

Estimates of genetic parameters for visual scores and daily weight gain in Brangus animals

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(Received 5 March 2010; Accepted 28 August 2010; First published online 5 January 2011)

(Co)variance components were estimated for visual scores of conformation (CY), early finishing (PY) and muscling (MY) at 550 days of age (yearling), average daily gain from weaning to yearling (GWY), conformation (CW), early finishing (PW) and muscling (MW) scores at weaning, and average daily gain from birth to weaning (GBW) in animals forming the Brazilian Brangus breed born between 1986 and 2002 from the livestock files of GenSys Consultores Associados S/C Ltda. The data set contained 53 683; 45 136; 52 937; 56 471; 24 531; 21 166; 24 006 and 25 419 records for CW, PW, MW, GBW, CY, PY, MY and GWY, respectively. Data were analyzed by the restricted maximum likelihood method using single- and two-trait animal models. Direct heritability estimates obtained by single-trait analysis were 0.12, 0.14, 0.13 and 0.14 for CY, PY and MY scores and GWY, respectively. A positive association was observed between the same visual scores at weaning and yearling, with correlations ranging from 0.64 to 0.94. Estimated correlations between GBW and weaning and yearling scores ranged from 0.60 to 0.77. The genetic correlation between GBW and GWY was low (0.10), whereas correlations of 0.55, 0.37 and 0.47 were observed between GWY and CY, PY and MY, respectively. Moreover, GWY showed a weak correlation with CW (0.10), PW (–0.08) and MW (–0.03) scores. These results indicate that selection of the traits that was studied would result in a small response. In addition, selection based on average daily gain may have an indirect effect on visual scores as the correlations between GWY and visual scores were generally strong.

Keywords: heritability, correlations, conformation, early finishing, muscling

Implications

Yearling visual scores of conformation, early finishing (precocity) and muscling and average daily gain from weaning to yearling are relatively easy to measure and are important traits for beef cattle production. Heritability estimates and genetic correlations between these traits as well as between them and weaning visual scores, and average daily gain from birth to weaning obtained for the Brangus breed in Brazil indicate that selection for average daily gain from weaning to yearling and visual scores at 550 days would result in small genetic changes in these traits. In addition, selection based on average daily gain from birth to weaning may promote a favorable correlated response in visual scores allowing greater economic returns for producers.

Introduction

The main selection criteria used in animal breeding programs for growth are weight and weight gain measured at certain

ages, an approach that has resulted in important economic benefits for beef cattle producers. However, selection of only these traits has been shown to be insufficient, as these traits do not describe the complete growth potential of the animals and do not provide any information on muscling, bones and frame. The use of visual scores has permitted the indirect evaluation of traits related to early finishing (precocity) and carcass composition of beef cattle. The scores of conformation (C), precocity (P) and muscling (M) were designed to estimate how much meat the animal would produce if slaughtered at the time of assessment, the capacity of the animal to deposit the minimum amount of fat necessary for slaughter at a non-elevated live weight, and the quantity of muscle mass in the carcass, respectively (Costa *et al.*, 2008). Nicholson and Butterworth (1986) emphasized the fact that a large number of animals can be evaluated visually without the need for weight recordings or other measurements, thus minimizing stress, in addition to the low cost of implementation of a score-based assessment system. Dal-Farra *et al.* (2002) suggested that selection based on C, P and M scores may be sufficient as long as the heritability estimates for

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these traits are similar to the estimates for weight gain. Cardoso *et al.* (2004) estimated heritabilities of 0.19, 0.25 and 0.26 for yearling C, P and M scores, respectively, in Angus cattle.

In addition, knowledge about genetic correlations between economically relevant traits is important for the design of selection programs as it permits the prediction of correlated genetic changes in these traits. In this respect, Cardoso *et al.* (2004) estimated genetic correlations ranging from 0.22 to 0.94 between the reported scores at 550 days, whereas these estimates ranged from 0.50 to 0.71 when correlated with weight gain from birth to weaning. On the other hand, the genetic correlation between the same visual scores observed at weaning and yearling age ranged from 0.90 to 0.99.

The objective of this study was to estimate heritabilities for visual scores of C, P and M at yearling and average daily gain from weaning to yearling in animals forming the Brangus breed, as well as the genetic correlations between these traits and between them and C, P and M scores at weaning and average daily gain from birth to weaning, in order to define selection criteria for this breed.

