

## Phenotypic and Genetic Association Between Meat and Carcass Traits with Growth Traits in Nellore Cattle

R. L. Tonussi<sup>1</sup>, A. F. B. Magalhães<sup>1</sup>, R. Espigolan<sup>1</sup>, D. G. M. Gordo<sup>1</sup>, W. B. F. Andrade<sup>1</sup>, G. C. Venturini<sup>1</sup>, L. A. L. Chardulo<sup>2</sup>, L. G. Albuquerque<sup>1,3</sup>, F. S. B. Rey<sup>1</sup>

<sup>1</sup>Sao Paulo State University (UNESP), Jaboticabal – Sao Paulo, Brazil. <sup>2</sup>Sao Paulo State University (UNESP), Botucatu – Sao Paulo, Brazil. <sup>3</sup>Researcher of CNPq and INCT-CA.

**ABSTRACT:** The aim was estimate genetic parameters for growth, carcass and meat traits in Nellore cattle. Records of weaning weight, yearling weight, weight gain from weaning to yearling, hot carcass weight, loin muscle area, backfat thickness and marbling score were used. A sample of one inch (2.54 cm) of *Longissimus dorsi* muscle was collected between the 12 and 13th ribs from the left carcass side. The contemporary groups (CG) were defined according to each trait. The (co)variance components and genetic parameters were estimated with an animal model by restricted maximum likelihood method using the computer program Wombat. The heritability estimates for the traits studied ranged from  $0.08 \pm 0.08$  to  $0.28 \pm 0.10$ . Estimates of genetic correlations ranged from  $-0.17 \pm 0.33$  to  $0.82 \pm 0.14$ . The growth, carcass and meat traits have enough variability genetic for response to selection.

**Keywords:** genetic correlation, heritability, loin muscle area, marbling score

### Introduction

Carcass traits such as hot carcass weight (HCW), loin muscle area (LMA) and backfat thickness (BFT) are used in the marketing of meat products, once these traits are indicators of the quantitative composition of carcass. The LMA is related to muscularity and the BFT is used as an indicator of the degree of carcass finish. Moreover, these traits can be used individually or combined in indexes or equations. The meat traits are the attributes that affect its texture and it may affect consumer preferences, for instance, the marbling score (MARB), which is an indicator of intramuscular fat, influences chewing and flavor (Thompson (2004)).

There are few studies estimating genetic parameters for carcass yield and meat quality traits measured in the *post mortem* period, probably due to the difficulty and cost of measuring these traits.

The growth traits such as weaning weight (WW), yearling weight (YW) and weight gain from weaning to yearling (GWY) are used as selection criteria in breeding programs in beef cattle. Selection for carcass yield and meat quality traits are still limited, however, measures of quality indicators, such as ultrasound and visual scores have been used to improve such traits (Yokoo et al. (2009)). Although there are some works studying the genetic association between growth traits and carcass traits assessed by ultrasound (Yokoo et al. (2010); Zuin et al. (2012)), there is little information regarding the impact of applying growth traits as selection criteria on carcass yield and meat quality

traits assessed in the *post mortem* period (Smith et al. (2007)).

Thus, the aim of this study was to estimate the phenotypic and genetic association between carcass yield and meat quality traits with growth traits in Nellore cattle, in order to provide information to improve these traits through selection.

### Materials and Methods

The records were obtained from eight farms participating in three beef cattle breeding programs (DeltaGen, Paint - CRV Lagoa and Nelore Qualitas). The animals were reared on pasture and were confined only for finishing on a period of approximately 90 days.

Records of 36,660, 35,742, 35,735, 1,441, 1,442, 1,435 and 1,610 for WW, YW, GWY, HCW, LMA, BFT and MARB were used, respectively.

Carcass yield and meat quality traits records were obtained in slaughterhouses in different regions of Brazil. The carcasses were chilled for a period of 48 hours. During boning, a sample of one inch (2.54 cm) of *Longissimus dorsi* muscle was collected between the 12 and 13th ribs from the left carcass side.

The LMA was measured by the quadrant points method (each square corresponds to one cm<sup>2</sup>), and the sum of all the squares corresponds to the *Longissimus* area. The BFT was assessed with a caliper, measured at an angle of 45 degrees from the geometric center of the sample. A visual grading scale (USDA - Quality and Yield Grade (1997)) varying from 0 to 9, was used to determine the MARB.

The contemporary groups (CG) were defined according to each trait. For WW, the CG was composed by farm and year of birth, management group at birth and weaning, and sex. For YW and GWY, it was added the management group at yearling to the CG. For carcass yield and meat quality traits the CG were defined by farm, year of birth and management group at yearling. Records above or below three standard deviations from the CG mean and CG with less than 3 animals were deleted.

