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Genetic analyses on bodyweight, reproductive, and carcass traits in composite beef cattle

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Abstract. In beef cattle, growth, reproductive, and carcass traits have been studied for improving productivity and quality of meat products. The aim of this study was to estimate genetic parameters for birth (BW), weaning (WW) and yearling (YW) weights, scrotal circumferences at weaning (SCW) and yearling (SCY), age at first calving (AFC), ribeye area (REA) and back fat thickness (BFT) in order to provide support for the evaluation program of the composite Canchim breed. Data on 12 967 (BW), 7481 (WW), 5131 (YW), 1447 (SCW), 1224 (SCY), 1400 (AFC), and 2082 (REA and BFT) animals were analysed using the Average Information Restricted Maximum Likelihood method under an animal model (single and multi-trait analyses). A substantial proportion of the variation in the bodyweights, scrotal circumferences and carcass traits was associated with the additive genetic term indicating that these traits may respond to the selection process. For AFC, a low heritability estimate was observed. Genetic correlations among bodyweights varied from 0.41 to 0.93. The genetic correlation among scrotal circumferences was 0.91. Important genetic correlations among YW, SCW, and SCY with AFC were observed (–0.48, –0.61, and –0.71, respectively), indicating that indirect responses to selection for these traits would be expected in the age of which the heifers calve. Furthermore, BFT presented an interesting result with calving performance due to the genetic correlation (–0.69) with AFC. Post-weaning weights showed moderate genetic correlations with REA. Many of the traits considered in the genetic evaluation of this breed are genetically correlated in a favourable manner. Genetic improvement through selection is expected for production, reproduction, and carcass traits in Canchim beef cattle.

Additional keywords: Canchim breed, genetic improvement, genetic parameters, selection.

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Introduction

Growth and reproductive traits are included in the selection criteria of breeding programs (Brumatti *et al.* 2011) due to their economic importance to the beef cattle industry. Enhanced reproductive indices have direct impact on the profitability of the production system, which may act on the longevity of the cows and higher quantity of animals for sale and selection (Krupa *et al.* 2005). Furthermore, carcass traits are of great interest to producers due to increasing demands for quality in the consumer market (Yokoo *et al.* 2010).

According to Luchiari Filho (2000), high quality carcasses should have adequate bone : muscle ratio and good fat coverage. Ultrasound measurements of the ribeye area and fat thickness are a non-invasive and affordable technology to evaluate carcass quality. Fat thickness is to some extent responsible for the conservation of physical and organoleptic traits of meat after slaughter and the ribeye area is located in the region of prime cuts

(Meirelles *et al.* 2010). Beef cattle breeders are concerned about providing suitable nutritional management systems as well as improving the genetic potential of livestock, especially in composite animals such as the Canchim in order to provide better products.

Thus, the aim of this study was to estimate genetic parameters for bodyweights, scrotal circumferences, age at first calving, ribeye area and fat deposition traits in order to provide support for the Canchim evaluation program.

Material and methods

Description of the data

The data contained animals from the Canchim breed (5/8 Charolais and 3/8 Zebu) and the MA genetic group (derived from mating between Charolais bulls and 1/2 Canchim + 1/2 Zebu dams) raised in Brazil. Details of the Canchim breed development

and management practices have been previously described in detail by Gianlorenço *et al.* (2003) and Andrade *et al.* (2008). The Brazilian Association of Canchim Breeders and Embrapa Southeast Livestock provided data on birthweight (BW), weaning (WW) and yearling (YW) weight, scrotal circumference at weaning (SCW) and yearling (SCY), age at first calving (AFC), ribeye area (REA), and back fat thickness (BFT).

The selection index known as 'genetic qualifying', which was developed through the Embrapa-Genepplus program, is used for selecting genetically superior dams and sires (ABCCAN-Embrapa-Genepplus 2015). This index is calculated from estimated breeding values for the following traits (with their respective weighting factors in brackets): BW (0.15), maternal ability at WW (0.20), YW (0.30), slaughter conformation at yearling (0.20), and SCY (0.15).

