

# Genetic associations between carcass traits measured by real-time ultrasound and scrotal circumference and growth traits in Nelore cattle<sup>1</sup>

M. J. Yokoo,\*† R. B. Lobo,‡§ F. R. C. Araujo,† L. A. F. Bezerra,‡ R. D. Sainz,# and L. G. Albuquerque\*<sup>2</sup>

\*Department of Animal Science, São Paulo State University, Jaboticabal, São Paulo, Brazil, CEP: 14.884-900; †Aval Serviços Tecnológicos S/S, Uberaba, Minas Gerais, Brazil; ‡Department of Genetic, University of São Paulo, Ribeirão Preto, São Paulo, Brazil; §National Association of Breeders and Researchers of Ribeirão Preto, São Paulo (ANCP), Brazil; and #Department of Animal Science, University of California, Davis 95616

**ABSTRACT:** The aim of the present study was to evaluate the genetic correlations among real-time ultrasound carcass, BW, and scrotal circumference (SC) traits in Nelore cattle. Carcass traits, measured by real-time ultrasound of the live animal, were recorded from 2002 to 2004 on 10 farms across 6 Brazilian states on 2,590 males and females ranging in age from 450 to 599 d. Ultrasound records of LM area (LMA) and backfat thickness (BF) were obtained from cross-sectional images between the 12th and 13th ribs, and rump fat thickness (RF) was measured between the hook and pin bones over the junction between gluteus medius and biceps femoris muscles. Also, BW (n = 22,778) and SC (n = 5,695) were recorded on animals born between 1998 and 2003. The BW traits were 120, 210, 365, 450, and 550-d standardized BW (W120, W210, W365, W450, and W550), plus BW (WS) and hip height (HH) on the ultrasound scanning date. The SC traits were 365-, 450-, and 550-d standardized SC (SC365, SC450, and SC550). For the BW and SC traits, the database used was from the Nelore Breeding Program—Nelore Brazil. The genetic parameters were estimated with mul-

tivariate animal models and REML. Estimated genetic correlations between LMA and other traits were 0.06 (BF), -0.04 (RF), 0.05 (HH), 0.58 (WS), 0.53 (W120), 0.62 (W210), 0.67 (W365), 0.64 (W450 and W550), 0.28 (SC365), 0.24 (SC450), and 0.00 (SC550). Estimated genetic correlations between BF and with other traits were 0.74 (RF), -0.32 (HH), 0.19 (WS), -0.03 (W120), -0.10 (W210), 0.04 (W365), 0.01 (W450), 0.06 (W550), 0.17 (SC365 and SC450), and -0.19 (SC550). Estimated genetic correlations between RF and other traits were -0.41 (HH), -0.09 (WS), -0.13 (W120), -0.09 (W210), -0.01 (W365), 0.02 (W450), 0.03 (W550), 0.05 (SC365), 0.11 (SC450), and -0.18 (SC550). These estimates indicate that selection for carcass traits measured by real-time ultrasound should not cause antagonism in the genetic improvement of SC and BW traits. Also, selection to increase HH might decrease subcutaneous fat as correlated response. Therefore, to obtain animals suited to specific tropical production systems, carcass, BW, and SC traits should be considered in selection programs.

**Key words:** *Bos indicus*, genetic correlation, genetic parameter, hip height, longissimus muscle area, rump fat thickness

©2010 American Society of Animal Science. All rights reserved.

J. Anim. Sci. 2010. 88:52–58  
doi:10.2527/jas.2008-1028

<sup>1</sup>Data first presented to the Genetic and Animal Breeding Post-Graduate Program at São Paulo State University (UNESP-FCAV). This research received financial support from Conselho Nacional de Desenvolvimento Científico e Tecnológico (CNPq-Brasil, No. 479692/2007-6). The authors acknowledge the Bacuri, Guaporé Pecuaría, Grupo Hofig Ramos, Rancho da Matinha, Colonial, São Dimas, Remanso, Passa Quatro, and Santa Marta farms for providing the animals and data to conduct this research. The authors thank Fundação de Amparo à Pesquisa do Estado de São Paulo (No. 05/58113-9) and CNPq-Brasil for providing the scholarships.

<sup>2</sup>Corresponding author: lgalb@fcav.unesp.br

Received March 11, 2008.

Accepted September 25, 2009.

## INTRODUCTION

In tropical countries, meat production is based mainly on *Bos indicus* (Zebu) cattle breeds and their crosses with *Bos taurus*. In these areas, BW and scrotal circumferences (SC) at different ages have been used as selection criteria in most of the existing breeding programs, ignoring carcass and other growth traits. Because BW at any age are genetically and positively correlated, selection for BW at young ages will result in larger birth and adult BW (Meyer, 1993; Kaps et al., 1999). Also, selection for faster growth will lead to large-frame ani-

mals that mature at heavier BW (Meyer, 1993; Nephawe et al., 2004; Yokoo et al., 2007). This strategy is especially inappropriate for extensive production systems. Increasing frame size will increase maintenance requirements and, in environments with limited feed resources (i.e., extensive production system in tropical areas), will decrease reproductive rates (Montaño-Bermudez and Nielsen, 1990; Jenkins and Ferrell, 1994; Beretta et al., 2002). Morris et al. (1993) suggested that environmental effects on pregnancy rate can be interpreted as an effect of food energy availability.

