

Phenotypic and genetic correlations for body structure scores (frame) with productive traits and index for CEIP classification in Nellore beef cattle

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ABSTRACT. The present study was carried out to estimate both (co)variance components and genetic parameters for frame scores obtained using two methods (FRAME_GMA and FRAME_BIF) as well as phenotypic and genetic correlations with traits such as weaning weight, weight gain from weaning to yearling, scrotal circumference, muscle score, and an empiric index for animal classification for the Special Certificate of Identification and Production (CEIP). Data on 12,728 animals, raised in Southeastern Brazil, with ages from 490 to 610 days were analyzed. Estimates of heritability for FRAME_GMA and FRAME_BIF in multi-trait analysis were 0.28 and 0.24, respectively. Genetic correlation coefficients between frame scores and the growth trait were of medium magnitude, which indicates that genetic selection for weight resulted in undesirable responses, increasing the animals' frames. Small changes should be expected in the frame of animals that have been submitted to a genetic selection regarding muscle score and scrotal circumference. The low magnitude of phenotypic and genetic

correlation between frame scores and the empirical selection index that classifies animals for CEIP, a Brazilian official certificate that recognizes the value of seedstock that is not registered at breeders associations, but is genetically evaluated, does not indicate important responses in giving a CEIP to animals that have been directly or indirectly selected for frame. Other studies must be performed to determine estimates of the genetic parameters for frame scores in other beef cattle populations.

Key words: Genetic and phenotypic correlation, Frame scores, Weight, CEIP, Nelore, Genetic improvement

INTRODUCTION

Body structure or frame is a complex trait, which is usually featured by the weight associated with maturity and gender (Cartwright, 1979), where its phenotypical expression is, *a priori*, a response of the growth process of the animal. Frame scores have been estimated in a subjective way through visual evaluations or through the formulas proposed by the American Beef Improvement Federation (ABIF, 2002). The use of these formulas, however, has proven to be less adequate than the mathematical models which have been specially developed for estimating the frame scores of Zebu livestock (Horimoto, 2005).

The evaluation of frame scores has been part of the American system of frame typing (United States Standards for Grades of Feeder Cattle) since 1979. In Brazil, there is an increasing interest in frame scores due to the nature of the observed correlations between frame and growth traits in beef cattle. In order to increase growth, body weight at early ages has been continually used as a selection criterion, which could promote an undesirable correlated response regarding the increase of the animal's frame (Cardoso et al., 1998; Arango and Plasse, 2002) associated with a negative impact on female reproductive efficiency (Vargas et al., 1999).

Few studies on beef cattle frame have been performed based on scores, most of them considering some characteristics indicative of frame, such as adult weight or hip height in the discussion of the relationships to the productive efficiency of the animals. The study of the magnitude of the relationships between frame scores and weight and reproductive traits of Zebu beef cattle and, above all, of a possible relationship to the index used in the classification of the animals for CEIP (Special Certificate of Identification and Production), is a must for accomplishing the control of this feature in genetic improvement programs.

The objectives of the present study were: to estimate (co)variance components and genetic parameters for frame scores using mathematical models developed for this data set and by the application of the formulas recommended by ABIF (2002), as well as for traits of weaning weight (WW), weight gain from weaning to yearling (WG₃₄₅) and hip height (H18), yearling weight (W18), scrotal circumference (SC18), and visual muscle score (MUSC18), measured at 18 months of age, and to estimate phenotypic and genetic correlation coefficients between frame scores and the empirical index used for classification of animals for the CEIP (I_CEIP), WW, WG₃₄₅, SC18, and MUSC18.

MATERIAL AND METHODS

Data from 12,728 Nellore animals measured for WW, W18, WG_345, SC18, MUSC18, and H18 were analyzed. These data were provided by two farms owned by Agro-Pecuária CFM Ltda., located in the middle-northwestern area of São Paulo State, and were records for 6,597 males and 6,131 females, born between 1995 and 2000. These records had a pedigree file of 30,081 animals from 7 different generations.

