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# Genetic parameters and response to selection for post-weaning weight gain, visual scores and carcass traits in Hereford and Hereford × Nellore cattle

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# ABSTRACT

The objective of this study was to estimate heritability, correlations and response to selection for postweaning average daily weight gain (ADG), visual scores of conformation (C), precocity (P) and muscling (M), longissimus muscle area (LMA), and backfat thickness (BFT) measured by ultrasound in Brazilian Hereford and Hereford × Nellore cattle. The components of (co)variance were estimated by the Bayesian method in two-trait analysis. The posterior means (±standard deviation) of heritability for ADG (0.164 $\pm$ 0.013), C (0.152 $\pm$ 0.014), P (0.194 $\pm$ 0.015), M (0.198 $\pm$ 0.015), LMA (0.232 $\pm$ 0.047) and BFT (0.136 $\pm$ 0.037) and their corresponding phenotypic standard deviation (standard deviation of posterior density) of 0.076 (0.0003) kg/day, 0.803 (0.003), 0.869 (0.005), 0.883 (0.007), 5.491 (0.069) cm<sup>2</sup> and 0.761 (0.009) mm support the utilization of these traits as criteria for selection, as long as the selection is done based on predicted breeding values. The genetic (orrelations ( $\pm$ standard deviation) between M and LMA (0.483 $\pm$ 0.098) and between P and BFT (0.403 $\pm$ 0.108) were favorable and indicate that part of the genes with additive effect on the visual scores also influenced the traits measured by ultrasound. The genetic correlations between M and P (0.814 $\pm$ 0.025) and between LMA and BFT (0.286 $\pm$ 0.200) suggest that the selection of animals with more developed muscle mass does not necessarily result in animals with less fat cover.

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# 1. Introduction

Brazil has the largest commercial cattle herd and is also the largest exporter of beef in the world (USDA-FAS, United States Department of Agriculture – Foreign Agricultural Service, 2009). Animal breeding programs and production of genetically superior animals certainly contribute to the country achieving this position. However, to maintain such a position, the components of the production network need to continue developing stock aimed at increasing production and final product quality with improved profitability of livestock.

In this context, the post-weaning average daily weight gain (ADG) is a trait economically important to the production system of beef because it is related to the time necessary for the animal to reach slaughter point, and it expresses the genetic potential of the animal itself. However, ADG by itself may not be sufficient as a trait indicative of carcass quality.

Carcass weight, the percentage of marketable cuts and meat tenderness are traits directly related to the quality and value of the carcass (Field, 2007). Since the measurements of these traits imply the slaughter of the animal, selection to improve the quality of the carcass can be made based on the results of progeny testing and analysis on molecular markers or on indicative traits measured in the live animal, such as visual scores and traits measured by ultrasound.

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The percentage of muscle, fat, bone and marketable cuts and the carcass value have phenotypic correlations that are moderate to high (0.4 to 0.8) with the visual scores and other traits measured by ultrasound in the live animal (Conroy et al, 2010). This suggests that the visual scores and the traits measured through ultrasound could be used as alternatives for selection to improve carcass quality.

In Brazil, some beef cattle breeding programs have performed visual evaluations for conformation (C), precocity (P) and muscling (M) since the 1970s. Evaluations for longissimus muscle area (LMA) and backfat thickness (BFT) measured with ultrasound began in the 1990s and gained momentum from 2000 on, with the adoption of this technique in several beef breeding programs.

Knowledge of genetic parameters and expected response to the selection for ADG, visual scores and carcass traits is fundamental to the design of animal breeding programs focusing on the quality of the carcasses produced in Brazil. Such information is useful for defining the most adequate selection criteria and predicting genetic values of the candidates for selection. The objective of this study was to estimate genetic parameters and selection response for the post-weaning average daily weight gain, visual scores and carcass traits evaluated through ultrasound in Brazilian Hereford and Hereford × Nellore cattle.

# 2. Materials and methods

Information regarding the performance of Hereford and Hereford × Nellore cattle participants in the Conexão Delta G breeding program was used to estimate (co)variances for the variables: post-weaning average daily weight gain (ADG, kg/day), visual scores of conformation (C), precocity (P) and muscling (M) and longissimus muscle area (LMA, cm<sup>2</sup>) and backfat thickness (BFT, mm) obtained through ultrasound.

The visual scores were utilized as alternatives to estimate the amount of meat on the carcass by length, body depth and muscle development, characterizing the conformation (C) measurement. Precocity (P) measurement represents the ability of the animal to display the lowest acceptable degree of finishing with a low body weight. The development of muscle mass determined the scores for muscling (M). The visual scores were assigned by livestock technicians, in which each contemporary group was assessed by a single technician, and on a scale of 1 to 5, where five represents the highest level of trait expression. The LMA and the BFT were measured with the use of ultrasound and specific software equipment in the region between the 12th and 13th ribs.