In general, crossbred animals from large-framed breeds produce carcasses with less subcutaneous fat and reduced carcass quality compared with medium-framed cattle (Camfield et al., 1997). Hip height (**HH**) is easily measured and less affected by environmental variations than BW (Baker et al., 1998) and therefore could be readily incorporated in cattle breeding programs.

Carcass traits can be quickly determined by real-time ultrasound (**RTU**), without the need for slaughtering the animals or assigning subjective visual scores. Carcass evaluation using RTU in live animals costs less than traditional progeny testing (Houghton and Turlington, 1992). Previous studies (Robinson et al., 1992; Herring et al., 1994) have shown that RTU provides accurate measures of live animal fat thickness and LM area (**LMA**), enabling estimation of breeding values for young animals before the first mating.

Considering the opportunities for entering new markets and the increasing demand for greater quality beef, carcass traits and HH (i.e., frame score) could be included in the Zebu breeding programs. Consequently, it is necessary to verify not only if these traits would be expected to respond to selection, but also to estimate the correlations among them and with traditional traits considered in tropical breeding programs. Therefore, the aim of the present study was to evaluate the genetic correlations of LMA and fat thicknesses over the 12th to 13th ribs (**BF**) and over the rump (**RF**) with BW and SC traits at different ages in Nelore cattle.

## MATERIALS AND METHODS

Data were obtained from an existing database used by the Nelore Breeding Program—Nelore Brazil (National Association of Breeders and Researchers, Ribeirão Preto, São Paulo, Brazil). On-farm data collection was conducted according to routine management procedures and conformed to the guidelines of NRC (1996).

Live-animal RTU records of 2,590 males and females ranging in age from 450 to 599 d and originating from 10 farms in 6 Brazilian states were collected. Longissimus muscle area and BF were obtained from cross-sectional images of the LM between the 12th and 13th ribs. Backfat thickness was estimated at the 3/4 position from the chine bone end of the LM using the cross-sectional LMA image. Moreover, RF was measured over the intersection between the gluteus medium and

biceps femoris muscles located between the hooks and pin bones.

An ALOKA 500V (Corometrics Medical Systems Inc., Wallingford, CT) apparatus equipped with a 3.5-MHz, 17.2-cm linear transducer (Aloka Co. Ltd., Tokyo, Japan) and an acoustic coupler (standoff pad) was used to obtain the RTU images, collected according to the Ultrasound Guidelines Council (**UGC**) approved methodology (<http://www.ultrasoundbeef.com/>), described in the Beef Improvement Federation guidelines (BIF, 1996). Records were stored using an image capture system (Blackbox, Biotronics, Ames, IA) and subsequently analyzed in a centralized laboratory responsible for the quality of the data (Aval Serviços Tecnológicos S/S, Uberaba, Minas Gerais, Brazil). Appropriate UGC-approved software with demonstrated accuracy and precision was used. Further details about the RTU measurements can be found in Yokoo et al. (2008).

Body weight (**WS**) and HH were also obtained at the time of scanning. Hip heights were measured directly over the hooks (hip bones) with the animal standing on a level surface, in accordance with the Beef Improvement Federation Guidelines (BIF, 2002). The animals with RTU, HH, and WS records were born between 2000 and 2002 and measured from 2002 to 2004.

Standardized BW and SC records of 22,778 and 5,695 animals, respectively, born between 1998 and 2003 in the same herds were also used. Body weights were standardized to 120 (**W120**), 210 (**W210**), 365 (**W365**), 450 (**W450**), and 550 (**W550**) d of age. The SC traits were standardized for 365 (**SC365**), 450 (**SC450**), and 550 (**SC550**) d of age and standardized for age and BW at 365 (**SCW365**), 450 (**SCW450**), and 550 (**SCW550**) d of age. Standardized BW and SC were measured every 3 mo from birth to 18 mo of age and from 12 to 18 mo of age, respectively. Age-standardized BW and SC were obtained as in BIF (2002). Additional details about standardized BW and SC traits can be found in Yokoo et al. (2007).

Contemporary groups (**CG**) were defined as the groups of animals of the same sex, reared within management group and born in the same herd, year, and season [spring (September, October, and November), summer (December, January, and February), autumn (March, April, and May), or winter (June, July, and August)]. Data from animals with records 3 SD above or below the mean of their CG were discarded. Contemporary groups containing progeny of only 1 sire and those with fewer than 3 animals were excluded for the RTU carcass traits, as well as HH and WS. For the remaining traits CG with fewer than 8 animals were eliminated. Table 1 shows a summary of the final data structure.

