Genetic parameter estimates for growth traits in Texel sheep of Brazil

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A B S T R A C T

The present study aimed to estimate the genetic parameters for direct and maternal influences on birth weight (BW), weaning weight (WW) and postweaning weight (PW) of Texel sheep, raised in an extensive system from Brazil. Data file used in this study consisted of 834 body weight records of 834 Texel lambs (376 males and 458 females) born from 2020 to 2021, offspring of 475 ewes and 45 rams. Multivariate animal model was conducted to estimate the variance components, heritability and genetic correlations using the restricted maximum likelihood method in ASReml-R software, while the effects of fixed factors were analyzed by the general linear model procedure of statistical analysis system. Five different animal models, with or without maternal genetic effect, maternal permanent environment effect and covariance between additive genetic and maternal genetic effects, were fitted on the growth traits data of the Texel sheep population. AIC and BIC test results were used to evaluate the best fit models for growth traits. The effect of lamb's sex was significant on BW, WW and PW while birth type and year of lambing effects were on all traits (P < 0.05). Model 4, incorporating direct additive genetic, maternal additive genetic and maternal permanent environmental effects showed the minimum AIC estimate for all growth traits. The direct additive genetic heritability for BW, WW and PW were 0.11 ± 0.03, 0.37 ± 0.05 and 0.31 ± 0.08, respectively and maternal heritability for these traits were 0.00 ± 0.00, 0.04 ± 0.02 and 0.00 ± 0.00, respectively. The total heritability estimates for BW, WW and PW were 0.11 ± 0.03, 0.39 ± 0.05 and 0.31 ± 0.08, respectively. The estimates of the direct additive genetic correlation between BW-WW, BW-PW and WW-PW were 0.68 ± 0.12, 0.66 ± 0.12 and 0.78 ± 0.07, respectively. The maternal permanent environmental correlation between BW-WW, BW-PW and WW-PW were 0.38 ± 0.27, 0.29 ± 0.20 and 0.74 ± 0.16, respectively. Phenotypic correlation ranged from 0.43 ± 0.03 to 0.75 ± 0.02. It is concluded that due to the existence of genetic variation for BB, WW and PW and strong genetic correlation among them, genetic progress for these traits is possible by selection in Texel sheep from Brazil.

1. Introduction

The Texel breed is one of the most important breeds in the southern region of Brazil, mainly raised for meat purpose. According to livestock census 2022, the total population in the southern region was approximately 4.3 million out of 21.51 million of the country's total sheep population [1]. This breed is medium size and has a white coat, with a muscular development, good rib eye area and ham with low fat deposition. It is a rustic and strong animal, producing well in extensive and semi-intensive systems [2,3]. Due to a significant increase in the sheep population in the southern region of Brazil, there is an increasing interest in genetic improvement for growth traits. In order to design effective selection programs to increase the efficiency of sheep production, estimates of genetic and environmental parameters of different component traits related to growth are needed. In addition, these parameters are necessary for the prediction of a response to selection.

Several studies have shown that many non-genetic factors such as sex, age, herd, type of birth and contemporary groups are known to affect significantly growth traits of lambs [4–6]. Furthermore, direct additive genetic effects and maternal genetic effects along with environmental effects also significantly affect early growth in lambs [5,7,8]. Hence, it is important to include these effects in the animal model to

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avoid biased estimates of genetic parameters [5,9]. Thus, to achieve optimum progress in a selection program, both direct and maternal components should be taken into account, especially in the presence of an antagonistic relationship between them [5,10].

On the other hand, the genetic parameters for growth traits are important for planning an efficient genetic improvement program and for making effective early decisions to enhance farm profitability [11]. However, there have been limited published results on genetic parameter estimates for birth, weaning and postweaning traits in Texel sheep and also because, genetic parameters may vary because of genotype, breed, location, period, herd, pedigree structure and the number of animals with productive records [8]. Hence, appropriate parameter estimates for growth traits for Texel sheep are important for adequate breeding strategies and for correct breeding value estimation. The aim of this study, therefore, was to estimate genetic parameters for growth traits weight as well as the genetic and phenotypic correlations among these traits sheep by fitting different models in Texel sheep.

