

GENETIC PARAMETERS FOR LIFETIME REPRODUCTIVE PERFORMANCE OF MERINO EWES

G.J. Lee, K.D. Atkins and M.A. Sladek

Cooperative Research Centre for Sheep Industry Innovation, NSW Department of Primary Industries, Orange Agricultural Institute, Forest Road, Orange, NSW 2800, Australia

SUMMARY

The genetic variation between ewes in lifetime (2-6 years of age) net reproductive performance, and its component traits, was estimated in each of 3 Merino research flocks. The heritability estimates for each of the lifetime reproductive traits were higher than published estimates based on single year records, and in line with expectation for traits with a repeatability of about 0.15. Therefore, a repeatability model for analysing reproductive performance seems adequate. The lifetime component traits (fertility, fecundity and survival) each had high positive genetic correlations (≥ 0.55) with net lifetime reproductive performance, indicating that all components contribute to genetic improvement in net reproductive performance.

INTRODUCTION

Reproduction rates in Australian sheep flocks are low nationally and have changed little in the last 30 years (ABARE 2008) despite the availability of genetic (Purvis *et al.* 1987) and within-year management options (Langford *et al.* 2004; Kleemann *et al.* 2006) to improve reproductive performance.

Improving reproductive performance increases productivity of the breeding ewe unit, more efficient use is made of available feed (proportionately less of the feed consumed is used for maintenance), more surplus animals are available for sale and greater selection pressure is available, increasing the potential for genetic gains. This can lead to increased profit (\$/ha) across the range of sheep breeding enterprises (Langford *et al.* 2004).

While there is a genetic influence on each component, heritability estimates are low (Safari *et al.* 2007b) and this in part is due to the nature of the annual expression of the traits. Using the high variability in annual records (Safari *et al.* 2005) for within-flock selection is likely to lead to permanent but relatively slow genetic improvement. Environmental sources (nutrition, management, health etc) contribute to the large variability in reproductive performance both between-ewes within years and within-ewe between years. Over a lifetime, the between-ewe variation in reproductive performance remains large (Lee *et al.* 2009), so combining a number of annual performances should improve precision in estimating the merit of individuals and potentially improve the rate of genetic improvement.

This study estimates the extent of genetic variation in the lifetime (2-6 years of age) reproductive performance of Merino ewes within 3 research flocks maintained at the Agricultural Research Centre, Trangie in central western NSW.

METHODS

Lifetime reproductive data (ages 2-6) were available from 3 flocks of Merino ewes (D-flock, C-flock and QPLU\$) run at the Agricultural Research Centre, Trangie. In each of these flocks, lambing and weaning performance of the ewes were routinely recorded. Lambing and weaning data for at least 3 joinings were available for 2430 D-flock ewes (born 1975-1983), 1819 C-Flock ewes (born 1984-1993) and for 3037 QPLU\$ ewes (born 1993-2002). Descriptions of flock structure and management have been provided elsewhere for D-flock (Mortimer and Atkins 1989), C-flock (Mortimer *et al.* 1994), and QPLU\$ (Taylor and Atkins 1997).

Statistical analyses. Data on the number of times each ewe was joined, the number of years the ewe lambled, the total number of lambs born, and the number of lambs weaned were obtained over the reproductive life (2-6 years of age) of the ewes in the flock. From these values lifetime fertility (ewes lambing/ewe joined), fecundity (lambs born/ewe lambing), lamb survival (lambs weaned/lamb born) and net reproduction (lambs weaned /ewe joined) were calculated (Lee *et al.* 2009).

Variance and co-variance components were estimated for lifetime net reproduction and the reproduction component traits (fertility, fecundity and lamb survival) using a mixed animal model within ASReml (Gilmour *et al.* 2002), fitting year of birth and genotype effects in univariate and bivariate analyses.

RESULTS AND DISCUSSION

Phenotypic variation. The means of net reproductive performance, and its component traits, over the ewes’ lifetime and the phenotypic variation are shown in Table 1. Within-flock phenotypic variation in each of the component traits was less than that in net reproduction. Among the component traits, phenotypic variation was least for fecundity, while survival was the most variable.

As expected, the phenotypic coefficients of variation observed for lifetime records of fertility, fecundity and net reproduction rate were substantially less (33-46%) than that observed by Safari *et al.* (2007a) for the annual records from these same flocks. Assuming equal variances across age expressions and unity genetic correlations between age expressions, the phenotypic variance for a mean (lifetime) trait compared with the phenotypic variance of a single age expression will be:

$$\sigma^2_{\mu} = \{ 1 + (n - 1) t \} / n * \sigma^2_x \dots\dots\dots(1)$$

where σ^2_{μ} = variance of lifetime mean
 σ^2_x = variance of single record
 t = repeatability
 n = number of records

Using n=4 and t=0.15 in equation (1) above shows that the phenotypic variance will be 0.36 of the annual record phenotypic variance or 0.6 ($\sqrt{0.36}$) for the standard deviation or coefficient of variation. The reduction in coefficient of variation of 33-46% is in broad agreement with the 40% reduction expected for the simple case above.