To find initial values to be used in pairwise analyses of combinations of BW and SC traits with each RTU carcass trait, the variance components were estimated in single-trait animal models using REML (Patterson and Thompson, 1971). A summary of initial single-trait

**Table 1.** Description of final data set of carcass traits as measured by ultrasound of the live animal, scrotal circumferences, and growth traits in Nelore cattle

Trait <sup>1</sup>	No. of records	Mean ± SD	$\hat{\sigma}_f^2$ <sup>2</sup>	$\hat{h}^2 \pm SE^3$	No. of sires	No. of dams	No. CG <sup>4</sup>
LMA, cm <sup>2</sup>	2,590	48.38 ± 8.72	30.21	0.29 ± 0.07	244	2,451	301
BF, mm	2,417	1.93 ± 1.09	0.60	0.50 ± 0.09	231	2,302	288
RF, mm	2,428	3.05 ± 1.97	1.00	0.39 ± 0.09	232	2,308	291
SC365, mm	5,377	209.68 ± 22.60	353.05	0.46 ± 0.05	372	3,917	169
SCW365, mm			245.18	0.46 ± 0.04			
SC450, mm	5,695	245.87 ± 30.22	607.29	0.51 ± 0.05	385	4,109	188
SCW450, mm			455.82	0.54 ± 0.05			
SC550, mm	1,771	276.78 ± 34.44	644.45	0.43 ± 0.09	204	1,543	129
SCW550, mm			486.36	0.52 ± 0.10			
HH, cm	2,356	136.06 ± 5.04	13.99	0.46 ± 0.09	226	2,308	250
WS, kg	2,551	323.93 ± 58.00	775.83	0.33 ± 0.08	231	2,416	308
W120, kg	22,778	128.78 ± 19.23	212.24	0.22 ± 0.03	540	11,759	630
W210, kg	17,068	186.72 ± 28.48	416.83	0.22 ± 0.03	490	9,699	534
W365, kg	13,973	250.39 ± 39.84	589.31	0.32 ± 0.03	473	8,121	556
W450, kg	11,957	298.47 ± 46.63	719.50	0.36 ± 0.04	451	6,896	443
W550, kg	4,254	347.14 ± 63.55	984.04	0.44 ± 0.05	249	3,096	201

<sup>1</sup>LMA = LM area; BF = backfat thickness; RF = rump fat thickness; SC365, SC450, and SC550 = standardized scrotal circumferences at 365, 450, and 550 d of age, respectively; SCW365, SCW450, and SCW550 = scrotal circumferences standardized for age and BW at 365, 450, and 550 d, respectively; WS and HH = BW and hip height obtained at the time of scanning, respectively; W120, W210, W365, W450, and W550 = standardized BW at 120, 210, 365, 450, and 550 d of age, respectively.

<sup>2</sup> $\hat{\sigma}_f^2$  = estimates of phenotypic variance in one-trait analyses.

<sup>3</sup> $\hat{h}^2$  = estimates of direct heritability in one-trait analyses.

<sup>4</sup>No. CG = number of contemporary groups.

genetic parameter values is presented in Table 1. Then, to minimize the influence of selection and culling, the multivariate (3-trait) animal models were fitted including W120 because all animals had records at this age. The heritability estimates were obtained by averaging the genetic and phenotypic variances obtained in the multivariate analyses. All analyses were done with the MTDFREML (multiple-trait derivative-free REML) program developed by Boldman et al. (1995), which employs a derivative-free REML method. Convergence was assumed to occur when the variance of the simplex ( $-2\log_e$  likelihood) reached  $1 \times 10^{-9}$ . The program was reinitiated after each convergence, using the previous estimates as initial values. This procedure was repeated until the differences in the  $-2\log_e$  likelihood values between the last 2 convergences were less than  $1 \times 10^{-4}$ . Approximate SE of the genetic correlations were estimated using the procedures described in Reeve (1955) and Robertson (1959). The relationship matrix included 3 generations of pedigree information and contained a total of 36,133 animals.

The models for all traits included a random animal genetic effect and CG as a fixed effect. For traits measured at or before 1 yr of age (W120, W210, and W365), random maternal genetic and permanent environment effects were added to the model. Initially, the covariance between direct and maternal genetic effects was set to zero as suggested by Benyshek et al. (1988), Meyer (1997), and Albuquerque and Meyer (2001). Subsequently, to verify the importance of the genetic correlations between W120, W210, and W365 maternal genetic effects and LMA, BF, and RF direct genetic

effects, analyses were performed estimating those particular covariances (i.e., without the constraint of zero covariance). Fixed effects considered for each trait were defined in preliminary analyses. The covariates, age of animal at scanning (linear effect) and age of dam (linear and quadratic effects), were considered for BF, RF, HH, and WS. For LMA only age of animal at scanning was kept in the model as a covariate. The fixed effect of age of dam class (6 classes: up to 35, 36 to 47, 48 to 59, 60 to 71, 72 to 119, and greater than 120 mo of age) was included in the W120, W210, and W365 models. Scrotal circumferences were analyzed with and without standardized BW at the respective ages as linear and quadratic covariates in the model.

