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Genetic Parameters of Growth Traits of Santa Gertrudis Cattle in Performance Tests

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ABSTRACT

Background: Genetic parameters are essential in genetic breeding programs. **Aim.** To estimate the genetic parameters of growth traits in Santa Gertrudis breed, evaluated in animals submitted to performance tests (PT).

Methods: A database made of 4 607 records from three genetic companies between 1981 and 2016 was used. The traits studied were birth weight (BW), weight at weaning (WW), final weight adjusted to 540 days of age (FW), mean daily gain (MDG), and weight by age (WBA). Same age groups were made according to the herd, year, and birth season (fourth-month period),\ combination, comprising no less than three animals. The (co)variance components were estimated in models single trait and multi trait; the genetic parameters were estimated using MTDFREML software.

Results: The h^2 estimated were, 0.08 ± 0.02; 0.18 ± 0.02; 0.28 ± 0.07; 0.05 ± 0.02, and 0.26 ± 0.07 for BW, WW, FW, MDG, and WBA, respectively. The genetic correlations were all positive, except between BW and MDG (-0.11), the others ranged between 0.10 (BW and WBA), and 0.98 (WW, FW; FW and MDG). The phenotypical correlations were lower than the genetic correlations.

Conclusions: FW in the PT, which is the main selection criterion, showed the greatest h^2, with positive genetic correlations to the other traits. Accordingly, a simultaneous improvement is expected in all of them. FW, MDG, and WBA are determined by the same additive genes.

Key words: heredity, performance tests, Santa Gertrudis breed (*Source*: *DeCS*)

INTRODUCTION

In order to formulate optimum genetic breeding programs, and evaluate the genetic progress of ongoing programs, it is important to estimate the genetic parameters, considering that they are

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specific to every population (Palacios-Espinosa *et al.,* 2010). The estimations of genetic parameters should be updated, due to changes undergone by the same population.

In Cuba, Santa Gertrudis breed was imported in the late 1935 by American farmer E.J. Baker, then proprietor of Turiguano Island. First, a total of 35 young males were imported, then 12 bullocks from King Ranch arrived on the island. Following several years of absorbing crossing with crossbred Zebu and already present on the island Red Polled, Santa Gertrudis was recognized as a pure Cuban breed, in December 1947. In 1955, the first cow was recorded in the Books of the Genealogical Record of the breed in Cuba. Today, it is present in several provinces, though the most important herds are found in Ciego de Avila (Turiguano), Santiago de Cuba (Vallina), and Pinar del Rio (Camilo Cienfuegos), in order of importance.

This breed has not been thoroughly studied in Cuba or the world; however, the first results of a study of genetic parameters date back to 1974, which were later updated by Iglesias *et al*. (2009), Morales *et al.* (2012), and Morales *et al*. (2013).

Santa Gertrudis was used in crossing projects to create new breeds, such as Caribe from Cuba, with a 5/8 Holstein, 3/8 Santa Gertrudis gene proportion, which showed positive results in terms of good adaptability to the Cuban conditions (López and Ribas, 1993). Hence, the aim of this paper was to determine the genetic parameters of growth traits, in Santa Gertrudis animals submitted to performance tests.

MATERIALS AND METHODS

The historic database of this population applied for estimation of genetic values and genetic trends in genetic breeding programs, was used. It comprises 4 607 records of animals submitted to performance tests, corresponding to pedigrees, the progenie from 286 studs and 2 463 cows. The tests were done during the 1981-2016 period. The animals belonged to companies Turiguano (Ciego de Avila), Camilo Cienfuegos (Pinar del Rio), and Vallina (Santiago de Cuba).

The traits studied were birth weight (BW), weight at weaning (WW), final weight in the performance test, adjusted to 540 days of age (FWA), mean daily gain (MDG), and weight by age (WBA). Same-age groups were made according to the combination herd, year, and birth season (fourth-month period), and comprised no less than 3 animals.