2. Materials and methods

2.1. Data records and animals

Data on Texel lamb growth was obtained from the database of ProAGO company - Programa de Avanço em Genética Ovina®, composed by the connection of six farm livestock participating in the genetic improvement program in Rio Grande do Sul state. Prior to the analysis, data were edited for consistency of dates and the pedigree. Records with inconsistent dates (outside the born year) and weights (≥ 3 standard deviation and ≤ 3 standard deviation of the average) were eliminated. After editing the data, the pedigree file presented 2.828 animals in the genealogy that was used to compute the numerator relationship matrix (NRM), and the pedigree description is summarized in Table 1. The data file consisted of growth records of 834 Texel lambs (376 males and 458 females) born from 2020 to 2021, offspring of 475 ewes and 45 rams and raised in an extensive system. Birth date, birth weight (BW), weaning weight (WW), postweaning weight (PW), genetic group or breed of lambs, and non-genetic factors like sex of lamb, herd and birth type "single, twin and triplets" were recorded for each lamb during this period. Body weights of lambs were measured using weighing balance. Lambs were separated into 24 contemporary groups (CG) composed by animals of the same sex, born in the same herd and in the same year and month. Body weights were recorded at various times during the lambs' lives, that is, birth weight was recorded up to 24h after birth; weaning weight at 90 days and the postweaning weight at 150 days of age. The balances for birth weight were digital and hand-type shapes with a maximum load capacity of 50 kg and precision of 10 g. For the other weights, the balances were used bar scales with a maximum capacity of 2000 kg and an accuracy of 10 g. The contemporary group was formed up of animals raised under the same feeding and health conditions, with an age difference not more than 60 days.

Table 1
Pedigree structure and descriptive statistics for growth traits in Texel sheep.

	N	Mean	SD	Min	Max	CV
Number of Sires	516	–	–	–	–	–
Number of Dams	1482	–	–	–	–	–
Number of Grand sires	215	–	–	–	–	–
Number of Grand dams	368	–	–	–	–	–
Number of progenies per sire	18	–	–	–	–	–
Number of progenies per dam	2	–	–	–	–	–
Birth weight (kg)	–	5.03	1.06	2.2	8.5	21.09
weaning weight (kg)	–	34.77	7.80	14.0	56.4	22.42
postweaning weight (kg)	–	43.06	8.68	18.0	85.0	20.15

2.2. Descriptive statistics

Table 1 shows the descriptive statistical results. The averages for BW, WW and PW were 5.03 ± 1.06, 34.77 ± 7.80 and 43.06 ± 8.68 kg, respectively, which are considered high because Texel sheep are medium to large animals. Theses finding are within the ranges reported in previous studies for the Texel breed [12–15]. Regarding CV, all traits showed similar variations ranged from 20.15 to 22.42 kg.

2.3. Statistical analysis

Initially, to assess the influence of fixed effects, such as sex ($i = 1$ and 2), type of birth ($j = 1$, 2 and 3) and year of lambing (k = 1 and 2) on BW, WW and PW, a least squares modeling was employed as follows:

$$y_{ijkl} = \mu + \alpha_i + \beta_j + \delta_k + \varepsilon_{ijkl}$$

where y_{ijkl} = lth growth trait (e.g.BW) of ith sex and jth type of birth and kth year of lambing, μ = population mean, α_i = ith sex effects, β_j = jth type of birth effects, δ_k = kth year of lambing and ε_{ijk} = random error attributed with each observation. Tukey test was used to test the significant differences between treatment means. This analysis was performed by Stats and Agricolae packages of the statistical software R version 4.3.2 [16].

Multivariate animal model analyses were conducted for all traits using ASReml-R software v.4.2 [17] to simultaneously estimate the variance components, heritability, genetic correlations and the random and fixed effects using the restricted maximum likelihood (REML) method. Five different animal models were fitted for each trait, by ignoring or including maternal additive genetic effect, covariance between direct-maternal additive genetic effect and maternal permanent environmental effect. These models are:

$$y = X\beta + Z_a a + e \qquad \text{Model 1}$$

$$y = X\beta + Z_a a + Z_m m + e \; \text{Cov}(a, m) = 0 \qquad \text{Model 2}$$

$$y = X\beta + Z_a a + Z_m m + e \; \text{Cov}(a, m) = A\sigma_{a,m} \qquad \text{Model 3}$$

$$y = X\beta + Z_a a + Z_m m + Z_c c + e \; \text{Cov}(a, m) = 0 \qquad \text{Model 4}$$

$$y = X\beta + Z_a a + Z_m m + Z_c c + e \; \text{Cov}(a, m) = A\sigma_{a,m} \qquad \text{Model 5}$$

