Genetic parameters for body measurements and ultrasound carcass traits in Nellore cattle[♣]

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Introduction

Carcass composition is an important trait because it determines the animal economic value to farmers and the beef industry (Berg and Butterfield 1976). Besides animal handling, nutrition and health, special attention must be given to carcass components, i.e. muscles, fat and bones, and their relationship in the carcass, because the proportion between these tissues will establish its commercial value. Many aspects have to be taken into account when the objective is to produce high quality carcasses, enclosing genetics and phenotypic aspects that can influence this trait. Therefore, understanding relationships among carcass traits is very important to guide beef quality genetic improvement programs. With this aim, Bergen et al. (2006) suggested that results with genetic selection for carcass traits can be satisfactory when indicative traits are used. Ribeye area (REA) for carcass leanness and fat thickness (FT) for the subcutaneous fat deposition are examples of indicative traits. Ultrasound has been extensively used to evaluate carcass composition as REA and FT and studies have demonstrated a high correlation between carcass traits (REA and FT) measured by this technique (in vivo) and those obtained directly in the carcass at slaughter (Silva et al., 2003), making possible to obtain fast and accurate information about the beef carcass composition and genetic differences among animals, to be included in genetic improvement programs (Wilson 1992). Additionally, body measurements such as rump height (HGT), rump length (LGT) and rump width (WDT) may be related to body percentage of muscles and fat because they are indicative of skeletal structure and frame as well. Consequently, those traits may be associated to the yield of commercial cuts of the carcass. Therefore, the aim of this study was to establish the genetic and phenotypic correlations for the ultrasound and body carcass measurements in Nellore cattle.

Material and Methods

Animals and traits. The estimations in this study were obtained using information of 2.190 Nellore young bulls, with 18 months of age, evaluated to body weight (BW), rump height

(HGT, measured at the *posterior superior iliac spine*), rump length (LGT, distance between posterior extremity of *tuber ischii* to anterior edge of *tuber coxae*), rump width (WDT, distance between extremities of the *tuber coxae*), ultrasound ribeye area (REA) and ultrasound fat tackiness (FT). The REA (cm^2) and FT (cm) was evaluated by ultrasound scanning at *Longissimus dorsi,* between 12ª and 13ª ribs, with an Aloka, model SSD 500 Micrus (Aloka Co. Ltd.) ultrasound equipment, equipped with a linear transducer of 3.5 mHz and 172 mm of length coupled to a acoustic guide to guarantee better contact to the animal surface. The digital images obtained by the measurements were saved in a microcomputer and analyzed subsequently.

Statistical Analysis. The genetic parameters were estimated by pedigree matrices composed by 14.722 animals, using multitraits analysis, with six traits simultaneously, using the VCE-6 software (Kovac and Groeneveld 2003).

Results and Discussion

Genetic and phenotypic correlations. The descriptive statistics to the traits evaluated in the study are showed in the Table 1.

Table 1: Descriptive statistics for ribeye area (REA), fat thickness (FT) body weight (BW), rump height (HGT), length (LGT) and width (WDT) in Nellore cattle.

Traits	Number of observations	Minimum	Maximum	Mean	Standard Deviation
REA, cm^2	2190	32.00	78.50	49.18	5.64
FT, cm	2190	0.00	2.80	0.22	0.55
BW, kg	2160	244.00	481.00	341.21	32.94
HGT, cm	2161	130.00	164.00	148.33	6.00
LGT, cm	2150	30.00	49.00	40.74	1.92
WDT, cm	2151	35.00	51.00	43.84	2.13
AGE_US[1], days	2190	493.00	726.00	573.00	30.60
AGE_WH[2], days	2190	464.00	703.00	546.89	30.91

1 = age at the REA, FT, LGT and WDT measurements. .
2 = age at the BW and HGT measurements.

Positive genetic correlations were observed between REA, BW, LGT and WDT (Table 2), showing that these traits are positively correlated with high value commercial cuts of the carcass, as REA is positively associated with lean meat yield. Considering that most of high value commercial cuts are located in the hindquarter, we can suppose that WDT and LGT can be adequate indicative measures of high value commercial cuts in beef cattle. It was found a high negative correlation between HGT and FT (-0.60), what can be explained by the fact that rump height reflects the individual frame and high-frame animals tend to storage fat at body weights higher than those observed for small-frame cattle. Furthermore, the genetic correlations between REA, BW, and HGT indicate that rump width and length may be associated with muscle yield in the carcass once REA, BW and HGT are negatively correlated with FT (Table 2). Figueiredo (2001) suggested that the FT can be reduced on the carcass when the animals are genetic selected for rump height. Eler et al. (1996) described

that the selection for increase REA could result in reduction of FT. Moreover, observing the genetic correlations between BW, HGT, LGT and WDT we can suppose that animals with high body weight and hump height could have higher rump length and width and, consequently, higher frame.

Table 2: Genetic parameters for ribeye area (REA), fat thickness (FT), body weight (BW), and rump height (HGT), lenght (LGT) and width (WDT) in Nellore cattle.[♦]

Traits	Traits					
	REA	FT	BW	HGT	LGT	WDT
REA	**0.31** **(0.05)**	-0.23 (0.11)	0.54 (0.08)	0.26 (0.13)	0.47 (0.08)	0.26 (0.11)
FT	-0.04	**0.06** **(0.03)**	-0.36 (0.11)	-0.60 (0.19)	0.22 (0.14)	-0.16 (0.23)
BW	0.36	0.09	**0.37** **(0.06)**	0.75 (0.07)	0.65 (0.06)	0.72 (0.08)
HGT	0.11	0.00	0.47	**0.18** **(0.05)**	0.39 (0.14)	0.81 (0.12)
LGT	0.19	0.09	0.55	0.30	**0.29** **(0.04)**	0.40 (0.11)
WDT	0.13	0.14	0.40	0.28	0.36	**0.13** **(0.03)**

[♦] Heritabilities on the diagonal, standard error in parenthesis, phenotypic and genetic correlations below and above the diagonal, respectively.

Heritabilities. The heritabilities for the traits evaluated in this study are in conformity to the values described in the literature, presenting moderated values to carcass and body weight at 18 months of age (Utera and Van Vleck et al. 2004; Horimoto et al. 2007). The heritability to FT estimated in this study is low (0.06), probably due to the low variability observed in the evaluated population (Table 1). This result can be explained by the fact that Nellore bulls (*Bos indicus*) storage subcutaneous fat in higher weights than steers of the same breed and cattle of British breeds. Variability of FT heritabilities (0.02 a 0.38) were also described by Crews and Franke (1998) evaluating composed animal groups with different participation of Brahman genetics (*Bos indicus*). The heritabilities values for LGT and WDT (0.29 and 0.13 respectively) indicate that satisfactory genetic progress can be attained by selection for LGT and WDT when the aim is to increase lean muscle yield, because genetic correlation of these traits with REA are positive (Table 2).

Conclusion

Measurements obtained at the rump have moderate to high genetic correlation with ribeye area and, therefore, they can be used as auxiliary tools in genetic selection programs for meat yield and carcass quality in beef cattle.

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