Outlier data had been eliminated from the data set based on the Theorem of the Central Limit. The contemporary groups considered were the non-genetic factors farm, year of birth, gender, and management group, variables where statistical significance had been identified by the application of the PROC GLM procedure from the Statistical Analysis System® program, version 8.02 (SAS, 2000). Contemporary groups that could negatively interfere with the analysis, such as groups composed of less than 4 animals, and groups composed of animals from only one sire and without any variability had been eliminated.

Two frame scores were estimated, FRAME_GMA and FRAME_BIF. In Table 1, the adjusted prediction formulas for estimating the FRAME_GMA scores by gender are presented, and they were developed as detailed in Horimoto (2005). FRAME_BIF was estimated as proposed by the ABIF (2002), and the formulas are presented in Table 2.

Table 1. Adjusted prediction formulas to estimate FRAME_GMA scores, by gender.

Gender	Formula
Male	$\hat{Y}_{FRAME_GMA} = -7.01993 + 0.06294 \cdot X_1 - 0.14870 \cdot X_2 + 0.00119 \cdot X_1 \cdot X_2$
Female	$\hat{Y}_{FRAME_GMA} = -93.47611 + 0.69992 \cdot X_1 + 0.14078 \cdot X_2 - 0.00093037 \cdot X_1 \cdot X_2$

$X_1 =$ H18 (cm); $X_2 =$ W18 (kg).

Table 2. Formulas used to estimate FRAME_BIF scores, by gender.

Gender	Formula
Male	$\hat{Y}_{FRAME_BIF} = -11.548 + 0.4878 \cdot X_1 - 0.0289 \cdot X_2 + 0.00001947 \cdot X_2^2 + 0.0000334 \cdot X_1 \cdot X_2$
Female	$\hat{Y}_{FRAME_BIF} = -11.7086 + 0.4723 \cdot X_1 - 0.0239 \cdot X_2 + 0.0000146 \cdot X_2^2 + 0.0000759 \cdot X_1 \cdot X_2$

$X_1 =$ H18 (inches); $X_2 =$ AgeH18 (days).

For estimating the genetic parameters, only integer values for FRAME_GMA and FRAME_BIF were taken. Phenotypic correlation coefficients moment-product of Pearson and Spearman between whole and decimal values were estimated for making this decision. Single-trait analysis was carried out for FRAME_GMA, FRAME_BIF, H18, WW, WG_345, SC18, and MUSC18, in addition to the multi-trait analysis between each frame score and the variables of WW, W18, WG_345, and SC18, using the restricted maximum likelihood procedure for animal models, available in the Multiple Trait Derivative Free Restricted Maximum Likelihood program (Boldman et al., 1995).

The models for analysis considered as fixed effects were contemporary groups and age classes of dams. The random effects included in the models were direct additive genetic effect for WW, WG_345, FRAME_GMA, FRAME_BIF, H18, W18, SC18, and MUSC18, maternal additive genetic effect for WW and WG_345 and permanent environmental effect for WW. The covariables included in the models of analysis were the ages at measurement (weaning or 18 months). Initial values of the (co)variance components, the priors, used in single-trait analysis were estimated using the PROC VARCOMP procedure from the Statistical Analysis System®, version 8.02 (SAS, 2000). The (co)variance estimates obtained in single-trait analysis were used as initial values for the multi-trait analysis.

When the I_CEIP was applied, 2,179 males born in 1998 were selected, the year when there was a larger number of males in the data set. The composition of the index is according to that proposed by Agro-pecuária CFM (2004), as presented below. In the calculation of I_CEIP, each component was obtained using the ratio between the expected difference in the progeny (DEP) divided by its genetic standard deviation, where a specific weight was attributed to each one. From the total animals that had their I_CEIP calculated, 23% had a higher index and were considered eligible for CEIP, totaling 490 young bulls.

$$I_CEIP = \frac{2. DEP_{WW}}{\sigma_g WW} + \frac{4. DEP_{WG_345}}{\sigma_g WG_345} + \frac{2. DEP_{MUSC18}}{\sigma_g MUSC18} + \frac{2. DEP_{SC18}}{\sigma_g SC18}$$

In order to verify the relationship between frame scores and productive efficiency in this Nellore population, phenotypic and genetic correlation coefficients of moment-product of Pearson and Spearman were obtained using the PROC CORR procedure from the Statistical Analysis System® program, version 8.02 (SAS, 2000), for each frame score (FRAME_GMA and FRAME_BIF), in relation to WW, W18, WG_345, SC18, MUSC18, and I_CEIP.

