

Genotype X Environment Interaction For Growth And Reproduction Traits Of Composite Beef Cattle In Brazil

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Introduction

Brazil has a great diversity of beef cattle production systems due to climatic, geographic, cultural and economic factors (Eler, J.P., Ferraz, J.B.S., Golden, B.L. *et al.* (2000); Toral, F.L.B., Silva, L.O.C., Martins, E.N. *et al.* (2004); Lopes, J.S., Rorato, P.R.N., Weber, T. *et al.* (2008)). The evaluation of genotype x environment interaction (GxE) is, therefore, relevant to breeding programs, since the best animals in a given environment, may not have the offspring of better performance when it is raised under a different environment than that their parents were selected. According to Alencar, M.M., Mascioli, A.S. and Freitas, A.R. (2005), this interaction may also cause changes in genetic, phenotypic and environmental variations and therefore result in significant changes in the genetic and phenotypic parameters estimation, implying possible changes in the selection criteria, according to the environment. Thus, the identification of these interactions should contribute to the selection efficiency in cattle. To verify the presence of GxE, Falconer (1952) proposed that the same trait in different environments could be interpreted as different traits, since the genes that control it in a given environment may be different, at least in part, from those who control it in another environment. The aim of this study was to characterize and define homogeneous environments of production in composite beef cattle in Brazil, in relation to climatic and geographical variables and verify the presence of GxE for post-weaning gain (PWG), muscle score (MUS) and scrotal circumference (SC) in these environments.

Material and methods

The dataset used in this study were from 30 farms located in the Brazilian states of Mato Grosso do Sul and Sao Paulo, participants of the Montana Tropical® composite breeding program, belonging to CFM-Leachman Cattle Ltda. It was used, 54,529, 53,611, 16,698 records, respectively, of PWD, MUS and SC of animals born between 1995 and 2008, progenies of 505 bulls and 37,690 cows on 2,164, 2,233, 2,762 contemporary groups. The

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complete pedigree included 430,005 animals. All observations were previously adjusted for maternal and individual breed composition and maternal heterozygosity. Information that exceeded 3 standard deviations above or below the average of the trait and contemporary groups with less than 10 animals were eliminated. The historical climate information (minimum average temperature, maximum average and average) and geographical (latitude, longitude and altitude) were obtained from the Agritempo (2009) Brazilian weather institute, but when the information was unavailable it was calculated as proposed by Neto et al. (2002). Initial analyses were based on hierarchical clustering centroid method and nonhierarchical k-means cluster analysis using the SAS program (2003). For both methods, the similarity coefficient used to evaluate the climatic and geographic similarity between the regions was the Euclidean distance. To set the number of groups and evaluate the quality of the group, it was used the root-mean-square standard deviation (RMSSTD) of all the variables that formed the group and R^2 . After the formation of groups were identified bulls with progeny in all groups to ensure connectivity between them. The genetic parameter estimation was analyzed with three-trait animal model using the program VCE-6 (Kovac and Groeneveld, 2003). The same trait was considered separately in relation to other groups of farms. The mathematical models included fixed effects of contemporary group (herd, year of birth, management group and sex) and the animal random effect, for PWG also were included ages at weaning and yearling (covariates with linear effect) and maternal effect, while for MUS and SC were included the covariates dam age (linear and quadratic), Julian date of birth (linear, quadratic and cubic) and age at measurement (linear).

Results and discussion

Three farm groups were formed (Figure 1), RMSSTD (0.51) and R^2 (0.76).