where y is the observation vector (e.g. between BW, WW and PW); β is a vector of fixed effects (sex, type of birth, age of dam and CG); $a \sim N(0, A\sigma_a^2)$ is a vector of direct additive genetic effects, $m \sim N(0, A\sigma_m^2)$ a vector of maternal additive genetic effects, $c \sim N(0, I_d\sigma_c^2)$ is a vector of maternal permanent environmental effects and $e \sim N(0, I_n\sigma_e^2)$ is a vector of random residual effects; X_b, Z_a, Z_m and Z_c are the incidence matrices that associate the elements of a, m and c respectively, with y. The σ_a^2, σ_m^2, σ_c^2 and σ_e^2, are direct additive genetic variance, maternal additive genetic variance, maternal permanent environmental variance and residual variance, respectively. A is the additive numerator relationship matrix, I_d and I_n are identity matrices that have order equal to the number of dams and number of records, respectively, and $\sigma_{a,m}$ denotes the covariance between direct additive genetic and maternal additive genetic effects. Estimates of direct heritability (h_a^2), maternal heritability (h_m^2) and ratio of maternal permanent environmental effect (c^2) were calculated as ratios of variances estimates: σ_a^2 (direct additive genetic), σ_m^2 (maternal additive genetic) and σ_c^2 (maternal permanent environmental), respectively, to the σ_p^2 (phenotypic variance). The total heritability (h_t^2) of the total genetic component was estimated [18] as: $h_t^2 = \left(\sigma_a^2 + 0.5\sigma_m^2 + 1.5\sigma_{am}\right) / \sigma_p^2$. The BIC (Bayesian information criterion) and AIC (Akaike information criterion) goodness-of-fit criteria were used to select the best model.

3. Results and discussion

3.1. Fixed effects

The least square means for growth traits of Texel sheep are presented in Table 2. The sex of the animals had a significant effect (P < 0.05) only on PW, with males being heavier than females, while BW, WW and PW at all ages were significantly affected by type of birth (P < 0.05). As expected, for BW, WW and PW, single lambs were heavier than twins, which in turn were heavier than triplets. A single lamb typically has a higher birth weight due to the condition where the dam provides direct nutrient intake to the lamb during pregnancy. Therefore, the birth weight of a single lamb is higher compared to twin and triplet lambs because they do not need to compete for nutrition during pregnancy [13, 19]. Similar results were reported in other sheep breeds [15,20]. Year of lambing had significant influence (P < 0.05) on BW, WW and PW of lambs. Lambs born in 2020 were heavier (3.42–6.19 %) than lambs born in 2021, this might be attributed to differences in climatic conditions, changes in flock management and the availability of green pastures from one year to another. Year of lambing differences have been reported by Tesema et al. [5] working with Dorper × indigenous sheep under extensive management.

3.2. Variance components and heritability estimates

Estimates of variance components and heritability estimates for BW, WW and PW are summarized in Table 3. As per the BIC criteria test, the model, which includes only direct additive and maternal genetic effects (model 2), was sufficient to explain the variation in the BW, WW and PW. However, based in AIC criteria a combination of direct additive, maternal genetic and maternal permanent environmental effect with $Cov(a, m) = 0$ (model 4) was the optimal model for the three traits by considering complex models. Similarly, Ehsaninia [21] proposed the same model for these traits in Sangsari sheep.

Based on optimal model the direct additive genetic (σ_a^2), maternal additive genetic (σ_m^2) and maternal permanent environmental (σ_c^2) variances, for BW, WW and PW found in this study were higher than the majority of findings reported in other latitudes to most other sheep breeds reported by several authors [22–24]. In Brazilian Texel and Polwarth crossbred sheep populations Amarilho-Silveira et al. [13,25] reported estimates of 0.001–0.069 and 0.147 to 0.164 for σ_a^2 and σ_c^2, respectively and estimates of 0.044–0.194 for σ_m^2 for BW. The findings reported in our study indicate that there is considerable direct additive genetic variability for BW, WW and PW, which could yield favorable outcomes when used in selection programs.

Direct heritability (h_a^2) estimate for birth weight (BW) from our study (0.11) was in agreement with those reported by Ahmad et al. [18] in Corriedale sheep from India, but lower than the results obtained by

Habtegiorgis et al. [26] who reported high estimates (0.25) of direct heritability for BW in Doyogena sheep population from Ethiopia. Similarly, Kannan et al. [27] reported high heritability $\left(h_a^2 = 0.21\right)$ in Mecheri sheep populations from India. Estimates lower than that from the present study has been reported in others studies. Boujenane and Diallo [28] reported low h_a^2 estimate (0.06) for BW in the Sardi sheep population of Morocco. In Dorper × indigenous sheep from Ethiopia, Tesema et al. [5] reported also low direct heritability (0.003).