The model for RTU carcass traits can be represented in matrix format as  $\mathbf{y} = \mathbf{X}\boldsymbol{\beta} + \mathbf{Z}\mathbf{a} + \mathbf{e}$ , where  $\mathbf{y}$  is the vector of observations,  $\boldsymbol{\beta}$  is the vector of unknown fixed effects,  $\mathbf{a}$  is the vector of unknown random effects that represent the breeding value of each animal,  $\mathbf{e}$  is the vector of unknown residual random effects, and  $\mathbf{X}$  and  $\mathbf{Z}$  are incidence matrices that relate the records to fixed and random genetic effects, respectively. The assumptions regarding the distributions of  $\mathbf{y}$ ,  $\mathbf{a}$ , and  $\mathbf{e}$  can be described as

$$\begin{bmatrix} \mathbf{y} \\ \mathbf{a} \\ \mathbf{e} \end{bmatrix} \sim N \left\{ \begin{bmatrix} \mathbf{X}\boldsymbol{\beta} \\ \mathbf{0} \\ \mathbf{0} \end{bmatrix}, \begin{bmatrix} \mathbf{Z}\mathbf{G}\mathbf{Z}' + \mathbf{R} & \mathbf{Z}\mathbf{G} & \mathbf{R} \\ \mathbf{G}\mathbf{Z}' & \mathbf{G} & \boldsymbol{\Phi} \\ \mathbf{R} & \boldsymbol{\Phi} & \mathbf{R} \end{bmatrix} \right\},$$

where  $\mathbf{G}$  is the variance-covariance matrix of the random effects of vector  $\mathbf{a}$ , and  $\mathbf{R}$  is the matrix of residual

**Table 2.** Estimates of genetic ( $\hat{r}_g$ ) and environmental ( $\hat{r}_e$ ) correlations between carcass traits as measured by ultrasound of the live animal and growth traits in Nelore cattle

Trait <sup>1</sup>	LMA, cm <sup>2</sup>		BF, mm		RF, mm	
	$\hat{r}_g \pm SE^2$	$\hat{r}_e$	$\hat{r}_g \pm SE^2$	$\hat{r}_e$	$\hat{r}_g \pm SE^2$	$\hat{r}_e$
W120, kg	0.53 ± 0.02	0.31	-0.03 ± 0.03	0.16	-0.13 ± 0.03	0.07
W210, kg	0.62 ± 0.02	0.27	-0.10 ± 0.03	0.22	-0.09 ± 0.03	0.08
W365, kg	0.67 ± 0.02	0.35	0.04 ± 0.03	0.29	-0.01 ± 0.04	0.21
W450, kg	0.64 ± 0.03	0.34	0.01 ± 0.04	0.36	0.02 ± 0.05	0.24
W550, kg	0.64 ± 0.03	0.34	0.06 ± 0.05	0.27	0.03 ± 0.05	0.12
WS, kg	0.58 ± 0.03	0.45	0.19 ± 0.05	0.31	-0.09 ± 0.05	0.41
HH, cm	0.05 ± 0.08	0.27	-0.32 ± 0.06	0.35	-0.41 ± 0.07	0.39

<sup>1</sup>LMA = LM area; BF = backfat thickness; RF = rump fat thickness; W120, W210, W365, W450, and W550 = standardized BW at 120, 210, 365, 450, and 550 d of age, respectively; WS and HH = BW and hip height obtained at the time of scanning, respectively.

<sup>2</sup>SE = approximate SE.

variances and covariances. The **G** and **R** matrices are described as  $\mathbf{G} = \mathbf{A} \otimes \mathbf{G}_0$ , where **A** is the relationship matrix, **G**<sub>0</sub> is the additive genetic variance-covariance matrix between traits, and  $\otimes$  is the direct product operator, and as  $\mathbf{R} = \mathbf{I} \otimes \mathbf{R}_0$ , where **I** is the identity matrix of the same order as **y**, **R**<sub>0</sub> is the matrix of residual variance-covariance between traits, **0** is the null vector, and  $\Phi$  is the null matrix.

### RESULTS AND DISCUSSION

For RTU carcass traits, SC and HH the estimates of heritability were moderate to high, varying from 0.35 to 0.63, indicating substantial additive genetic effects for these traits. Heritability estimates for standardized BW were moderate to high ranging from 0.23 to 0.49. All heritability estimates were within 1 SE of those obtained by single-trait analyses. The estimated genetic correlations between LMA and subcutaneous fat traits (BF and RF) were not significantly different from zero (0.06 ± 0.07 and -0.04 ± 0.06, respectively). The BF and RF are determined, largely, by the same groups of

genes ( $r_g = 0.74 \pm 0.03$ ). These results were already discussed in Yokoo et al. (2007, 2008).

The estimates of genetic and environmental correlations between RTU carcass traits and SC and growth traits in Nelore cattle are presented in Tables 2 and 3. The estimated genetic correlation between LMA and HH was not significantly different from zero (0.05 ± 0.08). Thus, selection for HH could be effective for changing animal size (frame) but would not be related to changes in LMA. This result is similar to those reported by Waldner et al. (1992) for Brangus, Riley et al. (2002) for Brahman, and Schenkel et al. (2004) for young *Bos taurus* beef bulls.

