RELIABILITY OF ESTIMATES OF CORRELATIONS BETWEEN REPRODUCTION AND PRODUCTION TRAITS FROM A MERINO RESOURCE FLOCK

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SUMMARY
Stochastic simulation was used to examine the reliability of estimating genetic parameters for fecundity (number of lambs born per ewe lambing) and fibre diameter in the CSIRO Fine Wool Project flock. The mean heritability estimates for fecundity and fibre diameter from 50 replicates of the simulation were similar to the true heritabilities as simulated. However, the genetic correlation between fibre diameter and fecundity was underestimated. The variation in estimates from across replicates was large. This highlights the difficulty of estimating correlation between fecundity and fibre diameter. More studies are required before the relationships between reproduction and production are known with certainty.
Keywords: sheep, variance components, fibre diameter

INTRODUCTION
With increasing emphasis on balancing reproduction and production in breeding programs for Australian Merino flocks it is important that the relationships between these traits are understood. A recent review of genetic parameters by Safari *et al.* (2005) highlighted that there are few reliable estimates of genetic correlations between reproduction and production traits in sheep. Even where estimates have been made they vary substantially. For example there was only one estimate of the correlation between fibre diameter and fecundity in sheep. A preliminary analysis of the correlations between fibre diameter and fecundity has been performed in the CSIRO Fine Wool Project. The genetic correlation estimated between fibre diameter and fecundity, defined as number of lambs born per ewe lambing, was 0.14 ± 0.07 (S. Dominik, *pers comm.*). This is lower than the estimate of 0.3 from Rao and Notter (2000), obtained by pooling data from three different breeds of sheep.

The CSIRO Fine Wool Project flock was designed to estimate genetic parameters for production traits where records were collected from animals born during the seven-year duration of the experiment. However, the suitability of this design for estimating parameters for reproduction was not initially considered. The data set used to estimate reproductive parameters is substantially smaller than that for production traits, as only lambing ewes contribute to the (co)variance component estimates. This study examines the reliability of estimating genetic correlations between fecundity and fibre diameter given the design of the CSIRO Fine Wool Project. A simulation study modelled a population structure that was similar to the CSIRO Fine Wool Project flock, enabling comparison of variance components estimated from simulated data with true variances as simulated data.

MATERIALS AND METHODS
Flock structure. The flocks modelled were based on the CSIRO Fine Wool Project flock. The structure and management has been described in detail by Swan *et al.* (2000).   The key elements of

this breeding program were as follows. All sheep were run on CSIRO field stations near Armidale, NSW, Australia, for seven years. Approximately 2200 Merino ewes representing 11 bloodlines were joined per year. Breeding ewes were run in four management groups, to which ewes from each bloodline were allocated randomly (stratified by sire and dam age) each year. Approximately seven sires were joined annually within each bloodline, one of which was used across all years as a link sire, while the remainder were replaced each year. Sires were selected to be representative of flock rams from their respective bloodline. The pedigree of introduced animals, including foundation ewes was unknown.

Stochastic simulation. Genetic parameters were obtained from Safari and Fogarty (2003) and are presented in Table 1. These parameters were calculated from a meta-analysis of literature estimates. For each animal, an array of normally distributed deviates was drawn from a random number generator. These deviates were then scaled to the appropriate variances by multiplication with Cholesky decompositions of the genetic and environmental (co)variance matrices. Phenotypes were generated as the sum of the mid-parent genetic value, a deviate representing Mendelian segregation, and an environmental deviate. The effect of inbreeding on the genetic variance was also accounted for when calculating the genetic values of the parents. The fixed effects of age of dam, sex, rearing type, and birth type were considered for both traits. Extra environmental variance was added to fecundity and fibre diameter to simulate the contemporary effect of management group within year which was assumed to be 20% of environmental variance.

Table 1. Heritability, phenotypic standard deviation genetic and phenotypic correlations between traits used in simulation

Trait	Abbreviation	Units	Heritability	Repeatability	Trait mean
Fibre diameter	FD	Micron	0.590	NA	19.0
Fertility	FERT	NEL/NEJ	0.080	0.13	0.87
Fecundity	FECUND	NLB/NEL	0.136	0.15	1.09
Survival	SURV	NLW/NLB	0.060	0.14	0.83

Genetic and phenotypic correlations (phenotypic above the diagonal, genotypic below and phenotypic standard deviation on the diagonal)

	FD	FERT	FERCUND	SURV
FD	**1.90**	-0.00061	0.0739	-0.00071
FERT	-0.0028	**0.628**	-0.0187	-0.1571
FERCUND	0.3061	-0.0366	**0.269**	0.0311
SURV	-0.0038	-0.5252	0.3512	**0.504**

Note; NEJ is number of ewes joined; NEL is number of ewes lambing; NLB is number of lambs born; NLW is number of lambs weaned.