Only the data from animals with known pedigree and members of the post-weaning contemporary groups with at least three observations were considered. For ADG, C, P and M, the post-weaning contemporary groups were formed by animals of the same contemporary group at weaning, raised on the same farm and part of the management post-weaning group, of the same sex and weighed on the same Julian date. The contemporary group at weaning was formed by animals of the same sex, born and weaned on the same farm and in the same year, raised in the same management group and weighed on the same Julian date at weaning. For LMA and BFT, the management group between the time of postweaning weighing and evaluation by ultrasound, and the Julian date of ultrasound were also included in the formation of the post-weaning contemporary groups. Table 1 provides a summary of the data structure studied in this work.

The database was composed of data from 47,563 animals belonging to Hereford (Her), 3/4Her, 11/16Her, 5/8Her, 9/16Her, 1/2Her, 3/8Her and 1/4Her genetic groups. Table 2 lists the numbers according to the genetic group of the animal.

The animals were born from 1974 to 2006 on 47 Brazilian ranches located between latitudes 14° S and 31.5°S, in the following states: RS, PR (South region), SP (Southeast region), MS, MT, GO (Central-West region) and BA (Northeast region). However, measurements by ultrasound were only taken on animals born from 1998 to 2005 on 22 ranches located between latitudes 21°S and 31.5°S, in the states of RS, PR, SP and MS.

The ages of the animals on the days of the measurements ranged between 370 and 670 days. The average  $\pm$  standard deviation of the ages in assessing ADG, C, P and M was 505  $\pm$  78 days, and for the assessments by ultrasound it was 541  $\pm$  58 days.

Under the matrix form, the general model considered in the analysis of two traits simultaneously was

$$\begin{bmatrix} y_1 \\ y_2 \end{bmatrix} = \begin{bmatrix} X_1 & 0 \\ 0 & X_2 \end{bmatrix} \times \begin{bmatrix} \beta_1 \\ \beta_2 \end{bmatrix} + \begin{bmatrix} Z_1 & 0 \\ 0 & Z_2 \end{bmatrix} \times \begin{bmatrix} a_1 \\ a_2 \end{bmatrix} + \begin{bmatrix} e_1 \\ e_2 \end{bmatrix}$$

in which:  $y_i$ , is a vector with the observations of trait i;  $\beta_i$ , is a vector with the "fixed" effect solutions (contemporary groups, month of birth, annual class of dam age at birth, linear effect of the animal composition (expected percent of Hereford genes in the calf), linear effect of the dam composition (expected percent of Hereford genes in the dam), and the linear effect of the age of the animal at the time of measurement);  $a_i$  is a vector with solutions of the random direct genetic additive effects;  $e_i$ , is a vector with the solutions of random residual effects; and  $X_i$ , and  $Z_i$  are incidence matrices that relate  $y_i$  with  $\beta_i$  and  $a_i$ , respectively.

#### Table 1

Number of observations and pedigree structure for each trait<sup>a</sup>.

	ADG	С	Р	М	LMA	BFT
Animals with records	45,773	47,253	41,589	41,402	4375	4363
Sires with progeny	1077	1078	988	975	294	294
Sires with progeny and personal data	263	261	258	257	36	36
Dams with progeny	34,092	34,881	31,443	31,310	3596	3587
Dams with progeny and personal data	4805	5082	3769	3733	199	195
Animals in the relationship matrix	80,867	80,867	80,867	80,867	80,867	80,867

<sup>a</sup> ADG, post-weaning average daily weight gain; C, conformation; P, precocity; M, muscling; LMA, longissimus muscle area; BFT, backfat thickness.

 Table 2

 Number of observations for each trait <sup>a</sup> according to the genetic group (GG) of the animals.

GG	ADG	С	Р	М	LMA	BFT
1/4Her	501	518	518	518	73	73
3/8Her	107	108	108	108	5	5
1/2Her	13,007	13,242	13,242	13,239	446	444
9/16He	r 1498	1612	1612	1612	69	69
5/8Her	7840	7999	7999	7998	1099	1091
11/16H	er 1838	1871	1871	1870	186	186
3/4Her	2202	2282	2283	2283	534	533
Herefor	d 18,780	19,621	13,956	13,774	1963	1962

<sup>a</sup> ADG, post-weaning average daily weight gain; C, conformation; P, precocity; M, muscling; LMA, longissimus muscle area; BFT, backfat thickness.

The assumptions for the random effects were:  $Var(a) = G \otimes A$ and  $Var(e) = R \otimes I$ , in which  $G = \begin{bmatrix} \sigma_{a_1}^2 & \sigma_{a_1a_2} \\ \sigma_{a_1a_2} & \sigma_{a_2}^2 \end{bmatrix}$ ;  $\sigma_{a_i}^2$ , is the additive genetic variance for trait i (i = 1 or 2);  $\sigma_{a_ia2}$ , is the additive genetic covariance between the traits 1 and 2; A, is the numerator relationship matrix;  $R = \begin{bmatrix} \sigma_{e_1}^2 & \sigma_{e_1e_2} \\ \sigma_{e_1e_2} & \sigma_{e_2}^2 \end{bmatrix}$ ;  $\sigma_{e_i}^2$ , is the residual variance for trait i;  $\sigma_{e_ie2}$ , is the residual covariance between traits 1 and 2; and I, is the identity matrix of order equal to the order of  $y_i$ .

