Linear And Threshold Models For Genetic Evaluation Of Slaughter Conformation At Yearling Age In Nellore Cattle[*]

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Introduction

Several indirect evaluations of early termination and carcass composition traits in beef cattle are proposed in the literature. Among these the slaughter conformation minimizes stress, cost and allows the evaluation of a large number of animals without excessive handling.

In Brazil, beef cattle genetic improvement programs usually utilize linear models for genetic evaluation of animals. However, some important economic traits, such as slaughter conformation, show discrete distribution of data, which violates some assumptions of linear mixed model. Therefore, linear procedures may be considered as not suitable for studying discrete traits (Gianola, 1982; Abdel-Azim and Berger, 1999) and threshold models are suggested to analyze them (Gianola, 1982; Gianola and Foulley, 1983; Gilmour et al., 1985; Hoeschelle and Tier, 1995).

Threshold model have ben used to estimate (co)variance components for discrete distribution traits of economic importance in livestock production. However, these models were not used for slaughter conformation study. The present study was carried out in order to obtain the heritability of slaughter conformation at yearling age using linear and non linear models, as well as to compare the use of such models for genetic evaluation in Nellore cattle.

Material and methods

A total of 8,193 records of slaughter conformation at yearling age (SCY) were used to obtain inferences about heritability and breeding values by linear and threshold models. The environmental systematic effects for SCY consisted of contemporary groups defined by sex, season of birth, year of birth, farm, feeding regime and evaluation date. Visual scores of slaughter conformation (harmonic animals in musculature, fat trim and structure of the carcass) were defined by comparing animals of the same contemporary group. This trait presents six categorical values (1 to 6), being the value 6 designated to the most desirable phenotype.

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For the linear model, the inference of (co)variance component was performed using the program GIBBS2F90 (MISZTAL, 2009). The burn-in was defined by the method of Raftery & Lewis (1992), implemented in the BOA package (Smith, 2007) of the program R (R Development Core Team, 2008). The thinning interval was obtained according to the methodology described by Van Tassel et al. (1998). Posterior mean and the HPD95% interval of heritability were obtained from the posterior distribution of this parameter. For the threshold model, the posterior distributions of parameters of interest was obtained using the program THRGIBBS1F90 (Tsuruta and Misztal, 2009). The burn-in and the thinning interval were defined as described for the linear model.

The linear model used was:

$$y = Xb + Z_1a + Z_2m + e,$$

where y is a the vector of phenotypic records, b is a vector of “fixed“ effects (contemporary group, linear and quadratic effects of age of dam at evaluation, linear effect of age of animal at evaluation), a is a vector of additive genetic effect, m is a vector of additive maternal genetic effect, e is a vector of model residuals. X, Z_1 and Z_2 are incidence matrices. The conditional distribution of y, given the location parameters b, a, m, and the dispersion parameter σ_e^2 can be described as $y \mid b, a, m, \sigma_e^2 \sim N(Xb + Z_1a + Z_2m, I\sigma_e^2)$. Scaled inverted chi-square distribution was assumed as a prior distribution of additive genetic, additive maternal and residual variances. A “non-informative“ distribuition was assumed as a prior distribution of “fixed“ effects. The assumed prior distribution of additive genetic and additive maternal genetic effects, conditionally on the dispersion parameters for each effect, were $p(a \mid \sigma_a^2) \sim N(0, A\sigma_a^2)$ and $p(m \mid \sigma_m^2) \sim N(0, A\sigma_m^2)$. Threshold model assumes that observed variables are determined by a underlying continuous distribution and a set of fixed thresholds, $t_1 < t_2 \ldots < t_{m-1}$, with $t_0 = -\infty$ and $t_m = +\infty$, where m is the number of categories. To make the model identifiable, the first threshold was imposed to be 0 and the second was imposed to be 1 (Van Tassel et al., 1998). Uniform prior distribution was assumed for the other thresholds.

