

## Genetic and environmental trends of early growth traits in the Elsenburg Dormer sheep stud

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Data from the Elsenburg Dormer sheep stud were used to estimate genetic and environmental change in early growth traits from 1943 to 1990. Best linear unbiased predictions (BLUP) of breeding values were obtained by Restricted Maximum Likelihood (REML) procedures fitting a direct additive and maternal additive genetic model. Environmental change, calculated as the difference between phenotypic and genetic values, was found to be negative for all traits studied. Genetic trends were smaller but significantly positive. The higher maternal trends reveal that the biggest genetic improvement was in the additive genetic ability of ewes to produce faster growing or heavier lambs. The relative low but linear genetic trends suggest that selection pressure on these traits was low during the 48 years, probably owing to higher selection emphasis on traits other than the growth traits studied.

Data van die Elsenburg Dormerskaapstoet is gebruik om die genetiese en omgewingsveranderinge in vroeë groei-eienskappe vanaf 1943 tot 1990 te beraam. Beste lineêre onsydige beramers (BLUP) van teelwaardes is verkry deur Bepaalde Maksimum Aanneemlikheid (REML)-prosedures deur 'n model wat direkte additiewe sowel as materne additiewe waardes as toevallige effekte ingesluit het. Omgewingsveranderinge, bereken as die verskil tussen fenotipiese en genetiese waardes, was negatief vir al die eienskappe. Genetiese tendense was kleiner maar betekenisvol positief. Die hoër tendense vir maternale waardes dui daarop dat die beste genetiese vordering gemaak is in die additiewe genetiese vermoë van oëie om vinniger-groeiende of swaarder lamms te lewer. Die relatiewe lae maar lineêr-betekenisvolle genetiese tendense dui aan dat seleksiedruk op hierdie eienskappe baie laag was gedurende die afgelope 48 jaar, moontlik as gevolg van hoër seleksiedruk op ander eienskappe as groei-eienskappe.

**Keywords:** Dormer sheep, early growth traits, genetic and environmental trends.

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### Introduction

The primary goal of animal breeders is to maximize the rate of genetic improvement through selection. In a meat sheep enterprise, this implies maximizing genetic improvement of meat production. Achieving this goal will depend mainly on the accuracy of selecting superior parents for the next generation. To determine the effectiveness of genetic selection, genetic trends in the population under consideration must be monitored.

Until recently, no appropriate procedures were available to determine which part of the total phenotypic change was in fact genetic. Henderson (1973) first described the use of mixed linear models for animal breeding, and this methodology is now being applied in animal genetic evaluation programmes all over the world. An appropriate animal model in particular, incorporates all known relationships in the population and is currently the most effective method of separating genetic and environmental effects (Henderson, 1973; Wiggans & Misztal, 1987). The statistical and genetic properties of an animal model have been well documented (Henderson, 1988; Kennedy *et al.*, 1988). Other effects such as maternal genetic effects, which is especially important in early growth traits such as those in this study, can be accounted for by simply fitting them as additional random effects.

The purpose of this study was to assess genetic change in early growth traits in a closed sheep breeding population by

partitioning the phenotypic trend into its causal components, i.e. environmental and genetic effects.

### Material and Methods

#### Data

Records used in this study were obtained from the registered Elsenburg Dormer sheep stud, and were collected from 1943 to 1990. A detailed description of the history, management and selection practices of the animals is given by Van Wyk *et al.* (1993a). The size of the stud was maintained at approximately 180 breeding ewes annually and 7 ram families.

The traits considered were birth weight (BW), weaning weight (WW), average daily gain (ADG) (0–100 days) and the Kleiber ratio (KL) ( $ADG/WW^{0.75}$ ), as described by Van Wyk *et al.* (1993a). WW was adjusted to a 100-day equivalent before analysis.

#### Statistical analysis

Direct and maternal breeding values were calculated for each trait by single trait mixed model analyses. The inclusion of two random effects per trait would make a multiple trait analysis prohibitive, since the coefficient matrix would be extremely large. Also, the genetic correlation between BW and the other traits was unreliable because of large standard errors (Van Wyk *et al.*, 1993c). A multiple-trait analysis was in any

case not possible because the method of estimation used yielded a non-positive-definite matrix.