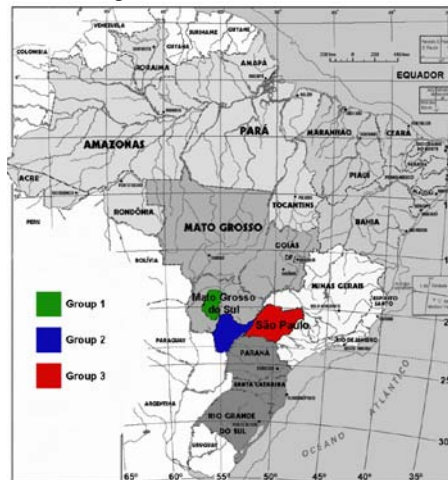


Figure 1: Farm groups distribution

The first group was characterized by the lower latitudes, altitudes and higher temperatures (Table 1). The second group was characterized by lower longitude, higher altitude and medians temperatures, while the third group had the most noticeable characteristics as higher

latitude, median longitude and altitude, and lower temperatures. It was identified 104 bulls, sires of 46,338 animals in the three groups.

Table 1: Climate and geographical average of the respectively formed groups

Cluster	Latitude	Longitude	Altitude	Mín. temp.	Max. temp.	Average temp.
1	20.46	55.81	188	19.19	30.76	23.57
2	20.88	49.95	456.87	16.82	30.38	23.62
3	21.95	54.37	449.85	17.26	28.85	21.99

Genetic parameters for the studied traits in the three groups are presented in Table 2. Except for estimates of PWG direct heritability in groups 1 and 2, the other estimates were similar to those obtained by Gressler, S.L., Bergmann, J.A.G., Pereira, C.S. *et al.* (2000), Van Melis, M.H., Eler, J.P., Silva, J.A. II V. *et al.* (2003) and Mourão (2005).

Table 2: Genetic parameter estimation of post-weaning gain (PWG), muscle score (MUS) and scrotal circumference (SC) of the respectively groups

Traits	h^2_d (s.e.)	h^2_m (s.e.)	h^2_t	Groups	r_g (s.e.)
PWG 1	0.06(0.01)	0.01(0.00)	0.04	1,2	0.72(0.09)
PWG 2	0.09(0.01)	0.03(0.00)	0.09	1,3	0.51(0.12)
PWG 3	0.18(0.01)	0.07(0.01)	0.12	2,3	0.62(0.07)
MUS 1	0.12(0.01)	-	-	1,2	0.81(0.05)
MUS 2	0.18(0.00)	-	-	1,3	0.99(0.01)
MUS 3	0.15(0.01)	-	-	2,3	0.85(0.05)
SC 1	0.21(0.03)	-	-	1,2	0.93(0.06)
SC 2	0.25(0.02)	-	-	1,3	0.91(0.05)
SC 3	0.32(0.02)	-	-	2,3	0.79(0.09)

h^2_d = direct heritability; h^2_m = maternal heritability; h^2_t = total heritability; r_g = genetic correlation

The coefficients of heritability for PWG and SC were higher for group 3, consisting of municipalities of the Sao Paulo state and characterized by a milder climate. For MUS, the highest heritability estimated was obtained for group 2, followed by group 3, which are in nearby regions and with similar climate. The lowest estimates of heritability were obtained for group 1, which is characterized by warmer weather and diversity of farming conditions. The results suggested that the response to selection for the studied traits is greater for environments with a milder climate. According to Falconer and Mackay (1996), the heritability is a property of the herd and the environment that the animal is subjected; while the environmental variance is dependent on the production and management - higher environmental variation reduces the heritability, higher environmental uniformity increase the heritability. According to DeNise, R.S.K., Torabi, M., Ray, D.E. *et al.* (1988), these differences between heritability coefficients may be due to the action of different sets of genes on the traits. These differences also reflect the possible heterogeneity of variances among environments.

The estimations of genetic correlations were high for MUS and SC and inferior than 0.80 for PWG. According to Robertson (1959), genetic correlation values below to 0.80 are evidence of the existence of GxE. In the present study, the GxE was most evident for PWG between groups 1 and 3, which are located in regions that were more distinct from each other with respect to geographical and climatic variables.

Conclusion

Multivariate clustering procedures are useful to characterize homogeneous environments of production. It was found GxE only for the PWG between the three farm groups, showing that the genetic evaluation of animals, in this case, should be made regionally or GxE interaction be included in the mathematical model.

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