Estimation Of Genetic Parameters For Yearling Weight, Mature Weight, Hip Height And Calving Success In Nellore Cattle Using A Multiple-Trait Threshold Model

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Introduction

Growing traits has continued to be an important part of breeding objective in cattle breeding programs, although it is established that selection for growth at young age leads to greater weights due to high correlation between weights at weaning or yearling and mature weight (Archer et al., 1998, Mercadante et al., 2004). Relationships among growth and reproductive traits, as well experimental results in terms of selection effects for increasing weight on reproductive performance of cows have not been well documented in *Bos indicus* populations. In 1976, a selection experiment for increasing yearling weight (YW) in Nellore Zebu breed, with the maintenance of a control population, was established at the Estação Experimental de Zootecnia de Sertãozinho (EEZS), São Paulo State, Brazil. The experiment aimed to determine the response to selection for higher weights in breeds of interest in tropics, since the few selection experiments available in the literature have been conducted on British breeds. Direct responses on YW and correlated responses on economic important traits were described through the years and recently by Bonilha et al. (2008). Several previous studies of traits related to size and reproductive performance of cows have used linear models or univariate treshold models (Mercadante et al., 2004). Therefore, the objective of this study was to estimate heritabilities and genetic correlations for growing and reproductive traits using a THRGIBBSF90 program (Misztal et al., 2009) that allows combination of categorical and continuous traits.

Material and methods

Records of 5844 Nellore males and females from three lines selected for yearling weight were used to evaluate the genetic parameters of yearling weight (YW), mature weight (MW), hip height (HH) and calving success (CS) (Table 1). All details concerning formation of these lines were described by Razook et al. (1998). The analysis carried out in a four-trait threshold linear model. The (co)variance components were obtained by THRGIBBSF90 (Misztal et al., 2009), a software that estimates (co)variance components in threshold animal mixed models, and allows combination of categorical and continuous traits. Random effects were animal additive genetic, maternal additive genetic for YW and permanent

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environmental for MW, HH and CS besides the residual effect. Fixed effects for YW were contemporary group (line, yr of birth and sex), month of birth (8, 9, 10, and 11 mo) and class of age of dam (3, 4…≥10 yr of age). For MW, HH and CS, fixed effects were contemporary group (line and yr of breeding season), previous reproductive status (calved or no calved) and class of age (2, 3… ≥10 yr of age). Analyses were run as a single chain of 100,000 cycles. A burn-in and stationary stage was monitored by graphical inspection, tracing plots of sampled values vs. iterations. Samples kept computing posterior means, standard deviations and credible regions were obtained as results of Gibanal program (Van Kaam, 1997).

Table 1. Number of animals, records, contemporary groups, unadjusted means, standard deviations and minimum and maximum values for Yearling Weight (YW), Hip Height (HH), Mature Weight (MW) and Calving Success (CS).

Trait	Animals	Records	GC	Means	SD	Min	Max
YW (kg)	5844	5844	144	288.02	44.34	153.56	435.80
HH(cm)	1445	6275	78	142.10	4.94	124.00	163.00
MW(kg)	1714	8987	78	401.35	65.39	203.00	609.00
CS(%)	1753	9100	77	0.75	0.42	0	1

Results and discussion

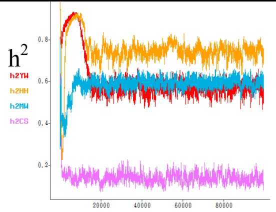
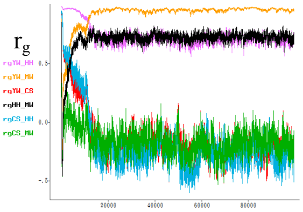
Posterior means, SD and median as well as greatest posterior density intervals at 95% for heritabilities, proportions of maternal genetic effect (YW) and permanent animal environment (HH, MW and CS) as well as genetic correlations were shown in Table 2. In addition, traces of heritabilities and correlations obtained by Gibbs samples were also shown in Table 2.