The following mixed linear model was used to describe the data:

$$y = Xb + Z_1a + Z_2m + e$$

where  $y$  is a vector of observations of BW, WW, ADG and KL,  $b$  is a vector of fixed effects consisting of year-season of birth, age of dam, sex of lamb and birth status of animals as identified by Van Wyk *et al.* (1993a),  $a$  is a random vector of direct additive genetic effects of the animals,  $m$  is a random vector of the maternal additive genetic effects,  $e$  is the random vector associated with residual errors and  $X$ ,  $Z_1$ ,  $Z_2$  are incidence matrices relating observations to the effects in the model.

The model applied in this study is a direct animal additive and maternal additive genetic model. It was therefore assumed that all genetic effects, both direct and maternal, stem from a large number of additive loci.

The variance-covariance matrices were assumed to have the following structure:

$$\begin{aligned} \text{Var}(a) &= Z_1AZ'_1\sigma_a^2, \text{Var}(m) = Z_2AZ'_2\sigma_m^2 \\ \text{Cov}(a,m) &= Z_1AZ'_2\sigma_{am} \text{ and } \text{Var}(e) = I\sigma_e^2, \text{ with} \\ \text{Var}(y) &= Z_1AZ'_1\sigma_a^2 + Z_2AZ'_2\sigma_m^2 + Z_1AZ'_2\sigma_{am} + I\sigma_e^2 \end{aligned}$$

where  $A$  is Wright's numerator relationship matrix with inbreeding included,  $I$  is an identity matrix,  $\sigma_a^2$ ,  $\sigma_m^2$  and  $\sigma_e^2$  are the direct and maternal additive genetic variance and residual variance components, respectively, and  $\sigma_{am}$  is the covariance between additive direct and additive maternal effects. The relationship matrix was constructed using full pedigree information and inbreeding was taken into account.

Breeding values were obtained as a by-product from the DFREML programme of Meyer (1989; 1991) used in the estimation of variance-covariance components (Van Wyk *et al.*, 1993b).

Genetic trends were calculated as the regression of average predicted breeding values on year of birth.

There are different ways of defining and computing environmental trends. The most common is to regress the year-season solution on the year-season number. This, however, is only the year-season effect and not the total environmental effect, since adjustments are made for known environmental effects. It was therefore decided to calculate the environmental trend by subtracting the genotypic (breeding value) from the phenotypic value.

The generation interval was calculated as the average actual age of the parents when the progeny were born.

With a combined standardized selection differential of 1.509, as calculated for this stud by Van der Merwe (1976), a generation interval of 3.31 years,  $h^2$  of 0.12 (Van Wyk *et al.*, 1993b) and a coefficient of variation of 19.01% (Van Wyk *et al.*, 1993a), the expected annual genetic response in WW – if this was the only trait considered in selection – was estimated as 1.04%. The actual response obtained was compared with this estimated response.

## Results and Discussion

Genetic and environmental trends are presented in Table 1. Linear regressions produced good fits as indicated by the high

**Table 1** Genetic and environmental trends for birth weight (BW), weaning weight (WW), average daily gain (ADG) and Kleiber ratio (KL)

Trait	Linear trend				
	Genetic				Environmental
	Animal <sub>D</sub> <sup>a</sup>	Sire	Dam <sub>D</sub>	Dam <sub>M</sub> <sup>b</sup>	
BW (kg/yr)	0.023	0.020	0.020	0.004	-0.021
SE <sup>c</sup>	0.001	0.001	0.001	0.000	0.002
WW (kg/yr)	0.071	0.081	0.062	0.105	-0.137
SE	0.002	0.002	0.003	0.005	0.024
ADG (g/d/yr)	0.670	0.764	0.580	0.836	-1.350
SE	0.016	0.015	0.030	0.043	0.243
KL	0.0157	0.018	0.013	0.013	-0.036
SE	0.001	0.001	0.001	0.001	0.008

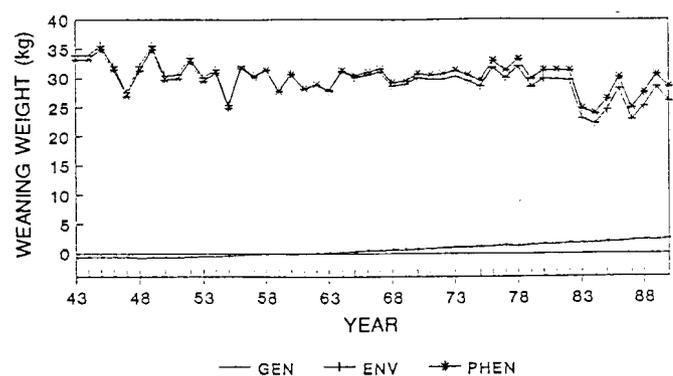
<sup>a</sup> D = Direct additive.

