Sire × contemporary group interaction to model genotype by environment interaction in genetic evaluations

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Objective

1) to evaluate the importance of genotype × production environment interaction for the genetic evaluation of weaning weight (WW) in a population of composite beef cattle, and 2) to investigate the importance of sire × contemporary group interaction (S×CG) to model genotype by environment interaction (G×E) in routine genetic evaluations.

Introduction

The production environment of beef cattle in Brazil is characterized by wide diversity and G×E should therefore be a matter of concern to breeders and producers. The most common manifestations of G×E are sire × herd, sire × season of birth, and sire × contemporary group interactions. However, beef cattle breeding programs have generally neglected the possible effects of sire × environment interaction.

Material and methods

Records of WW from 140,247 animals (purebred, crossbred, and composite) born between 1995 and 2008 on 47 farms located in the Brazilian states of Goiás, Minas Gerais, Mato Grosso do Sul, Mato Grosso, Pará, Rio Grande do Sul, and São Paulo were used. These animals participate in the Montana Tropical Composite Breeding Program, from partners of the CFM-Leachman Pecuária Ltda.. The pedigree file included 277,598 animals.

The standard model for WW included the fixed effects of contemporary group (farm, year of birth, management group and sex), and covariates age at weaning (linear), age of dam at calving (linear and quadratic), individual and maternal breed composition and individual and maternal heterozygosis (linear). The random effects of direct additive genetic, maternal genetic and maternal permanent environmental were also included.

Analyses were performed with different definitions of production environments based on the generalized least squares solutions of contemporary group effects. Thus, records of animals in a favorable environment were assigned to either trait 1, in an intermediate environment to trait 2 or in an unfavorable environment to trait 3. In summary, six analyses were preformed [three definitions of production environments (single, two or three environments) - S×CG included or omitted from the model].

The (co)variance components were estimated using Bayesian approach in single-, bi- or three- trait animal models. The models were compared by the accuracy of breeding values, error of prediction, squared bias, residual variance and deviance information criterion (DIC).

Results and discussion

The posterior mean of genetic correlation between direct effects was 0.76 ± 0.05, 0.63 ± 0.08, and 0.83 ± 0.03 between environments 1 and 2, 1 and 3, and 2 and 3, respectively, a fact that may lead to changes in the ranking of sires across environments. When S×CG was included in two- or three-trait analyses, the mean of direct genetic correlations were 0.93 ± 0.02, 0.93 ± 0.03, and 0.98 ± 0.01 between environments 1 and 2, 1 and 3, and 2 and 3, respectively, suggesting that there was no evidence of a genotype × production environment interaction. The model including S×CG contributed to prevent overestimation of the accuracy of breeding values of sires. The mean changes in accuracy for all sires were -5% and -4% for direct and maternal EBV, respectively. Therefore, in the present population, accuracy estimates might be overestimated when the effect of S×CG is not included in the genetic evaluation model of WW. Furthermore, the model including S×CG provided a lower error of prediction for both direct (-18.1%) and maternal breeding values (-19%), lower squared bias (-4.5%), residual variance (-3.5%) and DIC (-0.3%) than the model omitting S×CG.

Conclusions

The genotype × production environment interaction should not be neglected in the genetic evaluation of WW in the present population of beef cattle. The inclusion of S×CG in the model is a feasible and plausible alternative to model the effects of G×E in genetic evaluations.
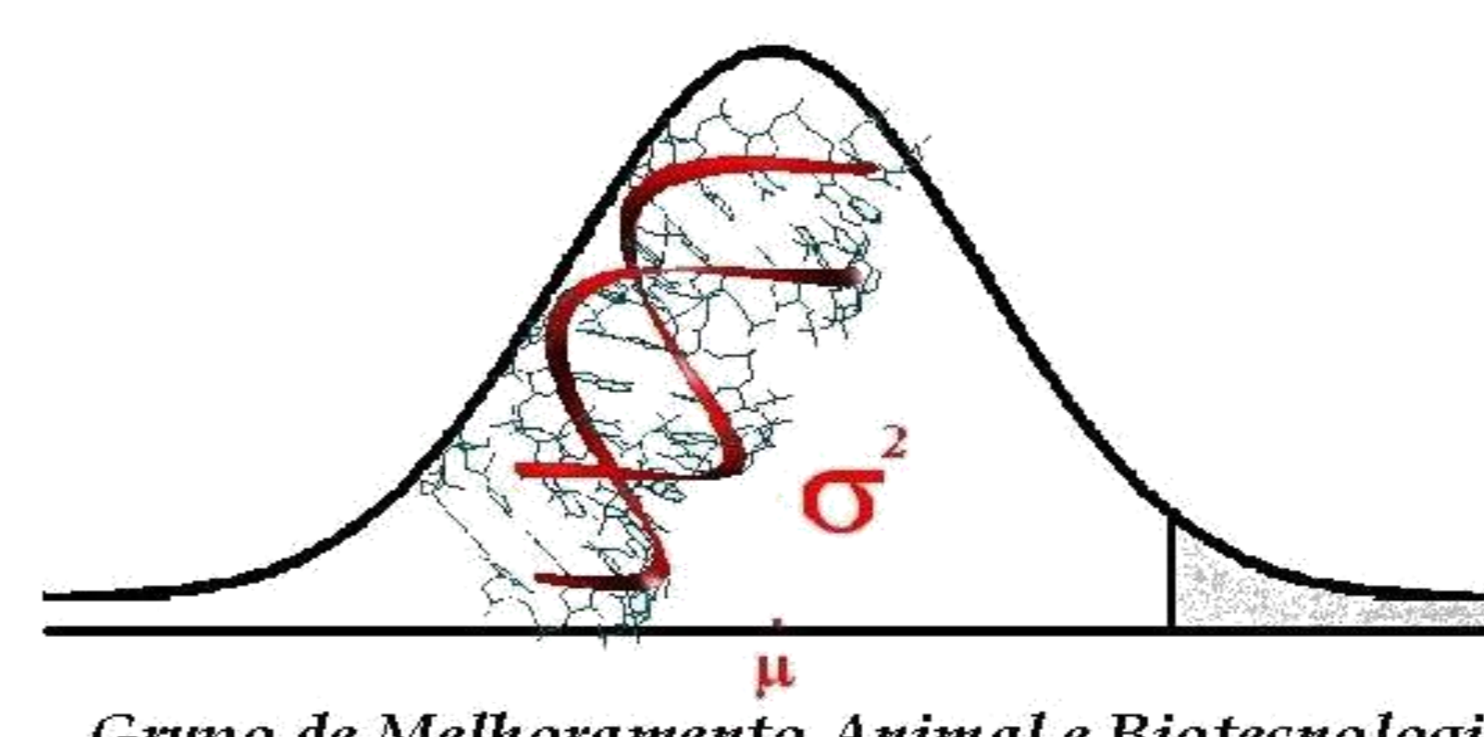
Acknowledgements

Montana Sires

GMA
Grupo de Melhoramento Animal de Mato Grosso

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Grupo de Melhoramento Animal e Biotecnologia

Montana Dams