PRELIMINARY GENETIC PARAMETERS FOR CLEAN FLEECE WEIGHT, FIBRE DIAMETER, HOGGET WEIGHT AND NUMBER OF LAMBS BORN IN MERINOS

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SUMMARY

The Australian Sheep Industry Cooperative Research Centre has amalgamated data from 6 Merino sheep research resource flocks. The data base comprises 2,112 sires, 22,141 dams and up to 94,000 records for each of a comprehensive range of production traits with deep animal pedigrees. Genetic parameters and in particular genetic correlations are being estimated to fill identified knowledge gaps in the literature. This paper reports estimates of heritability and genetic and phenotypic correlations for clean fleece weight, fibre diameter, hogget weight and number of lambs born as well as other variance components. Results show that while estimates of heritabilities are similar to the mean estimates obtained from the literature review, there are some important differences for genetic correlations. The size and depth of pedigree in the data set has allowed complex models to be fitted and genetic correlations to be estimated with high precision.

Keywords: heritability, genetic correlations, sheep

INTRODUCTION

Development of effective genetic evaluation and improvement programmes requires accurate knowledge of the genetic parameters (genetic variance of each trait and covariance among traits) for economically important production traits. Breeding objectives for Merino flocks are becoming more complex. Many breeders wish to incorporate a wider range of traits than simply fleece weight and fibre diameter, including wool quality, disease resistance, body weight, reproduction, meat and feed efficiency. Current development by the sheep industry of the Australian Sheep Genetic Database for genetic evaluation also requires an agreed genetic parameter matrix for a comprehensive range of traits relevant to Australian sheep populations. In their recent review of genetic parameters for production traits in sheep from the world literature over the last decade, Safari *et al.* (2005a) showed that there were more than 20 estimates of heritability for most wool and body weight traits, many of which were from Merino sheep populations. There were generally less and more variable estimates for reproduction, disease, carcass and meat traits. There was a dearth of estimates of genetic correlations (except within some wool and growth traits) between the various traits and especially between the trait groups. The estimates of genetic correlations generally had wide confidence intervals reflecting the large variation between estimates and relatively small data sets used in the estimation process. Safari *et al.* (2005b) used Monte Carlo simulation to study the impact of changes

in the genetic correlations under three selection index scenarios (fine wool, dual-purpose and meat). The correlations for reproduction with wool traits were sensitive under all objectives and those for reproduction with growth, worm resistance and carcass muscling were sensitive in at least some objectives. The correlation between growth and fibre diameter was highly sensitive in the fine wool objective. The results provide a logical basis for setting priorities for studies to obtain more accurate estimates of genetic correlations among sheep production traits. The Australian Sheep Industry CRC recognised the need to obtain accurate estimates of genetic correlations to fill the knowledge gap. The parties have pooled data from their research resource flocks that have deep pedigrees and extensive recorded data to achieve this objective. This study outlines the data sets from 6 of the reference flocks and provides preliminary estimates of genetic parameters for clean fleece weight (CFW), fibre diameter (FD), hogget weight (HWT) and number of lambs born per ewe joined (LB/EJ).

MATERIALS AND METHODS

Animals. The data were collected from six reference flocks as follows:

Trangie D flock. Established by the NSW Department of Primary Industries at Trangie Agricultural Research Centre in 1975 to study the variation between 15 different bloodlines (2 fine, 2 medium-wool non-Peppin, 9 medium-wool Peppin, one strong wool, and one Fertility).

Trangie C flock. Established in 1984 with 8 bloodlines (2 fine wool, 2 medium-wool non-Peppin, 3 medium-wool Peppin and one strong wool) from the Trangie D flock to study the outcome of crossing between bloodlines.

Trangie QPLUS flock. Established in 1993 to demonstrate simultaneous improvement in wool weight and fibre diameter in fine wool (8% micron premium and control),, medium wool (Industry, 3%, 8% and 15% micron premium and control) and broad wool (8% micron premium and control) populations and to evaluate a range of indices.