The maternal heritability (h_m^2) estimate for BW in the present study was close to the 0.017 reported by Ahmad et al. [18] in Corriedale sheep from India. However, higher h_m^2 estimates were also reported in other breeds. Kannan et al. [27] who evaluated Mecheri sheep from India finding estimates of 0.18. In contrast, Boujenane and Diallo [28] reported very low h_m^2 estimate of maternal heritability in Sardi sheep of Morocco. Similarly, Habtegiorgis et al. [26] and Tesema et al. [5] reported very low estimates of 0.05 and 0.06, in Doyogena and Dorper breeds, respectively.

Direct heritability (h_a^2) estimate for weaning weight (WW) from our study (0.37) was higher than those published by Ahmad et al. [18] in Corriedale sheep (0.12) from India, by Tesema et al. [5] in Dorper × indigenous sheep (0.14) from Ethiopia, by Habtegiorgis et al. [26] in Doyogena sheep (0.17) from Ethiopia and by Kannan et al. [27] in Mecheri sheep (0.21) from India. Very low h_a^2 estimates were also reported in other breeds. Boujenane and Diallo [28] worked with Sardi sheep from Morocco observed values for h_a^2 estimate of 0.03.

The maternal heritability (h_m^2) estimate for WW in the present study of 0.04 was lower than the 0.08 reported by Kannan et al. [27] in Mecheri sheep from India, and also lower than those of 0.07 reported by Boujenane and Diallo [28] in Sardi sheep from Morocco. Ahmad et al. [18] in Corriedale sheep from India reported a very low h_m^2 estimate of 0.006 and Tesema et al. [5] reported estimate of 0.00 in Dorper × indigenous sheep from Ethiopia. However, higher h_m^2 estimates were also reported in other breeds. In Doyogena sheep from Ethiopia, Habtegiorgis et al. [26] reported h_m^2 estimates of 0.16.

Direct heritability (h_a^2) estimate for postweaning weight (PW) from our study (0.31) was higher than those published by Kannan et al. [27] in Mecheri sheep (0.12) from India, by Habtegiorgis et al. [26] in Doyogena sheep (0.14) and by Ahmad et al. [18] in Corriedale sheep (0.16) from India. Very low h_a^2 estimates were also reported in other breeds. Boujenane and Diallo [28] worked with Sardi sheep from Morocco observed values for h_a^2 estimate of 0.05.

The maternal heritability (h_m^2) estimate for PW in the present study was close to the 0.001 reported by Ahmad et al. [18] in Corriedale sheep from India, but lower than those of 0.02 reported by Habtegiorgis et al. [26] in Doyogena sheep from Ethiopia, by Boujenane and Diallo [28] in Sardi sheep (0.01) from Morocco. However, higher h_m^2 estimate was also reported by Kannan et al. [27] in Mecheri sheep (0.11) from India.

Maternal permanent environmental effects (c^2) were low for all the three growth traits indicating that in the existing management conditions, good maternal environment pose positive effects on lambs from birth to adult age. were low for all the three growth traits indicating that in the existing management conditions, maternal environment pose less effects on lambs from birth to post weaning age.

The estimate of total heritability (h_t^2) for BW in the present study (0.11) was very close to that reported by Tesema et al. [5] (0.10) but greater than the value (0.07) reported by Ahmad et al. [18] working with Corriedale sheep from India and by Boujenane and Diallo [28] in Sardi sheep (0.09) from Morocco. Higher estimates of heritability for BW were also reported by Habtegiorgis et al. [26] in Doyogena sheep (0.21) from Ethiopia and by Ehsaninia [21] who reported an estimate of 0.36 in Sangsari sheep breed from Iran. The estimates of total heritability (h_t^2) for WW (0.39) and for PW (0.31) were greater than those published in others sheep breeds [5,22–24]. The high estimates of total

Table 2
Least-squares mean ± standard error of growth traits, according fixed effects in Texel sheep.