For the composition of the relationship matrix, a recursive algorithm was used to keep only the individuals with data (47,563), and their ancestors, in the pedigree base. In addition, individuals who did not have data nor were dams of animals with data, who did not have at least one known ancestor, and were linked to only one animal in the database, were also excluded from the pedigree record and the descendant's pedigree. These procedures were repeated until there were no more animals of this type. In this way, a relationship matrix was formed, containing only genealogical data on animals considered informative, i.e., 80,867 animals.

The (co)variance components were estimated by the Bayesian method, using the INTERGEN program (Cardoso, 2008), in two-trait analysis. Inference was based on Markov chain Monte Carlo (MCMC) with chains of 230,000 cycles with a burn-in period of 30,000 cycles and a thinning interval of 100 cycles. The convergence of the chains was evaluated using the R program (The R Foundation for Statistical Computing, 2009) with the BOA package (Smith, 2005), which generates convergence diagnostics according to Geweke (1992) and Heidelberger and Welch (1983). In the Geweke test, initial values of the Markov chain are compared with final values of the chain in order to detect convergence failures. P-values lower than 0.05 indicate the existence of evidence against the convergence of chains. The Heidelberger and Welch test uses Cramer-von Mises statistics to evaluate the null hypothesis of stationarity of the sample generated. If there is evidence of nonstationarity, the test is repeated after eliminating the first 10% of iterations. This process is continued until the resulting chain is approved in the test or until more than 50% of iterations are discarded.

After obtaining samples of posterior density of (co) variance components, the expected responses to direct and indirect selection and the relative efficiency of indirect

selection were calculated for the traits considered in each sample. The direct response to mass selection was calculated as  $\Delta G_{x,x} = i_x \times h_x^2 \times \sigma_{p_x}$  where:  $i_x$ , is the selection intensity considered for the trait x (retention of 10% of the males,  $i_m = 1.75$ , and 50% of the females,  $i_f = 0.80$ );  $h_x^2$ , is the heritability; and  $\sigma_{p_x}$  is the phenotypic standard deviation of the trait under selection. The correlated response was calculated as  $\Delta G_{x,y} = i_y \times h_x \times h_y \times r_a \times \sigma_{p_x}$ , where: y, is the trait under selection; x, is the trait indirectly selected; and  $r_a$ , is the genetic correlation between x and y. Considering the same intensity of selection for the traits x and y, the relative efficiency of indirect selection, in relation to direct selection, was calculated for each trait as  $\frac{\Delta G_{xy}}{\Delta G_{xy}} = r_a \frac{h_y}{h_c}$ .

#### 3. Results and discussion

The mean ( $\pm$  standard deviation) of ADG obtained in this work (0.397 $\pm$ 0.175 kg/day) was close to the values of 0.387 kg/day and 0.43 kg/day, reported by Bailey et al. (1991) and Phillips et al. (2001), which analyzed data of Hereford cattle fed on a diet with an intermediate energy level for a period of 168 days post-weaning, and of Hereford × Brahman and Hereford × Angus crossbreds grazed on native pastures in the southeast United States, respectively.

The means ( $\pm$  standard deviation) of visual scores were  $3.090 \pm 1.056$ ,  $3.376 \pm 0.966$  and  $3.248 \pm 0.985$  for conformation, precocity and muscling, respectively. The visual scores are assigned in relation to the contemporary group, and the animal considered as reference receives a score of three. Differences between observed means and expected means for the visual scores of the yearling animals are found in the literature (Cardoso et al., 2004). Part of these differences can be attributed to the differences between technicians during the evaluation (Conroy et al., 2010). The possibility of separation of animals that were assessed in the same group, depending on the definition of the contemporary group used, and the subsequent exclusion of data from those animals grouped into new groups and that did not meet the requirements during the edition of the files, could also contribute to the fact that the observed mean is different than the expected mean for the visual scores.

The estimated means ( $\pm$  standard deviation) for the LMA (49.539 $\pm$ 11.417 cm<sup>2</sup>) and BFT (2.435 $\pm$ 1.071 mm) are similar to the values of 46.0 cm<sup>2</sup> and 2.23 mm, respectively, obtained by Tarouco et al. (2006) on a sample of Brazilian Braford and Hereford cattle approximately 530 days old.

According to the Geweke and Heidelberger and Welch tests, the number of rounds, burn-in period and number of samples in the Markov chains were sufficient to ensure convergence for all chains. Table 3 presents the posterior density estimates of the components of variance and heritabilities for the traits considered in this study. Those posterior density estimates were calculated with all samples obtained from two-trait analysis (10,000 samples for each trait).

The heritability estimate for ADG was in agreement of the value of 0.16 reported by Fan et al. (1995) for the postweaning ADG in Hereford bulls in Canada and within the range of 0.07 and 0.20 reported by Cardoso and Tempelman (2004) for post-weaning weight gain in Hereford and Hereford × Nellore cattle in Brazil. The heritability estimate from

#### Table 3

Descriptive statistics of posterior density estimates of additive  $(\sigma_a^2)$ , residual  $(\sigma_e^2)$  and phenotypic  $(\sigma_p^2)$  variances and heritabilities  $(h^2)$  for post-weaning average daily gain (ADG), visual scores of conformation (C), precocity (P) and muscling (M) and ultrasound measurements of longissimus muscle area (LMA) and backfat thickness (BFT) in Brazilian Hereford and Hereford × Nellore cattle.

