Estimation Of Genetic Parameters For Growth Traits In Brangus Cattle

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Introduction

It is well known that the prediction of breeding values requires accurate (co)variance components. If the heritability estimates used in the analysis are too high, they could lead to an over estimation of the genetic progress, while inaccurate covariance components could lead to inaccurate breeding values, especially for growth traits, where erosion of records over time takes place because of selection. There is very little or no information regarding genetic parameters for growth traits for Brangus cattle in the literature available. Currently the South African Brangus Cattle Breed Society makes use of BREEDPLAN generic (co)variance components and heterosis estimates (Graser *et al* 2005) for similar composite type breeds in Australia in their prediction of breeding values. The purpose of this study was to estimate (co)variance components specific for the South African Brangus cattle breed.

Material and Methods

Data for this study were obtained from the Brangus Cattle Breeders' Society of South Africa. The first Brangus herd in South Africa, which is a cross between Brahman and Angus cattle, was established in 1963 in Ladysmith, Kwazulu Natal. However, the Breed Society was only established in 1986. Currently there are 135 breeders with 22300 registered cattle in South Africa. It is also one of the fastest growing breeds in terms of numbers in the country.

Fifty five thousand weight records of birth weight (BW), weaning weight (WW), yearling weight (YW) and eighteen month weight (FW) were available to estimate (co)variance components and subsequent genetic parameters. All incomplete records as well as records outside the normal biological boundaries were disregarded. The classifications of weight classes were done following the Breedplan genetic evaluation system (BREEDPLAN User Manual, 2001). The age ranges for different traits were: weaning weight (80 – 300 days); yearling weight (301- 500 days) and Eighteen month weight (501 – 900 days). Herds with less than three years of recording as well as contemporary groups with less than five records were also removed from the final data used for the analysis. The final dataset consisted of data from 34 herds, collected over a period of 23 years (1986-2008). A total of 711 sires and 171 sires of sires as well as 7516 dams were present in the data.

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A summary of the data used in the analysis is presented in Table 1. To assess the influence of non-genetic factors on the different weights for inclusion in the model an analysis of variance was done using the GLM procedure in SAS (2009). A significance level of $P<0.01$ was used as criteria for inclusion. The following factors were tested: Herd-year-season concatenation (500 levels), sex (2 levels) and breed composition (12 levels) as fixed effects and age at recording (except BW) as linear regressors as well as age of dam (both linear and quadratic regressors).

Table 1 Descriptive statistics for the different traits in the analysis

Trait	N	Aver (kg)	SD (kg)	Min (kg)	Max (kg)
BW	12329	33.02	4.50	15	53
WW	17747	219.45	46.58	48	458
YW	7698	298.16	64.72	110	638
FW	4561	391.45	77.22	194	780

The Brangus is a composite breed and in South Africa an open register system is used. This means that new animals with very little information can enter the dataset. As different breeds are involved it also means that heterosis can play a role in the estimation of the genetic parameters. It is therefore important to include breed composition in the analysis. Twelve different breed compositions were identified.

Taking into consideration both the distribution of records over a twelve month period as well as the weaning weights of the calves, two distinct seasons were identified. The months from September to March were classified as season one, while April to August were classified as season two. Age of dam was expressed in years starting with dams of two years and younger. All dams older than 6 years were grouped together.

(Co)variance components as well as heritabilities were estimated using the ASREMLprogram (Gilmour *et al* 1999). The Log likelihood ratio test (Swalve, 1993) was used to obtain the most suitable model for the multivariate analysis. The estimates obtained in the univariate analysis also act as starting values for the multivariate analysis. Only the most complete model is presented.

$$Y = X\beta + Z_1a + Z_2m + Z_3c + Z_4cxs + \varepsilon \ \{\text{with cov } (a, m) = A\sigma_{am}\}$$

Where: -

Y = vector of observation,
β = vector of fixed effects influencing growth,
a = vector of direct additive effects,
m = vector of random maternal additive (dam) effects,
c = vector of random permanent maternal environmental effects,
cxs = vector of additional random effects of herd-year-season x sire interaction,
ε = is vector of residuals and where
X, Z_1, Z_2, Z_3 and Z_4 are incidence matrices relating observations to their respective fixed and random effects.

Results and Discussion

All non-genetic factors tested were significant for all the traits under consideration and were thus included in the subsequent (co)variance analyses. A summary of the heritability estimates and subsequent ratios obtained in the univariate analysis using the best models according to the log likelihood ratio test are presented in Table 2.

Table 2 Heritability estimates obtained from the univariate analysis (SE in brackets)

	BW	WW	YW	FW
Direct heritability	0.16 (0.019)	0.10 (0.021)	0.05 (0.024)	0.17 (0.046)
Maternal heritability	0.01 (0.009)	0.06 (0.016)	0.08 (0.024)	0.06 (0.023)
Permanent maternal environmental ratio	0.10 (0.007)	0.10 (0.015)	0.01 (0.025)	0.00 (0.000)
HYSXS ratio	0.04 (0.010)	0.10 (0.008)	0.06 (0.011)	0.05 (0.016)

The covariance between direct and maternal genetic effects was not significant in the final model for all traits. The inclusion of both permanent maternal environment and HYSXS interaction as additional random factors lead to a substantial reduction in both the direct- and maternal genetic variances and the subsequent heritability estimates in all the traits. The high maternal- and low direct heritability estimates for YW did come as a surprise. Although a carryover effect is described in the literature (Meyer *et al.,* 1993), the fact that such a large proportion of the total variance in both YW and FW weight could be ascribed to maternal variance was also a surprise. In general the estimate falls into the range of parameters described in the literature (Koots *et al.,* 1994a). However, convergence problems and the low parameter estimates obtained do suggest the use of more simple models in preference to the final models considered in the above univariate analyses.

