

# Genetic parameters for growth, reproductive, and carcass traits in Tabapuã cattle

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**ABSTRACT** - We aimed to estimate genetic parameters for growth, reproductive, and carcass traits in Tabapuã cattle. Phenotypic data were collected between 1990 and 2019 in 1,218 farms, and the pedigree file had 340,868 animals. The traits evaluated were body weight at 120 (W120), 210 (W210), 365 (W365), and 550 (W550) days of age; age at first calving (AFC), scrotal circumference at 365 days of age (SC365), ribeye area (REA), backfat thickness (BF), and rump fat thickness (RF). The (co)variance components were estimated using the restricted maximum likelihood method, considering single and two-traits animal models. For all traits, the models considered fixed, direct additive genetic, and residual random effects. In addition, for W120 and W210, the maternal additive genetic and maternal permanent environmental effects were also included. Heritabilities for W120, W210, W365, W550, SC365, REA, BF, and RF were of moderate magnitude (0.15, 0.16, 0.23, 0.19, 0.22, 0.36, 0.31, and 0.27, respectively). Low heritability was observed for AFC (0.07). The genetic correlations between growth traits were higher than 0.90, while AFC and SC365 presented negative moderate correlation (-0.66). The REA showed low genetic correlations with BF (0.07) and RF (0.07), whereas BF and RF were highly correlated (0.77). Considering the heritability estimates, selection for AFC would result in limited genetic gain, while for the other traits, it would be satisfactory. Based on the high genetic correlations between growth traits, selection of Tabapuã animals can be performed at younger ages. Additionally, animals can be indirectly selected for AFC through SC365, and only one fat thickness trait may be used in the selection process considering the high genetic correlation and similar heritability values for BF and RF.

**Keywords:** backfat thickness, genetic correlations, heritability, scrotal circumference, weight, Zebu beef cattle

## 1. Introduction

Zebu breeds represent the majority of Brazilian beef herds due to their greater tolerance to endo- and ectoparasites, heat, solar radiation, and humidity, traits of great importance for production systems in tropical environments (Rosa et al., 2013). According to the Associação Brasileira dos Criadores de Zebu (ABCZ, 2021), there are currently nine registered Zebu breeds in Brazil. Among them, Tabapuã stands up for presenting good reproductive efficiency, high growth rates, and good quality carcasses (Evangelista et al., 2020; ABCT, 2020; ABCZ, 2021).

To implement a beef cattle breeding program, it is important to establish the selection objectives and criteria, as well as estimate the genetic and phenotypic parameters related to the target traits (Marques et al., 2013). In Tabapuã breed, the selection criteria mainly involve growth, reproductive, and carcass traits, which are equally important to achieve the productive and reproductive selection objectives in the breed.

Growth traits are related to the economic efficiency of the system, with emphasis on the weights at weaning, yearling, and 550 days of age (Evangelista et al., 2020). Regarding the reproductive traits, age at first calving (AFC) and scrotal circumference (SC) are widely considered as selection criteria for beef cattle. The inclusion of reproductive traits in breeding programs is essential to improve the herd reproductive efficiency, decreasing the generation interval (Bernardes et al., 2015). The carcass traits have been recently included in beef cattle selection programs. Ribeye area (REA) is closely related to the animal's potential for muscularity, growth, weight gain, and muscle:bone ratio (Sugisawa et al., 2013). In addition, backfat (BF) and rump fat (RF) thickness are indicative of carcass degree of finishing and equally important to aid the setting of the ideal moment for slaughtering animals of different genetic groups (Rosa et al., 2014).

The knowledge of genetic parameters for these traits is crucial for the selection of genetically superior animals and, consequently, for achieving greater genetic progress in beef production. Nonetheless, to our knowledge, studies on genetic parameters for these traits are still scarce in Tabapuã cattle, especially for reproductive and carcass traits. In this way, we aimed to estimate genetic parameters for weight at 120 (W120), 210 (W210), 365 (W365), and 550 (W550) days of age, AFC, SC at 365 days (SC365), REA, BF, and RF in Brazilian Tabapuã herd.

## 2. Material and Methods

The data were provided by ABCZ. Phenotypic information (Table 1) of growth, reproductive, and carcass traits from Tabapuã animals were collected between 1990 and 2019 in 1,218 farms located in 23 Brazilian states and the Federal District. The pedigree file had 340,868 animals.

