

## Genotype x ecological region interaction in the Nguni cattle breed

M. van Niekerk, F.W.C. Naser<sup>#</sup> and J.B. van Wyk

Department of Animal, Grassland and Wildlife Sciences, University of the Free State, P.O. Box 339, Bloemfontein 9300, South Africa

---

### Abstract

Weaning weight (WW) records were used to investigate the presence of a genotype x ecological region interaction as well as the magnitude and significance of such an interaction. Records from herds were allocated to one of three veld types that described the specific region in which each herd was situated, i.e. sweetveld (Region 1), sourveld (Region 2) and mixed veld (Region 3). The data set consisted of 2136 records for Region 1, 3984 for Region 2 and 11432 for Region 3. Weaning weight data from each region was considered as separate traits and two trait analyses of the three different regions were carried out to determine (co)variance components. Weighted direct heritability estimates for WW ranged from 0.23 to 0.45. Direct genetic correlations of Regions 2 and 3 with Region 1 were significant and were 1.00 and 0.71 respectively. This indicates that no G x E occurred between Regions 1 and 2, but indeed between Regions 1 and 3. The genetic correlation between Regions 2 and 3 (0.60) were not significantly different from 0.

---

**Keywords:** Genotype x environment interaction, growth traits, beef cattle

<sup>#</sup> Corresponding author. E-mail: naserfw.sci@mail.uovs.ac.za

### Introduction

Nguni cattle, like most other beef producing breeds, are kept under a wide variety of extensive environments throughout Southern Africa. The specific differences of these environments may have a greater effect on some genotypes than others (Falconer & Mackay, 1997). This could cause a change in the order of merit, as some genotypes might be more sensitive than others to environmental differences. Thus, it will be of economic importance to identify the presence of a genotype by environment interaction (G x E), as this will influence the genetic progress in a breeding program.

The aim of this study was to determine whether any G x E is present and if present, what the magnitude and significance of the interaction is in the Nguni breed.

### Material and Methods

Weaning weight (WW) records from Nguni herds participating in the National Beef Cattle Improvement Scheme (NBCIS) from 1960 to 2001, were used. Records from herds were allocated to one of three veld types according to Tainton (1999) (sweetveld - Region 1, sourveld - Region 2 and mixed veld - Region 3). Incomplete records were discarded. After editing the numbers of records for Regions 1, 2 and 3 were 2136, 3984 and 11432, respectively. Herds that were linked to less than two other herds through shared sires were excluded. The number of shared sires was 13 for Regions 1 and 2, 23 for Regions 1 and 3 and 17 for Regions 2 and 3. The greatest number of records was found in Region 3 as the Bartlow Combine Nguni Stud, a former government herd, contributed 78% of the records in this region. A more detailed description of the data set is given by Van Niekerk (2003). Heterogeneous variances were found to be non-significant as tested by correcting the y-value with the standard deviation of each contemporary group. The method used to estimate the existence as well as the magnitude of G x E was suggested by Falconer (1952) and reviewed by Mathur (2002). (Co)variance components and heritability estimates were obtained through two trait analyses of the three different regions using the ASREML program (Gilmour *et al.*, 1999). Fixed effects included were herd-year-season and sex with the direct genetic effect of animal as random. The model used in the two trait analyses of Regions 1 and 3 and of Regions 2 and 3 included a direct additive effect, the permanent environmental effect of the dam and the herd-year-season x sire interaction (HYSxS) effect. The two estimates for every region were weighted using the equations of Koots *et al.* (1994) as some corresponding estimates from the respective regions differed considerably. The same model was also used for Region 1 in the two trait analyses of Regions 1 and 2, but because of convergence problems the permanent environmental effect of the dam was excluded for Region 2. Convergence problems also prevented the use of a three trait analysis. The corresponding standard errors were not weighted since the values were similar.

