Genetic and Phenotypic Correlation Between Gestation Period and Growth Traits Pre and Post Weaning

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ABSTRACT: The objectives in this study were to estimate genetic and phenotypic correlations among gestation length as calf trait (GLcalf) and growth traits of weight gain pre weaning: birth weight (BW), weight at 120 days (W120) and weight 210 days (W210), and traits growth post weaning: weight at 365 days (W365) and weight at 450 days (W450) in animals Nelore breed participating in a cattle breeding program in Brazil. Estimation of genetic parameters was performed using the Restricted Maximum Likelihood Method (REML) for animal models, using the WOMBAT software. Genetic and phenotypic association between GLcalf and BW were 0.15 and 0.17 respectively, which would bring favorable results for the system creates by reducing the period of gestation. GLcalf already correlations between age and the other were positive and low magnitude (0.03 – 0.10), which does not promote significant changes in the different weights. Therefore the reduction of the gestation length as calf trait can be included as selection criterion for Nelore cattle.
Keywords: correlations genetics, genetic associations, selection in beef cattle

Introduction

The knowledge of the productive and reproductive performance information of animals and breeding techniques may contribute with Brazilian cattle productivity the increasing, and can accurately define the objectives and criteria of selection for traits of economic importance within each production system.

The reproductive traits are one of the factors that limits the productivity increasing as are features that suffer environmental influences, not allowing significant gains by direct selection. However, the productive trait is completely the opposite and therefore it received greater emphasis in animal breeding programs in Brazil.

According to Rocha et al., 2005, the gestation length has positive genetic association with the weight traits, among then the birth weight receives more attention because both evaluated jointly receive a major economic importance within the production system liked to calving ease and neonatal mortality. Therefore, monitoring is done through the knowledge of the magnitude and direction of genetic associations between such features, which con promote significant gains in indirect manner.

Thus, the objective in this study was to estimate genetic and phenotypic correlations among gestation length as calf trait and growth traits of weight gain pre weaning and post weaning traits growth.

Material and Methods

Animals and data file. The present study was conducted using data in animals of Nelore breed that participated in the Nelore Brazil Program. The traits studied were: gestation length was analyzed as calf trait (GLcalf) and growth traits of weight gain pre weaning: birth weight (BW), weight at 120 days (W120) and weight 210 days (W210), and traits growth post weaning: weight at 365 days (W365) and weight at 450 days (W450).

Data editing and contemporary groups. Preliminary analyses of all traits were performed to eliminate inconsistent data. A least square analysis, using the GLM procedure of the SAS computer software (SAS 9.1, SAS Institute, Cary, NC, USA), aided in defining the fixed effects considered in the models.

Assumptions for the fixed-effects model. Residual normality was verified for each trait using Guided Data Analysis – SAS (SAS 9.1, SAS Institute, Cary, NC, USA). The assumptions of variance analysis on each trait were investigated and observations with standardized residuals above 3.5 or below -3.5 standard deviations were excluded.

Statistical analysis. Estimation of genetic parameters was performance using Restricted Maximum Likelihood Method (REML) for multi-trait animal models, using WOMBAT software, described by Meyer (2007). For BW, W120 and W210 the maternal genetic effect and permanent environmental effects for traits pre weaning weight was included in the mixed model, for GLcalf, W365 and W450 the model which included only direct genetic effect. For all traits a linear and quadratic effect of the covariate dam age was considerate.

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Results and Discussion

The heritability found for the traits under study (Table 1) indicated that these would respond to selection and that the proportion of phenotypic variance was sufficient for it to be attributable to the additive effects of the genes, thereby ensuring efficiency in this selection.

The genetic associations between GLcalf with the pre and post weaning weight traits were positive and with low magnitude, where the selection for reducing the gestation length could reduce the weights at different ages. This positive correlation would contribute to reduce birth weight and calving ease consecutively higher and lower facility of calving problems which is in agreement to the results found by Mucari et al. (2011) for Canchin cattle.

However, the genetic and phenotypic correlations evidence in this study decreased with increasing age and low magnitude, which would not reduce the weights of the animals at these ages, affecting the profitability of the production system.

Conclusion

The reduction of the gestation length as calf trait can be included as selection criterion for Nelore cattle because it could promote the reduction of birth weight, without significantly affecting the weights in the upper ages.

Acknowledgments

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Literature Cited

Meyer, K. Wombat (2007). University of New England. Armidale, Australia, 66p.

Mucari, T. B.; Alencar, M. M., Barbosa, P. F. et al. (2011). Rev. Bras. Zoot., 40:1211-1216.

Rocha, J.C. M. C.; Tonhati, H., Alencar, M. M. et al. (2005). Arq. Bras. Med. Vet. Zootec., 57:784-791.

SAS System for Windows®. Version 9.1.2003. SAS Inst., Cary, NC, USA.

Table 1. Estimates of genetic parameters in Nelore cattle

TRAIT	h^2d (std)	h^2m (std)	rg (std) GLcalf	rf (std) GLcalf
GLcalf	0.46 (0.03)	------	------	------
BW	0.34 (0.04)	0.08 (0.01)	0.15 (0.09)	0.17 (0.02)
W120	0.23 (0.01)	0.08 (0.01)	0.10 (0.04)	0.10 (0.01)
W210	0.25 (0.01)	0.08 (0.01)	0.06 (0.05)	0.06 (0.01)
W365	0.44 (0.01)	------	0.07 (0.03)	0.04 (0.01)
W450	0.44 (0.01)	------	0.07 (0.04)	0.03 (0.01)

Std: Standard errors; h^2d: heritability direct; h^2m: heritability maternal; Rg: genetic correlations; Rf: phenotypic correlations; GLcalf: calf trait; BW: birth weight; W120: weight at 120 days; W210: weight 210 days, W365: weight at 365 days; W450: weight at 450 days.