There was a negative and moderate genetic correlation between HH and both subcutaneous fat traits (BF, -0.32 ± 0.06; RF, -0.41 ± 0.07). As in the present work, Schenkel et al. (2004) and Nephawe et al. (2004) also estimated negative correlations between HH and BF, but although significantly different from zero, their estimates were of smaller magnitude (-0.17 and -0.16, respectively). When analyzing the genetic correlations between subcutaneous fat and height measured at different body locations, such as hump height or wither

**Table 3.** Estimates of genetic ( $\hat{r}_g$ ) and environmental ( $\hat{r}_e$ ) correlations between carcass traits as measured by ultrasound of the live animal and scrotal circumferences in Nelore cattle

Trait <sup>1</sup>	LMA, cm <sup>2</sup>		BF, mm		RF, mm	
	$\hat{r}_g \pm SE^2$	$\hat{r}_e$	$\hat{r}_g \pm SE^2$	$\hat{r}_e$	$\hat{r}_g \pm SE^2$	$\hat{r}_e$
SC365, mm	0.28 ± 0.05	0.13	0.17 ± 0.04	-0.15	0.05 ± 0.05	0.00
SC450, mm	0.24 ± 0.05	0.25	0.17 ± 0.05	-0.20	0.11 ± 0.05	-0.09
SC550, mm	0.00 ± 0.07	0.48	-0.19 ± 0.06	0.08	-0.18 ± 0.07	0.24
SCW365, mm	-0.11 ± 0.04	-0.01	0.14 ± 0.04	-0.34	0.10 ± 0.05	-0.13
SCW450, mm	0.00 ± 0.05	0.03	0.14 ± 0.05	-0.46	0.11 ± 0.05	-0.17
SCW550, mm	0.00 ± 0.06	0.26	-0.12 ± 0.06	-0.05	0.00 ± 0.07	0.17

<sup>1</sup>LMA = LM area; BF = backfat thickness; RF = rump fat thickness; SC365, SC450, and SC550 = standardized scrotal circumferences at 365, 450, and 550 d of age, respectively; SCW365, SCW450, and SCW550 = scrotal circumferences standardized for age and BW at 365, 450, and 550 d, respectively.

<sup>2</sup>SE = approximate SE.



height, Aass (1996) and Smith et al. (2007) also found moderately negative genetic correlations of  $-0.29$  and  $-0.20$  between these traits, respectively. However, some authors (e.g., Waldner et al., 1992; Bergen et al., 2005) reported that the genetic correlation between HH and BF was close to zero ( $-0.07$  and  $0.01$ , respectively). Therefore, our results suggest that long-term selection for taller animals would tend to produce animals with less subcutaneous fat (i.e., later maturing in terms of carcass finishing). Although the Nelore breed shows lean to fat ratios intermediate between British and Continental breeds (Cundiff, 2004), in general they reach slaughter BW with less subcutaneous fat than that necessary to minimize carcass evaporative weight loss during the cooling process. This is largely due to management practices in tropical areas, where animals are finished on pasture or in short-period feeding based on conserved forage, such as silage or sugar cane (Albuquerque et al., 2006). In these areas, for Zebu breeds, both traits (HH and subcutaneous fat) should be considered as selection criteria, and appropriate selection indexes should be developed for this specific production system.

The estimation of the genetic correlation between direct and maternal effects using field data are not simple, with strong dependence on the data structure. Gerstmayr (1992) reported that a large proportion of dams without their own performance and a small number of progeny per dam negatively affected the reliability of the estimated parameters. Published estimates are generally negative and increased magnitude (Benyshek et al., 1988; Gerstmayr, 1992; Meyer, 1997).

To detect possible genetic correlations between the weaning weight maternal effect and the RTU carcass traits direct genetic effects, models allowing them to fluctuate were used, as reported by Splan et al. (2002). The estimate of W210 direct and maternal genetic correlation was negative and moderate ( $-0.32 \pm 0.02$ ), and including this effect in the model changed the direct correlation estimates between W210 and the RTU carcass traits only slightly. The estimated correlations between W210 and LMA, BF, and RF direct effects were  $0.52 \pm 0.02$ ,  $-0.15 \pm 0.03$ , and  $0.09 \pm 0.03$ , respectively. In addition, correlation estimates between W210 maternal genetic effect and LMA, BF, and RF direct effects were  $0.43 \pm 0.04$ ,  $0.31 \pm 0.06$ , and  $0.00 \pm 0.06$ , respectively. Similar results were found for W120 and W365. Positive, but less than in the present work, genetic correlation estimates between direct carcass traits (LMA and BF) and maternal genetic weaning weight effects were reported by Splan et al. (2002) in crossbred cattle. These results suggest that LMA and BF direct effects are partially determined by the same group of genes as BW maternal genetic effects. Because these correlations are not large in magnitude and the heritabilities of maternal effects are low (ranging from  $0.09 \pm 0.03$  to  $0.16 \pm 0.03$ ), selection for maternal ability would not be expected to result in important changes in carcass traits measured by RTU. On the other hand,

when selection is applied to improve maternal ability (a very important trait in tropical areas), antagonistic effects on carcass traits are not expected either.