Ribeye area, BF, and RF records were obtained *in vivo* by ultrasound. Ribeye area and BF were measured between the 12th and 13th ribs, in the *longissimus dorsi* muscle, and RF was measured in the *gluteus medius* and *biceps femoris* muscles junction, located between the ischium and the ileum, parallel to the vertebra. In the analyses, only animals with measurements between 12 and 24 months of age were considered.

Data quality control analysis was performed to remove inconsistent information in the pedigree and phenotype files. The Interquartile Range (IQR) rule was used to remove outliers for all traits using a boxplot graphic, i.e., phenotypes below the lower ( $Q1 - 1.5 \times (Q3 - Q1)$ ) or above the upper bounds

**Table 1** - Number of animals (N), number of contemporary groups (CG), mean, standard deviation (SD), minimum (Min), maximum (Max), and coefficient of variation (CV, %) values of growth, reproductive, and carcass traits in Tabapuã cattle

Trait	N	CG	Mean	SD	Min	Max	CV (%)
W120 (kg)	83,294	4,486	128.16	21.98	67.63	189.53	17.15
W210 (kg)	74,537	4,065	188.91	31.99	100.70	278.20	16.93
W365 (kg)	44,583	3,261	250.23	49.74	103.60	398.20	19.88
W550 (kg)	24,859	2,069	332.38	62.90	159.00	510.20	18.92
AFC (days)	44,418	4,670	1212.50	230.0	618.00	1,921.0	18.97
SC365 (cm)	6,128	498	22.06	2.82	14.36	30.00	12.78
REA (cm <sup>2</sup> )	2,424	48	57.18	10.50	27.68	87.74	18.36
BF (mm)	2,330	48	3.02	1.31	0.76	7.10	43.31
RF (mm)	2,339	48	3.83	1.47	0.76	8.13	38.39

W120 - weight at 120 days; W210 - weight at 210 days; W365 - weight at 365 days; W550 - weight at 550 days; AFC - age at first calving; SC365 - scrotal circumference at 365 days; REA - ribeye area; BF - backfat thickness; RF - rump fat thickness.

( $Q3 + 1.5 \times (Q3 - Q1)$ ) of the boxplot were removed, in which  $Q1$  and  $Q3$  are the first and third quartiles of the boxplot, respectively, and  $Q3 - Q1$  is the IQR. In addition, observations that were not within the range of three standard deviations from the trait mean within each contemporary group (CG) were removed from the database. Contemporary groups with less than three observations were also excluded from the analyses (Silva et al., 2017). The data were edited using the R software (R Core Team, 2021).

The months of birth were grouped into four seasons of birth: season 1, from November to January; season 2, from February to April; season 3, from May to July; and season 4, from August to October. These seasons were defined by grouping the animals born in a close period, with a maximum difference of 120 days of age. The cows' ages at calving were grouped into 14 classes, so that class 1 considered cows with age at calving below 30 months; the subsequent classes were formed considering intervals every 12 months, and class 14 considered cows with age at calving greater than 174 months (Table 2). The CG for the growth and reproductive traits were formed by combining the herd and year and season of birth. For carcass traits, the CG were formed by the herd, year and season of birth, and date of measurement. The CG and the classes of cows' ages at calving concatenated with progeny's sex were defined as fixed effects in the model.

For the growth traits, a linear adjustment was performed to standardize the data to a common age endpoint, allowing for the fairest comparison among animals, since the animals are not necessarily weighted at the same age (BIF, 2018). The adjustments were performed according to the Beef Improvement Federation guidelines (BIF, 2018), as follows:

$$W120 = \frac{W120^* - BW}{N1} \times 120 + BW, \quad (1)$$

in which  $W120$  is the weight adjusted to 120 days,  $BW$  is the calf's weight at birth,  $W120^*$  is the weight of the animal on the weighing day, and  $N1$  is the number of days from birth to the weighing day. As the animals had no information on birth weight, 31 kg for females and 33 kg for males were set, as proposed by ABCZ based on the data evaluated in the Tabapuã cattle breeding program ([https://www.abczstat.com.br/comunicacoes/sumario/apresentacao/raca\\_tabapua.pdf](https://www.abczstat.com.br/comunicacoes/sumario/apresentacao/raca_tabapua.pdf)).

$$W210 = \frac{W210^* - BW}{N2} \times 210 + BW, \quad (2)$$

in which  $W210$  is the weight adjusted to 210 days,  $W210^*$  is the weight of the animal on the weighing day, and  $N2$  is the number of days from birth to the weighing day.

