AN INVESTIGATION OF THE POTENTIAL FOR EARLY (INDIRECT) SELECTION IN AUSTRALIAN MERINO SHEEP

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SUMMARY

Six models were used in Restricted Maximum Likelihood (REML) analyses to estimate direct-genetic, maternal-genetic and maternal-environmental variances for body weight, greasy and clean fleece weight and fibre diameter, measured in Merino sheep between birth and 22 months of age. Maternal-genetic effects were important for body weight performances measured at any age, and for greasy fleece weight at 4 and clean fleece weight at 10 months of age. The results of bivariate analyses of performance at different ages within each trait suggest that early (indirect) selection for body weight will achieve a substantial proportion of direct response at later ages. For fleece traits, selection at 4 months will not be very useful, but selection at 10 months will achieve more than three-quarters of direct response at 22 months.

INTRODUCTION

It is possible that selection in Merino sheep could be improved by selecting on performance measured prior to first mating. In order to investigate this possibility, we need estimates of the importance of maternal effects (both genetic and environmental) and of the genetic and phenotypic correlations between early and later performance. There are several published estimates of maternal effects from univariate analyses of production traits of sheep, including two for Australian Merino sheep (Mortimer and Atkins 1994; Swan and Hickson 1994). However, there have been no bivariate studies of performance at different ages, and hence there are no estimates of genetic and phenotypic correlations. In this paper, we summarise the results of univariate and bivariate animal-model analyses of body-weight and fleece traits measured from birth to 22 months of age.

MATERIALS AND METHODS

A base population of 40 rams and 1200 ewes, which consists of 4 different bloodlines of Merinos, namely three medium-wool Peppin (Pye, Plevna and Trangie) and one fine-wool Saxon bloodline, was established in 1987 at the University of Sydney's Pye Farm which is located near Camden, N.S.W., Australia. Management procedures and performance-recording details for this flock have been described by Raadsma and Nicholas (1993). The traits considered in this study were body weight (B), greasy (G) and clean (C) fleece weights and fibre diameter (F) measured at the ages shown in Table 1, from 1988 to 1991 inclusive. The numbers of records ranged from 1,660 (for C10M and F10M) to 4,292 (for B0M); the number of sires represented ranged from 124 to 163. Initial least-squares analyses determined the importance of all relevant fixed effects and all two-way interactions, and the data were pre-adjusted for significant interactions. Restricted Maximum Likelihood (REML) analyses were then conducted, based on a derivative-free algorithm using the Simplex method and fitting Meyer's (1989) six animal models, which involve various combinations of direct and maternal effects. The significance of (co)variance components in each model was tested by a Likelihood Ratio Test (LRT). The most appropriate model for each measurement of each trait is the one which gives the highest log likelihood. For each trait, bivariate analyses for all pairwise combinations of performance were performed based on the model that gave the highest log likelihood for each measurement of performance in the univariate analyses and the magnitude of the estimated parameters.

RESULTS

Comparison of log likelihoods obtained from the six models indicates that maternal-genetic effects are a significant source of variation for all ages of body weight performances, but are not significant for fleece traits except at 4 months. Allowing for direct-maternal genetic covariance (model 4) gave significant increases in log likelihood for all early performances for all traits. Fitting the most comprehensive model (model 6) did improve the log likelihood for some traits, but none of them was significantly better than model 4. The estimates of direct heritability (h^2), maternal heritability (m^2) and direct-maternal genetic correlation (r_{AM}) for each performance for each trait are presented in Table 1. For the bivariate analyses, the estimates of h^2, m^2, r_{AM}, together with direct-genetic, phenotypic, maternal-genetic, and direct-maternal genetic correlations, are shown in Table 1. These estimates are the first from bivariate analyses under different animal models for production traits in Merino sheep. Estimates of all parameters of all performances are very similar to those obtained from the univariate analyses. Genetic correlations are all positive, and low to high in magnitude, ranging from 0.20 (B0M and B22M) to 0.97 (B10M and B16M). B4M has positive and high maternal-genetic correlations with other body weight performances at later ages, which is basically indicating a carry-over of maternal influence until B4M. All phenotypic correlations are positive, and low to moderate in magnitude, ranging from 0.21 (B0M and B22M) to 0.67 (F10M and F22M).