Weaning and yearling ages were on average 236 ± 27 days and 502 ± 79 days, respectively. Ultrasound measurements were obtained using the Piemedical Scanner 200 Vet with linear transduction of 18 cm and 3.5 MHz, and the ALOKA 500V with linear probe of 17.2 cm and 3.5 MHz, which was positioned over the *longissimus dorsi* muscle in the region between the 12th and 13th rib (Yokoo *et al.* 2010). The average age for the ultrasound measure was 555 ± 87 days. Data on BW was obtained from 1992 to 2012. For WW and YW, data was obtained from 1996 to 2012. For SCW and SCY, the animals were born from 2003 to 2011. For AFC and ultrasound traits, animals were born from 1996 to 2009 and from 2005 to 2012, respectively.

Contemporary groups

Data quality control was carried out using the SAS software (SAS 9.3, SAS Institute, Cary, NC, USA). The least-squares method

was used to evaluate the environmental effects. Significant effects ($P < 0.01$) were used to define contemporary groups (CG). Animals without pedigree information, CG with less than two animals, and sires with less than three offspring were excluded. The significant ($P < 0.01$) fixed terms included in the genetic models for each trait are presented in Table 1.

The season of birth was defined as spring (September–November), summer (December–February), autumn (March–May) and winter (June–August). The diet at weaning and yearling consisted of five classes (pasture, fertilised pasture, fertilised and rotational pasture, irrigated pasture, and feedlot). Genetic groups were defined for the Canchim and MA animals. Observations for which the standardised residuals (normalised data obtained by the z-scores statistic) were greater than 3.5 or lower than -3.5, (which correspond to 0.22% of the data for each trait) were considered outliers and excluded. The descriptive statistics of the evaluated traits after data quality control are presented in Table 2.

Genetic parameters

The genetic parameters were estimated by Average Information Restricted Maximum Likelihood method under an animal model (single and multi-trait analyses). The total number of animals in the relationship matrix was 20 041. Analyses were conducted using the software WOMBAT (Meyer 2007) using the convergence criterion of 10^{-9} .

The inclusion of maternal genetic and/or maternal permanent environmental random effects was previously evaluated for bodyweight and scrotal circumference traits using the likelihood ratio test (Dobson 1990). Due to limited pedigree structure, the statistical model for BW, WW, and SCW was extended to include the additive genetic, maternal genetic, and

Table 1. Significant ($P < 0.01$) fixed terms and coefficient of determination (R^2) included in the genetic models for each trait
BW, birthweight; WW, weaning weight; YW, yearling weight; SCW, scrotal circumference at weaning; SCY, scrotal circumference at yearling; AFC, age at first calving; REA, ribeye area; BFT, back fat thickness; (+), fixed effect considered in the contemporary group; *, linear effect; **, linear-quadratic effect

Effects	Traits							
	BW	WW	YW	SCW	SCY	AFC	REA	BFT
Fixed effects considered in the contemporary groups								
Sex	+	+	+	-	-	-	+	+
Year of birth	+	+	+	+	+	+	+	+
Season of birth	+	-	-	-	-	-	-	-
Farm of birth	+	+	+	+	+	+	+	+
Farm at weaning	-	+	+	+	+	+	+	+
Farm at yearling	-	-	+	-	+	+	+	+
Diet at weaning	-	+	-	+	-	-	-	-
Diet at yearling	-	-	+	-	+	-	+	+
Genetic group	-	+	+	+	+	+	+	+
Covariates								
Age of the dam at calving**	+	+	+	+	-	-	-	-
Age at weaning*	-	+	-	+	-	-	-	-
Age at yearling*	-	-	+	-	+	-	-	-
Age at ultrasound measurement*	-	-	-	-	-	-	+	+
Coefficient of determination (R^2)								
	0.37	0.53	0.73	0.39	0.28	0.39	0.81	0.61

Table 2. Descriptive statistics on the resulting unadjusted values after data quality control and statistical modelling for bodyweight, reproductive, and carcass traits. The unadjusted values were used for genetic analysis of the traits considered