	ADG	С	Р	М	LMA	BFT			
Mean	Mean (standard deviation)								
$\sigma_a^2$	9.43E-4 (7.73E-5)	9.82E-2 (9.41E-3)	1.46E-1 (1.24E-2)	1.54E - 1(1.31E - 2)	7.00 (1.50)	7.89E-2 (2.20E-2)			
$\sigma_e^2$	4.82E-3 (6.68E-5)	5.46E-1 (8.14E-3)	6.10E-1 (1.21E-2)	6.26E-1 (1.24E-2)	23.16 (1.29)	5.00E-1 (2.11E-2)			
$\sigma_p^2$	5.76E-3 (4.42E-5)	6.44E-1 (4.84E-3)	7.56E-1 (9.44E-3)	7.80E-1 (1.16E-2)	30.16 (0.76)	5.79E-1 (1.42E-2)			
$h^2$	0.164 (0.013)	0.152 (0.014)	0.194 (0.015)	0.198 (0.015)	0.232 (0.047)	0.136 (0.037)			
95% h	ighest posterior density inte	rval							
$\sigma_a^2$	7.91E-4 to 1.09E-3	7.95E-2 to 1.17E-1	1.22E-1 to 1.70E-1	1.29E-1 to 1.80E-1	4.37 to 10.13	3.52E-2 to 1.23E-1			
$\sigma_e^2$	4.69E-3 to 4.95E-3	5.30E-1 to 5.62E-1	5.85E-1 to 6.32E-1	6.00E-1 to 6.49E-1	20.62 to 25.62	4.57E-1 to 5.41E-1			
$\sigma_p^2$	5.68E-3 to 5.85E-3	6.35E-1 to 6.54E-1	7.35E-1 to 7.71E-1	7.54E-1 to 7.97E-1	28.70 to 31.67	5.52E-1 to 6.06E-1			
$h^2$	0.139 to 0.188	0.125 to 0.180	0.164 to 0.224	0.167 to 0.228	0.148 to 0.328	0.063 to 0.209			

the current study could be considered to be low. However, considering the elevated phenotypic variability observed in this population, selection for the higher ADG could help increase the mean of this trait and reduce the time for the animal to reach the minimum weight for slaughter.

The heritability estimates for the visual scores were lower than the values of 0.24  $\pm$  0.02 (C), 0.31  $\pm$  0.02 (P), and 0.32  $\pm$ 0.02 (M) estimated by Boligon et al. (2011) for Nellore cattle. For the Angus breed, Cardoso et al. (2004) also estimated higher heritability values for C (0.19), P (0.25) and M (0.26), both using the same scale as that in the present work. In general, the low heritability estimates for the visual scores could reflect an elevated environmental variance. The implementation of more stringent environmental control through better definition of contemporary groups, more standardized nutritional and health conditions and maximizing the accuracy of the measurements (Cardoso et al., 2004), could help to improve the identification of the genetic differences between the animals. In the current study, the great range in ages at the time of the visual appraisal also contributed to elevate the environmental variance but it was necessary to avoid a significant reduction in the dataset.

The mean heritability estimates for LMA and BFT were low and the 95% highest posterior density interval include the values of 0.20 (LMA) and 0.10 (BFT) obtained by Tarouco et al. (2006) from a sample of Braford and Hereford cattle from Brazil. MacNeil and Northcutt (2008) obtained heritability estimates for LMA and BFT in the Angus breed ranging between 0.18 and 0.33 and between 0.26 and 0.46, respectively, depending on the sex of the animal. In the Nellore breed, Yokoo et al. (2008) estimated heritabilities of 0.35 (LMA) and 0.51 (BFT), which are above the upper limit of the 95% highest posterior density interval. The low heritability estimates for the traits assessed through ultrasound may partly be the result of the intense selection of the animals before these measurements. Pre-selection before ultrasound evaluation is a common practice to reduce measuring costs. Thus, in most cases, the animals evaluated must show satisfactory weight and body condition and belong to the major genetic groups involved in the formation of the Braford breed. Taking these considerations into account, the heritability estimates for average daily weight gain, visual scores and ultrasound measurement of carcass traits in Brazilian Hereford and Hereford × Nellore cattle, found in this study, are consistent with the results found in literature.

#### Table 4

Descriptive statistics of posterior density estimates of genetic (above the diagonal) and phenotypic correlations (below the diagonal) for post-weaning average daily gain (ADG), visual scores of conformation (C), precocity (P) and muscling (M) and ultrasound measurements of longissimus muscle area (LMA) and backfat thickness (BFT) in Brazilian Hereford and Hereford × Nellore cattle.