RESULTS AND DISCUSSION

The descriptive statistics for H18, AgeH18, WW, AgeWW, W18, WG_345, SC18, and MUSC18 are presented in Tables 3 and 4, respectively for males and females.

After the application of the formulas, shown in Tables 1 and 2, scores for FRAME_GMA and FRAME_BIF were determined to be 12,635 and 12,084, respectively. The descriptive statistics for these scores are shown in Table 5. Mercadante et al. (2004), also studying FRAME_BIF scores in Nellore breed, reported lower values than the ones found in this study (6.07 ± 0.99) for females aged between 16 and 21 months. The lower variability of the FRAME_BIF scores, reflected by the coefficient of variation, agrees with the results obtained by that study.

Phenotypic correlation coefficients of Pearson and Spearman between decimal and integer values of both frame scores, determined as 0.93 to 0.99 in males and females, justified the decision of working just with the whole values of FRAME_GMA and FRAME_BIF scores for estimating genetic parameters.

The estimates of (co)variance components and heritability obtained through single trait-analysis are shown in Table 6. In two-trait analysis with WW, heritability estimates for direct additive genetic effect for FRAME_GMA and FRAME_BIF are 0.28 and 0.24, respectively.

Table 3. Descriptive statistics for hip height (H18), age at the measurement of hip height (AgeH18), weaning weight (WW), age at weaning (AgeWW), weight (W18), weight gain from weaning to yearling (WG_345), scrotal circumference (SC18), and visual muscle score (MUSC18) for males.

Variable	N	\bar{X}	SD	CV	MIN	MAX
H18 (cm)	6586	138.7	4.60	3.3	123.0	152.0
AgeH18 (days)	6586	531.9	29.50	5.5	490.0	610.0
WW (kg)	6357	200.1	25.70	12.9	117.0	270.0
AgeWW (days)	6357	200.6	19.80	9.9	146.0	270.0
W18 (kg)	6242	319.6	38.80	12.1	200.0	424.0
WG_345 (kg)	6219	121.1	36.00	29.8	-22.4	257.6
SC18 (cm)	6539	27.7	3.20	11.4	18.0	37.0
MUSC18	6591	6.0	0.95	15.9	1.5	9.0

N = number of observations; \bar{X} = mean; SD = standard deviation; CV = coefficient of variation (%); MIN = minimum value; MAX = maximum value.

Table 4. Descriptive statistics for hip height (H18), age at the measurement of hip height (AgeH18), weaning weight (WW), age at weaning (AgeWW), weight (W18), weight gain from weaning to yearling (WG_345), and visual muscle score (MUSC18) for females.

Variable	N	\bar{X}	SD	CV	MIN	MAX
H18 (cm)	6099	134.8	4.2	3.1	122.0	148.0
AgeH18 (days)	6099	534.3	28.8	5.4	490.0	610.0
WW (kg)	5908	187.1	21.7	11.6	117.0	267.0
AgeWW (days)	5908	206.4	19.6	9.5	139.0	312.0
W18 (kg)	5837	292.5	31.6	10.8	194.0	407.0
WG_345 (kg)	5808	110.3	27.3	24.7	-2.7	206.2
MUSC18	6129	6.1	1.0	16.4	2.0	9.0

N = number of observations; \bar{X} = mean; SD = standard deviation; CV = coefficient of variation (%); MIN = minimum value; MAX = maximum value.

Table 5. Descriptive statistics for FRAME_GMA and FRAME_BIF scores, by gender.