The (co)variance components and genetic parameters were estimated with an animal model (three-traits analyses) by restricted maximum likelihood method using the computer program Wombat (Meyer (2007)). All the analyses included the WW as anchor trait. The genetic additive direct and residual random effects were considered in the model. For WW, the maternal genetic and maternal permanent environmental random effects were also included in the model. For WW, YW and GWY were used

as fixed effects the CG and the age of animal at yearling as covariate (linear and quadratic). For carcass yield and meat quality traits the fixed effects of CG, class of slaughter age and length of feedlot period nested in farm-year, were considered in the model. The LMA and BFT were adjusted for HCW. The model can be represented in matrix notation as:

$$\mathbf{y} = \mathbf{X}\mathbf{b} + \mathbf{Z}_1\mathbf{a} + \mathbf{Z}_2\mathbf{m} + \mathbf{Z}_3\mathbf{c} + \mathbf{e}$$

where  $\mathbf{y}$  = matrix of observed traits,  $\mathbf{b}$  = matrix of fixed effects,  $\mathbf{a}$  = matrix of direct additive genetic effects,  $\mathbf{m}$  = matrix of maternal additive genetic effects,  $\mathbf{c}$  = vector of maternal permanent environmental effects,  $\mathbf{e}$  = vector of residual effects, and  $\mathbf{X}$ ,  $\mathbf{Z}_1$ ,  $\mathbf{Z}_2$  and  $\mathbf{Z}_3$  are incidence matrices relating  $\mathbf{b}$ ,  $\mathbf{a}$ ,  $\mathbf{m}$  and  $\mathbf{c}$  to  $\mathbf{y}$ . In this study, it was assumed that  $E[\mathbf{y}] = \mathbf{X}\mathbf{b}$ ;  $\text{Var}(\mathbf{a}) = \mathbf{A} \otimes \mathbf{S}_a$ ;  $\text{Var}(\mathbf{m}) = \mathbf{A} \otimes \mathbf{S}_m$ ;  $\text{Var}(\mathbf{c}) = \mathbf{I} \otimes \mathbf{S}_c$ ;  $\text{Var}(\mathbf{e}) = \mathbf{I} \otimes \mathbf{S}_e$ , where  $\mathbf{S}_a$  is the additive genetic covariance matrix;  $\mathbf{S}_m$  is the matrix of maternal genetic variance;  $\mathbf{S}_c$  is the matrix of variance of maternal permanent environment;  $\mathbf{S}_e$  is the residual covariance matrix;  $\mathbf{A}$ , the numerator relationship matrix additive genetic;  $\mathbf{I}$ , the identity matrix; and  $\otimes$ , the direct product of matrices. It was further assumed that,  $\mathbf{a}$ ,  $\mathbf{m}$ ,  $\mathbf{c}$  and  $\mathbf{e}$  are not correlated.

## Results and Discussion

### Heritability estimates

The heritability estimates for growth traits (WW, YW and GWY) were moderate, indicating that the use of these traits as selection criteria in breeding programs can promote genetic progress (Table 1). The heritability estimates for these traits are consistent with those reported in the literature for Nellore (Laureano et al. (2011)); Wenceslau et al. (2012)).

**Table 1.** Additive and phenotypic variance and heritability estimates for carcass, meat and growth traits

Trait	$\sigma_a^2$	$\sigma_p^2$	$h^2$	SE
HWC	75.8	274.45	0.28	0.10
LMA	10.36	54.12	0.19	0.11
BFT	0.30	3.89	0.08	0.08
MARB	0.02	0.13	0.15	0.09
WW	49.5	228.97	0.22	0.02
YW	237.30	955.21	0.25	0.02
GWY	0.00052	0.0033	0.16	0.02

$\sigma_a^2$ =additive genetic variance;  $\sigma_p^2$ =phenotypic variance;  $h^2$ =heritability; SE=standard-error; HCW = hot carcass weight; LMA=loin muscle area; BFT=backfat thickness; MARB=marbling score; WW=weaning weight; YW=yearling weight; GWY=gain of weaning to yearling

The heritability estimates for carcass yield traits ranged from low to moderate (Table 1). The BFT had the lowest heritability estimate. HCW and LMA should respond to selection more quickly when compared to BFT. Higher heritability estimates for these traits in *Bos indicus* were reported by Riley et al. (2002); Smith et al. (2007) and Rezende et al. (2009). A possible explanation for the low heritability estimate for BFT is due to the low number of phenotypic records and data structure.