**Table 2 - Classes of age at calving of Tabapuã cows**

Class	Age range (months)
1	<30
2	30-42
3	42-54
4	54-66
5	66-78
6	78-90
7	90-102
8	102-114
9	114-126
10	126-138
11	138-150
12	150-162
13	162-174
14	>174

$$W365 = \frac{W365^* - W210}{N3} \times 155 + W210, \quad (3)$$

in which  $W365$  is the weight adjusted to 365 days,  $W365^*$  is the weight of the animal on the weighing day, and  $N3$  is the number of days from weighing at 210 days to the weighing day.

$$W550 = \frac{W550^* - W365}{N4} \times 185 + W365, \quad (4)$$

in which  $W550$  is the weight adjusted to 550 days,  $W550^*$  is the weight of the animal on the weighing day, and  $N4$  is the number of days from weighing at 365 days to the weighing day.

Scrotal circumference was adjusted using a logistic model (Nelder, 1961), as follows:

$$SC_t = \frac{A}{1+B(\exp(-kt))} + e, \quad (5)$$

in which  $SC_t$  is the SC measured at  $t$  days of age;  $A$  is the estimated SC at maturity;  $B$  indicates the proportion of mature testis with an asymptotic size to be obtained after birth, established by the initial values of SC and  $t$ ;  $k$  is the maturation index, indicating the rate at which SC approaches  $A$ ; and  $e$  is the random error. The adjustment by logistic regression is a method used in the official genetic evaluations of Tabapuã breed.

For all weights and SC adjustments, only animals that had measurement records within the range of  $\pm 45$  days (BIF, 2018) in relation to the standard age of measurement were considered. According to BIF, calves within a test group should have a maximum age range of 90 days, i.e., a range of  $\pm 45$  days from the date considerate for weight.

The (co)variance components were estimated using the restricted maximum likelihood (REML) method (Patterson and Thompson, 1971), considering single and two-traits animal models in BLUPF90 software (Miszta et al., 2015). Convergence achievement was assumed when the differences between the logarithm of the restrict likelihood function over sequential iterations were equal to or less than  $10^{-9}$  (default threshold value). Heritabilities were obtained from the variance components estimated in the single-trait analyses for all traits, whereas the correlations were obtained from the (co)variance components estimated in the two-traits analyses for all traits.

The two-traits model can be described as follows:

$$\mathbf{y} = \mathbf{X}\boldsymbol{\beta} + \mathbf{Z}_1\mathbf{d} + \mathbf{Z}_2\mathbf{m} + \mathbf{Z}_3\mathbf{pm} + \mathbf{e}, \quad (6)$$

in which  $\mathbf{y}$  is the vector of observations,  $\boldsymbol{\beta}$  is the vector of fixed effects,  $\mathbf{d}$  is the vector of direct additive genetic random effect,  $\mathbf{m}$  is the vector of maternal additive genetic random effect,  $\mathbf{pm}$  is the vector of maternal permanent environmental random effect, and  $\mathbf{e}$  is the vector of residual random effect;  $\mathbf{X}$ ,  $\mathbf{Z}_1$ ,  $\mathbf{Z}_2$ , and  $\mathbf{Z}_3$  are incidence matrices for fixed, direct additive genetic, maternal additive genetic, and maternal permanent environmental random effects, respectively. The same effects were considered in single and two-traits models; nevertheless, the model terms related to the maternal additive genetic and permanent environmental effects were added only for W120 and W210 traits.

The assumptions for the distributions of random effects in the two-traits model were set as follows:

$$\begin{bmatrix} \mathbf{d} \\ \mathbf{m} \end{bmatrix} \sim N(\mathbf{0}, \mathbf{G} \otimes \mathbf{A}), \quad \mathbf{pm} \sim N(\mathbf{0}, \mathbf{P} \otimes \mathbf{I}_v), \quad \text{and} \quad \mathbf{e} \sim N(\mathbf{0}, \mathbf{R} \otimes \mathbf{I}_n),$$

in which  $\mathbf{G}$  is the (co)variance matrix of direct and maternal additive genetic random effects (only when considered in the model),  $\mathbf{P}$  is the (co)variance matrix of maternal permanent environmental random effect,  $\mathbf{R}$  is the (co)variance matrix of residual random effects,  $\mathbf{A}$  is the numerator relationship matrix,  $\mathbf{I}_v$  is the identity matrix with order equal to the number of mothers ( $v$ ),  $\mathbf{I}_n$  is the identity matrix with order equal to the number of observations ( $n$ ), and  $\otimes$  is the Kronecker product.