DISCUSSION

Within models, in all performances for all traits, ignoring the maternal effects results in upwardly biased estimates of direct additive genetic effects. This bias was largest for early ages. Except for B4M and G4M which showed estimates of m^2 (0.42 and 0.31) greater than h^2 (0.27 and 0.21, respectively), all performances of all traits had a value of m^2 smaller than h^2. Estimates for r_{AM} were negative for B0M (-0.43), B4M (-0.59) and B10M (-0.29), and were positive and strong for B16M and B22M (1.00). For greasy and clean fleece weights, all estimates of r_{AM} were negative, but for fibre diameter they were positive. These results are similar to those obtained by Swan and Hickson (1994) for Merino sheep, in which maternal-genetic effects were a significant source of variation in B4M and G4M (the earliest measurements taken in their study), and in body weight at 12 months of age. However, they found a positive r_{AM} for B4M and B12M. For the other measurements of performance studied by Swan and Hickson (1994), namely greasy fleece weight and fibre diameter at 12 months, their results are similar to those reported for the nearest comparable measurements in the present paper (G10M and F10M), i.e. none of the maternal effects was important for these traits after weaning. The other comparable study in Merino sheep is by Mortimer and Atkins (1994), who fitted only the maternal-genetic effect and the interaction between direct and maternal-genetic effects for body weight and fleece traits measured at 16 months of age. Our results are similar to their reports for B16M, namely a significant maternal-genetic effect, but are somewhat different from their findings for greasy and clean fleece weight, the nearest measurement to our data-set.

For all traits, the correlations between performance at different ages decreased as the time between measurements increased. Similar values were obtained for sire-model estimates, by Lewer et al. (1994) for genetic and phenotypic correlations for body-weight traits in Western Australian Merino sheep, except for genetic correlations between B0M and body weights at 11 and 14 months, which were reported negative. The estimates in Table 1 lead to the following predictions of the relative efficiency of indirect selection at early ages compared with direct selection at 22 months of age: selection at 4 months (55% for body weight, 19% for greasy fleece weight); selection at 10 months (77% for body weight, 73% for greasy fleece weight and for clean fleece weight, 80% for fibre diameter). For direct selection at 10 months, the relative efficiency of indirect selection at 4 months is 83% for body weight and 21% for greasy fleece weight.

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Table 1: Estimated genetic and phenotypic parameters for production traits from univariate and bivariate analyses

Trait	Body weight					Greasy fleece weight			Clean fleece weight		Fibre diameter	
Age	B0M[¶]	B4M	B10M	B16M	B22M	G4M	G10M	G22M	C10M	C22M	F10M	F22M
	Univariate estimates											
h^2	0.30	0.27	0.24	0.33	0.32	0.21	0.29	0.37	0.30	0.37	0.54	0.67
m^2	0.29	0.42	0.15	0.08	0.07	0.31	0.11	-§	0.17	-	-	-
σ_{AM}	-0.43	-0.59	-0.29	-	-	-0.86	-0.36	-	-0.58	-	-	-
	Bivariate estimates											
	h^2 (bold) on the diagonal; genetic correlations above and phenotypic correlation below the diagonal											
0M	**0.30**	0.52	0.43	0.35	0.20							
4M	0.36	**0.28**	0.77	0.59	0.61	**0.21**	0.51	0.26				
10M	0.26	0.53	**0.24**	0.97	0.92	0.31	**0.30**	0.83	**0.33**	0.77	**0.55**	0.87
16M	0.26	0.48	0.53	**0.34**	0.92							
22M	0.21	0.44	0.50	0.61	**0.34**	0.30	0.53	**0.38**	0.55	**0.37**	0.67	**0.65**
	m^2 (bold) on the diagonal, and maternal-genetic correlations below the diagonal											
0M	**0.29**											
4M	0.65	**0.41**				**0.29**						
10M	0.30	0.85	**0.14**			0.99	**0.10**		**0.14**			
16M	0.06	0.61	0.71	**0.07**								
22M	0.25	0.80	0.91	0.88	**0.07**	-	-	-	-	-		
	r_{AiMi} (bold) (i=j) on diagonal, (i>j) above diagonal and (i<j) below diagonal											
0M	**-0.44**	-0.49	-0.19	0.39	0.21							
4M	-0.31	**-0.57**	0.02	0.28	0.19	**-0.82**	-0.36	0.25				
10M	0.27	-0.82	**-0.27**	0.02	0.00	-0.90	**-0.41**	0.22	**-0.63**	0.01		
16M	0.07	-0.23	-0.11	-	-							
22M	0.01	-0.71	-0.37	-	-	-	-	-	-	-		

¶ M = months of age.

§ Not estimated, because the model that gave the highest log likelihood did not include maternal effects.