Fixed effects	N	BW	WW	PW
Sex				
Male	376	4.74 ± 0.07[a]	34.72 ± 0.59[a]	45.25 ± 0.61[a]
Female	458	4.50 ± 0.07[b]	31.59 ± 0.58[b]	38.24 ± 0.60[b]
Birth type				
Single	400	5.56 ± 0.05[a]	37.19 ± 0.37[a]	45.86 ± 0.38[a]
Twins	410	4.63 ± 0.05[b]	33.05 ± 0.36[b]	41.32 ± 0.38[b]
Triplets	24	3.68 ± 0.19[c]	29.22 ± 1.49[c]	38.06 ± 1.55[b]
Year of lambing				
2020	496	4.68 ± 0.07[a]	33.91 ± 0.56[a]	42.35 ± 0.58[a]
2021	338	4.52 ± 0.08[b]	31.87 ± 0.61[b]	40.73 ± 0.64[b]

N: Number of observations, BW: birth weight, WW: weaning weight, PW: postweaning weight. Different letters along the same column are significantly different (P < 0.05).

Table 3
Estimates of (Co) variance components, genetic parameters and the goodness-of-fit criteria for growth traits in Texel sheep with different models.[a].

Traits	Models	σ_a^2	σ_m^2	σ_c^2	σ_{am}	σ_e^2	σ_p^2	$h_a^2 \pm$ SE	$h_m^2 \pm$ SE	$h_t^2 \pm$ SE	$c^2 \pm$ SE	BIC	AIC
BW	1	0.86				0.13	3.91	0.22 ± 0.03				4708.35	4675.87
	2	0.48	0.22			0.25	3.61	0.13 ± 0.04	0.06 ± 0.02	0.16 ± 0.03		4483.51	4440.20
	3	0.44	0.26		0.50	0.26	3.77	0.12 ± 0.04	0.07 ± 0.02	0.15 ± 0.03		4488.98	4440.26
	4	**0.39**	**0.00**	**0.27**		**0.23**	**3.57**	**0.11 ± 0.03**	**0.00 ± 0.00**	**0.11 ± 0.03**	**0.07 ± 0.02**	**4484.77**	**4425.22**
	5	0.39	0.01	0.26	0.26	0.23	3.62	0.11 ± 0.03	0.00 ± 0.01	0.11 ± 0.03	0.07 ± 0.02	4491.29	4426.33
WW	1	39.49				7.54	83.85	0.47 ± 0.03				7379.29	7346.81
	2	34.19	4.52			7.92	83.20	0.41 ± 0.04	0.05 ± 0.02	0.44 ± 0.04		7375.24	7331.94
	3	29.74	8.34		4.77	8.70	83.22	0.36 ± 0.06	0.10 ± 0.03	0.41 ± 0.04		7378.65	7329.94
	4	**29.55**	**3.11**	**4.53**		**8.38**	**80.72**	**0.37 ± 0.05**	**0.04 ± 0.02**	**0.39 ± 0.05**	**0.06 ± 0.03**	**7385.49**	**7324.88**
	5	28.14	6.59	2.65	3.28	8.77	81.77	0.34 ± 0.06	0.08 ± 0.04	0.38 ± 0.05	0.03 ± 0.03	7389.83	7325.96
PW	1	41.88				16.01	94.71	0.44 ± 0.06				7379.29	7346.81
	2	41.53	0.46			15.90	94.46	0.44 ± 0.08	0.00 ± 0.02	0.44 ± 0.07		7375.24	7331.94
	3	32.97	5.60		4.77	18.41	93.42	0.35 ± 0.09	0.06 ± 0.04	0.38 ± 0.08		7378.65	7329.94
	4	**27.53**	**0.00**	**8.77**		**18.60**	**90.04**	**0.31 ± 0.08**	**0.00 ± 0.00**	**0.31 ± 0.08**	**0.10 ± 0.03**	**7385.49**	**7324.88**
	5	26.64	1.63	7.83	3.28	18.87	90.60	0.29 ± 0.08	0.02 ± 0.02	0.30 ± 0.07	0.09 ± 0.04	7389.83	7325.96

BW: birth weight, WW: weaning weight, PW: postweaning weight, σ_a^2: direct additive genetic variance, σ_m^2: maternal additive genetic variance, σ_c^2: maternal permanent environmental variance, σ_{am}: direct–maternal genetic covariance, σ_e^2: residual variance, σ_p^2: phenotypic variance, h_a^2: direct heritability, h_m^2: maternal heritability, c_m^2: ratio of maternal permanent environmental effect, h_t^2: total heritability, AIC: Akaike Information Criterion, BIC: Bayesian Information Criterion. Bold values indicate estimates from the best model.
The best-fitted model is highlighted in bold.
 [a] : Variance components of weights are in kg^2.

for WW and PW finding in the present study were influenced by the direct additive genetic variance and hence increase the potential response to selection [9].