The MDG (g.day^{-1}) at the end of the test was calculated as:

$$MDG = \frac{FW - SW}{TD} * 1000$$

Where: FW: final weight; SW: starting weight in the test; TD: test days.

Meanwhile, weight by age (g.day^{-1}) was calculated:

$$WBA = \frac{FW}{FA} * 1000$$

Where FA is the age at test end.

The weight adjusted to 540 days of age was done in keeping with the following formula:

$$\mathbf{YW18} = \left(\frac{\mathbf{W18} - \mathbf{WA}}{\mathbf{YWI} - \mathbf{W18}}\right)\mathbf{X\ 175} + \mathbf{AW}$$

Where:

YW = weight recorded at 1 year

W18=weight recorded at 18 months

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

The calves included in the performance test were weighed by separate using a 1 000 kg scale at the beginning, approximately between 10 and 15 days after weaning. Then weighing was done monthly until the end of the test, at about 18 months of age.

The data were analyzed through MTDFREML (Boldman *et al.*, 1995). A single trait animal model was used at the beginning to estimate the variance components and the genetic parameters; then a multi trait model was used. Both included the same-age group (herd-year-fourth-month period), as fixed effects. The random effects were considered as the direct additive genetic effects, and residual error. The statistical model used as a matrix was as following:

Single trait:

$$\mathbf{y = Xb + Za + e}$$

Where: y = trait vector studied

X and Z= matrices of incidence

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

a= vector of random effects on the animal

e= residue vector

Then, a multi trait model was used, including paired traits:

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,

$$\begin{bmatrix} y_1 \\ y_2 \end{bmatrix} = \begin{bmatrix} X_1 & 0 \\ 0 & X_2 \end{bmatrix} \begin{bmatrix} b_1 \\ b_2 \end{bmatrix} + \begin{bmatrix} Z_1 & 0 \\ 0 & Z_2 \end{bmatrix} \begin{bmatrix} a_1 \\ a_2 \end{bmatrix} + \begin{bmatrix} e_1 \\ e_2 \end{bmatrix}$$

Where: y_i = vector of observations of the i^{th} trait.

b_i = fixed effects vector of the i^{th} trait.

a_i = random effects vector on the animal of the i^{th} trait.

e_i = random residual effects vector of the i^{th} trait.

X_i and 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 multi trait. The variance and covariance components, and genetic parameters were estimated using the restricted maximum likeness (REML), and the free algorithm of derivatives through MTDFREML software (Boldman, *et al.* 1995).

RESULTS AND DISCUSSION

The general results of traits are shown in Table 1. Except for the birth weight (BW), with biological limitations, all the others showed high variation coefficients, mainly MDG, thus indicating existing differences not only within a company, but also between them.

A BW of 32.75 kg is similar to the one reported by Kebede and Komlosi (2015), in a Hungarian stud (32.9 kg), but higher than the one reported by Ossa, Suárez, and Pérez (2007) in Romosinuan cattle (30.65 kg). In dual purpose systems in Venezuela, Salamanca, Quintero, and Benítez (2011) reported 28.92 kg, whereas Garay *et. al.* (2014) reported 30.4 kg in a crossbred herd, in Colombia.

Table 1. General statigraphs of the traits studied

Traits	Mean	SD	VC (%)
Birth weight (kg)	32.75	3.26	9.96
Weight at weaning (kg)	179.13	39.16	21.86
Final weight at performance test (kg)	330.87	58.03	17.54
Mean daily gain in the test ($g.day^{-1}$)	450.28	192.98	42.86
Weight by age in the test ($g.day^{-1}$)	558.76	140.50	25.14

The WW (179.13 kg) was higher than the values reported by Morales *et al.* (2012), and Morales (2013), in the same breed, in Cuba. Higher results were reported in Australia, by Bradfield, Graser, and Johnston (1997), and Hernández-Hernández *et al.* (2015); Cárdenas, Kú, and Magaña (2015) reported weights at weaning in Brahman cattle (188.0 and 166.0 kg, respectively), within a similar value range to the findings of this study. Domínguez-Viveros *et al.* (2013), in Tropicarne cattle, in Mexico, with a mean of 183.2 kg. Whereas Montes, Vergara, and Barragán (2011) found higher weights than the reports made in Brahman cattle (238.5 kg).