The heritabilities were calculated as follows:

$$h^2_d = \frac{\sigma^2_d}{\sigma^2_p}, \quad (7)$$

in which  $h^2_d$  is the direct heritability,  $\sigma^2_d$  is the direct additive genetic variance, and  $\sigma^2_p$  is the phenotypic variance.

$$h^2_m = \frac{\sigma^2_m}{\sigma^2_p}, \quad (8)$$

in which  $h^2_m$  is the maternal heritability,  $\sigma^2_m$  is the maternal additive genetic variance, and  $\sigma^2_p$  is the phenotypic variance.

The correlations were obtained as follows:

$$r_G = \frac{Cov_{d(1,2)}}{\sigma_{d1} \cdot \sigma_{d2}}, \quad (9)$$

in which  $r_G$  is the genetic correlation,  $Cov_{d(1,2)}$  is the direct genetic covariance between traits 1 and 2,  $\sigma_{d1}$  is the direct additive genetic standard deviation of trait 1, and  $\sigma_{d2}$  is the direct additive genetic standard deviation of trait 2.

$$r_p = \frac{Cov_{p(1,2)}}{\sigma_{p1} \cdot \sigma_{p2}}, \quad (10)$$

in which  $r_p$  is the phenotypic correlation,  $Cov_{p(1,2)}$  is the phenotypic covariance between traits 1 and 2,  $\sigma_{p1}$  is the phenotypic standard deviation of trait 1, and  $\sigma_{p2}$  is the phenotypic standard deviation of trait 2.

$$r_{dm} = \frac{Cov_{dm}}{\sigma_d \cdot \sigma_m}, \quad (11)$$

in which  $r_{dm}$  is the correlation between direct and maternal additive genetic effects,  $Cov_{dm}$  is the covariance between direct and maternal additive genetic effects,  $\sigma_d$  is the standard deviation for direct additive genetic effect, and  $\sigma_m$  is the standard deviation for maternal additive genetic effect.

### 3. Results

Direct heritability estimates for growth traits were of moderate magnitude, with the lowest and highest values found for W120 (0.15) and W365 (0.23), respectively (Table 3). For reproductive traits, those estimates were low for AFC (0.07) and moderate for SC365 (0.22), and for carcass traits, they were also moderate, ranging from 0.27 to 0.36 (Table 3).

**Table 3** - Estimates of direct additive genetic ( $\sigma^2_d$ ), maternal additive genetic ( $\sigma^2_m$ ), maternal permanent environmental ( $\sigma^2_{pm}$ ), residual ( $\sigma^2_e$ ), and phenotypic ( $\sigma^2_p$ ) variances, direct ( $h^2_d$ ), and maternal ( $h^2_m$ ) heritabilities and standard errors (SE) of the respective heritabilities for growth, reproductive, and carcass traits of Tabapuã cattle obtained by single-trait animal models

Trait	$\sigma^2_d$	$\sigma^2_m$	$\sigma^2_{pm}$	$\sigma^2_e$	$\sigma^2_p$	$h^2_d$	SE	$h^2_m$	SE
W120	46.24	19.86	34.48	217.97	318.55	0.15	0.002	0.06	0.001
W210	104.97	39.15	67.42	425.38	636.93	0.16	0.003	0.06	0.002
W365	312.01	-	-	1018.10	1330.11	0.23	0.003	-	-
W550	320.16	-	-	1382.40	1701.56	0.19	0.004	-	-
AFC	2236.90	-	-	29132.00	31368.90	0.07	0.002	-	-
SC365	0.95	-	-	3.27	4.22	0.22	0.008	-	-
REA	14.27	-	-	25.73	40.00	0.36	0.014	-	-
BF	0.23	-	-	0.52	0.75	0.31	0.014	-	-
RF	0.38	-	-	1.03	1.41	0.27	0.014	-	-

W120 - weight at 120 days; W210 - weight at 210 days; W365 - weight at 365 days; W550 - weight at 550 days; AFC - age at first calving; SC365 - scrotal circumference at 365 days; REA - ribeye area; BF - backfat thickness; RF - rump fat thickness.

