Genetic parameters for growth traits in South African Limousin cattle

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Abstract

Accurate genetic parameters are vital for genetic prediction, selection on breeding values and creation of selection objectives. Consequently, records for birth weight (BW), 200 (WW), 400 (YW) and 600 (FW) day weight were analyzed to obtain heritability estimates. These records originated from Limousin herds with performance data on the South African Limousin Cattle Breeders' Society's database for the period 1980 to 2006. The dataset consisted of 26533 BW, 9756 WW, 6558 YW and 3329 FW records. Log likelihood ratio tests were used to indicate the most suitable model for each trait. Models tested included a herd-year-season by sire interaction (HYSxS) and permanent maternal environmental effect as additional random factors. Single trait analyses yielded direct heritability estimates of 0.09 and 0.19 for BW and WW, respectively while corresponding maternal heritability estimates were 0.05 and 0.12. A strong negative association was found between direct and maternal effects with a genetic correlation of –0.64 and –0.70 for BW and WW, respectively. Direct heritability estimates for YW and FW were 0.16 and 0.24, respectively. Direct genetic correlations of BW with YW and FW were 0.37 and 0.33, respectively. Direct genetic correlations of WW with YW and FW were 0.99 and 0.93, respectively while the correlation between YW and FW was 0.92. Heritability estimates indicate that genetic progress of the above traits will be slower than might be envisaged by some authors, due to lower direct estimates. The strong negative relationship between direct and maternal effects needs to be deliberated when defining selection objectives.

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Introduction

Maximum genetic response is favourable for traits of economic importance. The ability of an animal to put on weight up to a predefined age has a direct effect on the profitability of cattle producers and does not need any deliberation. It is however necessary that clear and well-defined selection objectives are compiled to insure that response to selection leads to overall improvement of animal production through increased profitability. Accurate heritability and genetic correlation estimates are very important to predict possible outcomes based on these selection objectives.

The importance of selection objectives is clearly outlined by many authors. Kluyts (2004) stated that the development of breeding objectives can be described in terms of various phases. These phases include, amongst others, the derivation of economic values after which the estimation of genetic parameters should follow (Kluyts, 2004). Notter *et al*. (1979) concluded that maternal and terminal sire breeds differ with respect to important economic traits with high economic values. For terminal sire breeds these traits included growth rate and mature size (Notter *et al*., 1979). Arango *et al*. (2002) showed that Limousin-sired cows as well as other continental European breeds tended to be heavier than breeds of British origin. This confirms the widely acknowledged classification of the Limousin breed as a sire breed, which is also the case in South Africa and justifies the necessity for genetic parameters for growth traits for the breed in South Africa. With more accurate information available for breeding, better selection decisions can be taken. This will result in more effective decisions and improve the chances of maintaining or increasing profitability in the short and long term (Kluyts, 2004).

The aim of the study was to derive heritability estimates and genetic correlations for growth traits in South African Limousin cattle, in an attempt to predict direct and correlated responses for the purpose of developing selection objectives.

Materials and Methods

Records from Limousin herds with performance data on the South African Limousin Cattle Breeders' Society's database for the period 1980 to 2006 were used in this study. Birth weight (BW), 200 (WW), 400 (YW) and 600 (FW) day weight were analyzed. Incomplete records were discarded. After editing, the dataset consisted of 26533 BW, 9756 WW, 6558 YW and 3329 FW records. (Co)variance components and heritability estimates were obtained through single trait analyses using the ASREML program (Gilmour *et al.*, 1999). Log likelihood ratio tests were used to determine the most suitable model for each trait (Table 1). The models described by Meyer (1992) were extended by including the herd-year-season x sire interaction (HYSxS) as an additional random effect. Herd-year-season and sex were included as fixed effects. Genetic correlations were obtained through two trait analyses with the same dataset as used in single trait analyses.

Table 1 Most suitable model for each trait as indicated by log likelihood ratio test (single trait analyses)

Effects	BW	WW	YW	FW
Direct	yes	yes	yes	yes
Maternal	yes	yes	-	-
Covariance between animal effects	yes	yes	-	-
Permanent maternal environment	yes	yes	-	yes
Herd-year-season x sire	yes	-	yes	-

BW – birth weight, WW – weaning weight, YW – yearling weight, FW – final weight, "yes" – effect was included in the analyses of the corresponding trait

Results and Discussion

The estimates from the HYSxS interaction were 0.13 and 0.07 (Table 3) for BW and YW respectively and were significant in these two traits. Van Niekerk *et al.* (2004) reported a value of 0.07 for both BW and YW in Nguni cattle while Pico (2004) obtained a value of 0.05 and 0.06 for BW and YW, respectively in South African Brahman cattle. The lower HYSxS interaction estimates which were obtained by other authors for BW may be explained by the fact that *Bos taurus africanus* and *Bos indicus* cattle are more adapted to harsh (high stress factors, e.g. heat and tick infestation) environments than *Bos taurus* cattle, as indicated by Vercoe & Frisch (1992). This is supported by Bishop (1993) when concluding that where environments differ sufficiently to make adaptation to environmental stresses necessary, genotype by environment interaction may be sufficiently important to consider when undertaking genetic improvement. However, it is not clear why HYSxS interactions are not significant for WW and FW. The inclusion of the HYSxS interaction led to a significant improvement in the log likelihood for BW and YW when the model used is compared with a similar model without the HYSxS interaction. This was also true for the estimates where in BW, there was a reduction in the direct heritability (0.21 to 0.09), maternal heritability (0.08 to 0.05) and direct-maternal correlation (-0.77 to -0.64) when the HYSxS interaction was included. In YW there was a reduction in the direct heritability of 0.18 to 0.16. Van Niekerk (2003) (Nguni cattle) found the same results for the corresponding traits and estimates. Neser *et al.* (1996) (Bonsmara cattle) also found a reduction in the direct additive variance when a HYSxS interaction was included while Robinson (1996) showed that direct-maternal correlation may be negative because of additional sire or sire x environment variation. Also in agreement with Neser *et al.* (1996) there is an increase in the error variance of BW when the HYSxS interaction was included, using the "best" model compared to a similar model without the HYSxS interaction. For YW however, there was a reduction in the error variance. Notwithstanding, when the error variance is expressed as a proportion of the total variance, there was a reduction in both BW (from 0.77 to 0.73) and YW (from 0.82 to 0.77).

