Genetic parameters and genetic trends in a Guzera purebred cattle population in Brazil

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Introduction

Large numbers of observations are required to genetically characterize beef cattle populations. In Brazil, where breeders' associations or government organizations supervise the implementation, performance test and official record keeping and processing of data. The Experimental Station of Sertãozinho (Estação Experimental de Zootecnia de Sertaozinho - EEZS), a research unit of the Instituto de Zootecnia, combines research and technical assistance and makes scientific work realistic and shortens the time gap between the availability of research results and their practical application.

The EEZS has the purpose of maintaining and studying beef cattle resources especially *Bos indicus*. Since 1933 the Station has maintained purebred herds of Caracu (taurus adapted), Gir, Guzerá and Nelore for beef production.

In extensive regions of Brazil, the beef production based on Zebu cattle is characterized by low production levels. However, technology is available to increase yields, particularly by selection and crossbreeding. Since the successful implementation of crossbreeding programs in such ecosystems seems to be limited, genetic improvement of these herds will rely principally on selection. Economically relevant growth traits in the Brazil beef commercialization system are weaning weight and weight at 18 mo of age. A fraction of calves is sold at weaning as feeders and the remaining ones are kept as replacement heifers and sires or sold as finished animals at 36 mo of age.

The objective this research was to describe such a stratified herd in terms of (co)variances and genetic parameters and to measure genetic trends for body weights over a 25-year period.

Material and methods

General description of herds. The Zebu herds (Gir, Guzerá and Nelore) started to be formed in Sertãozinho (SP) in 1933. All the herds were constituted mostly by the purchasing of bulls and cows from private breeders. They were maintained at the Station as a purebred population and also in some crossbreeding experiments. At this time, the main selection was based on phenotypic racial traits, under the influence of the importation, because breeders were looking for "racial purity". In 1976 a selection project was initiated having as selection criteria yearling weights and in 1980 the Zebu selection lines were established. All the details concerning the formation of these lines were described by Mercadante *et al.* (2003). The Guzerá (GuS) herd size was fixed at 120 cows and 6 bulls (2 and 3 years old). The breeding season was 90 days starting in November (Spring). A single sire natural mating group was used composed of 15 cows for a 2-year-old bull or 25 for a 3-year-old. Close relationship between bulls and cows was avoided by examining the pedigrees. The cows and calves were maintained in similar pastures (mostly *Panicum maximum*) throughout the suckling period. No creep feeding was used and the weaning was around 210 days age. The males started the performance test just after weaning up to 13 months (168 days of feeding) and the females remained on pastures until 18 months.

Selection criteria and performance records. For all the breed herds, male selection was based on high selection differentials for final weight on test corrected to 378 days (Y378) and females were selected based on weight at 550 days (Y550). Annually about 7-10% of the males and 55% of the females were selected from the contemporary groups. The annually culling rate was 20% for females, according to pregnancy status and age (more than 10 years), and 50% for males, aged 3 years. The traits measured and analyzed were birth weight (BW), 120 days weight (W120), weaning weight (W210) and yearling weight for males (Y378) and for females (Y550).

Statistical analyses. A full 5-trait REML estimate was obtained using the program REMLF90 (Misztal et al., 2002).

The model of analysis included the fixed effects contemporary group, defined as animals born in the same year (1957 to 2005), month of birth (8, 9, 10 and 11) and age of dam (3, 4, … ≥ 13 yr of age). The random effects were additive genetic direct and maternal, permanent environmental and residual. The model for W378 and W550 did not include the fixed effects of age of dam and the additive genetic effects of maternal and permanent environmental. The number of levels for the animal additive genetic effect was 6,043. A summary of data structure is presented in Table 1.

Results and discussion

In Table 1 In order to maximize the genetic gains, only animals with the highest deviations from the mean should have been used as parents of the next generation. However, for females, considering the low rates of reproduction in the tropics, potential selection intensity is less. The comparison of periods of time (1980/2005) gives an idea of part of the genetic change that occurred in the Guzera cattle population.

Table 1: Summary of data structure

Trait	N[a]	Mean (kg)[b]		
		1980	2005	Overall
BW	3,378	26.7 ± 3.8	27.4 ± 4.1	27.7 ± 4.1
W120	4,019	103.0 ± 18.1	106.9 ± 16.0	116.3 ± 21.8
W210	3,852	157.0 ± 22.1	176.5 ± 22.3	177.6 ± 29.6
Y378	1,536	269.3 ± 23.7	324.2 ± 34.4	293.8 ± 46.6
Y550	1,307	231.6 ± 24.7	276.3 ±26.2	257.6 ± 39.4

[a] Number of observations.

[b] Means ± standard deviations in 1980, 2005 and overall.

The inbreeding was maintained for the herd at a reasonable level (1981 = 7.0 and 2005 = 4.5). The lowest values, in 2005, are explained by the introduction of heifers from another herd.

Table 2 presents heritability estimates and genetic and phenotypic correlations for traits. Heritability estimates for traits were all moderate or high. There was an increasing trend for heritability estimates with age after BW, with a maximum heritability of 0.44 for W378. The heritability and correlations estimates are in agreement with those reported in the literature for growth traits obtained in selection experiments and from field data.