Estimates of genetic correlations between growth traits were favorable, positive, and high, ranging from 0.90 to 0.98 (0.98, 0.95 and 0.90 between W120 and the traits W210, W365, and W550, respectively; Table 4). Phenotypic correlations were also favorable, but with lower magnitude, ranging from 0.46 to 0.71 (0.71, 0.54, and 0.46 between W120 and the traits W210, W365, and W550, respectively). The genetic correlation between AFC and SC365 was negative and moderate (-0.66), while the phenotypic correlation was low (-0.09). The genetic correlations between AFC and the growth traits and REA were negative and low to moderate, ranging from -0.31 to -0.54 (-0.31, -0.42, -0.54, -0.54, and -0.49 between AFC and the traits W120, W210, W365, W550, and REA, respectively). Estimates of genetic correlation between SC365 and the growth traits were favorable and low to moderate, ranging from 0.34 to 0.51 (0.34, 0.43, 0.51, and 0.40 between SC365 and the traits W120, W210, W365, and W550, respectively). The genetic correlations between REA and the growth and reproductive traits were low, ranging from -0.39 to 0.42. Genetic correlation estimates between REA and BF were of low magnitude (both 0.07), and between BF and RF, it was favorable and of high magnitude (0.77) (Table 4). The correlations between AFC and fat traits were positive and low.

Correlation estimates between direct and maternal additive genetic effects for W120 and W210 were negative and low (-0.35 and -0.30, respectively).

**Table 4** - Estimates of genetic (above diagonal) and phenotypic (below diagonal) correlations with respective standard errors (in parentheses) for growth, reproductive, and carcass traits of Tabapuã cattle obtained by two-traits animal models

Trait	W120	W210	W365	W550	AFC	SC365	REA	BF	RF
W120	-	0.98 (0.001)	0.95 (0.002)	0.90 (0.004)	-0.31 (0.01)	0.34 (0.02)	0.27 (0.03)	0.38 (0.02)	0.11 (0.03)
W210	0.71 (0.0004)	-	0.98 (0.001)	0.95 (0.002)	-0.42 (0.01)	0.43 (0.01)	0.42 (0.02)	0.28 (0.02)	0.11 (0.03)
W365	0.54 (0.001)	0.69 (0.001)	-	0.99 (0.002)	-0.54 (0.01)	0.51 (0.01)	0.08 (0.03)	0.23 (0.03)	0.12 (0.03)
W550	0.46 (0.002)	0.58 (0.001)	0.85 (0.0003)	-	-0.54 (0.02)	0.40 (0.02)	0.19 (0.03)	0.13 (0.03)	0.14 (0.04)
AFC	-0.12 (0.002)	-0.15 (0.001)	-0.26 (0.002)	-0.28 (0.002)	-	-0.66 (0.02)	-0.39 (0.03)	0.44 (0.03)	0.39 (0.04)
SC365	0.29 (0.002)	0.36 (0.002)	0.46 (0.002)	0.41 (0.004)	-0.09 (0.002)	-	0.08 (0.03)	-0.22 (0.03)	-0.20 (0.03)
REA	0.26 (0.005)	0.31 (0.005)	0.38 (0.005)	0.48 (0.005)	-0.49 (0.01)	0.11 (0.01)	-	0.07 (0.03)	0.07 (0.03)
BF	0.09 (0.004)	0.06 (0.003)	0.19 (0.01)	0.31 (0.01)	-0.03 (0.01)	0.04 (0.01)	0.17 (0.005)	-	0.77 (0.01)
RF	0.03 (0.004)	0.04 (0.005)	0.12 (0.01)	0.21 (0.01)	-0.01 (0.01)	-0.02 (0.01)	0.19 (0.005)	0.58 (0.003)	-

W120 - weight at 120 days; W210 - weight at 210 days; W365 - weight at 365 days; W550 - weight at 550 days; AFC - age at first calving; SC365 - scrotal circumference at 365 days; REA - ribeye area; BF - backfat thickness; RF - rump fat thickness.