Table 1. Mean and coefficient of variation of lifetime net reproductive performance and its component traits in 3 flocks of Merino ewes

	D-flock		C-flock		QPLUS	
	mean	CV %	mean	CV %	mean	CV %
Fertility – ewes lambing/ewe joined	0.725	32.8	0.852	24.4	0.771	31.7
Fecundity – lambs born/ ewe lambing	1.374	24.3	1.398	22.5	1.471	24.4
Survival – lambs weaned/lamb born	0.732	34.7	0.770	30.5	0.714	39.6
Net reproduction - lambs weaned/ ewe joined	0.739	52.9	0.929	43.4	0.825	56.2

Heritability. Estimates of the heritability of lifetime net reproduction ranged from 0.108 to 0.193 across the 3 flocks. Both fertility and lamb survival heritability estimates had the largest range

between the flocks (0.012 to 0.196 and 0.036 to 0.195, respectively). Heritability estimates for lifetime fecundity were the most consistent between the flocks and indicated moderate levels (0.19 to 0.26, ± 0.04-0.05) of genetic variation.

Table 2. Heritability (diagonal, bold), genetic (below diagonal) and phenotypic (above diagonal) correlations (±se) for lifetime net reproductive performance and each of its components in Merino ewes from 3 flocks

		Fertility	Fecundity	Survival	Net
D-Flock	Fertility	0.196 0.043	0.047 0.023	0.192 0.021	0.702 0.011
	Fecundity	-0.024 0.169	0.191 0.045	-0.132 0.021	0.390 0.018
	Survival	0.791 0.349	0.173 0.381	0.036 0.038	0.630 0.013
	Net	0.811 0.072	0.550 0.136	0.776 0.171	0.172 0.043
	C-Flock	Fertility	0.012 0.032	0.122 0.025	0.200 0.024
C-Flock	Fecundity	0.628 0.804	0.260 0.052	-0.074 0.024	0.496 0.019
	Survival	1.032 0.895	-0.389 0.227	0.078 0.043	0.666 0.014
	Net	1.070 0.578	0.687 0.136	0.614 0.183	0.108 0.043
	QPLUS	Fertility	0.135 0.036	0.125 0.020	0.162 0.020
QPLUS	Fecundity	0.436 0.150	0.196 0.037	-0.053 0.019	0.430 0.016
	Survival	0.274 0.163	0.139 0.145	0.195 0.040	0.690 0.010
	Net	0.667 0.094	0.638 0.099	0.782 0.062	0.193 0.036

The average estimate of heritability for lifetime net reproduction, 0.16 across the 3 flocks, was higher than the estimate derived from annual records of these flocks (0.05, Safari *et al.* 2007b). Similarly, the average lifetime fecundity heritability of 0.21 was higher than the pooled estimate of annual records for the 3 flocks (0.074, Safari *et al.* 2007b). Given the assumptions of a repeatability model, the expected heritability for the mean (lifetime) trait compared with the heritability of a single age expression will be:

$$h^2_{\mu} = n / \{ 1 + (n - 1) t \} * h^2_x \quad \dots\dots\dots(2)$$

where h^2_{μ} = heritability of lifetime mean
 h^2_x = heritability of single record

For n=4 and t=0.15 in equation (2), the expected heritability of the lifetime trait will be 2.8 times that of the single record. Increases in heritability of 3.2 and 2.9 times for net reproduction rate and fecundity respectively, lend further support to the adequacy of the repeatability model for reproductive traits.

Phenotypic and genetic correlations. The phenotypic correlations (Table 2) of net reproductive performance with each of the component traits were moderate to high and positive, but for each flock were lowest for the relationship of fecundity with net reproduction (0.39 to 0.50). Phenotypic correlations of fertility with each of the other component traits were positive but low (<0.2), while survival and fecundity had a low negative correlation (-0.05 to -0.13) within each flock.

Across all flocks, the genetic correlations of each of the component traits with lifetime net reproduction were positive and high (≥ 0.55). However, the genetic correlations among the component traits were imprecise and/or inconsistent between the flocks.

CONCLUSION

Collecting and updating reproductive performance over the lifetime, as opposed to using annual records, will have the benefits in the current generation through improving the accuracy of selection for ewes to remain in the breeding flock, and will substantially improve the accuracy of selection of young animals (particularly rams in ram breeding flocks and ewes in commercial flocks) by including the dam's reproductive performance as a selection criterion in the index. Further, given the size of the genetic correlations of net reproduction with the component traits, using lifetime net reproductive performance will achieve the best overall response in reproduction rate rather than just focussing on fertility (wet-dry data), litter size (pregnancy scanning) or lamb survival alone.

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