South Australian Base flock (SA-BASE). Established in 1989 from 4 bloodlines (Medium/Broad wools) to estimate genetic parameters for wool and skin traits.

South Australian Selection Demonstration flock (SA-SDF). Established in 1997 from 4 bloodlines (Medium/Broad wools) to demonstrate outcomes from alternative breeding strategies, technology transfer, and generate genetically diverse flocks.

CSIRO Fine flock. Established in 1991 from 11 industry bloodlines to study the variation between and within bloodlines.

Data from the West Australian Katanning base and selection flocks are also being incorporated but none of their data are included in these results. The number of records from each flock and summary statistics for each trait analysed are shown in Table 1. A total of 2,112 sires and 22,141 dams were represented in the data with 1,573 sires and 9,145 of dams originating from the base populations.

Data analysis. Variance components were estimated by REML (Gilmour *et al.* 2002) in a series of bivariate analyses. The model included flock (6 levels), bloodline (40 levels), birth rearing type (3 levels) sex (3 levels), year of measurement (40), dam age (6 levels) and animal age (6 levels) as fixed effects. Additive animal genetic effect, animal permanent environmental effect, maternal genetic effect, maternal environmental effect and litter effects were fitted as random. Genotype was included as a random effect to account for the non-additive components in the Trangie C flock.

$$y = X\beta + Z_1 a + Z_2 m + Z_3 a_{pe} + Z_4 m_{pe} + Z_5 l + e$$

Where y is the vector of observation, ß is the vector of fixed effects, a and m are vectors of direct and maternal genetic effects, a_{pe} and m_{pe} are vectors of animal and dam permanent environmental effects, l the vector of litter effects, **X**, **Z_1**, **Z_2**, **Z_3**, **Z_4**, **Z_5**, are incidence matrices relating observations and effects and e is the vector of random residuals.

Table 1. Flocks and summary statistics for clean fleece weight (CFW), Fibre diameter (FD), Hogget weight (HWT) and lambs born per ewe joined (LB/EJ)

Flock	Statistics	CFW (kg)	FD (μm)	HWT (kg)	LB/EJ
Trangie D	Records	17,695	17,664	3,792	14,418
	Mean (sd)	3.56 (0.8)	21.78 (2.1)	38.25 (7.4)	1.02 (0.8)
Trangie C	Records	16,015	15,993	9,556	6,534
	Mean (sd)	3.62 (0.8)	21.07 (2.1)	46.39 (8.5)	1.20 (0.7)
Trangie QPLUS	Records	27,802	27,829	12,978	14,799
	Mean (sd)	4.34 (1.2)	21.61 (2.4)	53.65 (0.4)	1.13 (0.8)
SA-BASE	Records	15,093	15,140	5,800	10,636
	Mean (sd)	4.18 (1.3)	23.50 (2.5)	51.41 (7.3)	1.13 (0.7)
SA-SDF	Records	5,804	5,820	-	785
	Mean (sd)	4.99 (0.9)	20.58 (2.0)	-	1.02(0.6)
CSIRO Fine	Records	13,972	13,375	4,281	9,282
	Mean (sd)	2.73 (0.7)	18.37 (1.6)	34.08 (6.1)	0.86 (0.5)
Total[A]	Records	94,163	93,606	35,714	56,423
	Mean (sd)	3.90 (1.1)	21.33 (2.5)	47.39 (1.1)	1.06 (0.7)

Total records used in bivariate analysis

RESULTS AND DISSCUSSION
All fixed effects were significant (P<0.01) with dam age having a quadratic effect on all traits and animal age on CFW, FD and LB/EJ. The final model for LB/EJ included additive animal genetic and animal permanent environmental effects. For CFW, FD and HWT, inclusion of additive animal genetic effect, animal permanent environmental effect, maternal genetic effect, and litter effects improved the log likelihood significantly. The estimates of direct heritability and genetic and phenotypic correlations from the bivariate analyses of the combined data are shown in Table 2. The comprehensive and large size of the combined data set is reflected in the very low standard errors for all the heritability estimates (all <0.01). The estimates of heritability for CFW (0.33), FD (0.57), HWT (0.43) and LB/EJ (0.075) are very close to the mean estimates (0.36, 0.59, 0.41 and 0.10 respectively) for wool breeds from the literature (Safari *et al.* 2005a).

