Genotype-Environment Interaction of Santa Gertrudis Cattle in Cuba

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ABSTRACT

Background: The existence of genotype-environment interaction (GEI) implies the occurrence of a change of merit order under different environmental conditions, which may be important from the economic and practical standpoints. The aim of this research was to determine the possible existence of GEI in Santa Gertrudis cattle, in Cuba.
Methods: The weights of 18-month old males and females were adjusted to 540 days of age (AW). The animals belonged to three cattle raising companies, with 4 529 animals born between 1981 and 2016 from 161 studs. The data were narrowed down, removing the studs with less than 10 descendants and same-age group (SA), with less than three animals. Two data sets were made: animals with a high final adjusted weight (HAW), and low adjusted weight (LAW), which were above and under the mean, respectively. A single-character animal model was used, considering SA (herd-year-season) and sex as fixed effects; animal and residue were deemed as random effects. A two-trait model included the same effects: HAW and LAW, as two independent traits. Regarding the studs represented in the two environments, the Pearson and Spearman correlations were estimated among their genetic values.
Results: The single-trait heredities (h2) were, 0.37 ± 0.09, and 0.14 ± 0.04, and 0.22 ± 0.09, and 0.11 ± 0.04, in the two-trait model for PAA and PAB, respectively. The genetic correlation was 0.82, but the Pearson and Spearman correlations were, 0.04 and 0.18, which indicated a variation in stud merit order and GEI.
Conclusions: Heredities for the AW were moderate, and higher under better conditions, regardless of the model. This methodology demonstrated that under contrasting environments there is evidence of GEI upon changes in stud merit order.

Key words: *genetic parameters, weight adjusted to 540 days*

INTRODUCTION

Genotype-environment interaction (GEI) is one of the complications of animal selection processes, with significant implications. The existence of genotype-environment interaction (GEI) implies the occurrence of a change of merit order under different environmental conditions, which may be important from the economic and practical standpoints. Menéndez-Buxadera and Mandonnet (2006) provided evidence of that in dairy cattle in different countries. Suárez, Zubizarreta, and Pérez (2009) found that GEI in dairy Cuban Siboney cattle, they considered two handling levels for the calving interval, and more recently, Rodríguez and Guerra (2013) reported GEI in Cuban Zebu cattle. Likewise, de Souza *et al.* (2018) found GEI in Nellore cattle, in three regions of Brazil.

Accordingly, the aim of this paper was to evaluate the existence of GEI in Santa Gertrudis Cattle in Cuba, by estimating the genetic patterns evaluated in performance at grazing, considering two levels of production.

MATERIALS AND METHODS

Information was gathered from 4 529 animals (male and female), including 3 133 descendants from 161 studs born between 1981 and 2016 in three breeding companies. At 18 months, their weights were adjusted to 540 days.

The animals included in performance trials had been weaned between 6 and 7 months, and chosen for the trial in grazing conditions (*Cynodon nlemfuensis Panicum máximum*), with the addition of mineral

salts *ad libitum* for approximately 12 months. The animals belonged to these companies: Turiguanó, Camilo Cienfuegos, and Vallina.

The information was split into two data sets: above the mean for the trait studied, and below the mean, whose weights were adjusted high to 540 days (HAW), and adjusted low to 540 days (LAW). These were considered two different traits to contrast the extreme values only. A similar procedure had been used by Rodríguez and Guerra (2013) in Zebu, but they just considered the gains. The database was narrowed down by removing the studs with less than 10 descendants and same-age group, with less than three animals. Table 1 shows a description of each data subset containing the essential information.

Table 1. Genetic composition for the two environments

Environment	n	No. SA	No. of male parents	No. of female parents
High	1 489	134	132	1 258
Low	2 002	144	161	1 664

SA= same age groups

Weight was adjusted at 18 months of age (540 days), based on the formula below:

$$PA18 = \left(\frac{P18 - PA}{IPA - P18}\right) X\ 175 + PA$$

Where:

YW=weight recorded at 1 year

W18=weight recorded at 18 months

YWI-W18=day interval since the date in which weight was recorded, until weight was recorded at 18 months.

