BAYESIAN ANALYSES OF HETEROGENEOUS VARIANCES AMONG GENERATIONS OF BRAZILIAN CANCHIM BEEF CALVES

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INTRODUCTION

In the genetic evaluations, the models usually assume homogeneous variance through subclasses of identified factors. However, several studies have reported heterogeneous genetic and residual variances in analyses of many animal production traits (Weigel and Gianola, 1993). Different regions, birth years, feeding systems, genetic variability within herds and production levels can have heterogeneous variance among their subclasses (Ibáñez *et al.*, 1996; De Veer and Van Vleck, 1987).

Synthetic breeds are usually formed from selection of crossbred animals. Crossbred populations in general have relatively high genetic variability. However, selection changes gene frequencies and consequently it tends to reduce the genetic variability. Furthermore, the herds have had their environment modified over time by improvement in feeding and management. Therefore, data from different generations of a single population can have heterogeneous variances.

Ignoring heterogeneity of variance can reduce the efficiency of genetic evaluation procedures and consequently response to selection (Hill, 1984). Thus, the aim of this study was to evaluate the occurrence of heterogeneous variance of yearling live weight among the first six generations of Brazilian Canchim breed.

MATERIAL AND METHODS

Canchim breed. The synthetic Canchim bred was initially formed in 40's from 65 bulls (53 Charolais, 8 Indubrasil and 4 Guzera) and 145 cows (127 Indubrasil, 9 Guzera and 9 Nelore). Officially, the first generation of Canchim calves (5/8 Charolais and 3/8 zebu) born in 1953 and mating have been made only among these animals and their offspring. Inbreeding mating has been avoided. In the last 20 years, the selection has been based on yearling live weights (Alencar et al., 1981).

Data file. The study analyzed live weight at 365 days of age of 6,496 Canchim beef calves from the herd of São Carlos Unity of EMBRAPA (Brazilian Agricultural Research Institution). After the first generation, we defined the generation for an animal by the integer number resulted from adding 1 to the average of its parents' generation. Thus, an animal that has the father from the generation 1 and the mother from the generation 2 is classified into generation 3. With this definition we split the animals into six generations with 1347, 1070, 1645, 1355, 756 and 323 animals, successively from the first to the sixth generation.

Variance components estimation. The Bayesian estimation of (co)variance components employed the MTGSAM (Multiple Trait Gibbs Sampling in Animal Models) software (Van Tassel and Van Vleck, 1996). The heterogeneous variance was considered in the analyses by

using a multi-trait model that defined that each trait is composed by the observations in a specific generation. The single-trait (for homogeneous variance) and multi-trait animal models included the additive genetic effect and the fixed effects of sex, month and year at birth and calving age as a linear and quadratic covariate. Flat prior distributions was assumed for the fixed effects, normal distribution was assumed for the additive genetic effect, Inverted Wishart distribution was assumed for genetic (co)variance and inverted chi-square distribution for residual variance. The Gibbs sampler was run 830,000 rounds with the first 30,000 rounds discarded for burn-in and a thinning interval equal to 1,000 rounds. Thus, 800 samples were taken for each parameter.

Heterogeneous variance behavior. In each valid sample of the Gibbs chain, the generalized least square method was employed to estimate a quadratic regression equation ($y = b_0 + b_1X + b_2X^2$) for the genetic and residual variance (y) as function of the generation (X). The shape (the sign of b_1 and b_2) of the quadratic curve of each sample was compared to the average quadratic curve and the number of coincidences was computed.

Selection evaluation. A consequence of ignoring heterogeneity of variance was verified by computing the number of common animals in the selected groups when 10% of males and 30% of females were selected by the breeding values predicted with the single-trait model and the breeding values for the sixth generation predicted with the multi-trait model.

RESULTS AND DISCUSSION

The analysis with the single-trait model estimated the posterior mean estimate equal to 454.52, 680.36 and 0.40 respectively for the genetic variance, residual variance and heritability. These values are similar to those estimated by Freitas and Vencovsky (1993) and are smaller than the values estimated by Mascioli *et al*. (1996).

Table 1 shows the posterior mean estimate for genetic and residual variances, heritability and genetic correlations in each generation obtained with the multi-trait model.

The genetic variances decrease from the first to the fifth generation and raise up in the sixth generation. This characterizes a quadratic behavior of the heteroskedasticity over generations. Similar behavior was found in 78.9% of the samples. The reduction of the genetic variation in the first generations can be associated with the loss of genetic variability due to selection. In the other hand, the increase in from the fifth to the sixth generation can be caused by the improvement of production system and data collecting process. This may allowed identifying more precisely the genetic differences between animals. Furthermore, an improved environment can allow that some genes have their expression magnified.

Residual variance estimates in the first three generations were stable (homogeneous), increased from the third to the fifth and decreased in the sixth generation. Similar behavior was found in 75% of the samples. Pasture degradation in the first generations and possible technologic improvement in the last generations can be the explanation for this residual variance behavior.

The heritability estimates in all generation were higher than the value estimated by single-trait model. In the first three generations the values were stable, decreased in the fourth and fifth generations and raised up in the sixth generation, when it reached .59.

The genetic correlation estimates decrease with the increase of the distance between generations. This indicates that observations from different generations should be differently weighted.

Table 1 – Posterior mean estimates for genetic and residual variance, heritability and genetic correlation for body weight at 365 days of age for the 6 generations

Generation	1	2	3	4	5	6
			Genetic variance			
	628.9	555.8	537.0	472.4	454.5	593.9
			Residual variance			
	536.8	534.8	512.9	605.1	642.9	407.1
		Heritability (diagonal) and genetic correlation (off-diagonal)				
1	**0.54**					
2	0.67	**0.51**				
3	0.50	0.61	**0.51**			
4	0.50	0.50	0.69	**0.44**		
5	0.44	0.49	0.52	0.57	**0.41**	
6	0.33	0.37	0.45	0.52	0.52	**0.59**

Only 62.5% of animals in the selected grouped formed by the 10% of the males with the higher breeding values predicted by the single-trait model were the same animals in the selected group by the multi-trait model. When we selected 30% of the females, only 64% of the selected animals were common in the groups formed by both models.

CONCLUSION

The results found in this study indicate that genetic evaluation of Brazilian Canchim breed should consider heterogeneous variances over generations.

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