Overall, the direct heritability findings from our study, suggest that incorporating WW and PW trait into a selection program could lead to a significant genetic improvement in Texel sheep populations from Brazil. However, the results of maternal heritability imply that direct selection based on BW and PW may result in low genetic response and, therefore, could not be recommended as a selection criterion in a genetic improvement program. On the other hand, the low h_m^2 estimates reported in the present study would indicate little influence of the maternal genotype on BW.

3.3. Genetic correlations

Estimates of phenotypic, direct additive genetic, maternal permanent environmental and residual correlations between BW, WW and PW from bi-trait analysis with model 4 are presented in Table 4. The direct additive genetic correlations between BW WW and PW were positive and high, ranging from 0.66 to 0.78. These results are very close to those of 0.63 obtained by Kannan et al. [27] in Mecheri sheep from India, Ehsaninia [21] who reported an estimate of 0.67 in Sangsari sheep breed from Iran, and by Boujenane and Diallo [28] in Sardi sheep (0.72) from Morocco. However, our direct additive genetic correlation estimates

Table 4
Estimates of phenotypic, direct additive genetic, maternal permanent environmental and residual correlations between traits from bi-trait analysis with model 4.

Trait1	Trait2	r_p	r_a	r_c	r_e
BW	WW	0.45 ± 0.03	0.68 ± 0.12	0.38 ± 0.27	−0.17 ± 0.24
BW	PW	0.43 ± 0.03	0.66 ± 0.12	0.29 ± 0.20	−0.31 ± 0.29
WW	PW	0.75 ± 0.02	0.78 ± 0.07	0.74 ± 0.16	0.67 ± 0.11

BW: birth weight, WW: weaning weight, PW: postweaning weight. r_p: phenotypic correlations between traits 1and 2; r_a: direct additive genetic correlation between traits 1 and 2; r_c: maternal permanent environmental correlation between traits 1and 2; r_e: residual environmental correlation between traits 1and 2;.

between BW and WW were higher than those reported by Habtegiorgis et al. [26] and Tesema et al. [5] who reported estimates of 0.23 and 0.43, in Doyogena and Dorper breeds, respectively. The direct genetic correlation between BW and PW found in the present study (0.66) was higher to the reports by Kannan et al. [27] and Habtegiorgis et al. [26] who reported estimates of 0.25 and 0.17, in Mecheri and Doyogena breeds, respectively. However, was lower than those reported by Boujenane and Diallo [28] in Sardi sheep (0.68) from Morocco. The direct genetic correlation estimates between WW an PW reported in our study (0.78) was close to the 0.70 reported by Kannan et al. [27] in Mecheri sheep from India, but was lower than the result reported by Fitzmaurice et al. [14] who published estimate of 0.94 in purebred Texel, Suffolk and Charollais lambs. Habtegiorgis et al. [26] and Boujenane and Diallo [28] reported lower estimates (0.35 and 0.55) than those reported in the present study in Doyogena and Sardi breeds, respectively. The moderate to high phenotypic correlation estimates between three traits also imply that can very well be selected on the phenotypic improved performance in terms of growth traits for future improved production performance.

Estimates of maternal permanent environmental correlation (r_C) were moderate and positive among BW and WW and PW, and high among WW and PW.

The results of the present study showed that due to moderate to higher positive genetic correlation, selection for any of the studied traits can result in an increase of phenotypic magnitudes and genetic potentials for other body weight traits. As pointed out by Amarilho-Silveira et al. [25], birth weight has a high correlation with other weight-related characteristics, so that lambs with higher birth weights would also have higher weights in the subsequent stages of growth compared to lambs with lower birth weight.

4. Conclusion

Moderate estimates of direct heritability for WW and PW have indicated the presence of genetic variability in the Texel sheep population from Brazil. Therefore, it is possible to achieve significant genetic progress through selection for these traits. Maternal genetic effects were not significant on BW, WW, and PW. Additionally, the high and positive genetic correlation estimates among these traits suggest that selecting for one trait would indirectly result in positive selection for other traits

due to their correlated responses.

Ethical standards

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Consent for publication

The authors give their consent for publication.

Availability of data and material

The data will be made available on the request.

CRediT authorship contribution statement

Ali William Canaza-Cayo: Writing – original draft, Data curation, Conceptualization. **Fernando Amarilho Silveira:** Writing – review & editing, Formal analysis. **Roxana Churata-Huacani:** Writing – review & editing, Formal analysis. **Júlio Sílvio de Sousa Bueno Filho:** Writing – review & editing.

Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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