The genetic correlations of BW at different ages were moderate and positive with LMA and close to zero with subcutaneous fat traits (BF and RF). These estimates are close to several described in the literature (Waldner et al., 1992; Shepard et al., 1996; Wilson et al., 2001). However, Stelzleni et al. (2002), working with approximately 1,200 Brangus animals between 320 and 410 d of age, estimated a genetic correlation between BF and BW at scan date (0.42) greater than found in this study. Our results indicate that selection for BW would increase LMA in the medium or long term as a correlated response, but would not change subcutaneous fat. Usually, in most of the animal breeding programs in the tropics, the emphasis has been mainly on selection for BW, given that this trait is easy and inexpensive to measure in large populations. Nonetheless, this criterion is not effective to improve carcass merit, such as carcass fat cover, because that requires increasing subcutaneous fat (BF and RF) as well. Nephawe et al. (2004) showed that selection for mature BW or height could be effective for changing size but would not be expected to result in much change in carcass and meat composition traits, such as percentage retail product, marbling, and tenderness. Moreover, if HH is not considered as a selection criterion, the selection for BW will increase HH as a correlated response (Yokoo et al., 2007).

The estimated genetic correlations between carcass traits as measured by RTU of live animals and SC standardized to different ages (365, 450, and 550 d of age) and adjusted for BW were close to zero (Table 3). This indicates that selection for these carcass traits would not induce a change in SC and vice versa, and suggests few pleiotropic gene effects affecting these traits in Nelore cattle. Considering that SC is used as an indicator trait for sexual precocity (Toelle and Robison, 1985; Pereira et al., 2001), it may be expected that sexually precocious animals would begin carcass fat deposition earlier (Foster and Nagatani, 1999). Thus, a positive genetic correlation between SC and subcutaneous fat was anticipated, at least at younger ages, but this was not confirmed by the present study (Table 3).

These estimates agreed with those reported by Wilson et al. (2001) in *Bos taurus*. However, Turner et al. (1990) with Hereford and Johnson et al. (1993) with Brangus estimated negative and moderate to high genetic correlations between subcutaneous fat thickness and SC ( $-0.89$  and  $-0.33$ , respectively), and positive, low to moderate genetic correlations between LMA and SC ( $0.49$  and  $0.19$ , respectively). However, the data set analyzed by Turner et al. (1990) was relatively small (385 male animals). Estimates of genetic parameters for carcass traits as measured by RTU of live animal in Nelore cattle are rare, with only few estimates being reported, most of them in conference proceedings. The estimates obtained in the present study are similar

to those reported by Barbosa et al. (2005) in Nelore animals.

In this study, adjusting or not SC for BW had practically no effect on genetic correlation estimates with subcutaneous fat (BF and RF; Table 3). On the other hand, estimates of genetic correlations of SC at 365 and 450 d of age with LMA were greater when SC were not adjusted for BW than when they were adjusted (0.28 and 0.24, respectively; Table 3). These results could be expected, considering the genetic correlation between LMA and BW (Table 2). These values are similar to those described by Meyer et al. (2004) for Hereford cattle and Schenkel et al. (2004) for *Bos taurus* bulls.

In conclusion, beef production in the tropics depends mainly on *Bos indicus* (Zebu) breeds. There is a consensus that carcass merit is one of the traits that needs improvement in these breeds. One tool to evaluate carcass quality is RTU. The results of this study show that LMA and subcutaneous fat thickness measured by RTU can be used as selection criteria, allowing estimation of breeding values before the first mating and accelerating the response to individual selection. In breeding programs of most tropical countries, BW and SC, measured at different ages, have been used as selection criteria. Even though HH is not included in selection criteria, there is a tendency for breeders to favor larger framed animals (i.e., there is a positive genetic correlation between BW and HH); however, taller animals will deposit less subcutaneous fat. Selection for BW will lead to a correlated and desirable genetic response in LMA, but with no change in subcutaneous fat. Consequently, to improve carcass merit, such as fat cover, selection criteria should include carcass measures in addition to BW.