The mean of MDG 450.28 $g.day^{-1}$ coincides with the range described by Mascioli *et al.* (2000), of 344-576 g for this trait. The results of the current study were above the 356 g reported by Alencar, Oliveira, and Barbosa (2000) in grazing Canchim cattle, in Brazil; similar values were found in Zebu cattle by González (2009), with 468 g, and Morales (2013), in Santa Gertrudis cattle.

Regarding the other traits studied, WBA (558.76 g.day of age^{-1}) was inferior to the ones found in Cuba by Ceró (2007) in Chacuba (659 $g.day^{-1}$), González (2009) in Zebu (583 $g.day^{-1}$), and Morales (2013) (613.80 $g.day^{-1}$), showing certain worsening of test performance.

The mean FW value (330.87 kg), in turn, was lower than the one found in Cuban Zebu cattle by Villavicencio *et al.* (2007), with 343.3 kg, which was similar to the values reported by Trujillo *et al.* (2011), with 326.5 kg in Cuban Zebu, and Morales (2013) in Santa Gertrudis.

The results achieved in the single trait genetic analysis are shown in Table 2. All the heredity estimations were low, showing little additive genetic variation, and therefore, a high residual or environmental variability.

Table 2. Variance and heredity components of the traits analyzed

Traits	σ^2_A	σ^2_E	σ^2_P	$h^2 \pm SE$
BW	0.59	6.19	6.78	0.09 ± 0.03
WW	13.28	553.01	566.30	0.02 ± 0.02
FW	74.44	1 010.48	1 084.92	0.07 ± 0.02
MDG	367.30	8 442.26	8 809.56	0.04 ± 0.02
WBA	261.67	3 481.85	3 743.51	0.07 ± 0.02

Note: BW (birth weight), WW (weight at weaning adjusted to 205 days), FW (final weight in the performance test, adjusted to 540 days) MDG and WBA (mean daily gain and weight by age, respectively, in the performance test). σ^2_A, σ^2_E and σ^2_P, additive, residual, and phenotypical genetic variance, respectively; $h^2 \pm SE$ (heredity and standard error).

Regarding BW (0.09), a very similar result was achieved by Garay *et al*. (2016) in Brahman cattle, in Colombia. The other results confronted were higher: Aranguren-Méndez *et al.* (2006) in dual-purpose systems, in Venezuela (0.24); Ossa *et al.* (2007), in Romosinuano (0.17); Garay *et al.* (2014) in a multiracial herd (0.12, and Nandolo *et al*. (2016) in Malawi (0.33).

Table 3 shows the heredities and genetic and phenotypical correlations when the multi trait analyses were made, thus confirming the findings of Schaeffer (1999), that the models that include more than one trait simultaneously also increase heredity, in addition to the capacity to estimate the genetic correlations between traits. Except for BW and MDG, the other traits showed significant increases, coinciding with the reports found in the literature in these and other beef breeds.

Table 3. Genetic parameters estimated by multi trait models for growth traits

	BW	WW	FW	MDG	WBA
BW	**0.08 ± 0.02**	0.16 ± 0.03	0.17 ± 0.02	-0.11 ± 0.03	0.10 ± 0.03
WW	0.02 ± 0.02	**0.18 ± 0.02**	0.98 ± 0.04	0.48 ± 0.06	0.53 ± 0.30
FW	0.06 ± 0.02	0.49 ± 0.03	**0.28 ± 0.07**	0.98 ± 0.02	0.96 ± 0.01
MDG	0.01 ± 0.02	-0.08 ± 0.02	0.30 ± 0.02	**0.05 ± 0.02**	0.92 ± 0.11
WBA	0.02 ± 0.02	0.37 ± 0.02	0.99 ± 0.02	0.71 ± 0.01	**0.26 ± 0.07**

Note: In the heredity diagonal, above the diagonal line are the genetic correlations, below the diagonal line are the phenotypical correlations.