#### 4. Discussion

Most studies reporting genetic parameters for Tabapuã cattle only consider growth traits (Sakaguti et al., 2003; Campêlo et al., 2004; Ferraz Filho et al., 2004; Pereira et al., 2005; Ribeiro et al., 2007; Sousa Júnior et al., 2010; Caires et al., 2012; Menezes et al., 2013; Bernardes et al., 2015; Oliveira et al., 2015; Campos et al., 2016; Oliveira et al., 2017; Sousa Júnior et al., 2019). Reports are very scarce for reproductive traits (Pereira et al., 2005; Bernardes et al., 2015), and there are no studies for carcass traits in this breed.

According to Laureano et al. (2011), growth traits present genetic variability and respond to selection when included in breeding programs. In the present study, the moderate direct heritabilities

estimated for W120 and W210 (0.15 and 0.16, respectively) indicate that direct selection for these traits would result in satisfactory genetic gain. Similar results were obtained by Menezes et al. (2013) and Campêlo et al. (2004), who found direct heritability estimates of 0.18 and 0.17, respectively, for W120 in Tabapuã animals. For W210, higher heritability estimates (0.23 and 0.26) were reported by Laureano et al. (2011) and Oliveira et al. (2017), respectively, in Nellore herds. Since different populations were evaluated (Nellore animals) at different stages of selection, with distinct sample sizes, and considering statistical models with different effects, this variation in parameter estimates is expected (Oliveira et al., 2017).

The maternal heritability estimates for W120 and W210 were low (both 0.06). Nevertheless, the inclusion of the maternal additive effect in genetic evaluations is important to obtain more accurate estimates of additive genetic variance and greater genetic progress (Oliveira et al., 2017). The importance of the maternal effect in the initial growth stages of Tabapuã calves is evidenced in the present study when noting that the sum of maternal additive genetic and permanent environmental variances for W120 and W210 results in a slightly higher value than the direct additive genetic variance (Table 3). Oliveira et al. (2017) and Menezes et al. (2013) also estimated low maternal heritabilities (0.11 and 0.10, respectively) for W120 in Nellore and Tabapuã cattle, respectively. For W210, similar results were found by Laureano et al. (2011) and Oliveira et al. (2017), who obtained maternal heritability values of 0.08 and 0.12, respectively, in Nellore cattle.

For W365, the heritability estimate was of moderate magnitude (0.23). Ribeiro et al. (2007) and Caires et al. (2012) obtained heritabilities of 0.21 and 0.26, respectively, in Tabapuã cattle, similar to that observed in the present study, whereas Sakaguti et al. (2003) and Oliveira et al. (2017) obtained higher estimates, 0.36 and 0.37, for Tabapuã and Nellore animals, respectively. The heritability for W550 was also of moderate magnitude (0.19). Similar results were obtained by Ribeiro et al. (2007) and Laureano et al. (2011), who reported heritabilities of 0.17 and 0.24, for Tabapuã and Nellore cattle, respectively. On the other hand, Sakaguti et al. (2003) and Oliveira et al. (2017) found higher heritability estimates (0.36 and 0.34), in Tabapuã and Nellore animals, respectively. The heritabilities estimated for W365 and W550 show that there is genetic variability for these traits due to a moderate influence of genes of additive action; therefore, if direct selection is applied for these traits, moderate genetic gains would be achieved. It is worth mentioning that, among the growth traits, W365 presented the highest direct heritability (0.23; Table 3); however, care must be taken, since selection for post-weaning weights may increase the age at slaughter and the production costs over the years (Oliveira et al., 2017). In this way, it is still necessary to perform more studies to define the best age to select Tabapuã animals for weight. In addition, considering the importance of growth traits for Tabapuã animals and the sources of variation in different studies (distinct sample sizes, populations, statistical models, etc), the estimation of genetic parameters for these traits is still relevant in Tabapuã cattle.