Table 3 (Co) variance components and heritability estimates obtained in the multivariate analysis, using the best models, for each trait. (SE in brackets)

	BW	WW	YW	FW
Direct additive variance	2.815	182.839	431.562	554.309
Maternal additive variance	0.747	57.328		
HYSXS variance	1.397	102.415		
Error variance	10.526	500.632	1192.160	1404.140
Phenotypic variance	15.484	843.210	1623.700	1958.400
Direct heritability	0.18 (0.028)	0.22 (0.022)	0.27 (0.025)	0.28 (0.034)
Maternal heritability	0.05 (0.011)	0.07 (0.008)		
HYSXS ratio	0.09 (0.010)	0.12 (0.008)		

An increase in both the direct and maternal heritability estimates was observed in all the traits when changing from the univariate to the multivariate analyses (Table 3). The results correspond to results obtained by Bennet & Gregory (1996), and Van Niekerk *et al.* (2004). The increase in the heritability estimates can in part be explained by the moderate to high genetic correlation that exists amongst the different traits. This means that information in one trait is used as additional information in the other traits to obtain a more accurate prediction of the different (co) variance components.

The heritability estimates (both direct and maternal) for all the traits fall within the parameter range, albeit in the lower sector, described in the literature (Mohiuddin, 1993 and Koots *et al.*, 1994a).

The high value of the HYSXS ratio (0.12 –WW) indicated that some re-ranking of sires might occur over different contempory groups. This is higher than the value obtained by Neser *et al.*, (1996) in Bonsmara cattle as well as Pico *et al.*, (2004) in Brahman cattle.

Table 4 Genetic correlations between the different traits in the analysis. (SE in brackets)

	WW	YW	FW
BW	0.59 (0.0753)	0.52 (0.0793)	0.44 (0.0920)
WW		0.97 (0.0375)	0.90 (0.0548)
FW			0.79 (0.0483)

The direct genetic correlations between the different traits were all positive, ranging from moderate (0.44–BW and FW) to high (0.97–WW and YW). These results correspond to results obtained by Koots *et al.*, (1994b), Van Niekerk *et al.*, (2004) in Nguni cattle, Pico *et al.*, (2004) in Brahman cattle and Van Niekerk *et al.*, (2006) in Limousin cattle.

Conclusion

In animal breeding no decision can be taken in isolation and selection on one trait will have consequences on all other traits as well. This is clearly indicated by the moderate to high genetic correlation that exists between the traits. The estimation of (co)variance components should be seen as the first step in developing a proper breeding objective for the breed. Further research should also incorporate the use of random regression models to obtain proper growth curves for every animal in the breed. This means that the data for the study should be extended to include mature cow weight.

References

Bennett, G.L. and Gregory, K.E. (1996). *J. Anim. Sci. 74*, 2598-2611.

BREEDPLAN. (2001). Breedplan users manual. Version IV. November, 2001

Gilmour, A.R., Cullis, B.R., Welham, S.J. and Thompson, R. (1999). ASREML Manual.

Graser, H-U., Tier, B., Johnston, D.J. and Barwick, S.A. (2005). *Aust. J. Exp.Agric.* 45, 913-921.

Koots, K.R., Gibson, J.P. and Wilton, J.W. (1994a). *Anim. Breed. Abstr*. 62, 309-388.

Koots, K.R., Gibson, J.P. and Wilton, J.W. (1994b). *Anim. Breed. Abstr*. 62, 825-853.

Meyer, K., Carrick, M.J. & Donelly, B.J.P. (1993). *J. Anim. Sci.* 71, 2614-2622.

Mohiuddin, G. (1993). *Anim. Breed. Abstr*. 61, 495-522.

Neser, F.W.C., Konstantinov, K.V. & Erasmus, G.J. (1996). *S. Afr. J. Anim. Sci*. 26, 75-78.

Pico, B.A., Neser, F.W.C., Van Wyk, J.B. (2004). *S. Afr. J. Anim. Sci.* 34 (supplement 2) 44-46

SAS. (2009). SAS Institute Inc. SAS® Procedures Guide, Cary, NC.

Swalve, H.H. (1993). *J. Anim. Breed. Genet*. 110, 241-252.

Van Niekerk, M., Neser, F.W.C. & Van Wyk, J.B. (2004). S. Afr. J. Anim. Sci. 34 (Issue 6, Suppl. 2), 113-115.

Van Niekerk, M and Neser, F.W.C. (2006). *S. Afr. J. Anim. Sci.*,36: 5 (Supplement 1) 6-9