## LITERATURE CITED

- Aass, L. 1996. Variation in carcass and meat quality traits and their relations to growth in dual purpose cattle. *Livest. Prod. Sci.* 46:1–12.
- Albuquerque, L. G., M. E. Z. Mercadante, and J. P. Eler. 2006. Recent studies on the genetic basis for selection of *Bos indicus* for beef production. Pages 1–7 in Proc. 8th World Congr. Genet. Appl. Livest. Prod., Belo Horizonte, Minas Gerais, Brazil.
- Albuquerque, L. G., and K. Meyer. 2001. Estimates of direct and maternal genetics effects for weights from birth to 600 days of age in Nelore cattle. *J. Anim. Breed. Genet.* 118:83–92.
- Baker, J. F., T. S. Stewart, C. R. Long, and T. C. Cartwright. 1998. Multiple regression and principal components analysis of puberty and growth in cattle. *J. Anim. Sci.* 66:2147–2158.
- Barbosa, V., C. U. Magnabosco, C. U. Faria, R. D. Sainz, F. R. C. Araujo, and R. B. Lobo. 2005. Implementação da amostragem de Gibbs no estudo da correlação genética entre as características espessura de gordura e perímetro escrotal em touros da raça Nelore. Pages 1–5 in Proc. 42th Reunião Anual da Sociedade Brasileira de Zootecnia, Goiânia, Goiás, Brazil.
- Benyshek, L. L., M. H. Johnson, D. E. Little, J. K. Bertrand, and L. A. Kriese. 1988. Application of an animal model in the United States beef cattle industry. *Proc. Animal Workshop. J. Dairy Sci.* 71(Suppl. 2):35–53.
- Beretta, V., J. F. P. Lobato, and C. G. M. Netto. 2002. Produtividade e eficiência biológica de sistemas de produção de gado de corte de ciclo completo no Rio Grande de Sul. *Braz. J. Anim. Sci.* 31(Suppl. 2):991–1001.
- Bergen, R., S. P. Miller, and J. W. Wilton. 2005. Genetic correlations among indicator traits for carcass composition measured in yearling beef bulls and finished feedlot steers. *Can. J. Anim. Sci.* 85:463–473.
- BIF. 1996. Guidelines for Uniform Beef Improvement Programs, 7th ed. Beef Improvement Federation (BIF), Kansas State Univ., Colby, KS.
- BIF. 2002. Guidelines for Uniform Beef Improvement Programs, 8th ed. Beef Improvement Federation (BIF), Univ. Georgia, Athens, GA.
- Boldman, K. G., L. A. Kriese, L. D. Van Vleck, C. P. Van Tassell, and S. D. Kachman. 1995. A manual for use of MTDFREML. A set of programs to obtain estimates of variances and covariances [DRAFT]. USDA, ARS, Lincoln, NE.
- Camfield, P. K., A. H. Brown Jr., P. K. Lewis, L. Y. Rakes, and Z. B. Johnson. 1997. Effects of frame size and time-on-feed on carcass characteristics, sensory attributes, and fatty acid profiles of steers. *J. Anim. Sci.* 75:1837–1844.
- Cundiff, L. V. 2004. Encyclopedia of Animal Science “Beef cattle: Breeds and genetics”. W. G. Pond and A. W. Bell, ed. Cornell University, Ithaca, NY.
- Foster, D. L., and S. Nagatani. 1999. Physiological perspectives of leptin as a regulator of reproduction: Role in timing puberty. *Biol. Reprod.* 60:205–215.
- Gerstmayr, S. 1992. Impact of the data structure on the reliability of the estimated genetic parameters in an animal model with maternal effects. *J. Anim. Breed. Genet.* 109:321–336.
- Herring, W. O., D. C. Miller, J. K. Bertrand, and L. L. Benyshek. 1994. Evaluation of machine, technician, and interpreter effects on ultrasonic measures of backfat and longissimus muscle area in beef cattle. *J. Anim. Sci.* 72:2216–2226.
- Houghton, P. L., and L. M. Turlington. 1992. Application of ultrasound for feeding and finishing animals: A review. *J. Anim. Sci.* 70:930–941.
- Jenkins, T. G., and C. L. Ferrell. 1994. Productivity through weaning of nine breeds of cattle under varying feed availabilities. I. Initial evaluation. *J. Anim. Sci.* 72:2787–2797.
- Johnson, M. Z., R. R. Schalles, M. E. Dikeman, and B. L. Golden. 1993. Genetic parameter estimates of ultrasound-measured longissimus muscle area and 12th rib fat thickness in Brangus cattle. *J. Anim. Sci.* 71:2623–2630.
- Kaps, M., W. O. Herring, and W. R. Lamberson. 1999. Genetic and environmental parameters for mature weight in Angus cattle. *J. Anim. Sci.* 77:569–574.
- Meyer, K. 1993. Covariance matrices for growth traits of Australian Polled Hereford Cattle. *Anim. Prod.* 57:37–45.
- Meyer, K. 1997. Estimates of genetic parameters for weaning weight of beef cattle accounting for direct-maternal environmental covariances. *Livest. Prod. Sci.* 52:187–199.
- Meyer, K., D. J. David, and H. U. Graser. 2004. Estimates of the complete genetic covariance matrix for traits in multi-trait genetic evaluation of Australian Hereford cattle. *Aust. J. Agric. Res.* 55:195–210.
- Montaño-Bermudez, M., and M. K. Nielsen. 1990. Biological efficiency to weaning and to slaughter of crossbred beef cattle with different genetic potential for milk. *J. Anim. Sci.* 68:2297–2309.
- Morris, C. A., R. L. Baker, S. M. Hickey, D. L. Johnson, N. G. Cullend, and J. A. Wilson. 1993. Evidence of genotype by environment interaction for reproductive and maternal traits in beef cattle. *Anim. Prod.* 56:69–77.
- Nephawe, K. A., L. V. Cundiff, M. E. Dikeman, J. D. Crouse, and L. D. Van Vleck. 2004. Genetic relationships between sex-specific traits in beef cattle: Mature weight, weight adjusted for body condition score, height and body condition score of cows, and carcass traits of their steer relatives. *J. Anim. Sci.* 82:647–653.
- NRC. 1996. Institute of Laboratory Animal Resources. Commission on Life Sciences. Guide for the Care and Use of Laboratory Animals. Natl. Acad. Press, Washington, DC.