Estimated heritability for YW was 0.58 ± 0.03, and maternal genetic effect for YW showed substantial variance, about 10% of the total variance (Table 2). Lower results were reported by Mercadante et al. (2004) in study using data from the same experimental herd and considering male and female YW as different traits. Estimates reported by authors ranged from 0.36 ± 0.05 to 0.46 ± 0.05. Heritability values for HH were 0.76 ± 0.05, greater than 0.55 ± 0.06 showed by Mercadante et al. (2003). Estimated heritability was 0.59 ± 0.02 for MW (Table 2). This result agreed with conclusions by Arango and Plasse (2002) that found values for MW varying from 0.49 ± 0.10 to 0.68 ± 0.07 for Brahman experimental herd. Posterior means heritabilities estimated for all growing traits indicated the existence of significant genetic variance.

Great values of heritability for growth traits obtained in this study can be credited to the fact that data came from a simple herd, which, according to Rosa et al. (2001), allowed the environmental variations were better shaped, and also due to the use of repeated measures in multivariate model with a character preceding selection, as suggested by Kaps et al. (1999).

Conversely, heritability estimate for CS, 0.14 ± 0.03, obtained in this study are considered low for selections purposes, which agreed with conclusions obtained by Mercadante et al. (2003) that found low heritability for MW (0.11 ± 0.03).

Table 2. Estimates of heritabilities, proportions of maternal genetic effect ($m^{2)}$ and permanent animal environment (c^2), genetic correlations and histograms of the trace of heritabilities and genetic correlations.

Trait	Mean	SD	Median	CR_95%	Trace of h^2 and r_g
		Heritability			
h^2YW	0.58	0.03	0.58	0.54 - 0.63	
h^2HH	0.76	0.05	0.76	0.70 - 0.88	
h^2MW	0.59	0.02	0.59	0.54 - 0.64	
h^2CS	0.14	0.03	0.14	0.11 - 0.20	
m^2YW	0.10	0.01	0.59	0.08 - 0.12	
c^2HH	0.09	0.03	0.09	0.05 - 0.13	
c^2MW	0.06	0.01	0.06	0.05 - 0.09	
c^2CS	0.04	0.02	0.03	0.02 - 0.07	
		Genetic correlation			
r_g YW_HH	0.72	0.03	0.73	0.67 - 0.77	
r_g YW_MW	0.97	0.02	0.97	0.93 - 0.99	
r_g YW_CS	-0.21	0.07	-0.23	-0.30 - -09	
r_g HH_MW	0.74	0.03	0.74	0.70 - 0.78	
r_g HH_ CS	-0.27	0.11	-0.27	-0.44 - -0.14	
r_g MW_CS	-0.15	0.10	-0.18	-0.28 - 0.01	

YW: Selection Weight; HH: Hip Height, MW: Mature Weight; CS: Calving Success. In the heritability trace histogram: red = h^2YW; orange = h^2HH; blue = h^2MW; purple = h^2CS. In the genetic correlation trace histogram: purple = r_gYW_HH; orange = r_gYW_MW; red = r_gYW_CS; black = r_gHH_MW; blue = r_gHH_CS; green = r_gMW_CS.

Posterior means estimates of genetic correlations among growing traits were high. Values for genetic correlations between YW and HH; and HH and MW were, respectively, 0.72 ± 0.03 and 0.74 ± 0.03 (Table 2). For YW and MW genetic correlation was 0.97 ± 0.02. Such results suggested that genetic components of growing at early weights were, in great part, the same of those in later weights.

The genetic correlations among all growing traits and CS obtained in the present study were negative and moderate, ranging from -15 ± 0.10 for MW and CS to -0.27 ± 0.11 for HH and CS (Table 2). Negative correlations between reproductive and productive traits were reported by Scholtz and Roux (1984) and Luesakul-Reodecha et al. (1986). These results indicated that there is evidence of an antagonistic genetic relationship between growing and reproductive traits, however, Silva et al. (2006) and Phocas and Sapa (2004) have indicated that selection to heavy weight at young ages did not represent significant effect on reproductive performance of females.

Conclusion

The magnitude of the heritabilities and the antagonism between growing and reproductive traits implies in a necessity to combine selection of animals for growing and reproductive traits in a favorable way. The adoption of a selection index is expected to optimize genetic changes in growth and reproductive traits.

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