<sup>b</sup> M = Maternal additive.

<sup>c</sup> SE = Standard error.

$R^2$  values obtained, varying between 0.97 to 0.85 for genetic trends. In a fluctuating environment, environmental trend lines are not expected to produce such good fits and these varied between  $R^2 = 0.33$  and  $R^2 = 0.54$ . All the trends differed significantly ( $P < 0.001$ ) from zero. Genetic trends were all positive, whereas the environmental trends were all negative.

As shown by Wilson & Willham (1986), it is not necessary to remove environmental trends from phenotypic trends to obtain unbiased estimates of genetic trends, environmental trends could in itself be informative to a commercial breeder to monitor actual management effects and/or climatic changes. To illustrate this perspective in the stud under study, mean annual, phenotypic, genetic and environmental values are shown graphically on the same scale for WW in Figure 1.



**Figure 1** Annual mean phenotypic, genetic and environmental values for weaning weight.

ADG and KL followed similar patterns and are consequently not presented.

Figure 1 indicates a gradual decrease of about 2.0 kg in phenotypic value for WW from 1943 to 1982. There were, however, serious decreases of about 7.0 kg in the mid 1980s. Over a period of 48 years the phenotypic trend for WW

decreased by about 5.0 kg. The small positive contribution of about 3.0 kg of genetic trend to environmental trend, helped to counteract a larger decrease in phenotypic trend. Since animals were kept mainly on kikuyu grass pastures, fluctuations in environmental trend were caused mainly by fluctuations in annual rainfall which influence the amount and quality of the available forage. Also, several people were responsible for the management of the stud over the period of 48 years, and this could have contributed to certain unexplained fluctuations.

The genetic trend (Figure 1) showed a small but steady improvement in WW. The smoothness of the trend can be ascribed to the fact that selection response, estimated by mixed model methodology, lies between the true and predicted response and therefore tends to be smoother than the true response (Sorenson & Kennedy, 1986). In addition, the stud was closed for the whole period which resulted in a high relationship between animals and therefore a high correlation between their predicted breeding values.

The average annual genetic improvement of 0.02 kg, 0.07 kg, 0.67 g/d and 0.02 for BW, WW, ADG and KL, respectively, represented about 0.6%, 0.2%, 0.3% and 0.1% of the least-squares mean of all animals born during 1943 to 1990. As reported earlier, expected genetic gain in WW was estimated as 1.04% per year. Thus the Elsenburg Dormer stud has achieved about 19% of the possible gain in WW which represents the opportunity lost if increase in WW had been the sole objective. The low genetic gain in growth traits indicated that the selection differential was not maximized. Reduced selection pressure on these traits was mainly due to more emphasis placed on traits other than growth rate, such as conformation and visually assessed 'size'.

Prewaning growth rate of lambs is influenced not only by their own genotype but also by environmental influences which may be partly attributable to the genotype of the mother. The genetic trends (Table 1) show that the highest positive genetic increase was the genetic ability of ewes to produce faster growing or heavier lambs. The trend in direct and sire breeding values suggests that selection pressure on especially sires for the traits considered was low during the 48 years studied. This might be due to selection for a specific preconceived 'Dormer type' which is a prerequisite for registration. Apart from the emphasis placed on visual appearance in selection, the parentage of each possible sire was considered in an attempt to reduce the rate of inbreeding.

### Conclusions

The Elsenburg stud is not only the foundation Dormer stud, but an important source of genetic material to the Dormer sheep breed. The results obtained in this study therefore provide an important perspective on the development of this breed. Advanced scientific procedures have shown that the selection policy followed did not maximize possible genetic

gains in the traits studied. However, it was also illustrated that an environmental decline in the expression of these traits can be counteracted, however slightly, by an increase in genetic value.

There was very little, if any, direct selection for the traits studied and their positive genetic trends must mainly constitute a correlated response, most probably as a result of selection for visually assessed 'size'. The slight genetic increase in KL suggests a small possible increase in efficiency. However, the small environmental decrease in KL, together with the other traits, seems to suggest that efficiency as measured by KL was lower under poorer environmental conditions. More studies, especially on efficiency, are needed if the higher possible genetic progress by selection on BLUP of breeding values is to be properly exploited.

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