Genetic And Phenotypic Parameters For Yearling Weight, Scrotal Circumference And Frame Score In Simmental And Simbrah Beef Cattle From Mexico

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Introduction

Scrotal circumference and yearling weight are traits selected to increase fertility and growth rate in Mexico. Frame score can be used to project mature size, providing an indication for composition, and characterize performance potential and nutritional requirements of animals (Dhuyvetter (1995)). Few studies on beef cattle frame have been performed based on scores (Horimoto *et al*. (2007)), since considerable variation exists among cattle for frame size. It is important to study the magnitude of the relationship for frame score with other growth traits in animal breeding programs.

In Mexico, few estimates of genetic parameters for growth traits of different beef cattle populations exist (Ríos-Utrera *et al.* (2007)), and most of them have been obtained with single-trait animal models. Multi-trait animal models are preferable to single-trait models for unbiased (co)variance and genetic parameter estimation in animal populations (Thompson (2008)). The objective of this study was to estimate (co)variance components, heritabilities, and genetic and phenotypic correlations for yearling weight, scrotal circumference and frame score in Simmental and Simbrah cattle from Mexico.

Material and methods

Data. Field data for scrotal circumference, yearling weight and frame score as well as pedigree information were obtained from the Mexican Simmental – Simbrah Association for the period from 2006 to 2009. The information was edited to guarantee the quality of the data to be analyzed. Yearling weight records were adjusted to a 365-days basis and frame score was calculated according to the Guidelines for uniform beef improvement programs (BIF (2002)). Only male records of each breed were analyzed. Final data file included 3,208 records (1,949 and 1,259 Simmental and Simbrah records, respectively). The pedigree file consisted of 3,398 animals, 750 sires and 3,232 dams.

Statistical analyses. Each trait was analyzed with single-trait animal models to obtain starting values for the three-trait animal model. The models included fixed effects of herd-year-season for each trait, and the gene proportion of Simmental breed, heterozigozity and

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recombination losses effects as covariates (Dickerson (1973)). Additive genetic and residual effects were included as random effects. Covariance components were estimated by Restricted Maximum Likelihood (Graser *et al*. (1987)), using the ASReml program developed by Gilmour *et al*. (2006). Convergence was assumed to have been reached if the variance of minus twice the logarithm of the likelihood (-2logL) in the simplex was less than 10^{-2}. After first convergence, restarts were performed to verify that it was not at a local minimum.

Results and discussion

Descriptive statistics are presented in Table 1. Variance components and heritabilities are presented in Table 2. Genetic and phenotypic correlations obtained by using a three-trait animal model are presented in Table 3. Heritabilities estimated with single-trait animal models were similar to those obtained with the three-trait animal model.

Table 1: Descriptive statistics for the studied traits in Simmental and Simbrah cattle

Trait	n	Mean	Min	Max	SD	CV
Yearling weight (kg)	2,019	356.83	168.07	622.63	72.71	20.38
Scrotal circumference (cm)	3,208	30.53	18	44	4.67	15.30
Frame score (units)	3,208	5.25	0.52	9.5	1.55	29.59

Table 2: Variance components and heritabilities for the studied traits in Simmental and Simbrah cattle

Trait	σ^2_a	σ^2_e	σ^2_p	h^2
Yearling weight	376.3±130.9	755.8±116.8	1,132±43.8	0.33±0.11
Scrotal circumference	2.89±0.69	5.41±0.61	8.31±0.24	0.35±0.08
Frame score	0.37±0.08	0.51±0.07	0.89±0.03	0.42±0.08

σ^2_a is the additive genetic variance; σ^2_e is the residual variance; σ^2_p is the phenotypic variance; h^2 is the heritability.

Table 3: Genetic (above diagonal) and phenotypic correlations (below diagonal) for the studied traits in Simmental and Simbrah cattle

	Yearling weight	Scrotal circumference	Frame score
Yearling weight	-	0.42±0.02	0.41±0.02
Scrotal circumference	0.36±0.19	-	0.40±0.02
Frame Score	0.47±0.17	0.59±0.12	-

The estimate of heritability for yearling weight (0.33±0.11) is within the range (0.15 to 0.42) of estimated values using REML methodology in different beef cattle populations (Bishop (1992); Meyer (1992)). Also the heritability for scrotal circumference (0.35±0.08) was within the range (0.15 to 0.54) of published values in different beef cattle populations with REML methodology and animal models (Meyer *et al*. (1990); Gressler *et al*. (2006)).

The estimate of heritability for frame score (0.42±0.08) was similar to that estimated by Mercadante *et al*. (2004) (0.48±0.04), but greater than the obtained by Horimoto *et al*. (2007) (0.23±0.03) using a single-trait animal model and REML methodology.

All estimated genetic correlations for the studied traits were positive and of medium magnitude (ranged from 0.36 to 0.59). The genetic correlation between yearling weight and frame score was 0.47±0.17 (Table 3), indicating that selecting for yearling weight will increase the animal's frame. Our estimates agree with Mercadante *et al*. (2003), who found a positive yearly genetic trend of 0.25±0.03 cm when select for hip height, a measure indicative of frame size, in female Nellore cattle selected for yearling weight. Also with Horimoto *et al*. (2007), who estimated a positive covariate of 2.06 between the direct additive genetics effects for frame score with yearling weight.

The genetic correlation between yearling weight and scrotal circumference was 0.36±0.19 (Table 3). This agrees with many estimated values using paternal half-sib correlations in different beef cattle populations (Smith *et al*. (1989)), and was similar to that observed by Frizzas *et al*. (2009), using REML and an animal model in Nellore cattle.

The genetic correlation between frame score and scrotal circumference was 0.36±0.19 (Table 3), indicating that these traits were influenced by the same genes. Horimoto *et al*. (2007) estimated a genetic correlation between frame score and scrotal circumference as -0.02 and -0.01 using genetic correlation coefficients of moment-product of Spearman and Pearson, respectively. However more studies should be done for this trait in beef cattle populations.

Conclusion

Results showed that there are no genetic antagonisms between traits studied, indicating that animals selected for yearling weight could be directly selected for the increase of the body structure. Those genetic correlations also indicate the need for selecting animals using selection indices that properly weigh these three traits in order to maximize the economic response. Additional studies must be realized with multi-trait animal models in order to determinate the magnitude of associations of these traits in beef cattle populations.

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