Material and methods

Animals and data file

Records of conformation (CW), precocity (PW) and muscling (MW) at weaning, conformation (CY), precocity (PY) and muscling (MY) at yearling, average daily gain from birth to weaning (GBW) and average daily gain from weaning to yearling (GWY) of animals forming the Brangus breed were available. The animals were born between 1986 and 2002. These data were obtained from the Brangus and the Angus livestock files of GenSys Consultores Associados S/C Ltda. and refer to 110 commercial herds reared in the south, mid-west and southeast regions of Brazil. The animals were reared on pasture using different weaning and postweaning management systems in a heterogeneous climatic environment.

C, P and M scores were individually attributed to each animal using a method that evaluates animals in relation to their farm management group, that is, cattle of similar age and reared under the same environmental conditions. Scores ranging from 1 to 5 were attributed to animals by a trained person, usually a farm employee. A score of 1 was attributed to animals showing the worst phenotype of the trait within their farm management group. Animals below the average of their group received a score of 2. A score of 3 was attributed to cattle showing an average phenotype of the trait. Animals above the average of their group received a score of 4. Score 5 corresponded to the best expression of the trait (Costa *et al.*, 2008). GBW and GWY were calculated by linear interpolation using weaning and birth weight for GBW and yearling and weaning weight for GWY.

Inconsistency within the data were removed, resulting in files containing 53 683; 45 136; 52 937; 56 471; 24 531; 21 166; 24 006 and 25 419 observations for CW, PW, MW, GBW, CY, PY, MY and GWY, respectively.

Individual heterozygosity (IH) was calculated according to Teixeira and Albuquerque (2003) as follows: $IH = \text{sire breed} + \text{dam breed} - 2 \times (\text{sire breed} \times \text{dam breed})$, where

Table 1 Composition of the genetic groups and definition of direct and maternal additive effects in cattle forming the Brangus breed

Sire	Dam	Calf	Number of calves	Additive effect			
				Direct		Maternal	
				N	A	N	A
N	N	N	119	1	0	1	0
A	N	1N1A	19 130	1/2	1/2	1	0
N	A	1N1A	36	1/2	1/2	0	1
1N1A	N	3N1A	1002	3/4	1/4	1	0
3N1A	A	3N5A	7265	3/8	5/8	0	1
1N3A	N	5N3A	26	5/8	3/8	1	0
3N1A	N	7N1A	41	7/8	1/8	1	0
3N5A	A	3N13A	514	3/16	13/16	0	1
5N3A	A	5N11A	1234	5/16	11/16	0	1
3N5A	N	11N5A	13 056	11/16	5/16	1	0
5N3A	N	13N3A	906	13/16	3/16	1	0
11N5A	A	11N32A	315	11/32	21/32	0	1
11N5A	N	27N5A	123	27/32	5/32	1	0
A	A	A	12 724	0	1	0	1

N = Nelore; A = Angus.

Values in the genetic groups correspond to the portion of each breed in the composition of the groups, for example, 1N3A = 1/4 Nelore + 3/4 Angus.

breed = Zebu fraction of the individual. Maternal heterozygosity was not considered as only purebred Nelore or Angus cows were used as dams (Table 1).

The contemporary group at weaning consisted of animals of the same sex born on the same farm in the same season and year, and scored on the same day, farm and management group at weaning. At yearling, the same contemporary group as that used at weaning was defined, including the day, farm and management group at yearling. Contemporary groups containing fewer than five animals were eliminated. Dam age at calving ranged from 2 to 15 years, whereas the variable season of birth was divided into four periods of 3 months each, starting in January.

Statistical analysis

The (co)variance components of the variables studied were estimated by the derivative-free maximum likelihood method in single- and two-trait analyses using the MTDFREML program (Boldman *et al.*, 1995). The general model that was proposed included the contemporary group and the covariate age of dam in years (linear and quadratic effects), age of animal at weaning (linear and quadratic effects), age of animal at yearling (linear effect), in days, and IH (linear effect) as fixed effects, and direct and maternal additive genetic effects and maternal permanent environmental effects as random effects.

