

Influences of environmental descriptor for detect genotype by environmental interaction in Cuban Zebu population.

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ABSTRACT: Two different approaches: a character state model (**CSM**), and a reaction norm model (**RNM**) were tested in Cuban Zebu sires' progeny weight records. CSM considered the final weight in 2 environmental groups as different traits, and Spearman correlation between breeding values in both environments were tested. RNM considered a sire model with contemporary group as a fixed effect and the random regression of sire into the contemporary group averages standardized as environmental descriptor. Heritability estimates varied across the environmental groups in different ways depending on the model, and the order of fit of Legendre Polynomial. The highest heritability estimates were obtained by RNM model with 18 classes and third degree of Legendre polynomial ($h^2=0.26\pm 0.04$) and genotype-environmental interaction (GEI) was significant for CSM and RNM3, since for all other analyzes, r_g was close to 1. These results suggest that magnitude of GEI will vary depending on the statistical model used.

Keywords: Zebu.; GEI

Introduction

During the last few decades, Cuban Zebu's genetic improvement program has not favored phenotypic plasticity due to the standardized characteristic of the performance test in males for weaning weight under grazing. However, it's expected to find differences in progeny performance between different production levels because of changes in availability of Cuban's pastures between the dry and rainy seasons as well as different soils characteristics according to the region. Genetic-environmental interaction (GEI) can be measured by genetic correlation (r_g) between the same traits measured in two different environments and artificial insemination offers the possibility of comparing the performance of the descendants of a same bull under different environmental conditions. In past years, many papers had analyzed the random regression model with Legendre polynomials in order to evaluate environmental sensitivity, related to variations in slope coefficient of the reaction norm as an indication of the importance of genotype-environmental interaction (Kolmodin 2003; Fikse et al. 2003; Cardoso et al. 2008, Corrêa et al. 2009; Pegolo et al. 2009). Taking into account that in selection program of the best Cuban Zebu bulls, possible genotype-environment interaction is not considered, this paper aimed at evaluating the response of the progeny of Cuban Zebu sires according to the final live weight of the test using different environmental groups.

Materials and Methods

Two different approaches: a character state model (**CSM**), and a reaction norm model (**RNM**) were tested in Cuban Zebu sires' progeny weight records. Male final live weight records from performance test of 10 867 progeny were used. Animals were descendants of 223 Cuban Zebu sires, born between 1981 and 2009, in 6 cattle breeding enterprises all over the country. For both models, sires with less than 10 descendants and contemporary groups with less than five individuals were discarded. Environmental descriptor was created from the average weight gain value in test of each contemporary group. These mean values were standardized to a normal distribution, to determine the deviations of each contemporary group regarding the mean gain of the population ($491.8 \text{ g/d} \pm 126.76$). The obtained standardized value (from -2.19 to 2.35) was multiplied by 5 and only the integer part was used in order to work with whole numbers.

CSM considered the final weight in extreme environmental groups as different traits. The environmental groups were defined as: low with extreme negative values (gradient from -8 to -3), medium (gradient from -1 to 2) and high (gradient from 3 to 9) and information was divided in two data sets, since the medium environmental group was discarded (385 observations) to contrast only the extremes. Two single trait animal models were analyzed (**CSM**high and **CSM**low), according to environmental group (high and low) and Spearman correlation between breeding values concerning to the 203 sires common to both environments were tested. Single trait animal model considered contemporary group as a fixed effect (herd-year trimester of birth), the age at the end of the test, as a quadratic co-variable and the random effect of animals.

RNM take into account all requirements as for the CSM, but considered pedigree for a sire reaction norm model with a contemporary group as a fixed effect (herd-year trimester of birth), the age at the end of the test, as a quadratic co-variable and the random regression of the sires' progeny final weight records, into different combinations of classes and Legendre polynomial orders for the random regression.

Model **RNM**3, considered just 3 environmental classes and linear Legendre polynomial. Other group of models considered 8 classes and linear, quadratic y cubic Legendre polynomials (**RNM**8L1, **RNM**8L2 y **RNM**8L3), while a third group comprised 18 classes and the 3 types of Legendre polynomials (**RNM**18L1, **RNM**18L2 and **RNM**18L3).

Heritabilities, (co) variances and breeding values were obtained from the Wombat program (Meyer 2006).

Results and Discussion

According to the CSM, heritability in both environmental groups was moderate to low and slightly higher in the best environment (table 1). Espinoza-Villavicencio et al. (2008) found for this trait in Cuban Zebu, heritability of 0.19 using a single trait model. However, higher values were found by Menéndez-Buxadera et al. (2006) for live weight at different ages in the Cuban Zebu, using a multi-trait model (0.21 – 0.34), but in those cases, authors analyzed data belonging to only one Cuban enterprise.

Table 1. Heritability estimates ($h^2 \pm SE$, represented in the diagonal), Spearman correlation (above the diagonal) for final live weight in the Cuban Zebu in two environmental groups (EG) considering CSMhigh and CSMlow models.

