in YW model, supporting the superiority of this model over YWNM.

The Spearman's correlation found in the current study (0.99) suggests that the association between the classifications of the individuals evaluated using the YW and YWNM models is high. The observed percentages of common selected individuals in both models confirm this result, in which approximately 96% of animals were selected using the three evaluated percentage thresholds (1, 10, and 20%). Based on these results, we can infer that the model used (YW or YWNM) had a small effect on the identification of the best animals, resulting in the selection of the best animals using both models. Thus, both models were efficient to predict the genetic breeding values of animals in this population. On the other hand, based on the average ACC results, choosing the YW model would result in greater accuracies and less bias associated with the estimates.

5. Conclusions

The current study provides information on weaning weight and yearling weight traits of a composite population used to form the Purunã breed. The genetic parameters for yearling weight provided by models including and ignoring the maternal effect are inconsistent with specialized literature. The heritability estimates for yearling weight may have been influenced by the heterogeneity of the population, composed by several genetic groups, and by using a conventional animal model ignoring the heterozygosity effect, which may not have been the best fit model to evaluate the yearling weight in this population. The values of Deviance Information Criterion, model posterior probabilities, and accuracy of breeding values indicate that the yearling weight outperforms the model ignoring the maternal effect on yearling weight (YWNM), but the rank correlation and percentages of individuals selected in common suggest that the best animals would be selected independently of the model chosen.

Conflict of Interest

The authors declare no conflict of interest.

Author Contributions

Conceptualization: P.I. Otto. Data curation: P.I. Otto and A.L. Santos. Formal analysis: P.I. Otto, A.L. Santos, S.N. Oliveira and F.E.Z. Souza. Funding acquisition: P.I. Otto and D. Perotto. Investigation: P.I. Otto, A.L. Santos, D. Perotto, S.N. Oliveira and F.E.Z. Souza. Methodology: P.I. Otto, A.L. Santos, S.N. Oliveira and F.E.Z. Souza. Project administration: P.I. Otto. Resources: P.I. Otto and F.E.Z. Souza. Software: P.I. Otto and S.N. Oliveira. Visualization: F. Granzotto and F.E.Z. Souza. Writing-original draft: P.I. Otto. Writing-review & editing: P.I. Otto, F. Granzotto, D.O.R. Gobo and G. Thomazini.

