

ESTIMATION OF ADDITIVE AND DOMINANCE VARIANCES IN WOOL PRODUCTION TRAITS OF WESTERN AUSTRALIAN MERINO SHEEP

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INTRODUCTION

Genetic evaluations for Merino sheep have been largely restricted to additive animal models. Including nonadditive effects in genetic evaluations might improve estimation of additive effects and also aid in planning matings to improve progeny performance (Hayes and Miller, 2000). Considerable progress has been made in the study of nonadditive variation of farm animals (Henderson, 1985; Smith and Maki-Tanila, 1990; Hoeschele and VanRaden, 1991; Mizstal, 1997). Most studies on nonadditive effects have been in species other than sheep (Rye and Mao, 1998; Mizstal and Besbes, 2000). No information on nonadditive genetic effects in Merino sheep is available in the animal breeding literature.

The objective of the present study was to estimate additive, dominance and permanent environmental variances for wool production traits in Merino sheep.

MATERIAL AND METHODS

Data. The data consisted of records on greasy fleece weight (GFW), clean fleece weight (CFW), yield (Y) and mean fibre diameter (FD) from a resource flock held at Katanning in Western Australia. A total of four strains, each consisting of four daughter studs, were represented in the data. A detailed description of the data collection and flock history was given by Cloete *et al.* (2001). Nongenetic factors affecting the production traits included paddocks (85), year of birth (1982-1993), sex (male or female) and age of dam (2 to 4+ years) which were fitted as covariates. The distribution of records over sires and dams is presented in Table 1.

Table 1. Descriptive statistics of greasy fleece weight (GFW), clean fleece weight (CFW), yield (Y) and fibre diameter (FD)

Trait	Mean	SD	No. of sires	No. of dams	No. of progeny
GFW (kg)	4.71	0.99	435	3953	9337
CFW (kg)	3.32	0.75	435	3949	9284
Y (%)	70.60	4.98	435	3946	9288
FD (μm)	21.06	1.86	435	3949	9345

Models of analysis. All traits were analysed using three variants of an animal model. Model 3 was the most complete model; Models 1 and 2 were subsets of Model 3. The equation for model 3 is:

$$y = Xb + Za + Sd + Wl + Pc + e$$

where: \mathbf{y} is the vector of observations; \mathbf{b} is the vector of fixed effects; \mathbf{a} , \mathbf{d} , \mathbf{l} and \mathbf{c} are vectors of random additive, dominance, bloodline and common environmental effects; \mathbf{e} is the vector of random residual effects; \mathbf{X} , \mathbf{Z} , \mathbf{S} , \mathbf{W} and \mathbf{P} are incidence matrices corresponding to \mathbf{b} , \mathbf{a} , \mathbf{d} , \mathbf{l} and \mathbf{c} , respectively.

The second moments of the model were assumed to be:

$$\text{Var} \begin{bmatrix} a \\ d \\ l \\ c \\ e \end{bmatrix} = \begin{bmatrix} A\sigma_a^2 & 0 & 0 & 0 & 0 \\ 0 & D\sigma_d^2 & 0 & 0 & 0 \\ 0 & 0 & I\sigma_l^2 & 0 & 0 \\ 0 & 0 & 0 & I\sigma_c^2 & 0 \\ 0 & 0 & 0 & 0 & I\sigma_e^2 \end{bmatrix}$$

Where: σ_a^2 , σ_d^2 , σ_l^2 , σ_c^2 , σ_e^2 are additive, dominance, line, common environmental and residual variances, respectively; \mathbf{I} is an identity matrix, \mathbf{A} is the numerator relationship matrix and \mathbf{D} is the dominance relationship matrix. Model 2 was the same as Model 3 but without the common environmental effect; Model 1 included only an additive part of the direct genetic effect.

The method of estimating variance components was derivative-free restricted maximum likelihood (REML) as implemented in the DFREML program of Meyer (1997). Iterations were stopped when the variance of function values of the simplex was less than 10^{-8} .

Since the REML methodology requires the inverse of the dominance relationship matrix, the method of Hoeschele and VanRaden (1991) was used for calculation of the inverse. This method partitions dominance effects into sire-dam subclasses and constructs the inverse of the relationship matrix among both dominance and subclass effects. The inverse of \mathbf{D} was obtained by first computing the entire matrix followed by absorption of the sire-dam subclass effects into the dominance effects. Inbreeding was ignored since there were only 5 inbred animals in the entire data set. The above algorithm was coded in Fortran95 program with the use of sparse matrix technology.