The direct heritability estimates for BW (0.09), WW (0.19) and YW (0.16) (Table 2) are lower than the weighted mean heritability estimates of Koots *et al.*, (1994a) (0.31, 0.24 and 0.33, respectively). Bennett & Gregory (1996) found estimates of 0.47, 0.26 and 0.40 for birth weight, 200 day weight and 368 day weight, respectively (American Limousin cattle). The estimate for FW (0.24) (Table 2) is higher than the estimate reported by Pico (2004) (0.18).

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Table 2 Direct heritability estimates from single trait analyses (diagonal). Direct genetic correlations (above diagonal) and phenotypic correlations (below diagonal) from two trait analyses. Corresponding standard errors in brackets (s.e.)

Trait	BW	WW	YW	FW
BW	**0.09 (0.02)**	0.41 (0.15)	0.37 (0.10)	0.33 (0.09)
WW	0.16 (0.02)	**0.19 (0.04)**	0.99 (0.03)	0.93 (0.04)
YW	0.14 (0.01)	0.52 (0.01)	**0.16 (0.03)**	0.92 (0.04)
FW	0.08 (0.01)	0.49 (0.01)	0.73 (0.01)	**0.24 (0.05)**

BW – birth weight, WW – weaning weight, YW – yearling weight, FW – final weight

Table 3 Parameter estimates from single trait analyses. Corresponding standard errors in brackets (s.e.)

Parameter	BW	WW	YW	FW
Maternal heritability	0.05 (0.01)	0.12 (0.04)	-	-
Genetic correlation between animal effects	-0.64 (0.10)	-0.70 (0.11)	-	-
Permanent maternal environment / phenotypic variance	0.04 (0.01)	0.17 (0.03)	-	0.08 (0.03)
Herd-year-season x sire / phenotypic variance	0.13 (0.01)	-	0.07 (0.01)	-

BW – birth weight, WW – weaning weight, YW – yearling weight, FW – final weight, - effect not included in single trait analyses (see Table 1)

The maternal heritability estimate for BW (0.05) (Table 3) was lower than the estimate of Koots *et al*. (1994a) (0.13) while the estimate for WW (0.12) compared well with that of Koots *et al*. (1994a) (0.14). Permanent maternal environment expressed as a proportion of the phenotypic variance was 0.04, 0.17 and 0.08 for BW, WW and FW, respectively (Table 3). The estimate for WW corresponds well with the estimate by Neser *et al*. (1996) (0.15). This seems to be as important as the direct heritability in WW for South African Limousin cattle. Meyer (1992) reported a permanent maternal environmental estimate of 0.23 and stated that WW in Hereford cattle was primarily determined by this effect. Direct-maternal correlations for BW and WW were –0.64 and –0.70, respectively (Table 3). These estimates are higher than the estimates by Van Niekerk (2003) (BW ranged from –0.36 to –0.59, WW from –0.17 to –0.50) and Pico (2004) (BW ranged from –0.36 to –0.53 and WW from –0.02 to –0.30).

Genetic correlations among the different growth traits ranged from low (0.33) to high (0.99) (Table 2). All direct genetic correlations were significant except the correlation between BW and WW (0.41 ± 0.15). The direct correlations of BW with YW and FW were 0.37 and 0.33 (Table 2), respectively and are below the estimates of Pico (2004) (0.47 and 0.52, respectively). Koots *et al*., (1994b) reported an estimate of 0.55 between BW and YW. The direct correlations of WW with YW and FW were 0.99 and 0.93 (Table 2), respectively and correspond well with estimates of Pico (2004) (0.88 and 0.91, respectively), while Koots *et al*. (1994b) reported an estimate of 0.79 between WW and YW. The direct correlation between YW and FW was 0.92 (Table 2) and corresponds with the estimate of 0.83 of Pico (2004).

Conclusions

The direct heritability estimates for growth traits of the South African Limousin were lower than estimates from other authors for different breeds. This may suggest that genetic progress with reference to the direct genetic component of the South African Limousin could be slower than envisaged by other studies. One possible reason for this may be less genetic variation in the South African population. Maternal heritability estimates for BW were lower than estimates by other studies while the estimate for WW compared well with other studies. The genetic improvement of the milk production of cows seems possible,

although progress may be slow as the maternal estimate for WW was low. Genetic progress with reference to direct components of growth might be more progressive in some environments with certain sires as there was a significant interaction between contemporary groups and sires that explained part of the direct heritability estimate. However this was only the case with BW and YW and not in WW and FW The moderate to relatively strong negative direct-maternal correlation also needs to be deliberated on in breeding programs. Genetic correlations of BW with post-weaning weights (YW and FW) are low and genetic progress in these traits without the increase of BW, and consequently dystocia, seems possible. However, selection on WW will increase post-weaning weights (YW and FW) due to high direct correlations. This might increase mature weight and maintenance requirements that could decrease the efficiency (profitability) of beef production due to higher inputs. Genetic parameters estimated in this study should be seen and used as a step closer to composing a complete selection index with the aim of improving overall profitability.

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