

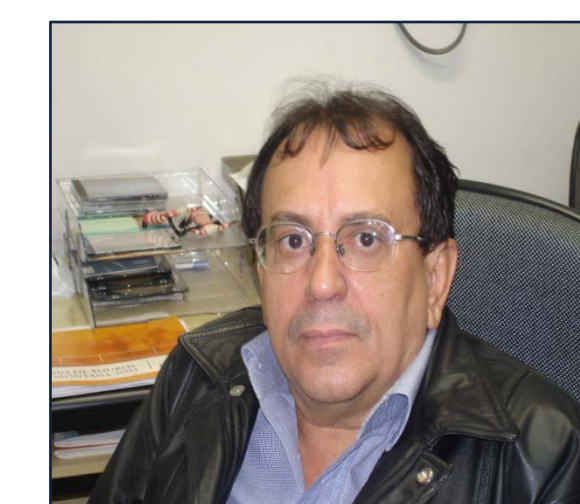


FOUR-TRAIT JOINT ESTIMATION OF VARIANCE COMPONENTS IN NELLORE CATTLE

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Poster Session 1

Objectives

The objective of this research was to estimate (co)variance components and genetic parameters jointly for 4 traits (used in a selection index) in a population of Nellore cattle reared in Brazil, considering management group at weaning as a random effect to increase the size of contemporary groups for post weaning traits.

Conclusions

The inclusion of weaning management group as random effect, in order to increase size of contemporary groups in joint estimation of (co) variance components was effective estimates of (co)variance components were all within reasonable interval, when compared to two-trait estimates.

Introduction

Brazil has the second largest bovine herd in the planet and is just after USA in beef production. The country's herd size is around 190 million heads and the most representative breed is Nellore, that influences around 80% of the Brazilian beef cattle population. In genetic evaluation programs, contemporary group sizes is always a problem, mainly if groups of consecutive ages are concatenated, breaking the original sizes. Besides that, to joint estimate (co)variance components was almost impossible for large datasets, due to memory requirements. The use of latest versions of software for estimation of those components of variance and genetic parameters and the use of the approach of considering weaning management group as random variable, instead of concatenating later ages management groups in the formation of contemporary groups was a very nice opportunity to estimate better parameters to be used in genetic evaluation of Nellore cattle reared in Brazil.

Methods

A. Data description and analyzed traits

Traits analyzed were weaning weight (WW, kg, N = 103,554), post weaning gain (PWG, kg, N = 81,908), scrotum circumference (SC, cm, N = 39,960) and muscle visual score (MUS, N = 72,787). The full animal model had 161,865 animals in A⁻¹.

B. Statistic model

Models of analysis considered, for each trait:

- Age of dam (linear and quadratic)
- Age at measurement (linear)
- Julian date (linear and quadratic)
- Contemporary group

Random effects considered were:

- Additive genetic direct
- Additive genetic maternal (not for MUS)
- Permanent environment (PE, not for MUS)
- Management group at weaning (MGW, not for WW).

C. Genetic analysis

The program used for the estimation was VCE 6.0 (Groeneveld, 2008).

Results

Direct heritability estimates (standard error) were:

- WW: 0.22 (0.006)
- PWG: 0.24 (0.006)
- SC: 0.402 (0.007)
- MUS: 0.236 (0.005)

Maternal heritability estimates were:

- WW: 0.086 (0.003)
- PWG: 0.036 (0.002)
- SC: 0.090 (0.003)

Correlation between direct and maternal genetic effects were low for majority of trait combinations, but around .5 between PWG and maternal WW, and MUS and maternal WW and -0.60 (0.026) between direct and maternal PWG and -0.71 (0.024) between maternal WW and PWG.

Ratios of random effect for MGW over phenotypic variance were 0.14 (0.005) for PWG, 0.04 (0.003) for SC and 0.04 (0.002) for MUS.

Ratios for PE were 0.12 (0.003), as concerned to WW, 0.04 (0.002), for PWG and 0.012 (0.002) for SC.

Genetic correlations between direct effects were all positive and of moderate, but between PWG and MUS, that correlation was 0.70 (0.018).