### Results and Discussion

Bishop (1993) concluded that for environments which differ only in the quality of nutrition available,  $G \times E$  for weight gain in beef cattle are likely to be small and probably will not be an important factor when making selection decisions. However, where environments differ sufficiently to make adaptation to environmental stresses necessary,  $G \times E$  may be sufficiently important to consider when undertaking genetic improvement. In Region 2 animals are not kept exclusively on natural grazing in the winter, as cultivated pastures and the feeding of supplements are not uncommon. If the recording of weights in Region 2 occurred under an 'artificial' environment where dipping and the feeding of supplements are practiced, differences between Regions 1 and 2 are not surprising. The issue of the contribution of one herd to most of the records in Region 3 is but one of the factors impairing the accuracy of the results obtained. These factors include unsatisfactory linkage of herds through sires used. There were only six sires with progeny in all three regions. In addition, due to limitations in the data set, records from sires with progeny in a minimum of two herds in different regions were not present. The restricted use of artificial insemination in the breed may have played a part.

The inclusion of the maternal genetic effect caused the parameters and/or log likelihood not to converge. Therefore this effect was excluded from final models. Weighted direct heritability estimates (Table 1) are higher than those estimated by Van Niekerk *et al.* (2004) (0.17) for WW. The increase in the direct heritability was evident in the two trait estimates where Region 1 and 2 were analyzed together. Here, the exclusion of the permanent maternal environmental effect with respect to Region 2 (see Material and Methods), caused a significant increase in the direct additive variance and subsequent heritability estimate. Koots *et al.* (1994) reported a weighted mean direct heritability of 0.24 for WW. The permanent maternal environment as a proportion of the phenotypic variance of Region 3 (weighted) (0.11) and Region 2 (unweighted) (0.10) is in agreement with the estimate by Van Niekerk *et al.* (2004) (0.14), while the estimate of Region 1 (weighted) (0.26) is well above. Estimates of the HYSxS interaction as a proportion of the phenotypic variance of Region 1, 2 and 3 (0.31, 0.39 and 0.31 respectively) are much higher than the corresponding estimate reported by Van Niekerk *et al.* (2004) (0.09). A conceivable reason may be the exclusion of the covariance between the two animal effects that caused an increase in the HYSxS interaction variance, as was the case in single trait analyses (Van Niekerk, 2003). Lee & Pollak (1997) reported corresponding results when a sire x year interaction was excluded.

**Table 1** Weighted direct heritability estimates (diagonal) and direct genetic correlations (off-diagonal) with corresponding average standard errors (s.e.) for weaning weight

Parameter	Region 1	Region 2	Region 3
Region 1	<b>0.23 (0.07)</b>	1.00 (0.33)	0.71 (0.19)
Region 2		<b>0.45 (0.04)</b>	0.60 (0.34)
Region 3			<b>0.25 (0.03)</b>

The results (Table 1) indicate that no genotype x ecological region interaction existed between Regions 1 and 2. However, a possible interaction existed between Regions 1 and 3 (0.71). Robertson (1959) suggests that if the genetic correlation between environments is less than 0.8, the genotype x environment interaction is of biological importance. Vercoe & Frisch (1992) concluded that a  $G \times E$  of small magnitude can only occur when genotypes with similar configurations of production potential and resistance to stress are compared, no matter how different the environments may be. In this regard, there is an indication of some difference in the genotypes between Regions 1 and 3 (Table 1). Consequently, there will be re-ranking in Region 1 when sires are selected in Region 3 and vice versa. The conclusion Vercoe & Frisch (1992) come to regarding low  $G \times E$ , might be explained by the fact that records for Region 3 mainly originated from one herd, namely the Bartlow Combine Nguni Stud. This may cause some bias, as the genetic correlation may well be a comparison between all the herds in Region 1 with one prominent herd in Region 3, which practised specific selection strategies, especially with respect to WW (Gertenbach & Kars, 1999). Therefore it might be a comparison with a herd with a specific genetic merit, which may differ, greatly from the rest of the breed. There are indications of differences in the production potential as well as resistance to stress between the Bartlow Combine stud and the rest of the breed. The direct genetic correlation between

Regions 2 and 3 was 0.60, but it did not differ from 0 ( $P > 0.05$ ). The inclusion of the HYSxS interaction effect is important as pointed out by Bertrand *et al.* (1985, 1987). These authors state that a genotype x environment interaction may in part be the cause of changes in sire ranking among contemporary groups, rather than changes in ranking of sires across the different environments. The exclusion of this interaction from the two trait analyses may thus have caused an apparent genotype x environment interaction. This is supported by results from Santa Gertrudis cattle suggesting an increase in the genetic correlation (0.63 to 0.83) between two different environments when a sire x contemporary group interaction was fitted (Bradfield *et al.*, 1997). Similar results were reported by Nephawe *et al.* (1999).