The single trait WW value was practically zero in the direct effect (0.02). The closest result found was a report made by Espinosa *et al.* (2007) in Cuban Zebu cattle (0.04± 0.02), and Guerra *et al.* (2010); Guillén *et al.* (2011), in Cuban Zebu cattle also found low values of direct heredity (0.06 ±0.01 and 0.08 ± 0.01, respectively). Comparable results (0.07) were reported by Vergara *et al.* (2016).

Coincidences were found in reference to multi trait (h^2 = 0.18) and the results reported by Aranguren-Méndez *et al.* (2006) (0.17); Morales (2013) in Santa Gertrudis (0.15), and Barbosa *et al.* (2017) in Nellore, in Brazil, (0.15), with the same result.

Other higher values were reported by Ríos Utrera *et al.* (2013) in Indubrazil cattle (0.27 ± 0.19), García *et al.* (2015) (0.17-0.30) in Costeno with Horns, using six different models, and Kebede and Komlosi (2015) (0.26), in Europe.

Such low final weight heredity in the performance test (0.07), which is the selection criterion) would justify the poor response to the selection achieved in this breed in time. Upon multi trait model analysis (Table 3), it was 0.28, and showed high and positive genetic correlations to WW, MDG, and WBA. Morales (2013) reported a slightly inferior value to 0.21, which is not justified with the poor genetic gain, though the results in Cuba have been higher in other breeds; Guerra *et al.* (2001), in Charolaise breed, reported estimates of 0.25, in relation to FW, whereas González-Peña *et al.* (2007) reported 0.21. In Chacuba cattle, Ceró (2007) reported 0.21, whereas González (2009) estimated a heredity of 0.23 in Zebu cattle.

Regarding MDG and WBA, Morales (2013) reported 0.14 and 0.22, respectively, much higher than the values reported in this paper, though they were very similar in WBA (Table 3). The genetic correlations were all positive, except between BW and MDG (-0.11), and varied from 0.10 (FW and WBA) to 0.98 (WW and FW; FW and MDG). Kebede and Komlosi (2015) reported a genetic correlation (0.28) between BW and MDG, one of the lowest values found. The phenotypical correlations were lower than the genetic correlations; the ones related to BW were practically zero, and the highest (0.99) was found between WBA and FW.

Between BW and WW, Neser *et al.* (2012), in Brangus cattle, reported a correlation (0.78) higher than the one found in this research. Also, between WW and MDG, Kebede and Komlosi (2015) found a much higher value (0.98). It must also be considered that weight at weaning in Simmental cattle, in Europe, is higher than the ones achieved in tropical conditions, and their late genetic determination of postweaning gain was high.

Schaeffer (1999) noted that in the analysis of multiple traits, all the traits were somehow benefited, and that they are more useful when the difference between genetic correlation and environmental correlation is the highest (greater than 0.5), or when one trait's heredity is much higher than another, thus benefiting the trait with the lower heredity.

Morales (2013) also found very high correlations in Santa Gertrudis, between FW, MDG, and WBA. Consequently, between WW and MDG (0.78); FW and MDG (0.91); and between FW and WBA (0.99), the values coincide with the values found in this study, ratifying that these characters are determined by the genes themselves.

CONCLUSIONS

Multi trait analyses were observed to benefit the estimates of heredity, mainly those with the lowest values.

The final weight in the performance test, which is the main selection criterion, showed the highest heredity, and had positive genetic correlations with the other characters, so a simultaneous improvement can be expected in all of them.

FW, MDG, and WBA are determined by the same additive genes, with high genetic correlations.

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AUTHOR CONTRIBUTION

Conception and design of research: MAST, MRC, MCGR, MSMG, data analysis and interpretation: MAST, MRC, redaction of the manuscript: MAST, MRC, MCGR, MSMG.

CONFLICT OF INTERESTS

The authors declare no conflict of interests.