RESULTS AND DISCUSSION

Estimates of variance components for the traits studied are shown in Table 2. Estimates of heritability for the additive direct effect are within the range of values reported previously (James *et al.*, 1990). Bloodline variance for clean fleece weight was surprisingly low, with high standard error. The estimates of dominance variances for GFW, CFW, Y and FD were 0.28, 0.34, 0.18 and 0.05, respectively. The percentage of total genetic variance accounted for by σ_d^2 was 45, 45, 25 and 8% for GFW, CFW, Y and FD, respectively.

Table 2. Estimates of variance components for wool production traits^A

Trait	Model	h^2	l^2	d^2	c^2	σ_e^2
GFW	1	0.35 ± 0.02	0.11 ± 0.02	-	-	0.28
	2	0.34 ± 0.02	0.11 ± 0.02	0.29 ± 0.07	-	0.13
	3	0.33 ± 0.03	0.14 ± 0.03	0.28 ± 0.08	0.0	0.13
CFW	1	0.43 ± 0.02	0.03 ± 0.02	-	-	0.14
	2	0.42 ± 0.02	0.03 ± 0.02	0.35 ± 0.09	-	0.05
	3	0.42 ± 0.03	0.03 ± 0.02	0.34 ± 0.09	0.0	0.05
Y	1	0.54 ± 0.05	0.12 ± 0.07	-	-	7.35
	2	0.54 ± 0.06	0.12 ± 0.06	0.18 ± 0.08	-	3.54
	3	0.53 ± 0.07	0.14 ± 0.07	0.18 ± 0.08	0.0	3.52
FD	1	0.55 ± 0.08	0.23 ± 0.07	-	-	0.65
	2	0.55 ± 0.08	0.23 ± 0.07	0.05 ± 0.01	-	0.52
	3	0.55 ± 0.08	0.23 ± 0.08	0.02 ± 0.01	0.01 ± 0.01	0.58

^AHeritabilities (\pm s.e.); h^2 is the heritability, l^2 is the bloodline variance as a proportion of total variance, d^2 is the dominance variance as a proportion of total variance, c^2 is the common environmental variance as a proportion of total variance

Apart from the variance for FD, our estimates are high compared with the estimates reported for other species (Rodriguez-Almeida, 1995; Tempelman and Burnside, 1991). We are unable to explain the high value of d^2 for CFW. This result is possibly due to some confounding sources that existed in the data.

Simultaneous estimation of additive and dominance variances has not been reported for wool production characteristics in sheep. In dairy and beef cattle, accounting for dominance effects generally had little influence on the estimates of additive genetic variances (Tempelman and Burnside, 1991; Rodriguez-Almeida *et al.*, 1995; Miglior *et al.*, 1995). The opposite was true in studies in poultry and fish (Rye and Mao, 1989; Wei and van der Werf, 1993). A comparison of variance components for the different models in our study revealed that the variance attributed to σ_d^2 under the dominance model was attributed mainly to σ_e^2 under the additive model. The differences could be attributed to a weakness of dominance information compared to other random effects (Mizstal *et al.*, 1997). In cattle, which are closer in reproductive performance to Merino sheep than poultry and fish, information on additive genetic variation is mainly provided from covariances between half-sibs, which will be inflated in the presence of interaction variances but not by dominance (Falconer, 1989).

The estimates of genetic variance components were not affected when common environmental effects were included into the model. For all traits studied common environmental variances were close to zero. Similar results were obtained for beef cattle (Rodriguez-Almeida *et al.*, 1995). Our findings contrast with those of Atkins and Ramsey (2001) who found significant maternal environmental variance for clean fleece weight. This could be attributed to differences in data structures and models for the estimation of variance components.

There are at least two possible reasons for further investigation in this area. Firstly, that the magnitude and the relationships between additive and nonadditive variances are affected by the population structure. From simulation Chang *et al.* (1990) concluded that a large number of families are required in order to obtain reliable estimates of nonadditive variances. Therefore, more animals are needed for analysis.

Secondly, the effect of epistatic interactions and inbreeding should also be considered. There is evidence in the literature that the inclusion of additive by additive effects into the model constantly led to a reduction in the additive variance estimates (Rodriguez-Almeida *et al.*, 1995; Miglior *et al.*, 1995).

CONCLUSION

The results indicate that dominance effects may exist for greasy and clean fleece weights and yield in Merino sheep. Studies involving larger data sets are needed as well as an investigation on the effect of epistatic interactions. The benefits of incorporating mate selection on total merit into a breeding program need to be examined to determine whether these benefits will compensate for the computational cost involved in the implementation of models accounting for nonadditive genetic effects.

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