	ADG	С	Р	М	LMA	BFT			
Mean (standard deviation)									
ADG	-	0.580 (0.048)	0.233 (0.056)	0.210 (0.057)	0.033 (0.104)	0.079 (0.140)			
С	0.401 (0.005)	-	0.565 (0.045)	0.686 (0.035)	0.410 (0.108)	0.176 (0.125)			
Р	0.351 (0.005)	0.590 (0.004)	-	0.814 (0.025)	0.363 (0.103)	0.403 (0.108)			
Μ	0.337 (0.005)	0.648 (0.003)	0.689 (0.003)	-	0.483 (0.098)	0.045 (0.134)			
LMA	0.194 (0.015)	0.297 (0.015)	0.241 (0.015)	0.263 (0.015)	-	0.286 (0.200)			
BFT	0.129 (0.016)	0.165 (0.015)	0.206 (0.015)	0.116 (0.016)	0.185 (0.017)	-			
95% highest p	osterior density interval								
ADG	-	0.493 to 0.676	0.117 to 0.337	0.102 to 0.320	-0.171 to 0.217	-0.193 to 0.329			
С	0.392 to 0.410	-	0.478 to 0.651	0.619 to 0.756	0.209 to 0.622	-0.052 to 0.422			
Р	0.342 to 0.362	0.583 to 0.597	-	0.764 to 0.859	0.142 to 0.556	0.191 to 0.604			
Μ	0.327 to 0.348	0.642 to 0.654	0.683 to 0.695	-	0.287 to 0.668	-0.223 to 0.278			
LMA	0.164 to 0.222	0.269 to 0.324	0.213 to 0.271	0.235 to 0.293	-	-0.100 to 0.643			
BFT	0.097 to 0.158	0.134 to 0.194	0.176 to 0.236	0.086 to 0.148	0.145 to 0.214	-			

Posterior density estimates of the genetic and phenotypic correlations for post-weaning average daily gain, visual scores and ultrasound measurements are presented in Table 4.

The genetic correlations of ADG with the visual scores were positive, with the highest estimate obtained between ADG and C. The phenotypic correlations were also positive. These results are consistent with those obtained by Cardoso et al. (2004), in spite of the differences in the magnitudes of the estimates.

In young animals, the nutrient intake is directed to various tissue synthesis such as bone, muscle and fat. Immediately after weaning, the bone is not fully developed and the animal must mobilize nutrients for its synthesis before initiating a more rapid deposition of muscle tissue and, finally, of adipose tissue (Lawrence and Fowler, 2002). Since the visual scores of conformation, muscling and precocity are, by definition, associated with the development of animal bone (length and body depth), muscle development and adipose tissue development, respectively, higher ADG genetic correlations would, indeed, be expected from weaning to approximately 505 days of age with C, then with M and, finally, with P.

The highest genetic and phenotypic correlations were estimated between the visual scores. All of the correlations were positive, agreeing with the results of Cardoso et al. (2004), and suggest that selection for improved C, or P, or M in Brazilian Hereford and Hereford × Nellore cattle will result in favorable correlated responses in others. This result may reflect both pleiotropic effects and genetic linkage in groups of genes that affect the expression of C, P and M, as much as in difficulties of visual evaluation of animals with different body types. In addition, the selection carried out on the animals that have the best combinations of traits that are important to their producers and with the highest scores of C, P, and M, in the herds for this study, may also contribute to the high genetic correlations estimated for these traits.

The genetic correlations of ADG with LMA and BFT were close to zero and the phenotypic correlations were of low magnitude. These results suggest that these traits are controlled by groups of different genes and that selection to increase the average daily gain post-weaning, in isolation, isn't sufficient to improve the quality of the carcass in Brazilian Hereford and Hereford × Nellore cattle. However, it is important to note that low correlations of ADG with LMA and BFT can be partly explained by the fact that most of the animals evaluated have not yet met the minimum weight and fat cover requirements for slaughter.

The selection for the highest ADG could lead to carcass weight gain (Devitt and Wilton, 2001) without necessarily improving the meat and fat proportion in the carcass because the genetic correlations of ADG with P ( $0.233 \pm 0.056$ ) and with M ( $0.210 \pm 0.057$ ) are low and the genetic correlations of ADG with LMA ( $0.033 \pm 0.104$ ) and with BFT ( $0.079 \pm 0.140$ ) are null. It is also important to remark that selection for increasing ADG may result in increasing cow mature weight (Boligon et al., 2010) and this may not be desirable depending on the production system.

All of the correlations involving carcass traits and visual scores were positive, and the genetic correlations were  $0.483 \pm 0.098$ between M and LMA and  $0.403 \pm 0.108$  between P and BFT. For these same trait pairs in Nellore cattle, Yokoo et al. (2009) estimated values of 0.61 and 0.40, respectively. These results suggest that part of the genes with additive effects on the visual scores also influenced the traits measured by ultrasound and that M and P were efficient for predicting muscle and fat deposition in Brazilian Hereford and Hereford × Nellore cattle, respectively.

Both the visual scores as well as the traits obtained by ultrasound can be used to improve the carcass quality, in terms of dressing percentage and finishing. The visual scores are the result of the evaluation of the animals' development as a whole, but they are subject to the ability of the judges. On the other hand, even assuming that ultrasound permits a more objective evaluation of the carcass, this technique only takes one or two points of the carcass into consideration. It's possible that the joint use of these measurements will lead to better results in relation to using any of them alone and further works on selection indexes with visual scores and ultrasound traits are needed.