The reproductive trait AFC is of great economic importance for the production system. A shorter AFC would result in a shorter interval to return the investment, increased females' longevity, and greater number of calves produced. The heritability for AFC was of low magnitude (0.07), showing that if direct selection is performed for this trait, genetic gains will be limited. Similar results were obtained in Nellore cattle by Pereira et al. (2000), Oliveira et al. (2017), and Costa et al. (2020) (0.12, 0.15, and 0.08, respectively). In Tabapuã animals, Pereira et al. (2005) and Bernardes et al. (2015) also obtained low heritability values (0.03 and 0.09, respectively). Most of the beef cattle production in Brazil occurs in extensive systems, often characterized by periods of feed restriction and high temperatures that might influence the animals' reproductive performance (Oliveira et al., 2017). In this sense, the low heritability is expected for AFC, since it is highly influenced by several environmental factors and management practices. Therefore, optimal environmental and management conditions should be provided to the animals, so that they can express their full genetic potential (Nieto et al., 2013).

The heritability estimate for SC365 was of moderate magnitude (0.22), which allows moderate genetic gains by direct selection. The heritability estimated in this study was lower than those reported by Silva et al. (2000), in Canchim cattle, and by Oliveira et al. (2017), Buzanskas et al. (2017), and Abreu Silva et al. (2018), in Nellore cattle (0.30, 0.43, 0.45, and 0.50, respectively).

Considering the carcass trait REA, the heritability was moderate (0.36), which suggest that the insertion of this trait in Tabapuã cattle breeding program may result in satisfactory genetic gains. The heritability estimated in the present study is in accordance with Oliveira et al. (2017), Paula et al. (2015), and Buzanskas et al. (2017), who reported values of 0.30, 0.41, and 0.31, respectively, for REA in Nellore cattle.

For BF, the heritability was of moderate magnitude (0.31), showing that the environment does not exert great influence on this trait; therefore, it may show a good response to direct selection. Oliveira et al. (2017) reported a similar estimate (0.29) in Nellore animals; nevertheless, Buzanskas et al. (2017) and Paula et al. (2015) reported lower estimates, 0.18 and 0.20, respectively. The heritability for RF, as in the other carcass traits, was moderate (0.27). Paula et al. (2015) and Oliveira et al. (2017) reported similar values for RF in Nellore cattle (0.29 and 0.28, respectively), whereas Buzanskas et al. (2017) found a lower estimate (0.19), also in Nellore animals. The BF and RF are traits of great importance for meat quality, since besides preventing water loss from carcass during cooling, they also prevent browning (Sugisawa et al., 2013). The heritability estimates for carcass traits indicate that reasonable genetic gains can be obtained by direct selection.

Genetic correlation estimates between growth traits were high and positive (Table 4). These correlations were similar to those reported in literature for Tabapuã cattle: 0.89 (W120 × W365), 0.81 (W120 × W550), 0.88 and 0.93 (W365 × W550) (Sakaguti et al., 2003; Ribeiro et al., 2007), and for Nellore cattle: 0.70 (W120 × W365), 0.89 (W120 × W550), 0.97 (W210 × W365), 0.70 to 0.85 (W210 × W550) (Boligon et al., 2010; Laureano et al., 2011; Oliveira et al., 2017).

The phenotypic correlations between the growth traits (0.46 to 0.85; Table 4) were lower than the genetic correlations, indicating that the cause of environmental correlations influenced the phenotypic correlations. Selection for heavier animals at younger ages may not express a high phenotypic association; however, the genetic associations indicate that the same set of genes acts on different growth traits. Therefore, the results of the present study suggest that selection of Tabapuã cattle for body weight can be performed at younger ages, leading to favorable gains at later ages.

Favorable, negative, and low to moderate genetic correlations were observed between AFC and growth traits and between AFC and REA (Table 4), indicating that selection for heavier animals or with higher REA will show, as a correlated response, a low or moderate decrease in AFC. This reduction in AFC and consequent improvement of the herd reproductive indices may directly affect the economic efficiency of the production system.

The genetic correlation observed between AFC and SC365 was favorable, negative, and of moderate magnitude (−0.66). Other authors reported values ranging from −0.16 to −0.45 between these traits in Nellore cattle (Pereira et al., 2000; Oliveira et al., 2017; Costa et al., 2020). The genetic correlation estimated in the present study indicates that a set of genes responsible for SC expression may control the females' sexual precocity. Besides presenting low phenotypic correlation (−0.09), the favorable and moderate genetic correlation between these reproductive traits indicates that selection to increase SC365 in males may result in lower AFC in females, with the additional advantage of reducing the generation interval (Costa et al., 2020). Therefore, SC365 would be a good selection criterion to increase the herd reproductive efficiency, even more considering that AFC heritability (0.07) is much lower than the SC365 heritability (0.22).

