

## Genetic Correlations Estimate between Meat Tenderness, Growth and Carcass Traits in a Population of Polled Nellore Cattle in Brazil

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**ABSTRACT:** Growth, carcass and tenderness data from 415 Polled Nellore animals were analyzed in order to estimate the genetic correlations between tenderness (WBSF) and growth (ILW, FLW and ADG) and carcass (BF, RF and LMA) traits. The covariance components and genetic parameters were estimated using the Gibbs Sampling method. The heritability estimated for WBSF was of low magnitude ( $0.11 \pm 0.022$ ). The genetic correlations between WBSF and the other traits were of low magnitude, with values of -0.15; -0.18; -0.13; 0.10; -0.12 and 0.18, between WBSF and ILW, FLW, ADG, BF, RF and LMA, respectively. The results support the conclusion that selection for improved tenderness will not affect genetic progress in other economic traits and vice-versa, but more studies are required for a better knowledge of the genetic relationships between meat tenderness and other traits for Polled Nellore cattle.

**Keywords:** beef cattle; carcass; shear force

### Introduction

Brazil was the largest beef exporter in the world by volume in 2012, producing about 9.6 million tons of beef and, of these, approximately 1.8 million tons were destined for export (USDA (2013)). However, most of the beef exported by Brazil is considered of medium and low quality by international buyers, mainly due to low tenderness. Therefore Brazil lags behind other global beef exporters in export value, losing to countries such as the U.S. and Australia (IBGE (2011)). Most Brazilian beef comes from *Bos indicus* animals, known to be less tender than beef from *Bos taurus* beef breeds. However, research developed with Nellore cattle (Sainz et al. (2005)) has demonstrated the existence of genetic variability for beef tenderness, indicating that this trait can be improved through genetic selection.

Very few Brazilian structured Zebu herds include beef tenderness in their breeding programs, even though genetic improvement of beef tenderness in Zebu populations is of major importance. That is because Brazilian packers do not pay for meat quality as in other countries, rather they pay only for quantity. However, there are studies showing that consumers would be willing to pay more for meat quality, especially regarding meat tenderness (Boleman et al. (1997)).

Several researchers have studied carcass, food intake and growth traits, such as weight at different ages, growth curves and features related to growth rate of Nellore cattle (Hoque et al., (2009), Bouquet et al., (2010), Lopes et al., (2012)). However, research to evaluate meat quality, especially tenderness and its relationships with growth and carcass quality traits of Zebu cattle in Brazil, are limited. In this context, we aimed to estimate the (co)variance components and genetic parameters for meat tenderness, growth and carcass traits, so we can have a better knowledge of the genetic relationships between those traits in the Polled Nellore cattle breed.

### Materials and Methods

Data were obtained from two slaughters conducted in 2004 and 2008 that were part of a study by Marca OB Ranch, the Brazilian Agricultural Research Corporation – Embrapa, and the University of California - Davis for characterization and genetic selection for meat tenderness in Polled Nellore. Twenty two sires representing the main Nellore bloodlines were mated with 552 Polled Nellore cows. The progenies of these matings were raised on pasture, finished in feedlot for three months and slaughtered with ages ranging from 24 to 26 months old. Complete pedigree and phenotypic evaluations for carcass and meat tenderness data of 415 progeny of purebred Polled Nellore sires and dams were produced, forming a relationship matrix containing 956 animals.

The analyzed traits were: initial live weight (ILW); final live weight (FLW); average daily gain (ADG); longissimus muscle area (LMA); rump fat thickness (RF); backfat thickness at the 12<sup>th</sup>-13<sup>th</sup> rib (BF); and Warner-Bratzler shear force (WBSF), determined using the *Longissimus dorsi* muscle after ageing for seven days at 4°C (Wheeler et al. (2005)).

The variance components needed to obtain the genetic parameters were estimated by the Gibbs Sampling method (Van Tassel and Van Vleck (1996)), using the MTGSAM program. The basic linear model for single trait and bivariate analyses was:  $y = X\beta + Zu + e$ , where  $y$  = vector of the dependent variable,  $\beta$  = vector of fixed effects,  $X$  = incidence matrix that associates  $\beta$  with  $y$ ,  $Z$  =

incidence matrix that associates the vector  $u$  to  $y$ ,  $u =$  vector of additive genetic effects, and  $e =$  vector of residual effects. The linear model included additive genetic and residual random effects, fixed effects of sex and contemporary group (formed by year of slaughter and slaughter date) and the systematic effect of age as covariate. For the prior values of additive and residual (co)variances the uninformative or "flat" distribution was used. In the implementation of Gibbs Sampling a chain of 1,500,000 cycles was used, the first 500,000 cycles were discarded and the samples taken every 1,000 cycles, totaling 1,000 Gibbs samples. For convergence evaluation, the GIBANAL software (Van Kaam (1997)) was used.