The posterior mean of genetic correlation between LMA and BFT was positive and of low magnitude with a wide 95% highest posterior density interval including zero. Kemp et al. (2002), with Angus steers, and Tarouco et al. (2006) found genetic

#### Table 5

Descriptive statistics of posterior density estimates of expected direct (diagonal) and indirect (out of diagonal) response by generation for post-weaning average daily gain (ADG), visual scores of conformation (C), precocity (P) and muscling (M) and ultrasound measurements of longissimus muscle area (LMA) and backfat thickness (BFT) in Brazilian Hereford and Hereford × Nellore cattle.

Selection criteria	Response trait							
	ADG (kg/day)	С	Р	М	LMA (cm <sup>2</sup> )	BFT (mm)		
Mean (standard deviation)								
ADG (kg/day)	0.016 (0.001)	0.092 (0.010)	0.046 (0.012)	0.043 (0.013)	0.047 (0.145)	0.011 (0.019)		
С	0.009 (0.001)	0.156 (0.015)	0.107 (0.013)	0.132 (0.013)	0.543 (0.164)	0.025 (0.018)		
Р	0.004 (0.001)	0.100 (0.012)	0.215 (0.018)	0.180 (0.016)	0.543 (0.164)	0.065 (0.020)		
M	0.004 (0.001)	0.121 (0.012)	0.177 (0.016)	0.223 (0.018)	0.725 (0.179)	0.008 (0.022)		
LMA (cm <sup>2</sup> )	0.001 (0.002)	0.080 (0.024)	0.086 (0.026)	0.117 (0.029)	1.624 (0.337)	0.047 (0.035)		
BFT (mm)	0.001 (0.002)	0.027 (0.019)	0.074 (0.023)	0.009 (0.028)	0.337 (0.254)	0.132 (0.036)		
95% highest posterior density interval								
ADG (kg/day)	0.013 to 0.018	0.073 to 0.112	0.022 to 0.071	0.017 to 0.067	-0.245 to 0.304	-0.026 to $0.045$		
С	0.007 to 0.010	0.128 to 0.186	0.083 to 0.134	0.108 to 0.158	0.251 to 0.869	-0.008 to $0.062$		
Р	0.002 to 0.006	0.078 to 0.125	0.181 to 0.249	0.150 to 0.212	0.254 to 0.892	0.022 to 0.102		
M	0.002 to 0.006	0.100 to 0.145	0.146 to 0.208	0.187 to 0.256	0.397 to 1.080	-0.034 to 0.049		
LMA (cm <sup>2</sup> )	-0.003 to 0.004	0.035 to 0.125	0.035 to 0.136	0.065 to 0.173	1.025 to 2.323	-0.014 to 0.116		
BFT (mm)	-0.002 to $0.005$	-0.010 to 0.064	0.025 to 0.117	-0.040 to $0.057$	-0.118 to 0.817	0.061 to 0.205		

correlations of 0.23 and 0.32 between LMA and BFT, respectively. These results, in accord with the positive correlation between P and M, suggest that the selection to increase the amount of muscle in the carcass doesn't necessarily result in the reduction of subcutaneous fat in Brazilian Hereford and Herford × Nellore crossbred cattle. Regardless, it's important to stress the existence of negative estimates of genetic correlation between LMA and BFT (Bertrand et al., 2001), which suggests the need for more studies on these traits. As Tarouco et al. (2006) emphasized, the nutritional management of the animals can influence the expression of body composition traits, and, in this way, result in a genotype × environment interaction for different types of cattle in different nutritional management programs.

The expected direct and correlated responses are presented in Table 5 and expected relative efficiencies of indirect selection for the traits studied in this work are presented in Table 6.

Despite the low magnitude of heritability estimates (Table 3), the selection of 10% males and 50% females with higher phenotypic values of ADG, LMA and BFT can provide gains up to 4%, 3% and 5% respectively, per generation (2151 days sire–son; 2100 days sire–daughter; 1800 days dam–son and 1726 days dam–daughter), compared with the means observed for these traits. It's worth noting that these gains also depend upon the phenotypic standard deviations for the traits, which represented approximately 19% (ADG), 11% (LMA) and 31% (BFT) of the observed means.

Expectations for response to phenotypic selection for ADG, LMA and BFT are encouraging, but also depend on the correct identification and adjustment for fixed effects. For traits of low heritability, it would be interesting to increase the number of animals (candidates for reproduction and their progeny) with phenotypic data, and to consider the pedigree information to obtain (co)variance components and genetic values.

The results from Tables 5 and 3 show that it is also possible to obtain genetic gains around 5% to 7% per generation for visual scores. However, given the relative nature of these traits, the phenotypic averages for all of the contemporary groups (independent of generation) should remain constant and it would not be possible to identify phenotypic changes between

generations, unless the scoring system changes. In the field, there may be a tendency on the part of the technician to give a higher percentage of scores of 4 and 5 to animals from farms that practice selection based on these variables, rather than scores of 1 and 2. However, this practice should be avoided, since when it deals with relative traits, the reference is the group under evaluation and not the breed as a whole. As intense as the selection for C, P and M may have been in a herd, it will always have animals on all levels of the evaluation scale.