BW, birthweight; WW, weaning weight; YW, yearling weight; SCW, scrotal circumference at weaning; SCY, scrotal circumference at yearling; AFC, age at first calving; REA, ribeye area; BFT, back fat thickness; CG, contemporary groups; CV, coefficient of variation; R^2 , coefficient of determination

Traits	Number of animals	Number of males	Number of sires	Number of dams	Number of CG	Average	CV (%)	Minimum values	Maximum values
BW (kg)	12 967	1901	362	7634	936	34.70	13.79	15.00	54.00
WW (kg)	7481	1730	323	4656	736	202.00	18.07	94.00	326.00
YW (kg)	5131	1365	312	3427	609	305.00	20.93	127.00	514.00
SCW (cm)	1447	–	204	996	113	18.70	11.94	12.50	26.00
SCY (cm)	1224	–	230	980	86	29.20	10.81	20.00	41.00
AFC (months)	1400	–	177	1225	208	36.65	13.99	25.60	52.39
REA (cm ²)	2082	1077	257	1422	189	53.00	27.63	21.46	92.27
BFT (mm)	2082	1077	257	1422	189	2.20	34.60	0.60	4.36

Table 3. Variance components and heritability estimates obtained in single-trait analyses

BW, birthweight; WW, weaning weight; YW, yearling weight; SCW, scrotal circumference at weaning; SCY, scrotal circumference at yearling; AFC, age at first calving; REA, ribeye area; BFT, back fat thickness; σ_a^2 , additive genetic variance; σ_m^2 , additive maternal variance; σ_e^2 , environmental variance; σ_p^2 , phenotypic variance; h_a^2 , direct heritability estimate; h_m^2 , maternal heritability estimate; s.e., standard error

Traits	Variance components and heritability estimates					
	σ_a^2	σ_m^2	σ_e^2	σ_p^2	$h_a^2 \pm$ s.e.	$h_m^2 \pm$ s.e.
BW	4.36	1.34	10.23	15.94	0.27 \pm 0.03	0.08 \pm 0.01
WW	169.04	138.06	420.18	727.29	0.23 \pm 0.03	0.19 \pm 0.02
YW	360.13	–	863.00	1223.14	0.29 \pm 0.04	–
SCW	0.97	0.21	2.10	3.29	0.29 \pm 0.08	0.06 \pm 0.04
SCY	3.36	–	4.55	7.92	0.42 \pm 0.10	–
AFC	1.88	–	17.14	19.02	0.09 \pm 0.07	–
REA	15.62	–	29.04	44.67	0.35 \pm 0.06	–
BFT	0.05	–	0.19	0.24	0.20 \pm 0.06	–

residual random effects; and the fixed effects of CG and covariates. The statistical model for YW, SCY, AFC, REA, and BFT included the additive genetic and residual random effects, as well as the fixed effects of CG and covariates. Residual covariances between traits measured on opposite sex were set to zero.

Results and discussion

The observed average for bodyweight, reproductive, and carcass traits (Table 2) are in agreement with previous studies of the Canchim breed (Andrade *et al.* 2008; Baldi *et al.* 2010; Barichello *et al.* 2010; Buzanskas *et al.* 2010; Meirelles *et al.* 2010; Borba *et al.* 2011). The variance components and heritabilities estimated in single-trait analyses are presented in Table 3. A substantial proportion of the variation in the bodyweights, scrotal circumferences and carcass traits was associated with the additive genetic term indicating that these traits may respond to selection in Canchim cattle.