## Conclusions

No real genotype x ecological region interaction was found between Regions 1 and 2, suggesting that there will be no ranking order change between sires in these two regions. However, results show a genotype by ecological region interaction between Regions 1 and 3 indicating that there may be a change in the ranking order of sires. The high estimates of the HYSxS interaction as a proportion of the phenotypic variance in the different regions indicate that an apparent genotype x environment interaction may result from the re-ranking of sires between different contemporary groups. Moreover, the importance of the structure of the data in G x E studies was also considered. The extended use of shared sires and artificial insemination in the breed would have benefited the accuracy of the study. The classification of regions or environment in such studies also needs to be more precise – not just in terms of feeding, but also at the management level. This may lead to less confounding of genetics with respect to resistance to environmental stresses, which might be complicated by management practices such as dipping and feeding supplements.

## References

- Bertrand, J.K., Berger, P.J. & Willham, R.L., 1985. Sire x environment interaction in beef cattle weaning weight field data. *J. Anim. Sci.* 60, 1396-1402.
- Bertrand, J.K., Hough, J.D. & Benyshek, L.L., 1987. Sire x environment interaction and genetic correlations of sire progeny performance across regions in dam-adjusted field data. *J. Anim. Sci.* 64, 77-82.
- Bishop, S.C., 1993. Grassland performance of Hereford cattle selected for rate and efficiency of lean gain on a concentrate diet. *Anim. Prod.* 56, 311-319.
- Bradfield, M.J., Graser, H-U. & Johnston, D.J., 1997. Investigation of genotype x production environment interaction for weaning weight in the Santa Gertrudis breed in Australia. *Aust. J. Agric. Res.* 48, 1-5.
- Falconer, D.S., 1952. The problem of environment and selection. *Amer. Nat.* 86, 293-298.
- Falconer, D.S. & Mackay, T.F.C., 1997. *Introduction to Quantitative Genetics*. Longman, England.
- Gertenbach, W.D. & Kars, A.A., 1999. Toward the conservation of the indigenous cattle of Kwazulu-Natal. *S. Afr. J. Anim. Sci.* 29, 55-63.
- Gilmour, A.R., Cullis, B.R., Welham, S.J. & Thompson, R., 1999. *ASREML Reference Manual*. NSW Agriculture Biometric Bulletin No.3 NSW Agriculture, Orange Agricultural Institute, Forest Road, Orange 2800 NSW, Australia.
- Koots, K.R., Gibson, J.P., Smith, C. & Wilton, J.W., 1994. Analyses of published genetic parameter estimates for beef production traits. 1. Heritability. *Anim. Breed. Abstr.* 62, 309-338.
- Lee, C. & Pollak, E.J., 1997. Relationship between sire x year interactions and direct-maternal genetic correlation for weaning weight of Simmental cattle. *J. Anim. Sci.* 75, 68-75.
- Mathur, P.K., 2002. Methods for estimation and use of genotype-environment interactions. 7th Wrld Congr. Genet. Appl. Livest. Prod. August 19-23, Montpellier, France. CD-ROM communication No. 25-35.
- Nephawe, K.A., Nesor, F.W.C., Roux, C.Z., Theron, H.E. & Erasmus, G.J., 1999. Sire x ecological region interactions in Bonsmara cattle. *S. Afr. J. Anim. Sci.* 29, 189-201.
- Robertson, A., 1959. The sampling variance of genetic correlation coefficient. *Biometrics* 15, 469-485.
- Tainton, N., 1999. *Veld Management in South Africa*. University of Natal press. Scottsville, South Africa.
- Van Niekerk, M., 2003. A genetic evaluation of production traits in Nguni cattle. M.Sc. (Agric) thesis. University of the Free State, Bloemfontein, South Africa.
- Van Niekerk, M., Nesor, F.W.C. & Van Wyk, J.B., 2004. (Co)variance components for growth traits in the Nguni cattle breed. *S. Afr. J. Anim. Sci.* 34 (Suppl. 2), 113-115.
- Vercoe, J.E. & Frisch, J.E., 1992. Genotype (breed) and environment interaction with particular reference to cattle in the tropics. *Aust. J. Anim. Sci.* 5, 401-409.