The single-trait animal model used can be represented as

$$y = X\beta + Zg + Mm + Wp + e,$$

where y is a $n \times 1$ vector of records, β denotes the vector of fixed effects, X is a matrix that associates β with y , g is a

vector of random additive direct genetic effects, Z is a matrix that associates g with y , m is a vector of random maternal additive genetic effects, M is a matrix that associates m with y , p is a vector of random effects of maternal permanent environment plus non-additive genetic effects contributed by dams to records of their progeny, W is a matrix that associates p with y , and e is the vector of random residual effects, peculiar to observations, that are not explained by other parts of the model. Assumptions for this model are:

$$E[y] = X\beta,$$

$$E \begin{bmatrix} g \\ m \\ p \\ e \end{bmatrix} = \begin{bmatrix} 0 \\ 0 \\ 0 \\ 0 \end{bmatrix} \text{Var} \begin{bmatrix} g \\ m \\ p \\ e \end{bmatrix} = \begin{bmatrix} A\sigma_{gm1}^2 & A\sigma_{gm1} & 0 & 0 \\ A\sigma_{gm1} & A\sigma_{m1}^2 & 0 & 0 \\ 0 & 0 & I_c\sigma_{p1}^2 & 0 \\ 0 & 0 & 0 & I_n\sigma_{e1}^2 \end{bmatrix}.$$

The multiple-trait animal model can be represented as

$$\begin{bmatrix} y_1 \\ y_2 \end{bmatrix} = \begin{bmatrix} X_1 & 0 \\ 0 & X_2 \end{bmatrix} \begin{bmatrix} \beta_1 \\ \beta_2 \end{bmatrix} + \begin{bmatrix} Z_1 & 0 \\ 0 & Z_2 \end{bmatrix} \begin{bmatrix} g_1 \\ g_2 \end{bmatrix} + \begin{bmatrix} M_1 & 0 \\ 0 & M_2 \end{bmatrix} \begin{bmatrix} m_1 \\ m_2 \end{bmatrix} + \begin{bmatrix} W_1 & 0 \\ 0 & W_2 \end{bmatrix} \begin{bmatrix} p_1 \\ p_2 \end{bmatrix} + \begin{bmatrix} e_1 \\ e_2 \end{bmatrix},$$

where the subscripts 1 and 2 represent traits 1 and 2, respectively. As before, assumptions for this model are:

$$E \begin{bmatrix} y_1 \\ y_2 \end{bmatrix} = \begin{bmatrix} X_1 & 0 \\ 0 & X_2 \end{bmatrix} \begin{bmatrix} \beta_1 \\ \beta_2 \end{bmatrix}.$$

The co(variance) matrix for genetic effects is $G = G_0 \otimes A$, where

$$G_0 = \begin{bmatrix} \sigma_{g1}^2 & \sigma_{g12} & \sigma_{gm1} & 0 \\ \sigma_{g12} & \sigma_{g2}^2 & 0 & \sigma_{gm2} \\ \sigma_{gm1} & 0 & \sigma_{m1}^2 & \sigma_{m12} \\ 0 & \sigma_{gm2} & \sigma_{m12} & \sigma_{m2}^2 \end{bmatrix}$$

and $\otimes$ denotes the direct product operator.

As shown in G_0 , the direct genetic effect for one trait was assumed to be uncorrelated to the genetic maternal effect for the other trait. The (co)variance matrix for permanent environmental effects is $P = P_0 \otimes I_c$, where

$$P_0 = \begin{bmatrix} \sigma_{p1}^2 & \sigma_{p12} \\ \sigma_{p12} & \sigma_{p2}^2 \end{bmatrix}.$$

The residual (co)variance of random residual effects was assumed to be $R = R_0 \otimes I_n$, where

$$R_0 = \begin{bmatrix} \sigma_{e1}^2 & \sigma_{e12} \\ \sigma_{e12} & \sigma_{e2}^2 \end{bmatrix}.$$

In both models, c is the number of cows, n is the number of observations, A is the numerator relationship matrix, I are identity matrices of appropriate order. For the i^{th} trait, σ_{gi}^2 denotes the additive genetic variance, σ_{mi}^2 is the maternal additive genetic variance, σ_{gmi} is the covariance between direct and maternal additive effects, σ_{pi}^2 is the permanent environmental variance and σ_{ei}^2 is the residual variance.

Non-zero covariance between traits 1 and 2 was considered for direct additive (σ_{g12}), maternal additive (σ_{m12}), maternal permanent environment (σ_{p12}) and residual (σ_{e12}) random effects. For both models, covariance between direct or maternal effects and any of the remainder effects (i.e. p and e) was assumed to be zero, as well as the covariance between the random effects p and e .