EG	High	Low
High	0.22 ± 0.04	0.39
Low		0.15 ± 0.03

Spearman correlations between sires breeding values evaluated in both environmental groups were low. This suggests the presence of genotype-environment interaction and a change in the magnitude of the differences in the genetic merit of sires. Breeding values of the best 5% of sires in high environment are exposed in figure 1, showing a re-ranking of sires, when they are evaluated in low environment. Even when we considered environmental conditions as high and low, it's important to spell out the fact that Cuban Zebu performance test in males for weaning weight take place under natural grazing, therefore it is a harsh environment.

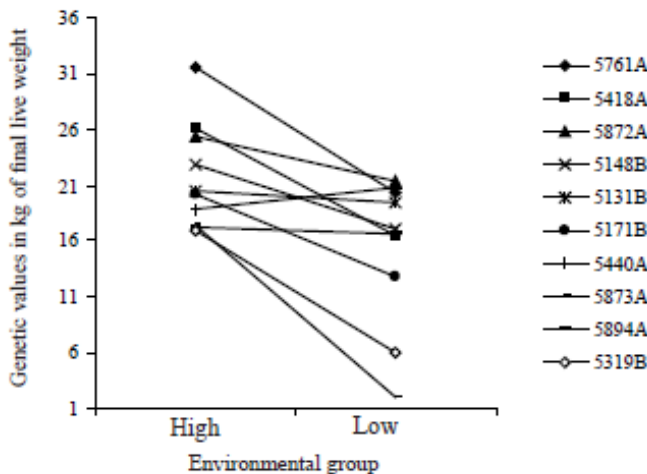


Figure 1. Breeding values of the best 5% of the sires in high environment according to CSM approach.

RNM Approach. Estimates of heritability by Model RNM3 are shown in table 2. Similar as for CSM, higher values were found in the best environmental group, and significant GEI was obtained between extreme environments.

Table 2. Heritability estimates ($h^2 \pm SE$, represented in the diagonal), genetic correlation (above the diagonal) and residual correlation (below the diagonal) for final live weight in the Cuban Zebu according to RNM3 model.

EG	Low	Med	High
Low	0.12 ± 0.04	0.86 ± 0.09	0.66 ± 0.23
Med	0.03 ± 0.00	0.15 ± 0.03	0.94 ± 0.04
High	0.03 ± 0.01	0.04 ± 0.01	0.26 ± 0.07

Increasing the number of environmental classes (8 and 18) revealed heritability estimates across the environmental gradient but no significant GEI, due to genetic correlations close to 1. Figure 2 illustrates heritability estimates for. RNM18L1, RNM18L2 and RNM18L3 models, and were similar to those obtained by models with 8 classes of environment (RNM8L1, RNM8L3 and RNM8L2). In cases of third degree polynomials, estimates were bigger, but extremes values were biased due to a few numbers of observations. Increasing of heritability estimates in better environments is consistent with results obtained by Kolmodin et al., 2002 & Fikse et al., 2003 with random regression models and linear Legendre polynomials. Our results for the second and third degree Legendre polynomials are contrary of those of Pegolo et al. 2009 in Brazilian Nellore cattle, with the higher heritability estimates in both extremes gradients, but they also find that the way of define the environmental descriptor interfered with estimation of genetic parameters of population.

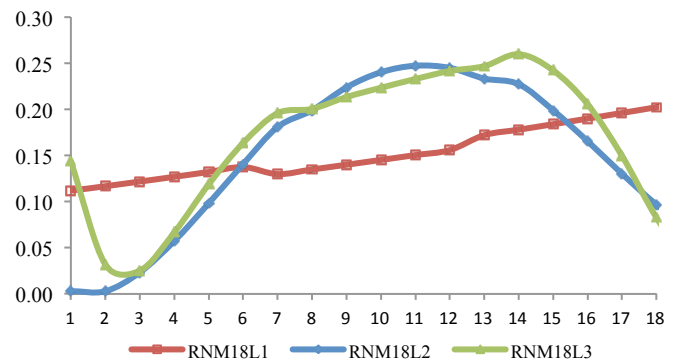


Figure 2. Heritability estimates for final live weight in Cuban Zebu according to RNM approach.

Table 3 illustrate the goodness of fit for all models considers in this study and RNM approach revealed the better adjustment and confirm the linear polynomial alternative as the better choice considering the easier biological interpretation.

Table 3. Number of parameters and goodness of fit criterion for the analyzed models (Logarithm of maximum likelihood, Akaike information criteria and bayesian information criteria).

Model	No. Parm	Max log L	-1/2 AIC & AICC	-1/2 BIC
CSMhigh	2	-19032	-19034	-19040
CSMlow	2	-19880	-19882	-19888
RNM3	4	-38473	-38477	-38491
RNM8L1	4	-40387	-40391	-40406
RNM8L2	7	-40382	-40388	-40414
RNM8L3	11	-40381	-40392	-40431
RNM18L1	6	-40384	-40390	-40412
RNM18L2	9	-40377	-40386	-40418
RNM18L3	13	-40376	-40389	-40436

Conclusions

The magnitude of Genotype-Environment Interaction and re-ranking of sires changes considerably depending on the model that is being used, and the way of define the environmental descriptor. In the national genetic improvement plan of Cuban Zebu, it is recommended to use RNM with 3 classes of environments, because it detects GEI between extremes environments, and make easier the model, not differing so much in goodness of fit criterion with those that enhance the number of classes.

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