A single-trait model was used for each of the two traits (environments), which considered the fixed effects of the same-age group (herd-year-birth season, as a four-month period), sex, and the random direct effects on the animal, and residues. The matrix notation was,

y = Xb + Za + e

Where: y= vector of adjusted weight records

X and Z= matrixes of incidence

b: vector of fixed effects (levels of same-age groups and sex)

a= vector of random effects on the animal

e= residue vector

Later, a multitrait model was used, including HAW and LAW.

Trait 1 $y_1 = X_1 b_1 + Z_1 a_1 + e_1$

Trait 2 $y_2 = X_2 b_2 + Z_2 a_2 + e_2$

The matrix notation was,

$$\begin{bmatrix} y_1 \\ y_2 \end{bmatrix} = \begin{bmatrix} X_1 & O \\ O & X_2 \end{bmatrix} \begin{bmatrix} b_1 \\ b_2 \end{bmatrix} + \begin{bmatrix} Z_1 & O \\ O & Z_2 \end{bmatrix} \begin{bmatrix} a_1 \\ a_2 \end{bmatrix} + \begin{bmatrix} e_1 \\ e_2 \end{bmatrix}$$

Where:

y_i = observation vector for the ith trait.

b_i = fixed effects vector for the ith trait.

a_i = random effects vector on the animal for the ith trait.

e_i = random residual effects vector for the ith trait.

X_i y Z_i are the matrix design relating the data to the fixed effects and the animals, respectively.

In all cases, the variance and covariance components were estimated, along with genetic parameters, heredity (h^2), and genetic correlations for the multitrait. The variance and covariance components, genetic parameters, and genetic values were estimated using the restricted maximum likelihood and the free algorithm of derivatives through MTDFREML software (Boldman, *et al.* 1995).

The Pearson and Spearman correlations were calculated for the genetic values of the parents evaluated in either environment as a possible signal of the existence of genotype-environment interaction, using the PROC CORR, SAS 9.4 (2013) procedure.

RESULTS AND DISCUSSION

Table 2 shows the general statgraphs of HAW and LAW. Greater variability was observed in HAW, the general means in the two groups of statistics were HAW 390.99 ± 64.68, and 286.15 ± 53.05 kg, including males and females. The HAW males weighed 74% more than the females, with 66% in LAW, logical indicators of higher growth potential in males; these differences were widened as the "handling" level increased.

Table 2. General statgraphs in the two environments

Environment	n	Mean (kg)	±SD	VC (%)	Min (kg)	Max (kg)
High	1 489	390.99	64.68	16.54	219	633
Low	2 002	286.15	53.05	18.54	112	340

Aranguren-Méndez *et al.* (2006), in double-purpose crossbred animals (Brahman and Holstein) reported adjusted weights to 540 days of 283.5 ± 38.2 kg for males, and 251.7 ± 34.1 kg for females, which were below the findings of this paper, considering the two sexes. Rodríguez Calvo *et al.* (2017) in Cuban Zebu cattle from 6 cattle ranches, found weight ranges of 255-327 kg at 18 months, below the mean values of Santa Gertrudis. De Souza *et al.* (2018) studied Nellore cattle in Brazil to demonstrate or not the existence of genotype-environment interaction, reported adjusted weights at 550 days in three regions of Brazil, which ranged between 301.1 ± 51.3 and 315.3 ± 53.2 kg. These values are way below the values attained in this paper, though the variation coefficients varied around 17%, very similar to this study. Differences in the behavior of these indicators in Nellore under different production systems were also found by Souza *et al.* (2003) and Conceição *et al.* (2005). Guillén Trujillo *et al.* (2012) on Zebu Bermejo, in Cuba, reported final weights in performance trials in several provinces (327.7 ± 52.3 kg), but below the reports made in Brahman from South Africa (360.8 kg), by Pico (2004). However, it was above the values reported in White Brahman, in Venezuela, by Plasse *et al.* (2002), with 297.4 kg, and in Cuba, by Espinoza-Villavicencio *et al.* (2008), with 326.5 kg.