A likelihood ratio test was used to compare the pre-weaning models and to evaluate the significance of maternal genetic random effects. As the latter effect was found to be non-significant ($P > 0.01$) for CW, PW and MW scores, it was not included in the models for these scores, but was included in the model for GBW. For yearling traits, maternal genetic and permanent environmental effects were also not included as they were not found to be important after weaning. The effect of age of dam at calving was taken as linear in the models for CY, PY and MY scores as the quadratic effect was not significant ($P > 0.05$) in a previous analysis using the GLM procedure of the SAS 9.1 program (SAS Institute Inc., Cary, NC, USA).

Single-trait analyses were first performed for all the traits that were studied. The variance components obtained with these analyses were used as initial values for the two-trait analyses. Genetic covariance between direct and maternal additive effects was set to zero (Muniz *et al.*, 2005).

Results and discussion

Table 2 shows the descriptive statistics of the traits studied. The estimates of variance components and direct additive heritability for weaning and yearling traits obtained with the single-trait models are shown in Tables 3 and 4. Similar direct heritability estimates of 0.17 ± 0.02 , 0.16 ± 0.02 , 0.15 ± 0.02 and 0.18 ± 0.02 were obtained for CW, PW and MW scores and GBW, respectively. For further details regarding these results see Costa *et al.* (2008). The same pattern was observed for the heritability estimates of yearling traits (Table 4).

The heritability estimates for yearling visual scores and GWY were lower than those observed for the weaning traits, suggesting that phenotypic selection for either weaning or yearling traits would result in a small response in the herds studied (Tables 3 and 4). The low estimates obtained were probably due to large variations in the environment to which the animals were exposed as they belonged to herds from three different regions of Brazil. It is possible that the models used were unable to completely remove all environmental variation.

The heritabilities for yearling traits found in this study (Table 4) were lower than those reported for the same traits by Cardoso *et al.* (2004), who estimated values of 0.19, 0.25,

Table 2 Descriptive statistics of weaning and yearling visual scores and weight gain in cattle forming the Brangus breed

Trait	N	Mean	Mode	Median	s.d.	Range	CV (%)
CW	53 683	3.42	3	3	0.946	1 to 5	27.62
PW	45 136	3.33	3	3	0.938	1 to 5	28.19
MW	52 937	3.36	3	3	0.967	1 to 5	28.77
GBW (kg/day)	56 471	0.663	0.658	0.666	0.132	0.328 to 1.492	19.94
CY	24 531	3.46	3	4	0.930	1 to 5	26.88
PY	21 166	3.44	3	3	0.874	1 to 5	25.34
MY	24 006	3.41	3	3	0.900	1 to 5	26.39
GWY (kg/day)	25 419	0.212	0.200	0.166	0.076	0.047 to 0.754	36.25

CW = conformation at weaning; PW = precocity at weaning; MW = muscling at weaning; GBW = average daily gain from birth to weaning; CY = conformation at yearling; PY = precocity at yearling; MY = muscling at yearling; GWY = average daily gain from weaning to yearling.

Table 3 Estimates of variance components and heritability obtained by single-trait analysis for weaning visual scores and weight gain in cattle forming the Brangus breed

Traits	$\hat{\sigma}_G^2$	$\hat{\sigma}_M^2$	$\hat{\sigma}_{EP}^2$	$\hat{\sigma}_E^2$	$\hat{\sigma}_P^2$	$\hat{h}_G^2 \pm \text{s.e.}$
CW	0.0983		0.0500	0.4254	0.5738	0.17 ± 0.019
PW	0.1025		0.0716	0.4796	0.6538	0.16 ± 0.019
MW	0.0952		0.0548	0.4773	0.6273	0.15 ± 0.017
GBW	0.0015	0.0002	0.0012	0.0059	0.0089	0.18 ± 0.018

$\hat{\sigma}_G^2$ = direct additive genetic variance; $\hat{\sigma}_M^2$ = direct additive maternal variance; $\hat{\sigma}_{EP}^2$ = permanent maternal environment variance; $\hat{\sigma}_E^2$ = residual variance; $\hat{\sigma}_P^2$ = phenotypic variance; $\hat{h}_G^2$ = direct additive heritability; CW = conformation at weaning; PW = precocity at weaning; MW = muscling at weaning; GBW = average daily gain from birth to weaning.