	Gender	N	\bar{X}	SD	CV	MIN	MAX
<i>FRAME_GMA</i>	Male	6541	7.0	2.4	34.5	1	12
	Female	6094	5.4	2.1	39.5	1	11
<i>FRAME_BIF</i>	Male	6276	6.3	0.9	14.7	3	9
	Female	5808	6.9	0.9	12.2	4	10

N = number of observations; \bar{X} = mean; SD = standard deviation; CV = coefficient of variation (%); MIN = minimum value; MAX = maximum value.

Heritability estimates for the direct additive genetic effect for frame scores calculated through multi-trait analysis regarding W18, WG_345 and SC18, showed the same values that were found in single-trait analysis. Heritability estimates for FRAME_BIF obtained through single- and multi-trait analysis were lower than those obtained by Mercadante et al. (2004) in a data set of 3,948 animals, which were respectively 0.48 ± 0.04 and 0.60 .

Table 6. Estimates of the covariance components obtained through single-trait analysis of the FRAME_GMA and FRAME_BIF scores, hip height (H18), weaning weight (WW), yearling weight (W18), weight gain from weaning to yearling (WG_345), scrotal circumference (SC18), and visual muscle score (MUSC18), obtained using the restricted maximum likelihood method.

Analysis	σ_a^2	σ_m^2	σ_{am}	σ_c^2	σ_e^2	σ_p^2	h_a^2
FRAME_GMA	0.63	-	-	-	1.78	2.40	0.26 ± 0.03
FRAME_BIF	0.10	-	-	-	0.35	0.45	0.23 ± 0.03
H18	2.45	-	-	-	7.25	9.71	0.25 ± 0.03
WW	63.80	3.70	6.39	38.79	118.17	230.85	0.28 ± 0.04
W18	161.40	-	-	-	319.91	481.31	0.34 ± 0.03
WG_345	104.26	40.75	-39.90	-	219.74	324.84	0.32 ± 0.05
SC18	3.68	-	-	-	3.02	6.69	0.55 ± 0.05
MUSC18	0.09	-	-	-	0.49	0.59	0.16 ± 0.03

σ_a^2 = direct additive genetic variance; σ_m^2 = maternal additive genetic variance; σ_{am} = covariance between the direct additive genetic effects and maternal ones; σ_c^2 = variance due to the permanent environmental effects; σ_e^2 = environmental variance; σ_p^2 = phenotypic variance; h_a^2 = estimate of the heritability for the direct additive genetic effects; - the last one is not included in the model.

Table 7 presents the estimates of the (co)variance components obtained through multi-trait analysis, where the frame score was the anchor trait.

(Co)variance estimates between frame scores (FRAME_GMA and FRAME_BIF) and growth traits (WW, W18 and WG_345) obtained through two-trait analysis showed that selection for weight will positively reflect on the increase of the animal's frame. These results are in accordance with Mercadante et al. (2003), who found a yearly genetic trend of changing hip height, a measure indicative of frame, of 0.25 ± 0.03 cm, for female Nellore cattle that had been selected for weight.

Table 8 presents phenotypic and genetic correlation coefficients of Pearson and Spearman between the frame scores and the traits I_CEIP, WW, WG_345, SC18, and MUSC18.

Genetic correlation coefficients between the frame scores and WW and WG_345 were of medium magnitude, indicating that genetic selection shows some undesirable responses in the increase of the animal's frame. For SC18 the positive and of low-magnitude genetic correlations regarding FRAME_GMA and the negative and close to zero ones related to FRAME_BIF, show few changes in the body structure of the animals under selection regarding scrotal circumference. The genetic correlation coefficients between frame scores and visual muscle score, negative and close to zero, do not show any significant changes in the visual muscle score.

Although the phenotypic and genetic correlation coefficients estimated between the FRAME_GMA scores and I_CEIP were higher when compared to those obtained related to

Table 7. Estimates of the (co)variance components obtained through two-trait analysis between the FRAME_GMA and FRAME_BIF scores and the weaning weight (WW), yearling weight (W18), weight gain from weaning to yearling (WG_345), and scrotal circumference (SC18) using the restricted maximum likelihood method.