Table 2: Heritability estimates (diagonal), phenotypic (above diagonal) and genetic (below diagonal) correlations among traits

Traits[a]	BW	W120	W210	W378	W550	BWm	W120m	W210m
BW	**0.34**	0.35	0.31	0.37	0.32			
W120	0.66	**0.19**	0.80	0.65	0.59			
W210	0.56	0.87	**0.22**	0.74	0.38			
W378	0.59	0.83	0.90	**0.44**	0.38			
W550	0.56	0.79	0.88	0.91	**0.40**			
BWm	0.05	0.32	0.40	0.31	0.26	**0.10**		
W120m	0.45	0.32	0.50	0.60	0.66	-0.16	**0.07**	
W210m	0.48	0.38	0.37	0.57	0.59	-0.27	0.89	**0.05**

[a] BW and BWm=birth weight and maternal, W120 and W120m=120 days weight and maternal, W210 and W210m=weaning weight and maternal, Y378 and Y550=yearling weight for males and females

[b] Means ± standard deviations in 1980, 2005 and overall.

Phenotypic correlation estimates among weights are given in Table 2. All of the phenotypic correlations were positive. Correlations among traits ranged from 0.31 between BW and W120 to 0.80 between W120 and W210. Genetic correlations among most pairs of traits were higher than the corresponding phenotypic correlations (Table 3). Weights measured at successive ages were highly correlated, ranging from 0.56 to 0.91. Since the yearling weights of males and females were obtained at distinct ages and with different postweaning management, their analysis indicated a below unit genetic correlation (0.91).

Maternal heritability for live weight declined with increasing age (Table 2). Maternal heritability for W120 and W210 was 52.6% and 45.5% of that for direct heritability. The interpretation of genetic parameter estimates for traits that are influenced by maternal effects in an animal model context is dependent on both the structure and the model used in the analysis. There are several reports concerning beef cattle that have shown inflated direct heritability estimates when maternal effects were not included.

The permanent environmental effects for traits were lower than 0.05, with negative correlations between BW and W120 and BW and W210 (-0.23 and -0.16, respectively) and positive between W120 and W210 (0.94). The values suggest that mothers which produce heavier calves, are not necessarily those mothers whose calves become heavier more rapidly after birth. The preferred model for the analysis of maternal traits included maternal genetic and permanent environmental effects.

The EPD mean for Y378 and Y550 at the start of the experiment (1978 to 1980) were – 9.03 kg and - 7.08 kg for females (Figure 1). After 25 yrs (2005) of selection for yearling weight, the EPD mean of Y378 and Y550 were 11.86 kg and 8.75 kg, respectively. In 2000, two sires selected (high selection differentials) had health problems and were replaced by others with less differential, a fact which resulted in a decrease in the EPD mean of traits of the progeny born in 2001. The results indicate that selection for yearling weight promoted high and consistent responses in the other weight. There was no correlated response in BW contrary to the other selected herds (Razook and Mercadante, 2007).

The genetic trends obtained after 25 yr for BW, W120, W210, Y378 and Y550 were 0.043 ± 0.001, 0.0250 ± 0.006, 0.407 ± 0.008, 0.848 ± 0.016 and 0.634 ± 0.013 kg/yr, respectively. For maternal traits, the genetic trends for BW, W120, W210 were 0.014 ± 0.001, 0.106 ± 0.003 and 0.116 ± 0.003. The results indicate that selection for yearling weight promoted high and consistent responses in the other weights, but had little impact on maternal traits.

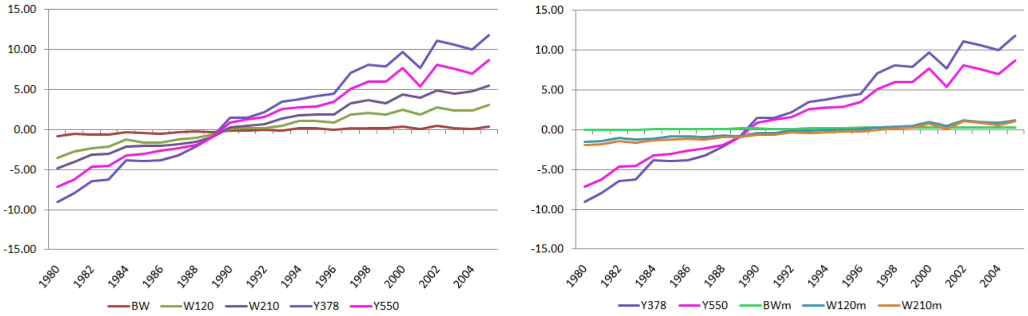

Figure 1: Genetic trends for birth weight (BW), 120 days weight (W120), weaning weight (W210), yearling weight for males (Y378) and females (Y550) (left) and means of EPD maternal for BW, W120 and W210 (right) in a Guzera breed cattle population.

Conclusion

A Guzera purebred cattle population in Estação Experimental de Zootecnia de Sertãozinho (SP-Brazil) has preserved these important breed herds, which were submitted to an effective selection program for growth traits with significant genetic changes.

References

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