Table 4 Estimates of variance components and heritability obtained by single-trait analysis for yearling visual scores and weight gain in cattle forming the Brangus breed

Trait	$\hat{\sigma}_G^2$	$\hat{\sigma}_E^2$	$\hat{\sigma}_P^2$	$\hat{h}_G^2 \pm \text{s.e.}$
CY	0.0560	0.4280	0.4840	0.12 ± 0.02
PY	0.0731	0.4623	0.5355	0.14 ± 0.02
MY	0.0665	0.4504	0.5170	0.13 ± 0.02
GWY	0.00019	0.0012	0.0014	0.14 ± 0.02

$\hat{\sigma}_G^2$ = direct additive genetic variance; $\hat{\sigma}_E^2$ = residual variance; $\hat{\sigma}_P^2$ = phenotypic variance; $\hat{h}_G^2$ = direct additive heritability; CY = conformation at yearling; PY = precocity at yearling; MY = muscling at yearling; GWY = average daily gain from weaning to yearling.

0.26 and 0.20 for CY, PY, MY and GWY, respectively, in Angus animals, and by Faria *et al.* (2009) for the visual evaluation of M in Nelore cattle at 15 and 22 months of age. Using Bayesian analysis, Faria *et al.* (2009) obtained mean heritability estimates of 0.38 and 0.21 for M at these two ages. In addition, mean estimates obtained for C at the same ages were 0.07 and 0.29, respectively. Pons *et al.* (1990a) reported a heritability of 0.34 for C. In two different studies involving Nelore animals, Eler *et al.* (1996a and 1996b) obtained heritability estimates ranging from 0.23 to 0.34 for postweaning C, P and M scores. The differences in heritability estimates for yearling visual scores between this study and the literature might be attributed to variations between observers, to genetic differences between populations, or even to differences in the visual evaluation system. Visual evaluation using scores varies among breeding programs. Scores might be attributed by one observer in one program and by three observers in another. In the latter case, the animal is scored by consensus among observers. A score ranging from 1 to 6 has been reported in some programs, whereas most programs report scores ranging from 1 to 5.

Higher heritabilities for average postweaning gain than those observed in this study have been reported by other investigators. In this respect, Koots *et al.* (1994) reported average heritability of 0.40 for postweaning weight gain of beef cattle. Kriese *et al.* (1991) obtained estimates of 0.31 and 0.15 for weight gain of Brahman and Brangus cattle from weaning to 365 days of age, respectively.

Table 5 shows the genetic and environmental correlation estimates between weaning and yearling traits obtained by two-trait analysis. Maternal effects were included in the model for GBW and maternal permanent environmental effects were only included in the models for weaning traits.

The estimated genetic correlations between the same visual scores obtained at weaning and yearling, for example, CW v. CY, were very strong (>0.83 ; Table 5). In the literature, this association was only reported by Cardoso *et al.* (2004), who obtained correlations between scores stronger than 0.90 in the Angus animals. Correlation estimates between the different scores obtained at weaning and yearling were also strong (>0.63 ; Table 5). We found no reports of such correlations in the literature.

The genetic correlation between pre- and postweaning average daily gains estimated in this study was 0.10 ± 0.008 (Table 5). This result suggests that the genes involved in pre-weaning growth are not the same or are not expressed during the yearling period, indicating that most genes responsible for the expression of GBW do not continue acting on the expression of GWY. Thus, animals that gain more weight from birth to weaning may not be the same as those that will gain more weight after weaning. However, although the estimated value indicates a very weak association between the two traits, it contradicts results from previous studies. In a review on genetic parameters of productive traits in beef cattle, Koots *et al.* (1994) found a mean genetic correlation of 0.39 between pre- and postweaning gains. In a recent study

Table 5 Estimates of genetic (r_a) and environmental (r_e) correlations (respective s.e.) between weaning and yearling visual scores and weight gain obtained by two-trait analysis for cattle forming the Brangus breed

Trait	r	CW	PW	MW	GBW	CY	PY	MY
CY	r_a	0.87 (0.0002)	0.64 (0.0004)	0.63 (0.0004)	0.75 (0.0003)			
	r_e	0.27 (0.0002)	0.20 (0.0003)	0.22 (0.0001)	0.25 (0.0001)			
PY	r_a	0.69 (0.0003)	0.90 (0.0001)	0.81 (0.0003)	0.60 (0.0005)	0.84 (0.0003)		
	r_e	0.19 (0.0006)	0.22 (0.0001)	0.21 (0.0008)	0.24 (0.0003)	0.40 (0.0006)		
MY	r_a	0.75 (0.0003)	0.80 (0.0002)	0.83 (0.0003)	0.63 (0.0004)	0.85 (0.0002)	0.91 (0.001)	
	r_e	0.20 (0.0008)	0.22 (0.0003)	0.25 (0.0001)	0.23 (0.0004)	0.22 (0.0001)	0.21 (0.0001)	
GWY	r_a	0.07 (0.001)	-0.08 (0.011)	-0.04 (0.001)	0.10 (0.008)	0.55 (0.006)	0.37 (0.008)	0.47 (0.008)
	r_e	-0.06 (0.002)	-0.08 (0.007)	-0.08 (0.001)	-0.17 (0.003)	0.28 (0.002)	0.31 (0.001)	0.27 (0.005)