In preserved herds of Colombian native breeds, as part of the program of genetic animals resources, Suárez and Pérez (2007) reported 247.2 ± 33.8 kg at 16 months, in a herd of Romosinuano Ossa cattle, and Martínez *et al.* (2009) in Santaminero native animals, reported mean values of 222.58 ± 39.6 kg, all inferior to the results in LAW, but in younger animals.

Table 3 shows the variance components and heredities of univariate analyses.

Possibly, the greatest variability observed in the low level influenced on higher variance components. Coincidentally, this phenotypical variability determined an h2 estimate, which was significantly lower than the high level.

Table 3. Variance components and heredities (± SE) in HAW and LAW

Estimates	HAW	LAW
σ^2_A	440	32 019
σ^2_E	755	196 688
σ^2_P	1 196	228 707
h^2 ± SE	0.37 ± 0.09	0.14 ± 0.04

σ^2_A= additive genetic variance, σ^2_E= residual variance, σ^2_P = phenotypical variance, $h^2 \pm SE$= heredities and standard error

In a single-trait analysis, Rodríguez and Guerra (2013) studied the final weight in performance trials of Cuban Zebu, and found heredities of 0.22 ± 0.04 at the high level, and 0.15 ± 0.03 at the low level; the same trend found in this research, though the difference between the ends was lower. The authors stated the existence of genotype-environment interaction. Also in Cuba, in Zebu, Espinoza-Villavicencio *et al.* (2008) and Guillén Trujillo *et al.* (2012), in univariate analyses, reported 0.28 heredity, more similar to the high levels found in Santa Gertrudis, and Rodríguez Calvo *et al.* (2017), using multi-trait models, reported 0.33 ± 0.07 heredity in weight at 18 months.

In single-trait determinations, Aranguren-Méndez *et al.* (2006), in double purpose crossbred cattle in Venezuela, reported a similar high level value to this study (0.38 ± 0.10). That population was considered genetically heterogeneous, and it influenced on genetic variability, which was above the values reported in Venezuelan Brahman (Plasse *et al.* 2002), or in Tabapua cattle (Ferraz *et al.* 2004), but similar to Hereford (Meyer *et al.* 1993). In Brazilian Nellore, Barbosa *et al.* (2017), taking into account weight adjustment at 550 days, reported $h^2=0.26$, which is a mid-point to the values found in this study.

In Colombian native cattle (Romosinuano), Martínez, Pérez, and Herazo (2006), and Ossa, Suárez, and Pérez (2007) considered weight adjustment at 16 months, and reported 0.33 ± 0.07 and 0.13 ± 0.05 heredities, in the same population, whereas Martínez *et al.* (2009), in Sammartinero cattle, in the eastern Colombian plains, reported $h^2 =0.18$.

Table 4 shows the results from the two-trait analysis, considering the two data sets as independent traits, according to Falconer and Mackay (2006), as a way to determine the possible genotype-environment interaction.

Table 4. Variance and covariance components, genetic parameters, and standard errors in HAW and LAW

Estimates	HAW	LAW
$\sigma2_A$	321	136
$\sigma a_{(AB)}$	171	
σ^2_E	1 117	1 098
$\sigma e_{(AB)}$	-99.6	
σ^2_P	1 439	1 233
$\sigma p_{(AB)}$	-26.6	
$h^2 \pm SE$	0.22 ± 0.09	0.11 ± 0.04
rg	0.82	
re	-0.09	
rp	-0.02	

σ^2_A= additive genetic variance, $\sigma a_{(AB)}$= genetic covariance, σ^2_E= residual covariance, $\sigma e_{(AB)}$= residual covariance, σ^2_P= phenotypical variance, $\sigma p_{(AB)}$= phenotypical covariance, $h^2 \pm SE$= heredity and standard error, rg, re, rp= genetic, residual, and phenotypical correlations, respectively.