## Results and Discussion

The variance components estimation for WBSF showed that this trait does not have significant values of additive genetic variance. This can be observed by the low additive genetic variance estimate (0.148) and the high residual (1.222) and phenotypic (1.370) variances presented. These values of direct additive genetic and phenotypic variances generated a heritability estimate of  $0.11 \pm 0.022$ , suggesting that only 11% of the WBSF genes have direct additive genetic effects, while 89% of the effects that control this feature are present in the residual, this being composed of epistatic, dominance, genotype-environment interactions and environmental effects.

The heritability estimate found in this study is similar to the value of 0.17 for Brahman animals and their crossbreds reported by Elzo et al. (1998). By contrast, previous studies with Brahman cattle have reported heritability values for WBSF as high as 0.29 (Smith et al. (2007)) and as low as 0.02 (Crews and Franke (1998)). Clearly, the heritability of meat tenderness varies widely. Various reports in the literature demonstrate heritabilities ranging from low to high magnitude, whether within or between breeds (Johnston et al. (2003), Minick et al. (2004), Boukha et al. (2011)). However, there are few studies that are directly comparable with the results found in this study, because most of the research with gene prospecting of meat quality features refers to *Bos taurus* breeds and their crossbreds with Zebu cattle (Elzo et al., (1998), Johnston et al. (2003)). That happens because taurine breeds have been selected, for some time now, in breeding programs that include carcass and meat quality as selection criteria, as opposed to zebu breeds, especially Nelore cattle.

The genetic correlations (Table 1) between the growth traits (ILW, FLW and ADG) and WBSF were negative and of low magnitude (-0.15, -0.18 and -0.13, respectively), indicating that selection for WBSF will not influence directly the selection for weight and *vice versa*. A negative and low magnitude (-0.12) correlation also occurred between WBSF and fat thickness measured on the rump (RF), indicating that the joint selection for these traits will not influence their phenotypic expression. For other carcass traits, BF and LMA, despite also being of low mag-

nitude, the genetic correlations with WBSF were positive (0.10 and 0.18, respectively). Although the positive genetic correlation estimate between WBSF and LMA can be explained by the increase in muscle size with age and consequently decreased meat tenderness, these results must be interpreted with caution due to the very large 95% confidence regions. Genetic correlations between WBSF and carcass traits (BF and LMA) were also observed by Koch et al. (1982) who obtained a value of -0.01 for genetic correlation between WBSF and BF, and a value of -0.02 between WBSF and LMA. Although these genetic correlations were negative, opposite to those obtained in this study, they were also of very low magnitude, indicating that the selection for WBSF should not influence the selection for the mentioned carcass traits.

**Table 1. Descriptive statistics of the (co) variance components and heritability estimates and genetic correlations between WBSF and ILW, FLW, ADG, BF, RF and LMA traits, in Polled Nelore cattle, obtained from bivariate analyses in animal model.**

Traits	(Co)variance components					Genetic parameters			
	$\sigma_{a_1}^2$	$\sigma_{a_2}^2$	$\sigma_{a_{12}}$	$\sigma_{e_1}^2$	$\sigma_{e_2}^2$	$h_1^2$	$h_2^2$	$r_{g_{12}}$	
WBSF <sup>1</sup> x ILW <sup>2</sup>	Mean	0.13	639.99	-1.32	1.24	83.97	0.09	0.88	-0.15
	SD	0.12	138.38	4.40	0.14	100.80	0.09	0.15	0.55
	CR	0.007	289.090	-10.31	0.931	0.01	0.01	0.44	-0.98
	95%	to 0.434	to 845.975	to 6.920	to 1.493	to 0.90	to 0.32	to 1.00	to 0.99
WBSF <sup>1</sup> x FLW <sup>2</sup>	Mean	0.16	1430.17	-2.61	1.22	363.55	0.11	0.79	-0.18
	SD	0.18	420.64	8.21	0.16	317.91	0.11	0.19	0.56
	CR	0.009	544.525	-21.11	0.823	0.730	0.01	0.34	-0.99
	95%	to 0.681	to 2065.225	to 12.330	to 1.476	to 1047.675	to 0.45	to 1.00	to 0.88
WBSF <sup>1</sup> x AG <sup>2</sup>	Mean	0.19	0.03	-0.01	1.20	0.02	0.13	0.61	-0.13
	SD	0.18	0.02	8.21	0.17	0.01	0.12	0.30	0.62
	CR	0.010	0.000	-0.110	0.830	0.000	0.01	0.06	-0.99
	95%	to 0.640	to 0.050	to 0.09	to 1.480	to 0.040	to 0.42	to 1.00	to 0.97
WBSF <sup>1</sup> x BF <sup>2</sup>	Mean	0.19	2.49	0.07	1.21	3.90	0.12	0.37	0.10
	SD	0.18	1.91	0.05	0.17	1.52	0.12	0.26	0.60
	CR	0.009	0.240	-0.794	0.843	0.235	0.01	0.04	-0.96
	95%	to 0.621	to 7.240	to 0.974	to 1.499	to 6.115	to 0.43	to 0.97	to 0.99
WBSF <sup>1</sup> x RF <sup>2</sup>	Mean	0.15	4.54	-0.11	1.23	1.48	0.11	0.74	-0.12
	SD	0.14	1.57	0.47	0.15	1.18	0.10	0.21	0.60
	CR	0.004	1.425	-1.079	0.894	0.030	0.01	0.26	-0.99
	95%	to 0.531	to 7.105	to 0.807	to 1.482	to 4.040	to 0.37	to 1.00	to 0.97
WBSF <sup>1</sup> x LMA <sup>2</sup>	Mean	0.20	17.23	0.29	1.18	38.81	0.14	0.29	0.18
	SD	0.22	16.23	1.35	0.19	13.17	0.14	0.25	0.63
	CR	0.008	0.525	-3.055	0.637	6.12	0.01	0.01	-0.97
	95%	to 0.895	to 59.345	to 3.327	to 1.479	to 56.43	to 0.54	to 0.90	to 0.99

