GENETIC PARAMETER ESTIMATES OF VISUAL SCORE TRAITS AND THEIR RELATIONSHIP WITH GROWING TRAITS IN BRAZILIAN NELORE CATTLE

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INTRODUCTION

The adoption of visual score traits is advantageous for genetic improvement of carcass-related traits (muscling and fat thickness) as compared with the traditional progeny tests and *post mortem* evaluation, due to reduction in time and costs to reach results. Existence of genetic variability of morphologic traits in Nelore cattle is indicated by the heritability estimates for carcass-related visual scores and body measurements (Lima et al., 1989; Eler et al., 1996; Koury Filho, 2001; Van Melis et al., 2003).

The objective of this study was to estimate genetic parameters of a new proposal of visual scores (body structure, E; finishing precocity, P; and muscling, M) used to evaluate beef cattle body proportions.

MATERIALS AND METHODS

Visual scores (E, P and M), measured at yearling age, were obtained from 1,367 males of five different herds which participate in the Brazilian Nelore Breeding Program, from February to May 2003. Trait E predicts the animal's lateral area, through the evaluation of body length and depth; P evaluates the proportion of body depth relative to legs height; and M evaluates animal's body volume and convexity of musculature. For each of these traits, animals received a score from 1 to 6, 1 representing the worst animal of the contemporary group and 6 the best. These three traits allow a spatial conception of the animal, since E predicts its lateral area, which looks like a rectangle, and when analyzed simultaneously with P, it will indicate the proportion of the sides of the rectangle. Inclusion of M will show the third dimension (Figure 1). Records on hind height (HH) and body weight (YW) were also available from 2,128 and 2,255 animals, respectively.

The (co)variance component and genetic parameter estimates were obtained by the restricted maximum likelihood methodology with one and two-trait models, which included fixed effects of contemporary group (herd, sex, year and season of birth and management group; 68 groups) and animal age as a covariate (linear and quadratic effects), and additive direct random effect, using MTDFREML (Boldman et al., 1995).

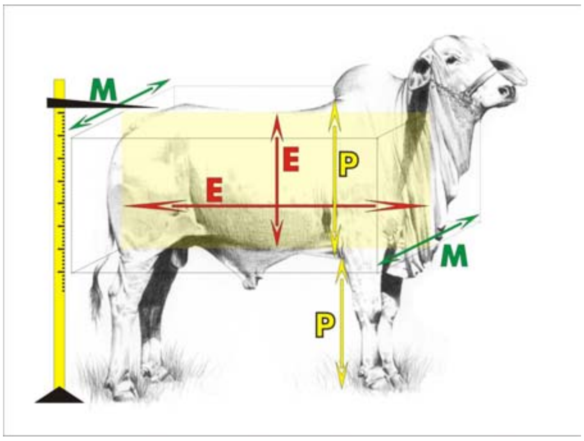

Figure 1. Schematic representation of different proportions to be evaluated by the visual scores E (body structure), P (finishing precocity) and M (muscling)

RESULTS AND DISCUSSION

The heritability values obtained in this study (Table 1) are explained by the high variability of morphological types existing in the Nelore breed, in which artificial selection is relatively recent (Magnabosco et al., 1997).

Table 1. Additive genetic variance component and genetic parameter estimates obtained by one and two-trait analyses of body structure (E), finishing precocity (P), muscling (M), hind height (HH), and yearling weight (YW)

	Variance component^A	Genetic parameters^B	
Trait	σ^2_a	h^2_d	e^2
E	0.429	0.24 ± 0,09	0.76 ± 0,09
P	1.498	0.63 ± 0,12	0.37 ± 0,12
M	0.962	0.48 ± 0,11	0.52 ± 0,11
HH	4.968	0.37 ± 0,08	0.63 ± 0,08
YW	230.744	0.29 ± 0,07	0.71 ± 0,07

$^A\sigma^2_a$ = additive direct variance component.
^{B} h^2_d = additive direct heritability; e^2 = proportion of the total variance due to residual effect.

Estimated heritabilities of P and M are higher than the estimates obtained for HH and YW, indicating that expected responses to direct selection for these visual score traits should be superior to those expected for growing traits.

The lower heritability estimated for E was expected, since different bio types can show similar scores for body structure, that is, taller, long bodied and shallow animals may have similar scores to smaller, shorter, and deeper animals. So, the visualization of the animal's biotype is possible only when P and E are analyzed simultaneously.

The high heritability estimate obtained for P (Table 1) is similar to the one obtained by Lima et al. (1989) for thorax depth (0.65 ± 0.22) evaluated visually. Heritability estimated for M is higher than the values obtained for muscling score in Nelore cattle, which ranged from 0.18 to 0.33 (Eler et al., 1996; Koury Filho, 2001; Van Melis et al., 2003).

Genetic correlation estimates among E, P and M were all positive (Table 2). For P and M the genetic correlation was higher, which was expected, since there was more coincidence of P and M scores.

Table 2. Genetic (above diagonal) and residual (bellow diagonal) correlations among body structure (E), finishing precocity, muscling (M), hind height (HH), and yearling weight (YW), obtained by two-trait analyses

Trait	E	P	M	HH	YW
E	-	0.49 ± 0.17	0.63 ± 0.15	0.57	0.83
P	0.43 ± 0,10	-	0.90 ± 0.05	-0.29	0.42
M	0.44 ± 0,08	0.56 ± 0.10	-	-0.33	0.50
HH	0.49	0.22	0.30	-	-
YW	0.68	0.58	0.62	-	-

The genetic correlation (0.57) between HH and E (Table 2) indicates that selection for higher animals should increase E. The negative genetic correlations between HH and P, and HH and M (Table 2) indicate that increasing hind height should result in slower finishing and lesser muscled animals.

All genetic correlations among visual scores and YW were positive (Table 2). When looking for morphologically equilibrated animals, it is possible to find animals with high breeding values for E, P and M. By identifying and using these animals, one can improve the traits E, P, M and YW simultaneously, so adoption of appropriate selection indices is recommended.

CONCLUSION

Body structure, finishing precocity and muscling, measured at yearling age, have enough additive genetic variability to show response to selection, and selection for anyone of them should result in favorable response in the others.

Selection for taller animals at yearling age should increase body structure and reduce finishing precocity and muscling.

More studies must be conducted before evidence showed in this work can be adopted.

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