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References

- Akanno, E. C.; Abo-Ismael, M. K.; Chen, L.; Crowley, J. J.; Wang, Z.; Li, C.; Basarab, J. A.; MacNeil, M. D. and Plastow, G. S. 2018. Modeling heterotic effects in beef cattle using genome-wide SNP-marker genotypes. *Journal of Animal Science* 96:830-845. <https://doi.org/10.1093/jas/skx002>
- Alencar, M. M.; Gonçalves, A. C.; Barichello, F.; Barbosa, P. F.; Barbosa, R. T.; Cruz, G. M. and Tullio, R. R. 2009. Desempenho de bezerros cruzados do nascimento à desmama. In: *Anais da 46ª Reunião Anual da Sociedade Brasileira de Zootecnia*. SBZ, Maringá.
- Araújo, R. O.; Rorato, P. R. N.; Weber, T.; Everling, D. M.; Lopes, J. S. and Dornelles, M. A. 2010. Genetic parameters and phenotypic and genetic trends for weight at weaning and visual scores during this phase estimated for Angus-Nellore crossbred young bulls. *Revista Brasileira de Zootecnia* 39:2398-2408. <https://doi.org/10.1590/s1516-35982010001100012>
- Baldi, F.; Alencar, M. M. and Albuquerque, L. G. 2010. Estimativas de parâmetros genéticos para características de crescimento em bovinos da raça Canchim utilizando modelos de dimensão finita. *Revista Brasileira de Zootecnia* 39:2409-2417. <https://doi.org/10.1590/S1516-35982010001100013>
- Barichello, F.; Alencar, M. M.; Torres Júnior, R. A. A. and Silva, L. O. C. 2010. Herdabilidade e correlações quanto a peso, perímetro escrotal e escores visuais à desmama, em bovinos Canchim. *Pesquisa Agropecuária Brasileira* 45:563-570. <https://doi.org/10.1590/S0100-204X2010000600005>
- Bueno, R. S.; Torres, R. A.; Ferraz, J. B. S.; Lopes, P. S.; Eler, J. P.; Mourão, G. B.; Almeida e Silva, M. and Mattos, E. C. 2012. Métodos de estimação de efeitos genéticos não-aditivos para características de peso e perímetro escrotal em bovinos de corte mestiços. *Revista Brasileira de Zootecnia* 41:1140-1145. <https://doi.org/10.1590/S1516-35982012000500009>
- Canaza-Cayo, A. W.; Lopes, P. S.; Cobuci, J. A.; Martins, M. F. and Silva, M. V. G. B. 2018. Genetic parameters of milk production and reproduction traits of Girolando cattle in Brazil. *Italian Journal of Animal Science* 17:22-30. <https://doi.org/10.1080/1828051X.2017.1335180>
- Cardoso, F. F. and Tempelman, R. J. 2004. Hierarchical Bayes multiple-breed inference with an application to genetic evaluation of a Nelore-Hereford population. *Journal of Animal Science* 82:1589-1601. <https://doi.org/10.2527/2004.8261589x>
- Chud, T. C. S.; Caetano, S. L.; Buzanskas, M. E.; Grossi, D. A.; Guidolin, D. G. F.; Nascimento, G. B.; Rosa, J. O.; Lôbo, R. B. and Munari, D. P. 2014. Genetic analysis for gestation length, birth weight, weaning weight, and accumulated productivity in Nellore beef cattle. *Livestock Science* 170:16-21. <https://doi.org/10.1016/j.livsci.2014.09.024>
- Corrêa, M. B. B.; Dionello, N. J. L. and Cardoso, F. F. 2006. Influência ambiental sobre características de desempenho pré-desmama de bovinos Devon no Rio Grande do Sul. *Revista Brasileira de Zootecnia* 35:1005-1011. <https://doi.org/10.1590/S1516-35982006000400010>
- Corrêa, M. B. B.; Dionello, N. J. L. and Cardoso, F. F. 2009. Caracterização da interação genótipo-ambiente e comparação entre modelos para ajuste do ganho pós-demama de bovinos Devon via normas de reação. *Revista Brasileira de Zootecnia* 38:1468-1477. <https://doi.org/10.1590/S1516-35982009000800010>
- Costa, R. B.; Misztal, I.; Elzo, M. A.; Bertrand, J. K.; Silva, L. O. C. and Łukaszewicz, M. 2011. Estimation of genetic parameters for mature weight in Angus cattle. *Journal of Animal Science* 89:2680-2686. <https://doi.org/10.2527/jas.2010-3574>
- Crews, D. H.; Lowerison, M.; Caron, N. and Kemp, R. A. 2004. Genetic parameters among growth and carcass traits of Canadian Charolais cattle. *Canadian Journal of Animal Science* 84:589-597. <https://doi.org/10.4141/A04-019>
- El-Saied, U. M.; de la Fuente, L. F.; Rodríguez, R. and San Primitivo, F. 2006. Genetic parameter estimates for birth and weaning weights, pre-weaning daily weight gain and three type traits for Charolais beef cattle in Spain. *Spanish Journal of Agricultural Research* 4:146-155. <https://doi.org/10.5424/sjar/2006042-186>
- Fernandes, H. D.; Ferreira, G. B. B. and Rorato, P. R. N. 2002. Tendências e parâmetros genéticos para características pré-desmama em bovinos da raça Charolês criados no Rio Grande do Sul. *Revista Brasileira de Zootecnia* 31:321-330. <https://doi.org/10.1590/S1516-35982002000200005>
- Fialho, F. R. L.; Rezende, M. P. G.; Souza, J. C.; Silva, R. M.; Oliveira, N. M. and Silveira, M. V. 2015. Performance in preweaning pure and crossbred calves in the Mato Grosso do Sul Pantanal region, Aquidauana, Mato Grosso do Sul State, Brazil. *Acta Scientiarum. Animal Sciences* 37:437. <https://doi.org/10.4025/actascianimsci.v37i4.28345>
- Geweke, J. 1992. Evaluating the accuracy of sampling-based approaches to the calculation of posterior moments. p.169-193. In: *Bayesian statistics 4*. Bernardo, J. M.; Berger, J. O.; Dawid, A. P. and Smith, A. F. M., eds. Oxford University Press, Oxford.
- Goldberg, V. and Ravagnolo, O. 2015. Description of the growth curve for Angus pasture-fed cows under extensive systems. *Journal of Animal Science* 93:4285-4290. <https://doi.org/10.2527/jas.2015-9208>
- Gomes, F. J.; Torres Júnior, R. A. A.; Menezes, G. R. O.; Oliveira, J. C. K.; Battistelli, J. V. F. and Rocha, T. F. 2013. Alternativas de raças usadas como paternas e maternas em cruzamentos triplos de bovinos de corte na fase de cria. In: *X Simpósio Brasileiro de Melhoramento Animal*. Uberaba, MG.

