

## GENETIC STABILITY OF TWO MERINO SHEEP CONTROL POPULATIONS

G.J.Erasmus

Dept. of Animal Science, University of the Orange Free State  
P.O.Box 339, Bloemfontein 9300, Republic of South Africa.

### SUMMARY

A mixed model analysis on three traits, employing a single trait animal model, was used to evaluate the genetic stability in two Merino sheep control populations. No significant trend in clean fleece weight or fibre diameter was detected in either of the populations, but a highly significant ( $P < 0.01$ ) positive trend for mature body weight was found in both. The trend is ascribed to natural selection and poor design in the one case, while the small trend in the other population is difficult to explain. It is concluded that mixed model analyses can be useful in checking the stability of control populations.

### INTRODUCTION

Control populations provide one method of evaluating genetic progress in selection experiments. The genetic stability of such a control population is of crucial importance if genetic gain in selected lines is to be quantified correctly. Control populations can be designed to minimize the possibilities of random genetic drift and directional genetic change as discussed by Hill (1972). This does not, however, guarantee genetic stability and the person analyzing the results often has no proof that the design has been strictly adhered to.

C.R.Henderson's mixed model methodology provides an alternative of separating genetic and environmental trends. It can be used to evaluate genetic trend without the use of a control population and also to detect possible genetic change in such a control.

The aim of this paper is to report on the genetic trend found by employing this methodology in two Merino sheep control populations in South Africa.

### MATERIAL AND METHODS

The "Klerfontein" control flock, initiated in 1961 and terminated in 1983, was used to monitor selection response in an arid environment (Erasmus, 1988). The flock consisted of 200 ewes and 10 rams. Ewes were replaced after five matings and rams were replaced annually. Replacements were merely chosen at random.

The "Tygerhoek" control flock, initiated in 1968, is used extensively in genetic research with the main objective being the evaluation of response to direct and indirect selection for wool production under favourable conditions (Heydenrich, du Plessis & Cloete, 1984). The flock consisted of 160 ewes and 16 rams until 1975 after which it was increased to 200 ewes and 20 rams. Ram replacements are chosen at random in such a way that each ram is replaced by a son and used for one season only. Ewes are normally replaced by a second daughter to reach mating age (Heydenrych, *et al.*, 1984).

For both flocks, single trait mixed model analyses for body weight, clean fleece weight and fibre diameter, all recorded at 18 months of age, were carried out. The following linear mixed model was fitted:

$$y_{ijk} = \mu + b_i + c_j + u_k + e_{ijk}$$

where:  $y_{ijk}$  = a measurement on the  $k^{\text{th}}$  individual born in the  $i^{\text{th}}$  year and belonging to the  $j^{\text{th}}$  handicap class,  
 $\mu$  = the population mean,  
 $b_i$  = the fixed effect of the  $i^{\text{th}}$  year of birth,  
 $c_j$  = the fixed effect of the  $j^{\text{th}}$  handicap class (sex, birth status and age of dam),  
 $u_k$  = the random effect (breeding value) of the  $k^{\text{th}}$  individual,  
 $e_{ijk}$  = random error.

Breeding value solutions were obtained using an animal model adaptation of the method devised by Schaeffer and Kennedy (1986).

#### RESULTS AND DISCUSSION

In the "Klerfontein" control flock the regression of mean annual predicted breeding values on year of birth was non significantly deviant from zero for both clean fleece weight and body weight. In the "Tygerhoek" control this was also the case with clean fleece weight, but fibre diameter showed a significant ( $P < 0.05$ ) positive trend mainly due to the high breeding values obtained for the 1974 progeny group. From 1974 onward the trend was non significant. The high breeding value in 1974 could be due to natural selection, since the mortality rate was the highest (60 %) yet recorded.

Body weight showed a highly significant ( $P < 0.01$ ) positive trend in both populations as illustrated in Figure 1.

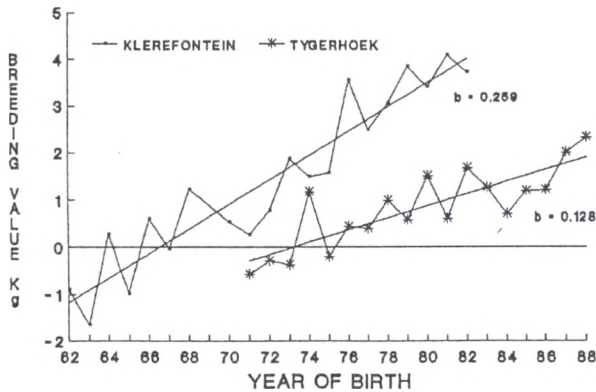


FIGURE 1: GENETIC TREND IN BODY WEIGHT IN THE "TYGERHOEK" AND "KLEREFONTEIN" CONTROL POPULATIONS.

In the "Tygerhoek" control, with an improved design, the genetic trend was far less than the "Klerefontein" one in spite of a higher heritability (0.511 vs. 0.247) being used in the mixed model equations. Any genetic trend in a control population is, however, a cause for concern.

The positive response in the "Klerefontein" control population can be ascribed partly to natural selection in a harsh environment where some sheep were at a sub - optimum body mass (Erasmus, 1988). The response in the "Tygerhoek" control is difficult to explain and warrants further investigation. It is interesting to note that the significant trend was only obtained after inclusion of the data of the last two birth years (1987 & 1988).

Although it can be argued that control populations are unnecessary when selection experiments are analyzed by mixed model methods, they can supply valuable additional information during the course of an experiment. Mixed model methodology can be used to good effect to check their stability. The results obtained in the two populations discussed suggest that when a mixed model analysis is not possible (for instance due to lack of records of parents), the results obtained should be interpreted with caution.

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