- Patterson, H. D., and R. Thompson. 1971. Recovery of inter-block information when block size are unequal. *Biometrics* 58:545–554.
- Pereira, E., J. P. Eler, F. A. A. Costa, and J. B. S. Ferraz. 2001. Análise genética da idade ao primeiro parto e do perímetro escrotal em bovinos da raça Nelore. *Arq. Bras. Med. Vet. Zootec.* 53:116–121.
- Reeve, E. C. R. 1955. The variance of the genetic correlation coefficient. *Biometrics* 11:357–374.
- Riley, D. G., C. C. Chase Jr., A. C. Hammond, R. L. West, D. D. Johnson, T. A. Olson, and S. W. Coleman. 2002. Estimated genetic parameters for carcass traits of Brahman cattle. *J. Anim. Sci.* 80:955–962.
- Robertson, A. 1959. The sampling variance of the genetic correlation coefficient. *Biometrics* 15:469–485.
- Robinson, D. L., C. A. McDonald, K. Hammond, and J. W. Turner. 1992. Live animal measurement of carcass traits by ultrasound: Assessment and accuracy of sonographers. *J. Anim. Sci.* 70:1667–1676.
- Schenkel, F. S., S. P. Miller, and J. W. Wilton. 2004. Genetic parameters and breed differences for feed efficiency, growth, and body composition traits of young beef bulls. *Can. J. Anim. Sci.* 84:177–185.
- Shepard, H. H., R. D. Green, B. L. Golden, K. E. Hamlin, T. L. Perkins, and J. B. Diles. 1996. Genetic parameter estimates of live animal ultrasonic measures of retail yield indicators in yearling breeding cattle. *J. Anim. Sci.* 74:761–768.
- Smith, T., J. D. Domingue, J. C. Paschal, D. E. Franke, T. D. Bidner, and G. Whipple. 2007. Genetic parameters for growth and carcass traits of Brahman steers. *J. Anim. Sci.* 85:1377–1384.
- Splan, R. K., L. V. Cundiff, M. E. Dikeman, and L. D. Van Vleck. 2002. Estimates of parameters between direct and maternal genetic effects for weaning weight and direct genetic effects for carcass traits in crossbred cattle. *J. Anim. Sci.* 80:3107–3111.
- Stelzleni, A. M., T. L. Perkins, A. H. Brown Jr., F. W. Pohlman, Z. B. Johnson, and B. A. Sandelin. 2002. Genetic parameter estimates of yearling live animal ultrasonic measurements in Brangus cattle. *J. Anim. Sci.* 80:3150–3153.
- Toelle, V. D., and O. W. Robison. 1985. Estimates of genetic correlations between testicular measurements and female reproductive traits in cattle. *J. Anim. Sci.* 60:89–100.
- Turner, J. W., L. S. Pelton, and H. R. Cross. 1990. Using live animal ultrasound measures of ribeye area and fat thickness in yearling Hereford bulls. *J. Anim. Sci.* 68:3502–3506.
- Waldner, D. N., M. E. Dikeman, R. R. Schalles, W. G. Olson, P. L. Houghton, J. A. Unruh, and L. R. Corah. 1992. Validation of real-time ultrasound technology for predicting fat thickness, longissimus muscle areas and composition of Brangus bulls from 4 months to 2 years age. *J. Anim. Sci.* 70:3044–3054.
- Wilson, D. E., G. H. Rouse, and C. L. Hays. 2001. Genetic Relationship between Live Animal Ultrasound Measures and Scrotal Circumference in Yearling Angus Bulls. Beef Research Report A.S. Leaflet R1737. Cooperative Extension Service, Iowa State Univ., Ames.
- Yokoo, M. J., L. G. Albuquerque, R. B. Lobo, L. A. F. Bezerra, F. R. C. Araujo, J. A. V. Silva, and R. D. Sainz. 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., L. G. Albuquerque, R. B. Lobo, R. D. Sainz, J. M. Carneiro Júnior, L. A. F. Bezerra, and F. R. C. Araujo. 2007. Estimativas de correlações genéticas entre altura do posterior, peso e circunferência escrotal em bovinos da raça Nelore. *Braz. J. Anim. Sci.* 36:1761–1768.