- Haile, A.; Joshi, B. K.; Ayalew, W.; Tegegne, A. and Singh, A. 2011. Genetic evaluation of Ethiopian Boran cattle and their crosses with Holstein Friesian for growth performance in central Ethiopia. *Journal of Animal Breeding and Genetics* 128:133-140. <https://doi.org/10.1111/j.1439-0388.2010.00882.x>
- Iversen, M. W.; Nordbø, Ø.; Gjerlaug-Enger, E.; Grindflek, E.; Lopes, M. S. and Meuwissen, T. 2019. Effects of heterozygosity on performance of purebred and crossbred pigs. *Genetics Selection Evolution* 51:8. <https://doi.org/10.1186/s12711-019-0450-1>
- Leite, M. C. P.; Martins, E. N.; Perotto, D. and Santos, A. L. 2010. Estimativas de parâmetros genéticos para características de crescimento de diferentes raças e cruzamentos de bovinos de corte envolvidos na formação da raça Purunã. In: VIII Simpósio Brasileiro de Melhoramento Animal. Maringá, PR.
- Lukaszewicz, M.; Davis, R.; Bertrand, J. K.; Misztal, I. and Tsuruta, S. 2015. Correlations between purebred and crossbred body weight traits in Limousin and Limousin-Angus populations. *Journal of Animal Science* 93:1490-1493. <https://doi.org/10.2527/jas.2014-8285>
- Madureira, A. P.; Oliveira, H. N.; Rosa, G. J. M.; Bezerra, L. F. and Marques, L. F. A. 2009. Inferência bayesiana na predição de valores genéticos do peso aos 365 dias de bovinos de corte. *Archivos de Zootecnia* 58:265-275.
- Mello, S. P.; Alencar, M. M.; Passafaro, T. L. and Toral, F. L. B. 2013. Parâmetros genéticos de relações de pesos, características de fertilidade e crescimento em vacas da raça Canchim. *Boletim de Indústria Animal* 70:235-241. <https://doi.org/10.17523/bia.v70n3p235>
- Mello, S. P.; Alencar, M. M.; Santos, D. C. C. and Toral, F. L. B. 2014. Análise genética de características de fertilidade, de crescimento e de produtividade em vacas da raça Canchim. *Arquivo Brasileiro de Medicina Veterinária e Zootecnia* 66:555-562. <https://doi.org/10.1590/1678-41626876>
- Miller, S. 2010. Genetic improvement of beef cattle through opportunities in genomics. *Revista Brasileira de Zootecnia* 39:247-255. <https://doi.org/10.1590/S1516-35982010001300027>
- Moreira, H. L.; Savegnago, R. P.; Freitas, L. A.; Lôbo, R. B.; Bezerra, L. A. F. and Paz, C. C. P. 2019. Breeding goals and economic values for Nellore cattle in a full-cycle production system. *Acta Scientiarum. Animal Sciences* 41:e43361. <https://doi.org/10.4025/actascianimsci.v41i1.43361>
- Moura, I. C. F.; Kuss, F.; Moletta, J. L.; Menezes, L. F. G.; Henrique, D. S.; Cherubin, A. A. and Paris, M. 2014. Eficiência produtiva e reprodutiva de vacas de corte Purunã de diferentes categorias. *Semina: Ciências Agrárias* 35:2555-2562. <https://doi.org/10.5433/1679-0359.2014v35n4Suplp2555>
- Mrode, R. A. 2014. *Linear models for the prediction of animal breeding values*. 3rd ed. CABI, Oxfordshire, UK.