The genetic (and phenotypic) correlations also had very low standard errors (<0.04) which are substantially lower than most reports in the literature. The genetic correlations for CFW with FD (0.23) and HWT (0.26) were similar to estimates from literature (0.28 and 0.21 respectively, Safari *et al.* 2005a). However the mean estimates from literature had large 95% confidence intervals (0.06 to 0.48 and -0.14 to 0.51 respectively,). The genetic correlation between FD and HWT was higher (0.29) than the literature mean of 0.15 with a wide confidence interval of -0.21 to 0.47. The genetic

correlation between LB/EJ and HWT (0.37) was more than double the literature mean of 0.15 which also had a very wide confidence interval of -0.38 to 0.61. The genetic correlations for LB/EJ with CFW and FD were close to zero, in contrast to the moderately negative literature means (-0.13 and -0.17) which were based on very few reports. The phenotypic correlations were similar to the means from the literature, except for those associated with LB/EJ which had literature means close to zero from very few reports.

Table 2. Direct heritability (se) (on diagonal), genetic (below) and phenotypic (above) correlations for clean fleece weight (CFW), fibre diameter (FD), hogget weight (HWT) and number of lambs born per ewe joined (NLB/EJ) and variance components[A]

	CFW	FD	HWT	LB/EJ
CFW	**0.33 (0.009)**	0.15 (0.005)	0.36 (0.005)	-0.19 (0.005)
FD	0.23 (0.018)	**0.57 (0.009)**	0.23 (0.006)	-0.07 (0.005)
HWT	0.26 (0.020)	0.29 (0.016)	**0.43 (0.001)**	0.58(0.010)
LB/EJ	0.05 (0.041)	-0.06 (0.030)	0.37 (0.036)	**0.075 (0.007)**
Variance components				
σ^2_p	0.487	2.701	17.618	0.478
h^2_m	0.024 (0.004)	0.020 (0.004)	0.048 (0.010)	-
c^2_a	0.214 (0.011)	0.107 (0.010)	-	0.100 (0.010)
L^2	0.047 (0.009)	0.039 (0.008)	0.044 (0.010)	-

[A] Phenotypic variance (σ^2_p) and maternal effect (h^2_m), permanent environmental effect of animal (c^2_a) and litter effect (L^2) as proportions of total variance

The mean variance components from the bivariate analyses (Table 2) showed the maternal effect accounted for about 2% of total variance for CFW and FD and almost 5% for HWT. They were obtained from the bivariate analyses without accounting for the covariance between direct and maternal genetic effects. However in the univariate analyses of CFW, FD and HWT the maternal effects accounted for a higher proportion of variance with a significant negative genetic correlation between direct and maternal genetic effects. Permanent environmental effect of animal accounted for 21% CFW, 11% FD and 10% LB/EJ of variance while the litter effect accounted for 4-5% of variance. These results illustrate the power of this large combined data set from research resource flocks with deep pedigree. The genetic correlations have been estimated with considerable precision, in contrast to most estimates in the literature. Further analyses are being undertaken to provide a genetic parameter matrix for a comprehensive range of production traits that is directly applicable to Australian Merino sheep. This will fill many of the gaps identified by Safari *et al.* (2005a), especially for the genetic correlations between the groups of production traits with high economic value that were identified as sensitive to selection under various breeding objectives (Safari *et al.* (2005b).

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