The genetic correlations between SC365 and growth traits were positive, favorable, and moderate (Table 4). In other studies, similar values were reported, ranging from 0.24 to 0.26 between W210 and SC365, and equal to 0.39 between W365 and SC365 (Laureano et al., 2011; Abreu Silva et al., 2018; Oliveira et al., 2017). These genetic correlations suggest that selection for SC365 would result in increased body weight. The correlations between SC365, REA, and fat traits were of low magnitude, indicating that different genes are controlling these traits. Therefore, genetic breeding programs that have a selection objective of increasing SC365 will not obtain satisfactory response for carcass traits. Similar genetic correlation estimates, ranging from 0.15 to 0.33 between SC365 and REA, −0.04 between SC365 and BF, and 0.05 between SC365 and RF, were reported (Marques et al., 2013; Buzanskas et al., 2017).

Positive and low genetic correlations were obtained between REA and fat thickness traits (Table 4). Similar genetic correlations, ranging from 0.05 to 0.17 for REA × BF and 0.02 to 0.23 for REA × RF, were reported in literature (Zuin et al., 2012; Marques et al., 2013; Buzanskas et al., 2017; Oliveira et al., 2017).

Favorable, positive, and high genetic correlation was estimated between BF and RF (0.77; Table 4). Oliveira et al. (2017), Zuin et al. (2012), and Buzanskas et al. (2017) reported similar values, ranging from 0.59 to 0.72, in Nellore cattle. The high genetic correlation between the fat thickness traits and similar heritability estimates (0.31 for BF and 0.27 for RF) suggest that only one trait could be used as selection criterion.

Correlation estimates between direct and maternal additive genetic effects for W120 and W210 were negative and of low magnitude. These correlations were lower than those found by Campêlo et al. (2004) for W120 (−0.40) and W240 (−0.48) in Tabapuã cattle. This negative correlation is in agreement with the results obtained for W205 in Tabapuã by Ferraz Filho et al. (2004) and Oliveira et al. (2015) (−0.42 and −0.32, respectively). Negative correlations between direct and maternal additive genetic effects can be biased due to selective reporting, which is not necessarily the result of antagonistic genetic relationships, as suggested by Mallinckrodt et al. (1995). Therefore, care must be taken when interpreting these correlations.

## 5. Conclusions

Considering the heritability estimates, selection of Tabapuã animals for age at first calving would result in limited genetic gains, whereas for scrotal circumference at 365 days and all growth and carcass traits, it would be satisfactory. In addition, the selection can be performed at younger ages, based on the high genetic correlations between growth traits. Furthermore, animals can be indirectly selected for age at first calving through selection for scrotal circumference at 365 days, since a favorable moderate genetic correlation was found between these traits. Finally, only one fat thickness trait may be used in the selection process, considering the favorable and high genetic correlations between these traits and the similar heritability estimates.

## Conflict of Interest

The authors declare no conflict of interest.

## Author Contributions

Conceptualization: T.C. Freitas, H.T. Ventura, F.F. Silva and P.S. Lopes. Data curation: H.T. Ventura. Formal analysis: T.C. Freitas, F.F. Silva, R. Veroneze, E.V. Costa and D.A. Silva. Funding acquisition: F.F. Silva, R. Veroneze and P.S. Lopes. Investigation: T.C. Freitas, H.T. Ventura, F.F. Silva, E.V. Costa and P.S. Lopes. Methodology: H.T. Ventura, F.F. Silva, R. Veroneze, E.V. Costa and P.S. Lopes. Project administration: H.T. Ventura, F.F. Silva and P.S. Lopes. Resources: F.F. Silva, R. Veroneze and P.S. Lopes. Software: H.T. Ventura, F.F. Silva, R. Veroneze, E.V. Costa and D.A. Silva. Supervision: H.T. Ventura, F.F. Silva and P.S. Lopes. Validation: T.C. Freitas, H.T. Ventura, F.F. Silva, D.A. Silva and P.S. Lopes. Visualization: T.C. Freitas, H.T. Ventura, F.F. Silva, D.A. Silva and P.S. Lopes. Writing – original draft: T.C. Freitas, F.F. Silva, D.B.D. Marques and P.S. Lopes. Writing – review & editing: F.F. Silva, D.B.D. Marques and P.S. Lopes.

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