- Orege, J. S. K.; Ilatsia, E. D.; Kosgey, I. S. and Kahi, A. K. 2009. Genetic and phenotypic parameters and annual trends for growth and fertility traits of Charolais and Hereford beef cattle breeds in Kenya. *Tropical Animal Health and Production* 41:767-774. <https://doi.org/10.1007/s11250-008-9250-2>
- Otto, P. I.; Guimarães, S. E. F.; Verardo, L. L.; Azevedo, A. L. S.; Vandenplas, J.; Soares, A. C. C.; Sevillano, C. A.; Veroneze, R.; Pires, M. F. A.; Freitas, C.; Prata, M. C. A.; Furlong, J.; Verneque, R. S.; Martins, M. F.; Panetto, J. C. C.; Carvalho, W. A.; Gobo, D. O. R.; Silva, M. V. G. B. and Machado, M. A. 2018. Genome-wide association studies for tick resistance in *Bos taurus* × *Bos indicus* crossbred cattle: A deeper look into this intricate mechanism. *Journal of Dairy Science* 101:11020-11032. <https://doi.org/10.3168/jds.2017-14223>
- Pereira, M. C.; Mercadante, M. E. Z.; Albuquerque, L. G.; Razook, A. G. and Figueiredo, L. A. 2006. Estimativas de parâmetros genéticos de características de crescimento em um rebanho Caracu selecionado para peso ao sobreano. *Revista Brasileira de Zootecnia* 35:1669-1676. <https://doi.org/10.1590/s1516-35982006000600013>
- Pereira, M. C.; Mercadante, M. E. Z.; Razook, A. G.; Figueiredo, L. A. and Albuquerque, L. G. 2008. Results of 23 years of selection for post-weaning weight in a Caracu beef herd. *South African Journal of Animal Science* 38:136-144.
- Prastowo, S.; Widowati, I. F. I.; Nuraini, D. M. and Widyas, N. 2021. Simulating allele frequency changes in Indonesian goat crossbreeding scenarios. *IOP Conference Series: Earth and Environmental Science* 637:012025. <https://doi.org/10.1088/1755-1315/637/1/012025>
- Prestes, A. M.; Oliveira, M. M.; Mello, F. C. B.; Rorato, P. R. N.; Lopes, J. S.; Feltes, G. L. and Bravo, A. P. 2019. Genetic evaluation models for post-weaning weight gain in a multibreed Angus-Nelore population. *Pesquisa Agropecuária Brasileira* 54:e00694. <https://doi.org/10.1590/S1678-3921.PAB2019.V54.00694>
- Queiroz, S. A.; Oliveira, J. A.; Costa, G. Z. and Fries, L. A. 2013. Efeitos ambientais e genéticos sobre escores visuais e ganho em peso ao sobreano de bovinos Brangus. *Archivos de Zootecnia* 62:111-121.
- R Core Team. 2018. *R: A language and environment for statistical computing*. R Foundation for Statistical Computing, Vienna. Available at: <<https://www.r-project.org/>>. Accessed on: Apr. 19, 2021.
- Raftery, A. E. and Lewis, S. M. 1992. Comment: One Long Run with Diagnostics: Implementation Strategies for Markov Chain Monte Carlo. *Statistical Science* 7:493-497. <https://doi.org/10.1214/ss/1177011143>
- Raidan, F. S. S.; Porto-Neto, L. R.; Li, Y.; Lehnert, S. A.; Vitezica, Z. G. and Reverter, A. 2018. Evaluation of nonadditive effects in yearling weight of tropical beef cattle. *Journal of Animal Science* 96:4028-4034. <https://doi.org/10.1093/jas/sky275>