For BW, WW, YW, and SCW the direct heritability estimates were in the range found in the literature for the Canchim breed, which ranged from 0.25 to 0.41 (BW), 0.23 to 0.48 (WW), 0.24 to 0.29 (YW), and 0.17 to 0.52 (SCW) (Alencar *et al.* 1993; Silva

et al. 2000; Gianlorenço *et al.* 2003; Andrade *et al.* 2008; Baldi *et al.* 2010; Buzanskas *et al.* 2010; Borba *et al.* 2011). Direct heritability estimates for BW obtained by Boligon *et al.* (2011), El-Saied *et al.* (2006), and Meyer (1995) were equal to 0.30 ± 0.01 , 0.36 ± 0.04 , and 0.38 for Nellore, Charolais, and Australian Angus cattle. Boligon *et al.* (2010), Meyer (1993), and Meyer (1995) estimated direct heritability in Nellore, Charolais, and Australian Angus of 0.33 ± 0.02 , 0.13 , and 0.23 ± 0.01 , for WW; and 0.37 ± 0.03 , 0.32 , 0.31 ± 0.01 , for YW.

For SCW, Boligon *et al.* (2011) and Morris *et al.* (2000) found heritability estimates of 0.39 ± 0.01 and 0.37 ± 0.06 , respectively for Nellore and Angus breeds. Alencar *et al.* (1993) and Borba *et al.* (2011) found lower heritability estimates for SCY in Canchim. According to Silva *et al.* (2013a) and Garmyn *et al.* (2011), heritability estimates for SCY in Nellore and Angus, respectively, were equal to 0.40 ± 0.02 and 0.46 ± 0.08

The heritability estimates for REA and BFT are in agreement with the ones obtained by Meirelles *et al.* (2010) in Canchim cattle. Heritability estimates varying from 0.18 to 0.68, for BFT, and from 0.29 to 0.64, for REA, were described for Simmental (Crews *et al.* 2003), Charolais (Chen *et al.* 2014), Guzerat (Lima Neto *et al.* 2009), and Nellore (Yokoo *et al.* 2010; Zuin *et al.* 2012).

Buzanskas *et al.* (2010) and Borba *et al.* (2011) found heritability estimates of 0.04 ± 0.01 and 0.05 ± 0.02 for AFC, respectively, using Bayesian methodology. Under the restricted maximum likelihood method, Baldi *et al.* (2008) and Silva *et al.* (2000) found heritability estimates equal to 0.10 ± 0.05 and 0.12 , respectively, slightly larger than our estimate of 0.09 obtained in single-trait analysis. The age at which heifers are exposed to the bulls is very challenging when evaluating AFC. Heifers that have early oestrus cannot be detected if not exposed, thus the variability of the trait could be influenced by non-genetic factors.

The maternal genetic effect was estimated for BW, WW, and SCW, respectively. The results for maternal heritability estimate for WW and SCW indicates that this effect could influence the performance of WW traits (Meyer 1992), however there has been some evidence for maternal effects on post-weaning growth (Mackinnon *et al.* 1991). In our study, the average number of calves per dam was equal to 1.69, 1.60, and 1.45, for BW, WW, and SCW, respectively. According to Pelicioni *et al.* (2003), the presence of cows with a low number of calves may present confounded effects between maternal genetic and maternal permanent environmental random effects when genetic evaluations are conducted.

The heritability estimates and genetic correlations obtained in multi-trait analysis are presented in Table 4. Due to the (co) variance structure considered in the multi-trait analysis, greater variation in the heritabilities estimates (direct and maternal) was observed for WW in comparison to the single-trait analysis. All other traits presented similar results in each analysis.

The genetic correlations among bodyweight traits were from 0.41 to 0.93, suggesting pleiotropic effects, especially between WW and YW. These estimates were similar to those presented by Baldi *et al.* (2010) in Canchim cattle. High genetic correlations among bodyweight traits were observed by Vargas *et al.* (2014), Naser *et al.* (2012), and Van Niekerk and Naser (2006) for Brahman, Brangus, and Limousin breeds. Silva *et al.* (2013b) estimated genetic correlations for Nellore cattle from birth to 550 days of age, which varied from 0.25 to 0.98. Selection of any of these traits would increase bodyweight gains at later ages.

