

# BIVARIATE ANIMAL MODEL ANALYSIS OF GROWTH WEIGHTS AND SCROTAL CIRCUMFERENCE OF NELLORE CATTLE IN BRAZIL

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## SUMMARY

Mixed model methodology under bivariate animal models was used to predict (co)variance components and genetic parameters of 11,070 field data records of calf weight at birth (BW), 120 (W120), 240 (W240), 365 (W365), 550 (W550) and 730 (W730) and scrotal circumference at 365 (SC365) and 550 (SC550) days of age. Herd-year-season, calving age of cow and sex were considered as fixed effects and genetic direct animal effect and error were considered as random. Heritabilities, genetic and environmental correlations were estimated from the appropriate (co)variances and phenotypic correlations were computed. All data came from 9 herds of purebred Nellore seedstock raised in tropical southeastern and northern Brazil and born from 1980 to 1993. Heritability estimates for direct effects were 0.29 (BW), 0.20 (W120), 0.25 (W240), 0.24 (W365), 0.26 (W550) and 0.21 (W730), 0.25 (SC365), and 0.43 (SC550). Genetic correlations between yearling scrotal circumference and other growth traits were positive, suggesting that selection for yearling scrotal circumference should not adversely affect other growth traits in Nellore Cattle. Environmental correlation estimates among those traits were high and positives.

## INTRODUCTION

Beef cattle production is very important in the tropics and appropriate knowledge of genetic parameters of growth traits and scrotal circumference is needed to establish the adequate selection programs. Best linear unbiased prediction (BLUP) of genetic parameters, now available with mixed model methodology under animal models, is becoming the method of choice of animal breeders (Henderson, 1988) and restricted maximum likelihood (REML) estimation of variance and covariance and prediction of breeding values is the most adequate method for unbalanced animal field data (Boldman and Van Vleck, 1991). The animal model is most advantageous for less heritable but highly variable traits (Meyer et al., 1991), like calf weights and scrotal circumference. However animal models have large computational demands and the modifications introduced by Boldman and Van Vleck (1991) to use a sparse matrix solver (Sparspak, George et al., 1980) brought high speed software to solve mixed models equations. Multivariate analysis under animal model has added value for traits, as they can change rank of animals, due to genetic correlations. Multiple trait derivative-free REML estimates can be obtained by using Boldman and Van Vleck's program (1993, 1994). Estimates of genetic and phenotypic parameters for

performance traits of beef cattle were reviewed by Mohiuddin (1993). Scrotal circumference estimates of heritability were obtained by animal model REML for Australian beef cattle by Meyer et al. (1990), while Kriese et al. (1991) studied some traits for Brahman and Brahman-derivative cattle. The objectives of this study were estimate variances and covariances, heritabilities and correlations among growth traits and scrotal circumference of Nellore cattle raised under tropical conditions.

### MATERIAL AND METHODS

Field data records on 11,070 registered Nellore Cattle, born from 1980 to 1993, were obtained from "Programa de Melhoramento Genético da Raça Nelore " (Lôbo, 1994), conducted by Genetic Department of the University of São Paulo, Brazil. The data set included records from 9 herds raised on pasture in tropical southeastern (8) and northern (1) Brazil, for birth weight (BW), weight at 120 (W120), 240 (W240), 365 (W365), 550 (W550), 730 (W730), and scrotal circumference at 365 (SC365) and 550 (SC550) days of age. Herd-year-season, calving age of cow and sex of calf were considered as fixed effects and genetic direct and error were considered as random. Data were analyzed using MTDFREML (Boldman and Van Vleck, 1993, 1994), that used a sparse matrix solver (Sparspak, George et al., 1980). The linear model was:

$$y = X\beta + Z\mu + e, \text{ where:}$$

- y = vector of dependent variables,
- X = matrix of incidence of fixed effects, for both dependant variables,
- $\beta$  = vector of fixed effects, including herd-year-season, calving age of cow and sex,
- Z = matrix of incidence of random effects, for both dependant variables,
- $\mu$  = vector of random effects genetic direct effects of animal,
- e = vector of random residual errors.

### RESULTS AND DISCUSSION

The number of observations and estimates of phenotypic and environmental variances, heritabilities and genetic correlations between W240 and BW, W120, W365, W550, W730, SC365 and SC550 from bivariate analysis are shown in Table 1.

The variance and covariance components found in the uni- and bivariate analysis were similar. The heritability estimates ranged from 0.17 to 0.29 for growth traits, and from 0.20 to 0.43 for scrotal circumference. Genetic correlation varied from 0.42 to 1.00 among growth traits, whereas scrotal circumference and weights ranged from 0.21 to 0.60. These results were very close agreement with literature estimates in Zebu cattle in the tropic (Eler et al, 1992, Mohiuddin, 1993, Mercadante, 1994).

**TABLE 1 - (Co)variances, heritabilities and correlations estimates for growth traits and scrotal circumferences from bivariate analysis.**

	N	$\sigma^2_{p1}$	$\sigma^2_{p2}$	$\sigma_{p1,2}$	$\sigma^2_{e1}$	$\sigma^2_{e2}$	$h^2_1$	$h^2_2$	$r_g$
<b>W240<sup>a</sup></b>	6,790	568.610	-----	-----	428.118	-----	0.25	-----	-----
<b>BW</b>	10,944	570.199	13.081	25.845	455.549	9.240	0.25	0.29	0.42
<b>W120</b>	7,641	585.360	224.435	275.071	433.265	177.468	0.26	0.21	0.86
<b>W365</b>	6,311	556.421	1102.376	630.449	436.377	830.718	0.23	0.25	0.93
<b>W550</b>	4,882	572.796	1779.522	697.232	437.485	1322.930	0.24	0.26	0.88
<b>W730</b>	2,340	565.646	2166.589	640.050	432.915	1782.137	0.23	0.18	1.00
<b>SC365</b>	1,082	568.439	3.973	24.919	428.441	3.118	0.25	0.22	0.57
<b>SC550</b>	987	568.705	8.757	32.355	427.644	4.999	0.25	0.43	0.42

N = Number of animals,  $\sigma^2_p$  = phenotypic variance,  $\sigma^2_e$  = environmental variance,

$\sigma_{p1,2}$  = phenotypic covariance,  $h^2$  = heritability,  $r_g$  = genetic correlation,

1 = weight at 240 days, 2 = another traits, <sup>a</sup> - Results of univariate analysis.

#### ACKNOWLEDGEMENTS

This research was supported by Financiadora de Estudos e Projetos - FINEP, Conv. no. 64.92.0196.00.

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