<sup>1</sup>: Warner-Bratzler shear force of the *Longissimus dorsi* (WBSF); <sup>2</sup>: initial live weight (ILW), final live weight (FLW), average daily gain (ADG), longissimus muscle area (LMA), backfat thickness at the 12th-13th rib

(BF), rump fat thickness (RF);  $\sigma_{a1}^2$ : additive genetic variance of 1;  $\sigma_{a2}^2$ : additive genetic variance of 2;  $\sigma_{a12}$ : additive genetic covariance between 1 and 2;  $\sigma_{e1}^2$ : residual variance of 1;  $\sigma_{e2}^2$ : residual variance of 2;  $h_1^2$ : heritability of 1;  $h_2^2$ : heritability of 2;  $r_{g12}$ : genetic correlation between 1 and 2; SD: standard deviation; CR: credibility region at 95%.

The heritability estimates obtained for the traits related to carcass quality by bivariate Bayesian analysis, measured *in vivo* by ultrasound, were 0.29, 0.37 and 0.74 for LMA, BF and RF, respectively. These values range from moderate (LMA and BF) to high (RF) magnitude, but the heritability estimates obtained in this study for the growth traits as ILW, FLW and ADG were of high magnitude, with values of 0.88, 0.79 and 0.61, respectively. Literature values of heritabilities for weight, especially for yearling weight and weight gain, vary widely. Bergmann (2003) reported variation from 0.08 to 0.83 for direct heritability for yearling weight in studies with various breeds of beef cattle, and the author further stated that due to the great use of the trait as a selection criterion, several authors have been concerned with obtaining more accurate estimates of the genetic parameters.

The heritabilities obtained in the present study indicate that these traits can be passed from one generation to the next, in other words, there may be genetic progress in applying the selection for the same. Thus, in a breeding program it will be possible to select and improve both carcass and / or growth traits as well as the tenderness trait, not through a correlated response, but rather due to the high heritabilities of the individual traits.

There was also a wide amplitude of values of the credibility region at 95% (CR 95%) in the bivariate analyses presented here, such as the correlation between WBSF and the initial live weight (ILW). This credibility region at 95% (95% CR) ranged from -0.98 to 0.99, indicating that the analyzed parameter can assume any value within that range. This high amplitude of the credibility region at 95% occurred with all analyzed parameters and may indicate that the collected data was insufficient to generate more consistent analyses and further studies should be conducted to obtain a greater volume of information on the meat tenderness trait. In general, when considering only the Zebu breeds, especially Nellore, studies addressing tenderness as an object of selection are rather scarce. However, experiments to evaluate this trait are of high cost and long duration, which further complicates large scale collection of tenderness data.

### Conclusion

The estimates of (co)variance components and genetic parameters for meat tenderness indicated that most of genes responsible for meat tenderness trait (WBSF) have no direct additive genetic effect. The selection for meat ten-

derness in Polled Nellore will not affect deposition of subcutaneous fat in carcass nor the animals' muscularity and *vice versa*.

Furthermore, results of this study also demonstrated no correlated response between tenderness and growth traits, such as weight and weight gain, indicating that joint selection for those traits will not influence phenotypic expression of tenderness. These results indicate that meat tenderness can be used as selection criteria in breeding programs independently of other selected traits.

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