The genetic correlation between SCW and SCY was high (0.91). Boligon *et al.* (2010) obtained genetic correlations of 0.80 ± 0.02 among scrotal circumferences measured at 9 and 18 months of age in Nellore cattle. High genetic correlations were observed between SCW and WW, and SCY and YW. For the Nellore breed, Boligon *et al.* (2010) obtained genetic correlations for scrotal circumference and bodyweight traits lower than ours. Selection to increase SCW or SCY will contribute positively and indirectly to bodyweight of Canchim animals. The genetic correlation between WW and SCW estimated by Barichello *et al.* (2010) in Canchim cattle was lower than ours.

Most of the genetic correlations with AFC were favourable, especially with YW, SCW, and SCY (-0.48 , -0.61 and -0.71 , respectively), which suggests indirect and favourable responses to selection. Similar genetic correlations among these traits were observed in the Canchim breed (Talhari *et al.* 2003; Borba *et al.* 2011) and Nellore breed (Barrozo *et al.* 2012; Chiaia *et al.* 2015). The genetic correlation between AFC and BFT (-0.69) indicated that selection for high fat deposition could result in lower ages at first calving. From a biological point of view, this favourable correlation could be due to the lipid production or fat deposition, which is directly linked to hormonal production and sexual development (Dias *et al.* 2009). According to Caetano *et al.* (2013), the genetic correlation between AFC and BFT was equal to -0.35 ± 0.08 in the Nellore breed.

The REA presented low to moderate genetic correlations with BW, WW, and YW. The genetic correlation among these traits increases as animals grow older, possibly due to muscular development, suggesting that selection for bodyweight could improve this carcass trait. For the Nellore breed, Yokoo *et al.* (2010) and Zuin *et al.* (2012) estimated genetic correlations of 0.69 ± 0.06 and 0.62 ± 0.02 between REA and WW, respectively. Meirelles *et al.* (2010) and Gordo *et al.* (2012) observed a genetic correlation of 0.62 ± 0.16 and 0.55 ± 0.04 between YW and REA in Canchim and Nellore cattle. The opposite trend was observed between REA with SCW and SCY, in which SCY resulted in a genetic correlation close to zero. Thus, REA and scrotal circumferences appear to be independent

Table 4. Direct and maternal heritability estimates (diagonal, in bold) and genetic correlations (above diagonal) with respective standard errors (\pm) obtained from multi-trait analysis

BW, birthweight; WW, weaning weight; YW, yearling weight; SCW, scrotal circumference at weaning; SCY, scrotal circumference at yearling; AFC, age at first calving; REA, ribeye area; BFT, back fat thickness

Traits	BW	WW	YW	SCW	SCY	AFC	REA	BFT
BW	0.26 ± 0.03^A 0.07 ± 0.01^B	0.42 ± 0.07	0.41 ± 0.07	0.07 ± 0.11	0.09 ± 0.10	0.14 ± 0.21	0.25 ± 0.11	0.18 ± 0.13
WW	–	0.35 ± 0.03^A 0.08 ± 0.01^B	0.93 ± 0.02	0.52 ± 0.09	0.43 ± 0.09	-0.23 ± 0.25	0.62 ± 0.09	0.38 ± 0.14
YW	–	–	0.32 ± 0.04^A	0.59 ± 0.09	0.47 ± 0.10	-0.48 ± 0.27	0.49 ± 0.11	0.43 ± 0.16
SCW	–	–	–	0.32 ± 0.06^A 0.06 ± 0.02^B	0.91 ± 0.06	-0.61 ± 0.39	0.09 ± 0.17	0.14 ± 0.20
SCY	–	–	–	–	0.49 ± 0.08^A	-0.71 ± 0.34	-0.02 ± 0.17	0.15 ± 0.19
AFC	–	–	–	–	–	0.11 ± 0.07^A	0.30 ± 0.32	-0.69 ± 0.35
REA	–	–	–	–	–	–	0.35 ± 0.07^A	0.27 ± 0.17
BFT	–	–	–	–	–	–	–	0.21 ± 0.06^A

^ADirect heritability estimate.

^BMaternal heritability estimate.