Additionally, Spearman correlation coefficient between posterior means of breeding values from both models was estimated, and proportion of animals in common among the top 20% breeding values was obtained.

Results and discussion

Posterior distributions of heritability for slaughter conformation at yearling age obtained from linear and threshold models are presented in figures 1 and 2.

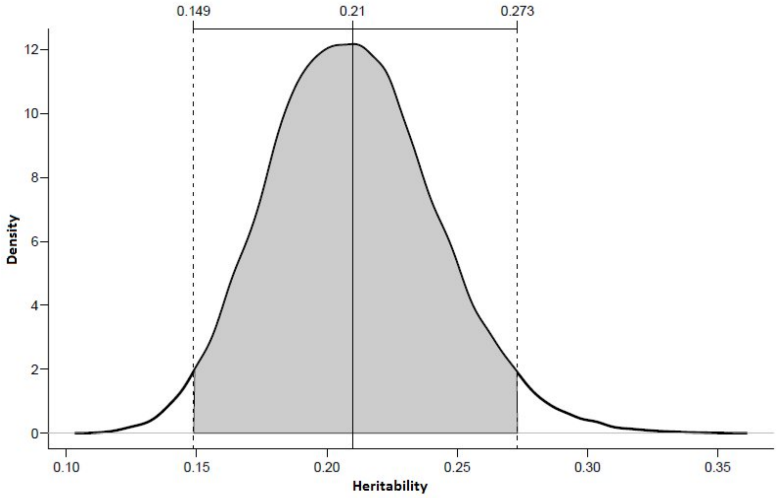

Figure 1: Marginal posterior distribution, mean and HPD 95% interval of heritability for slaughter conformation at yearling age obtained from linear model.

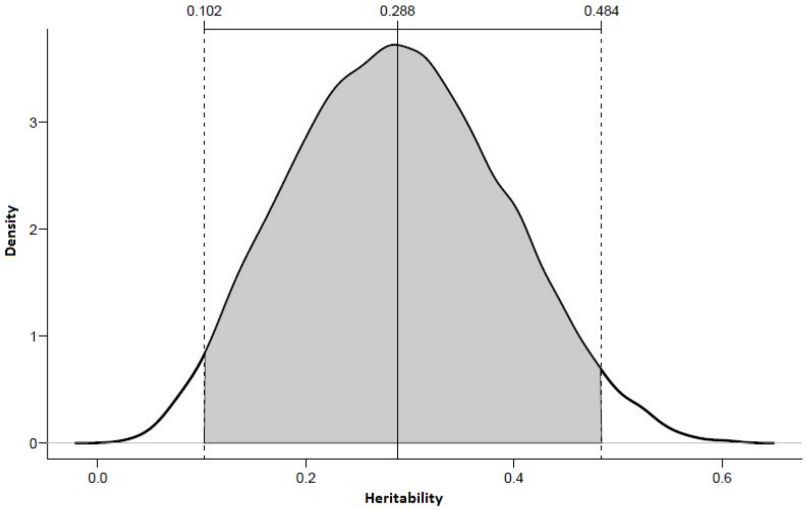

Figure 2: Marginal posterior distribution, mean and HPD 95% interval of heritability for slaughter conformation at yearling age obtained from threshold model.

The posterior mean of heritability obtained using threshold model (0.28) was higher than the estimated by the linear model (0.21). However, the HPD 95% intervals for this parameter obtained from both models were similar.

Spearman correlation between posterior means of breeding values from linear and threshold models was 0.99. This result suggests that both models can be used for SCY genetic evaluation of Nellore cattle. Among the 20% top posterior means of breeding values for both models, a high percentage of animals in common (95%) was observed.

Conclusion

No considerable changes between inferences for heritability of slaughter conformation at yearling age obtained from linear and threshold models were observed.

The choice between linear and threshold models had no influence on the ranking of the posterior means of breeding values for the studied trait. In spite of threshold model theoretical adequacy, the linear model analysis should be prioritized due to its lower operational and time cost.

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