The conversion of reproduction phenotypes from normally distributed deviates to categorical traits was performed following the method of Reverter *et al.* (2001). The threshold for fertility was calculated given the mean reproductive rate of 4-year-old dams as a base. The thresholds for

fecundity were calculated given average proportions of each litter size. Additionally, survival was simulated as a threshold trait with different levels of survival for each litter size. The average reproductive rates were calculated from the data and are presented in Table 1.

Statistical Analysis. Analyses were performed using ASREML (Gilmour *et al.* 2002). Hogget fibre diameter was fitted as a simple single record trait, while fecundity was modelled as a multiple record trait consisting of all parities of a dam. Single trait analyses were initially performed. A bivariate analysis was then performed between hogget fibre diameter (single record) and fecundity (multiple-record). The fixed effects fitted for each trait were bloodline, birth type, rear type, dam age and a contemporary group consisting of year of birth and management group. These models were fitted to each replicate of the simulation, and comparisons were made of the variation across replicates.

RESULTS AND DISCUSSION
The average heritability realised for fibre diameter and fecundity was 0.58 ± 0.047 and 0.12 ± 0.032 respectively which agreed with the true genetic parameters as simulated (Table 2). However, the genetic correlation between these traits was underestimated, the average estimate being 0.21 compared to the true correlation as simulated (0.3). There was substantial variation in the genetic correlation estimated from the 50 datasets (replicates), Figure 1 presents this variation in a histogram. The distribution of correlation estimates was approximately normal, hence a 95% confidence interval was calculated using the properties of a standard normal distribution. From this it was estimated that 95% of estimates lie between –0.06 and 0.48 which only represents a slightly higher range than the average standard error estimate from the analysis (-0.04 to 0.45). To check that the simulation was generating records with the correct genetic correlation between fecundity and fibre diameter, the correlation between underlying normal genetic values of all animals within a replicate were analysed and the correlation was 0.30 (SD$\pm$0.025) which is similar to the simulated value. Additionally the variances for each of the parameters contributing to the genetic correlation also agreed with the input parameters.

Table 2. Estimates of genetic parameters for fecundity and FD diameter (SD in brackets)

Heritability	Parameter estimates from observed data	Difference from simulated
Fibre diameter	0.58 (0.047)	0.0
Fecundity	0.12 (0.032)	0.01
Correlations		
r_G	0.214(0.122)	0.10
r_P	0.051(0.018)	0.02

Histogram of genetic correlation estimates between fecundity and fibre diameter
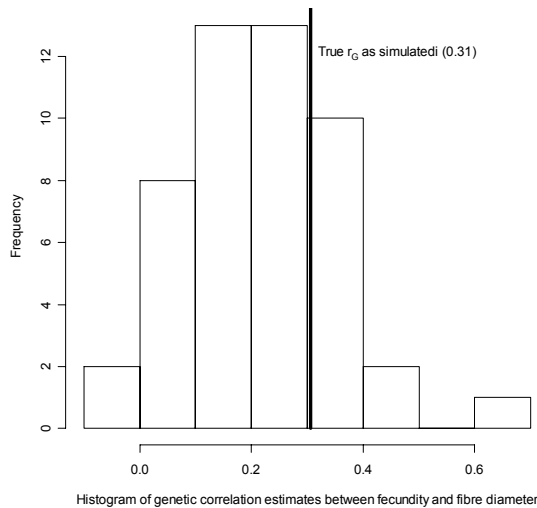
Figure 1 Histogram of estimates of genetic correlation fro 50 replicates of the simulation

There are at least three factors that could have contributed to the underestimate of the genetic correlation between fibre diameter and fecundity. Firstly, the design of the experiment may not allow the parameter to be more accurately estimated. Secondly, it could be a reflection of the small genetic variance for fecundity. Thirdly, given that the estimates for genetic variance were constrained to be above zero, the mean value of the variance could be biased upwards. This would lead, on average, to a decrease in the estimated genetic correlation as the genetic covariance is divided by a term containing this parameter when calculating the genetic correlation.

Given that there are currently only two studies where the genetic correlation between fibre diameter and fecundity have been estimated, more studies need to be performed before we can be confident in the correlations estimated between these traits. Given the increasing importance of balancing reproduction and production traits in Merino breeding programs, if more reliable estimates are required it will be necessary to collect more data containing both reproduction and production data, or to consider whether alternative reproduction traits exist that do not suffer the same bias in prediction of their correlation with fibre diameter.

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