The estimates of heredity were lower than the ones reported in single-trait estimations; consequently, the variance components were lower. The genetic correlation was high and positive, but residual and phenotypical correlations were close to zero on the negative side.

In a multi-trait analysis and research done to find evidence of possible genotype-environment interaction, Menéndez-Buxadera *et al.* (2006), in Cuban Zebu, reported heredities between 0.21-0.34. Guillén Trujillo *et al.* (2012), in analysis of final weight on performance trials of Cuban Zebu, reported 0.28 ± 0.10 heredity, adding that multivariate estimations were higher than the univariate estimations, and the former are more useful when the differences between the genetic and residual correlations is greater than 0.50, which was stated by Bennett and Gregory (1996). In this study, the bivariate estimates were lower

than the univariate estimates, which supports differences found in correlations to validate these results somehow.

Verde (2010), in Romosinuano cattle from Venezuela, analyzed the weight at 548 days, and found statistical genotype-environment interaction.

More recently, De Souza *et al.* (2018), on Nellore, on three Brazilian locations, and analyzing weight at 550 days, found high heredity values, between 0.60 and 0.62, thus confirming the results of Santos *et al.* (2012) in the north of Brazil, and they reported the existence of genotype-environment interaction. De Lira *et al.* (2013) studied the same breed in three Brazilian states and found 0.80 heredity in two of them, and 0.24 in Mato Grosso, which was similar to the high level found in Santa Gertrudis.

Souza *et al.* (2003) said that genetic correlations of the same trait below 0.80 in different environments is an indicator of genotype-environment interaction, which was corroborated by Nepomuceno *et al.* (2013). Although this is an important criterion, it should not be regarded as the only one; changes in the merit order must also be assessed among studs, considering their genetic values. The fact that in this study the genetic correlation was 0.82, indicates that the two traits are determined by the same genes that act additively, but the absence of genotype-environment interaction cannot be necessarily assured. It can be better assessed with the Pearson and Spearman correlations, considering the genetic values observed in both environmental conditions in studs with descendants living in the two environment sets.

Table 5 shows the results of Pearson and Spearman correlations, which were estimated in the 48 bulls represented in the two environment settings. They showed no association between the genetic values of the bulls from the two types of environment; i.e. the best animals in the high environment were not necessarily the best under other conditions.

Table 5. Correlations of Pearson and Spearman for the genetic values of bulls living in the two environmental settings

	HGV	LGV
HGV	-	0.04
LGV	0.18	-

Note: Pearson correlation above the diagonal and Spearman correlation below the diagonal. HGV= High genetic environment value; LGV= Low genetic environment value

Rodríguez and Guerra (2013) reported correlations of Pearson and Spearman of 0.46 and 0.39 in Cuban Zebu cattle, respectively, concluding that there is genotype-environment interaction between the two extreme environments used. Those values were greater than the values found in this study. Additionally, de Souza *et al.* (2018) concluded that they had found sufficient evidence of this interaction using the Pearson and Spearman correlation, with genetic values observed in Nellore bulls from three Brazilian states, which ranged between 0.28 and 0.31.