The selection to increase weight gain, visual scores or the carcass traits in Brazilian Hereford and Hereford × Nellore cattle should result in positive correlated response or little to no response, depending on the trait used as criteria for selection and the trait indirectly selected. For all of the traits studied, the direct selection was more efficient than indirect selection (Table 6). Of course, if both traits can be observed in all animals, direct selection unless the genetic correlation is high and the heritability of the indicator trait is much higher than that of the trait of concern.

Considering the possibility of different selection intensity for visual scores and ultrasound traits (approximately 10% of animals with muscling and precocity scores had LMA and BFT), the assumption of same intensity of selection for the traits *x* and *y* in calculating the relative efficiency of indirect selection could not be real. Then, we fixed  $i_y = 1.275$  (for y = M and P),  $\frac{\Delta G_{xy}}{\Delta G_{xx}} = 1$  and solved  $\frac{\Delta G_{xy}}{\Delta G_{xx}} = \frac{i_y \times h_x \times h_y \times r_{axy} \times \sigma_{px}}{i_x \times h_x^2 \times \sigma_{px}}$  to find  $i_x$  (*x* = LMA and BFT) in each MCMC sample. In this situation,  $i_x = \frac{1.275 \times h_y \times r_{axy}}{h_x}$ .

If animals with ultrasound traits are random sampled in Brazilian Hereford and Hereford × Nellore population and if selection intensities for LMA and BFT were less than 0.572 (standard deviation of 0.126, with 95% highest posterior density interval from 0.334 to 0.823) and 0.606 (standard deviation of 0.191, with 95% highest posterior density interval from 0.223 to 0.973), the indirect response to selection for M and P, respectively, will be more efficient than direct selection. However, in the present situation, the scanned animals are not part of a random sample because the producers pre-select the animals for scanning to reduce costs.

#### Table 6

Descriptive statistics of posterior density estimates of relative efficiencies of indirect selection (out of diagonal) by generation for post-weaning average daily gain (ADG), visual scores of conformation (C), precocity (P) and muscling (M) and ultrasound measurements of longissimus muscle area (LMA) and backfat thickness (BFT) in Brazilian Hereford and Hereford × Nellore cattle.

Selection criteria	Response trait								
	ADG	С	Р	Μ	LMA	BFT			
Mean (standard deviation)									
ADG	-	0.614 (0.061)	0.216 (0.054)	0.190 (0.053)	0.027 (0.086)	0.092 (0.171)			
С	0.550 (0.051)	-	0.500 (0.047)	0.607 (0.043)	0.339 (0.099)	0.187 (0.137)			
Р	0.252 (0.063)	0.639 (0.061)	-	0.809 (0.042)	0.333 (0.105)	0.476 (0.149)			
M	0.232 (0.064)	0.776 (0.056)	0.820 (0.038)	-	0.449 (0.099)	0.051 (0.162)			
LMA	0.041 (0.127)	0.503 (0.145)	0.400 (0.118)	0.524 (0.122)	-	0.390 (0.275)			
BFT	0.070 (0.122)	0.168 (0.121)	0.349 (0.104)	0.040 (0.113)	0.215 (0.160)	-			
95% highest pos	sterior density interval								
ADG	-	0.489 to 0.727	0.112 to 0.322	0.087 to 0.289	-0.142 to 0.179	-0.238 to 0.421			
С	0.447 to 0.643	-	0.410 to 0.593	0.529 to 0.691	0.149 to 0.530	-0.076 to 0.451			
Р	0.129 to 0.374	0.519 to 0.756	-	0.726 to 0.894	0.134 to 0.551	0.175 to 0.763			
M	0.113 to 0.363	0.661 to 0.874	0.748 to 0.897	-	0.262 to 0.645	-0.290 to 0.323			
LMA	-0.211 to 0.275	0.235 to 0.787	0.179 to 0.629	0.281 to 0.754	-	-0.139 to 0.867			
BFT	-0.162 to 0.295	-0.060 to $0.404$	0.135 to 0.532	-0.183 to 0.249	-0.086 to 0.551	-			

The average daily weight gain, the visual scores of conformation, precocity and muscling, and the traits evaluated through ultrasound (longissimus muscle area and backfat thickness) have genetic and phenotypic variability that support their inclusions in selection programs for Brazilian Hereford and Hereford × Nellore cattle, as long as the selection is based on predicted genetic values.

## 4. Conclusions

The selection for increasing the average daily weight gain from weaning to 505 days of age, alone, will result in modest or no change in longissimus muscle area and backfat thickness of the carcass of Brazilian Hereford and Hereford × Nellore cattle.

The selection to increase visual scores of muscling and conformation should promote positive correlated response in longissimus muscle area and backfat thickness of the carcass of Brazilian Hereford and Hereford × Nellore cattle.

The selection of Brazilian Hereford and Hereford × Nellore animals with more developed muscle mass does not necessarily result in animals with less fat cover.