Table 5. Environmental (above diagonal) and phenotypic (below diagonal) correlations obtained by multi-trait analysis

BW, birthweight; WW, weaning weight; YW, yearling weight; SCW, scrotal circumference at weaning; SCY, scrotal circumference at yearling; AFC, age at first calving; REA, ribeye area; BFT, back fat thickness

Traits	BW	WW	YW	SCW	SCY	AFC	REA	BFT
BW	–	0.20 ± 0.02	0.12 ± 0.03	0.12 ± 0.04	0.15 ± 0.05	–0.08 ± 0.05	–0.07 ± 0.04	–0.03 ± 0.04
WW	0.24 ± 0.01	–	0.62 ± 0.02	0.56 ± 0.04	0.43 ± 0.06	–0.12 ± 0.06	0.28 ± 0.04	0.03 ± 0.04
YW	0.19 ± 0.01	0.69 ± 0.01	–	0.39 ± 0.04	0.53 ± 0.06	–0.15 ± 0.06	0.46 ± 0.04	0.09 ± 0.05
SCW	0.09 ± 0.02	0.51 ± 0.01	0.44 ± 0.02	–	0.46 ± 0.06	–	–0.01 ± 0.07	–0.14 ± 0.09
SCY	0.12 ± 0.02	0.41 ± 0.02	0.50 ± 0.02	0.62 ± 0.01	–	–	0.36 ± 0.09	0.03 ± 0.08
AFC	–0.03 ± 0.03	–0.12 ± 0.03	–0.20 ± 0.04	–0.10 ± 0.06	–0.77 ± 0.42	–	–0.15 ± 0.09	0.03 ± 0.08
REA	0.03 ± 0.02	0.36 ± 0.02	0.47 ± 0.02	0.14 ± 0.03	0.21 ± 0.03	–0.06 ± 0.06	–	0.09 ± 0.06
BFT	0.02 ± 0.02	0.10 ± 0.02	0.17 ± 0.02	0.03 ± 0.03	0.06 ± 0.03	–0.07 ± 0.06	0.14 ± 0.02	–

traits. Marques *et al.* (2013) found low genetic correlation of scrotal circumference with REA in the Nellore breed.

Moderate genetic correlation between REA and AFC was observed. As the age at calving increases, an increase in bodyweight is expected. This indicates that females with higher REA may calve later in life; however, a high standard error was obtained for this genetic correlation. Caetano *et al.* (2013) observed a genetic correlation of -0.11 ± 0.04 between REA and AFC. The BFT presented moderate genetic correlation with WW and YW, whereas for the scrotal circumferences and BW it presented correlations of low magnitude. This indicates that at post-weaning ages the fat deposition could be beginning. For Brangus and Nellore breeds, Stelzleni *et al.* (2002) and Yokoo *et al.* (2010), respectively, found similar genetic correlations between BFT and YW.

Low and positive genetic correlations were observed among carcass traits, indicating no linear association and if selection were carried out, there would be minor changes expected among them. Similar results were observed by Meirelles *et al.* (2010), Chen *et al.* (2014), and Caetano *et al.* (2013) between REA and BFT, equal to 0.21 ± 0.24 , 0.19 ± 0.18 , and 0.19 ± 0.06 , for Canchim, Charolais, and Nellore breeds, respectively. Peters *et al.* (2014), using multivariate normal distribution analysis, obtained genetic correlation between REA and BFT equal to -0.41 ± 0.30 in beef cattle.

The environmental and phenotypic correlations obtained in multi-trait analysis are presented in Table 5. Environmental correlations between BW and AFC, BW and REA, BW and BFT, SCW and AFC, SCW and REA, SCW and BFT, SCY and REA, AFC and REA, and AFC and BFT presented opposite signs and similar magnitudes with the genetic correlations. The opposite signs indicate that genetic and environmental sources of variation affect the traits by means of different physiological mechanisms (Falconer and Mackay 1996).

Conclusion

Genetic improvement through selection is expected for production, reproduction, and carcass traits in Canchim beef cattle. Many of the traits considered in the genetic evaluation of this breed are genetically correlated in a favourable manner. Genetic parameter estimates indicate that improvement for carcass and reproduction traits could be achieved.

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