The MARB heritability estimate was moderate (Table 1). Similar result of heritability estimate for MARB in Brahman cattle were found by Wolcott et al. (2009) 0.17. For *Bos taurus*, the heritability estimates for marbling score reported in the literature ranged from 0.35 to 0.62 (McAllister et al. (2011); Lu et al. (2013)).

### Genetic and phenotypic correlation estimates

The estimates of genetic correlations between HCW and growth traits (WW, YW and GWY) were positive and moderate to high (Table 2). Thus, the selection that is usually practice for weights at different ages should lead to a correlated response in the same direction for HCW. In *Bos taurus*, Splan et al. (2002) also found positive and high genetic correlation estimate (0.70) between HCW and WW. The estimates of genetic correlation between HCW and YW agreed with that obtained by Ferriani et al. (2013) also working with Nellore (0.69). The estimated genetic correlation between HCW and GWY was lower than that found by Riley et al. (2002), in Brahman cattle (0.84).

**Table 2.** Phenotypic (rp) and genetic (rg) correlation estimates between carcass and meat traits with growth traits

traits		rp	rg
HCW	WW	0.52 ± 0.02	0.82 ± 0.14
	YW	0.44 ± 0.02	0.78 ± 0.10
	GWY	0.22 ± 0.03	0.30 ± 0.22
LMA	WW	-0.03 ± 0.04	-0.12 ± 0.25
	YW	-0.03 ± 0.04	-0.05 ± 0.23
	GWY	-0.03 ± 0.04	0.05 ± 0.25
BFT	WW	0.01 ± 0.03	-0.17 ± 0.33
	YW	0.05 ± 0.05	0.28 ± 0.36
	GWY	0.05 ± 0.05	0.74 ± 0.45
MARB	WW	-0.01 ± 0.04	-0.19 ± 0.24
	YW	0.01 ± 0.03	0.01 ± 0.23
	GWY	0.01 ± 0.03	0.21 ± 0.25

rp=phenotypic correlation; rg=genetic correlation; HCW = hot carcass weight; LMA=loin muscle area; BFT=backfat thickness; MARB=marbling score; WW=weaning weight; YW=yearling weight; GWY=gain of weaning to yearling

The genetic correlations obtained between (LMA and BFT) with WW were negative and low (Table 2), thus the selection for increased WW would not affect these traits. Probably, these results are explaining by the fact that LMA and BFT were adjusted for HCW, and this trait is correlated with WW and YW. Different results were reported by Arnold et al. (1991) and Splan et al. (2002) whom reported positive genetic correlations between LMA and WW, being 0.33 and 0.29, respectively, and by Wheeler et al. (2005) between LMA and YW (0.18). In these studies, LMA and BFT were adjusted for different effects (e.g. age at weaning and slaughter, days of fed and slaughter weight).

The genetic correlation estimate between LMA and GWY was close to zero (Table 2). Riley et al. (2002) working with Brahman cattle estimated higher genetic correlation (0.49) between LMA and GWY. The genetic correlation between BFT and GWY was high and positive

(0.74), similar to that reported by Riley et al. (2002) (0.58). Thus, selection for higher weight gain after weaning should lead to an increase in BFT.

The genetic correlation obtained between MARB and WW was low and negative (Table 2). Similar result (-0.12) was reported by Splan et al. (2002). The genetic correlation estimated between MARB and YW was nearly zero, indicating that the use of YW as a selection criterion do not lead to genetic changes in MARB. Similar results were reported by Arnold et al. (1991) and Wheeler et al. (2005) for taurine breeds, being the correlation estimates 0.20 and 0.10, respectively. The genetic correlation estimated between MARB and GWY was low and positive (Table 2), similar to those obtained by Riley et al. (2002) (0.28) and Smith et al. (2007) (0.27).

In general, the standard errors of genetic correlation estimates for carcass yield and meat quality traits were high, probably due to the low number of animals. However one should take into account that there are few studies for these traits in Nelore under tropical conditions.

The phenotypic correlation estimates between growth traits (WW, YW, GWY) with HCW were positive (Table 2) indicating that heavier animals will have higher carcass weight. However, the phenotypic correlation estimates between growth traits and other carcass yield and meat quality traits (Table 2) were close to zero, thus, the growth traits are not good indicators of meat quality traits.

### Conclusions

The growth (WW, YW and GWY), carcass (HCW and LMA) and meat (MARB) traits have enough variability genetic for response to selection.

Selection for higher WW, YW and GWY should promote genetic changes in the same direction for HCW. However, selection for growth traits would not affect MARB.

Selection for higher weight gain after weaning could induce a correlated response in BFT.

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