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#### References

- Bailey, D.R., Gilbert, R.P., Lawson, J.E., 1991. Post-weaning growth of unselected Hereford and Angus cattle fed two different diets. J. Anim. Sci. 69, 2403–2412.
- Bertrand, J.K., Green, R.D., Herring, W.O., Moser, D.W., 2001. Genetic evaluation for beef carcass traits. J. Anim. Sci. 79, E190–E200.
- Boligon, A.A., Albuquerque, L.G., Mercadante, M.E.Z., Lôbo, R.B., 2010. Study of relations among age at first calving, average weight gains and weights from weaning to maturity in Nellore cattle. R. Bras. Zootec. 39, 746–751.
- Boligon, A.A., Mercadante, M.E.Z., Albuquerque, L.G., 2011. Genetic associations of conformation, finishing precocity and muscling visual scores with mature weight in Nelore cattle. Livest. Sci. 135, 238–243.
- Cardoso, F.F., Cardellino, R.A., Campos, L.T., 2004. Componentes de (co)variância e parâmetros genéticos de caracteres pós-desmama em bovinos da raça Angus. R. Bras. Zootec. 33, 313–319.

- Cardoso, F.F., Tempelman, R.J., 2004. Hierarchical Bayes multiple-breed inference with an application to genetic evaluation of a Nelore-Hereford population. J. Anim. Sci. 82, 1589–1601.
- Cardoso, F.F. 2008. Manual de utilização do programa INTERGEN versão 1.0 em estudos de genética quantitativa animal. Embrapa Pecuária Sul, Bagé.
- Conroy, S.B., Drennan, M.J., Kenny, D.A., McGee, M., 2010. The relationship of various muscular and skeletal scores and ultrasound measurements in the live animal, and carcass classification scores with carcass composition and value of bulls. Livest. Sci. 127, 11–21.
- Devitt, C.J., Wilton, J.W., 2001. Genetic correlation estimates between ultrasound measurements on yearling bulls and carcass measurements on finished steers. J. Anim. Sci. 79, 2790–2797.
- Fan, L.Q., Bailey, D.R., Shannon, N.H., 1995. Genetic parameter estimation of post-weaning gain, feed intake, and feed efficiency for Hereford and Angus bulls fed two different diets. J. Anim. Sci. 73, 365–372.
- Field, T.G., 2007. Beef production and management decisions. Pearson Education Inc., Upper Saddle River.
- Geweke, J., 1992. Evaluating the accuracy of sampling-based approaches to calculating posterior moments. In: Bernardo, J.M., Berger, J.O., Dawid, A.P., Smith, A.F.M. (Eds.), Bayesian Statistics. Oxford University Press, Oxford, pp. 1–31.
- Heidelberger, P., Welch, P.D., 1983. Simulation run length control in the presence of an initial transient. Oper. Res. 31, 1109–1144.
- Kemp, D.J., Herring, W.O., Kaiser, C.J., 2002. Genetic and environmental parameters for steer ultrasound and carcass traits. J. Anim. Sci. 80, 1489–1496.
- Lawrence, T.L.J., Fowler, V.R., 2002. Growth of farm animals. CABI Publishing, Wallingford.
- MacNeil, M.D., Northcutt, S.L., 2008. National cattle evaluation system for combined analysis of carcass characteristics and indicator traits recorded by using ultrasound in Angus cattle. J. Anim. Sci. 86, 2518–2524.
- Phillips, W.A., Brown, M.A., Brown Jr., A.H., Coleman, S.W., 2001. Genotype×environment interactions for post-weaning performance in crossbred calves grazing winter wheat pasture or dormant native prairie. J. Anim. Sci. 79, 1370–1377.
- Smith, B.J., 2005. Bayesian output analysis program (BOA) version 1.1 user's manual. http://www.public-health.uiowa.edu/boa/2005Available from:, [Accessed 03/09/10].
- Tarouco, J.U., Silva, S.L., Ferraz, J.B.S., Balieiro, J.C.C., Roso, V.M., Mourão, G.B., Mattos, E.C., Tarouco, A.K., Eler, J.P., 2006. Genetic analysis of live ultrasound measurements on replacement bulls and heifers of Braford and Hereford cattle. Proceedings of the 8th World Congress on Genetics Applied to Livestock Production, Belo Horizonte.
- USDA-FAS (United States Department of Agriculture Foreign Agricultural Service), 2009. Livestock and poultry: world markets and trade. United States Department of Agriculture, Washington DC.
- Yokoo, M.J., Albuquerque, L.G., Lobo, R.B., Bezerra, L.A.F., Araujo, F.R.C., Silva, J.A.V., Sainz, R.D., 2008. Genetic and environmental factors affecting ultrasound measures of longissimus muscle area and backfat thickness in Nelore cattle. Livest. Sci. 117, 147–154.
- Yokoo, M.J., Werneck, J.N., Pereira, M.C., Albuquerque, L.G., Koury Filho, W., Sainz, R.D., Lobo, R.B., Araujo, F.R.C., 2009. Correlações genéticas entre escores visuais e características de carcaça medidas por ultrassom em bovinos de corte. Pesq. Agropec. Bras. 44, 197–202.