Analysis	σ_{a1}^2	σ_{a2}^2	σ_{m2}^2	σ_{a1a2}	σ_{a1m2}	σ_{a2m2}	σ_{e1}^2	σ_{e2}^2	σ_{e1e2}	σ_{p1}^2	σ_{p2}^2	σ_{p1p2}	
GMA x WW	0.68	69.50	11.26	4.63	0.99	4.12	26.56	1.76	120.16	5.99	2.44	231.59	11.11
GMA x W18	0.63	160.99	-	6.65	-	-	-	1.78	320.49	14.20	2.41	481.48	20.86
GMA x WG_345	0.63	111.40	26.94	4.14	-2.03	-32.19	-	1.78	219.89	7.41	2.41	326.05	10.53
GMA x SC18	0.62	3.65	-	0.15	-	-	-	1.78	3.02	0.59	2.41	6.67	0.74
BIF x WW	0.11	67.31	10.62	1.63	0.37	2.97	31.32	0.35	119.00	1.85	0.46	231.22	3.67
BIF x W18	0.10	161.14	-	2.06	-	-	-	0.35	320.31	4.28	0.45	481.45	6.33
BIF x WG_345	0.10	106.52	34.43	1.00	-0.59	-36.30	-	0.35	220.48	2.17	0.45	325.13	2.88
BIF x SC18	0.10	3.69	-	0.05	-	-	-	0.35	3.00	0.16	0.45	6.69	0.21

σ_a^2 = direct additive genetic variance; σ_m^2 = maternal additive genetic variance; σ_{aa} = covariance between the direct additive genetic effects; σ_{am} = covariance between the direct and maternal additive genetic effects; σ_e^2 = variance due to the permanent environmental effect; σ_e^2 = environmental variance; σ_e^2 = phenotypic variance; σ_{pp} = covariance between the phenotypic effects; - the last one is not included in the model; 1 = covariance components for the first characteristic of the analysis (GMA or BIF); 2 = covariance components for the second characteristic of the analysis.

Table 8. Phenotypic and genetic correlation coefficients of Pearson (P) and Spearman (S) between frame scores (FRAME_GMA and FRAME_BIF) and the empirical index for CEIP (I_CEIP), weaning weight (WW), weight gain from weaning to yearling (WG_345), scrotal circumference (SC18), and visual muscle score (MUSC18).

	Phenotypic correlation				Genetic correlation			
	FRAME_GMA		FRAME_BIF		FRAME_GMA		FRAME_BIF	
	P	S	P	S	P	S	P	S
I_CEIP	0.21	0.26	0.13	0.13	0.22	0.21	0.13	0.11
WW	0.45	0.39	0.41	0.25	0.40	0.40	0.30	0.29
WG_345	0.24	0.38	0.15	0.20	0.29	0.30	0.16	0.17
SC18	0.19	0.27	0.11	0.11	0.06	0.05	-0.01	-0.02
MUSC18	0.32	0.42	0.16	0.15	-0.01	0.00	-0.14	-0.12

the FRAME_BIF, the low magnitude of these estimates does not indicate important responses in giving a CEIP to animals that have been directly or indirectly selected for frame.

CONCLUSIONS

Heritability estimates and phenotypic and genetic correlation coefficients related to FRAME_GMA were always higher when compared to those obtained for FRAME_BIF, which suggests a better adaptation of FRAME_GMA scores to Zebu cattle data, allowing a greater response to genetic selection. The phenotypic and genetic correlation coefficients between the frame scores and the body weight show that the animals that have been submitted to weight selection may be indirectly selected for the augmentation of the body structure. Not very significant changes would be expected in the visual muscle score, scrotal circumference and classification index for giving a CEIP to animals selected for frame. Further studies must be performed to determine the magnitude of the estimates of the genetic parameters for frame scores in other populations of beef cattle.

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