- Ribeiro, V. M. P.; Raidan, F. S. S.; Barbosa, A. R.; Silva, M. V. G. B.; Cardoso, F. F. and Toral, F. L. B. 2019. Multiple trait and random regression models using linear splines for genetic evaluation of multiple breed populations. *Journal of Dairy Science* 102:464-475. <https://doi.org/10.3168/jds.2017-14321>
- Santos, G. C. J.; Lira, T. S.; Pereira, L. S.; Lopes, F. B. and Ferreira, J. L. 2011. Efeitos não genéticos sobre características produtivas em rebanhos Nelore criados na região Norte do Brasil. *Acta Veterinaria Brasilica* 5:385-392.
- Santos, A. L. and Perotto, D. 2019. AGPUR 2019 - Avaliação genética Purunã de 2019: Raça Purunã. IAPAR, Londrina.
- Sarmiento, J. L. R.; Pimenta Filho, E. C.; Ribeiro, M. N. and Martins Filho, R. 2003. Efeitos ambientais e genéticos sobre o ganho em peso diário de bovinos Nelore no estado da Paraíba. *Revista Brasileira de Zootecnia* 32:325-330. <https://doi.org/10.1590/S1516-35982003000200010>
- Schiermiester, L. N.; Thallman, R. M.; Kuehn, L. A.; Kachman, S. D. and Spangler, M. L. 2015. Estimation of breed-specific heterosis effects for birth, weaning, and yearling weight in cattle. *Journal of Animal Science* 93:46-52. <https://doi.org/10.2527/jas.2014-8493>
- Silva, F. F.; Rosa, G. J. M.; Guimarães, S. E. F.; Lopes, P. S. and de los Campos, G. 2011. Three-step Bayesian factor analysis applied to QTL detection in crosses between outbred pig populations. *Livestock Science* 142:210-215. <https://doi.org/10.1016/j.livsci.2011.07.012>
- Silva, J. A. II V.; Marcelo, E. T.; Ribeiro, C. B.; Maiorano, A. M.; Curi, R. A.; Oliveira, H. N. and Mota, M. D. S. 2012. Análise genética de características de crescimento e perímetro escrotal em bovinos da raça Brangus. *Pesquisa Agropecuária Brasileira* 47:1166-1173. <https://doi.org/10.1590/S0100-204X2012000800018>
- Silva Neto, W. A. and Bacchi, M. R. P. 2014. Growth of Brazilian beef production: effect of shocks of supply and demand. *Revista de Economia e Sociologia Rural* 52:209-228. <https://doi.org/10.1590/S0103-20032014000200001>
- Souza, J. C.; Ramos, A. A.; Silva, L. O. C.; Euclides Filho, K.; Alencar, M. M.; Wechsler, F. S. and Ferraz Filho, P. B. 2000. Fatores do ambiente sobre o peso ao desmame de bezerros da raça Nelore em regiões tropicais brasileiras. *Ciência Rural* 30:881-885. <https://doi.org/10.1590/S0103-84782000000500024>
- Spiegelhalter, D. J.; Best, N. G.; Carlin, B. P. and Van Der Linde, A. 2002. Bayesian measures of model complexity and fit. *Journal of the Royal Statistical Society Series B - Statistical Methodology* 64:583-639. <https://doi.org/10.1111/1467-9868.00353>
- Sushma, G.; Ramesh, B. G.; Vinoo, G. V.; Reddy, N. and Reddy, S. 2006. Influence of genetic and non-genetic factors of body weights and body measurements of Ongole cattle. *Indian Journal of Animal Science* 75:228-235.
- Szabó, F.; Szabó, E. and Bene, S. 2012. Statistic and genetic parameters of 205-day weaning weight of beef calves. *Archives Animal Breeding* 55:552-561. <https://doi.org/10.5194/aab-55-552-2012>
- Torres-Vázquez, J. A. and Spangler, M. L. 2016. Genetic parameters for docility, weaning weight, yearling weight, and intramuscular fat percentage in Hereford cattle. *Journal of Animal Science* 94:21-27. <https://doi.org/10.2527/jas.2015-9566>
- USDA. 2019. Brazil - Livestock and Products Semi-annual - 2019 Semiannual Livestock. United States Department of Agriculture - USDA.
- Utrera, Á. R.; Velázquez, G. M.; Tsurutac, S.; Bertrandc, J. K.; Murillo, V. E. V. and Bermúdez, M. M. 2007. Estimadores de parámetros genéticos para características de crecimiento de ganado Charolais mexicano. *Técnica Pecuaria en México* 45:121-130.
- VanRaden, P. M.; Olson, K. M.; Wiggans, G. R.; Cole, J. B. and Tooker, M. E. 2011. Genomic inbreeding and relationships among Holsteins, Jerseys, and Brown Swiss. *Journal of Dairy Science* 94:5673-5682. <https://doi.org/10.3168/jds.2011-4500>
- VanRaden, P. M.; Tooker, M. E.; Cole, J. B.; Wiggans, G. R. and Magonigal Jr., J. H. 2007. Genetic evaluations for mixed-breed populations. *Journal of Dairy Science* 90:2434-2441. <https://doi.org/10.3168/jds.2006-704>
- Weber, T.; Rorato, P. R. N.; Lopes, J. S.; Comin, J. G.; Dornelles, M. A. and Araújo, R. O. 2009. Parâmetros genéticos e tendências genéticas e fenotípicas para características produtivas e de conformação na fase pré-desmama em uma população da raça Aberdeen Angus. *Revista Brasileira de Zootecnia* 38:832-842. <https://doi.org/10.1590/S1516-35982009000500008>
- Williams, J. L.; Aguilar, I.; Rekaya, R. and Bertrand, J. K. 2013. Estimation of breed and heterosis effects for growth and carcass traits in cattle using published crossbreeding studies. *Journal of Animal Science* 88:460-466. <https://doi.org/10.2527/jas.2008-1628>