Fig. 1 shows the variability and changes in the merit order of 10 bulls whose genetic values had been chosen at random in both environments, which corroborated the aspects mentioned previously. For instance, 619B, 673 A, 678 A, and 621B performed better under the worst conditions.
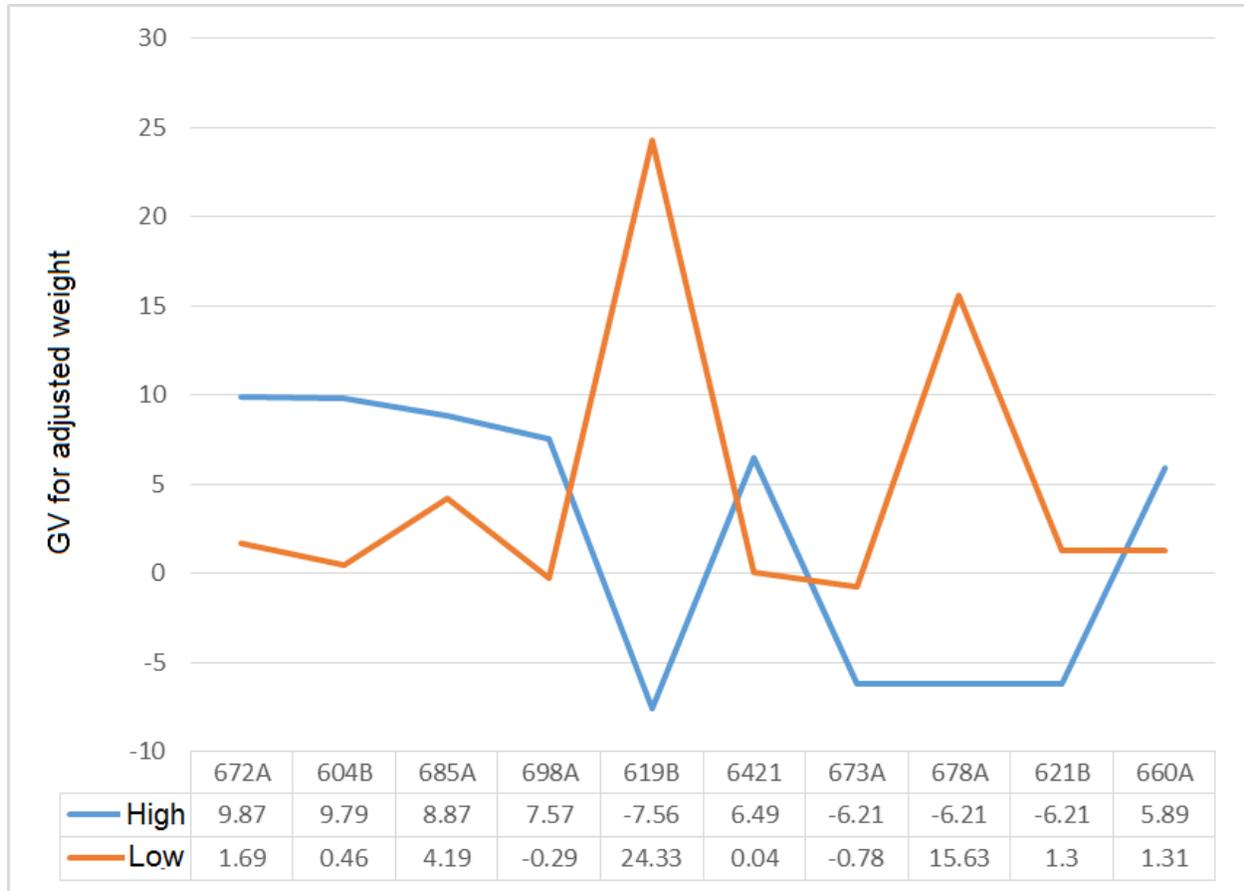
	672A	604B	685A	698A	619B	6421	673A	678A	621B	660A
High	9.87	9.79	8.87	7.57	-7.56	6.49	-6.21	-6.21	-6.21	5.89
Low	1.69	0.46	4.19	-0.29	24.33	0.04	-0.78	15.63	1.3	1.31

Fig. 1. Variations in genetic value (GV) from 10 bulls evaluated in contrasting conditions

Ambrosini *et al.* (2016) stated that changes in the merit order of studs, used as evidence of genotype-environment interaction must be particularly considered in unfavorable environmental conditions, where spotting the best animals is a difficult task.

CONCLUSIONS

Heredities of weight adjusted to 540 days of age were moderate, and always superior in the best conditions, regardless of utilizing a single trait or two trait model, the latter being inferior.

This methodology demonstrated that under contrasting environments there is evidence of genotype-environment interaction as a result from major changes in stud merit order.

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AUTHOR CONTRIBUTION

CONFLICTS OF INTEREST

None