CW = conformation at weaning; PW = precocity at weaning; MW = muscling at weaning; GBW = average daily gain from birth to weaning; CY = conformation at yearling; PY = precocity at yearling; MY = muscling at yearling; GWY = average daily gain from weaning to yearling.

of growth in beef cattle to detect SNP associations with body weight and weight gain at different ages, Snelling *et al.* (2010) also demonstrated that most of the SNPs showing highly significant associations between genotype and growth phenotypes coincided with previously described quantitative trait loci for growth or correlated traits. The estimated correlation might be explained in part by compensatory gain during the post-weaning period, that is, animals born to younger or older cows, which showed poorer growth during the preweaning period, presented accelerated growth after the cessation of feed restriction, reducing the intensity of the genetic association between these traits. The model possibly did not account efficiently for the environmental effects even when maternal permanent environmental effects and age of cow at calving were included. This hypothesis is supported by the environmental correlation estimate between GBW and GWY (-0.17 ± 0.016 ; Table 5), indicating weak antagonism between environmental and non-additive genetic effects that act on the two traits. However, this result agrees with Cardoso *et al.* (2004), Marcondes *et al.* (2000) and Sarmiento *et al.* (2003) who reported genetic correlation estimates of 0.23, 0.23 and 0.22, respectively, between pre- and postweaning weight gains.

GBW showed a strong positive genetic correlation with the visual scores of CY, PY and MY (0.75, 0.60 and 0.63, respectively). These correlations suggest that animals with good preweaning body development presented higher yearling scores because they had already achieved a better degree of performance than those presenting poorer GBW.

Very weak genetic correlations (basically zero) were observed between the visual scores evaluated at weaning and GWY indicating that selection for weaning visual scores will not influence postweaning gain.

Yearling visual scores were positively associated with genetic correlations higher than 0.84. However, these correlations were slightly weaker than those observed at weaning according to the results reported by Costa *et al.* (2008) for the same data. Similar to the weaning results, the magnitude of these correlations might be attributed to differences in the evaluation system. Pons *et al.* (1990b), studying Hereford animals at postweaning, estimated lower genetic correlations between the same scores ranging from

0.30 to 0.68. Eler *et al.* (1996b) obtained a genetic correlation of 0.86 between CY and PY, of 0.82 between CY and MY, and of 0.96 between PY and MY for Nelore animals. Similar results have been reported by Cardoso *et al.* (2004) for Angus cattle.

The genetic correlations between yearling visual scores and GWY were of medium magnitude and ranged from 0.37 to 0.55. The lowest correlation was observed between PY and GWY (0.37). This result might be explained by the fact that a higher GWY indicates faster weight gain irrespective of the biotype of the animal. However, animals presenting greater weight gain, lower rib depth and no carcass finishing receive lower PY scores. Similar genetic correlations have been reported by Koury Filho (2001) for Nelore animals. In contrast, Cardoso *et al.* (2004) estimated higher correlations for Angus cattle.

Environmental correlations between the traits (Table 5) ranged from -0.17 (GWY v. GBW) to 0.40 (PY v. CY). These estimates indicate a weak association between environmental effects for all traits and revealed that the environmental conditions provided for animals from birth to weaning are almost independent of those at yearling.

Conclusions

Visual scores for conformation, early finishing (precocity) and muscling at weaning and yearling might be included as selection criteria in the breeding program of the Brangus breed in Brazil in order to help producers meet industry expectations, although selection based on these traits will not result in large genetic changes in these traits. In addition, selection for weaning visual scores would have a marked effect on yearling visual scores, and selection for average daily gain during the preweaning period would result in a correlated genetic response in visual scores during life.

Acknowledgement

The authors are thankful to Gensys consultants associates LTDA for providing the data used in this research.

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