GENETIC PARAMETERS FOR PASTURE INTAKE AND WOOL GROWTH EFFICIENCY IN MERINO SHEEP

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SUMMARY
In this report, all of the known estimates of the genetic parameters for pasture intake by Merino sheep and its relationship with production traits were combined. Combining these estimates improved the precision of the genetic parameter estimates. The pooled estimates of heritability of digestible organic matter intake (DOMI), wool growth, wool growth efficiency and fibre diameter were 0.12 ± 0.04, 0.37 ± 0.05, 0.25 ± 0.05 and 0.66 ± 0.08, respectively. The genetic relationships of wool growth efficiency with wool growth and fibre diameter were 0.84 ± 0.20 and –0.03 ± 0.12, respectively, while those for feed intake (as DOMI) with wool growth and fibre diameter were –0.02 ± 0.17 and 0.40 ± 0.15.

Keywords: feed intake, genetic parameters, wool production, Merino.

INTRODUCTION
Feed is a major cost to the wool industry. In the past, geneticists have focussed on traits contributing to returns (e.g. fleece weight and growth rate) leading to "many simplified and optimistic predictions" of the economic outcomes from breeding programs (Ponzoni 1988). To reflect the profit equation (and not merely returns), breeding objectives need to include feed intake (cost). James (1986) has argued that it is preferable to include feed intake as a separate trait in the breeding objective rather than include it as an adjustment to the economic value of a production trait.

To date, feed intake has not been included as a separate trait because precise estimates of the heritability of feed intake and its genetic relationship with production traits have not been available. With these parameters, it would be possible to maximise genetic responses and profit, and understand the consequences on feed costs of selecting for wool production, wool quality, liveweight etc.

For general use in the industry, precise estimates of the genetic variation in feed intake and its covariation with the economically important traits over the lifetime are required (Piper 1991). Thus, the genetic parameters need to be estimated in a range of age groups. An earlier investigation of feed intake by grazing mature Merino ewes (Lee et al. 1995) demonstrated that feed intake was heritable and this was confirmed in a subsequent investigation (Lee 2000) which estimated genetic parameters in mixed-sex weaner sheep and in adult wethers. In general, there was good agreement between the parameter estimates derived from each of the age groups. However, in both reports, the sampling variance of the estimates of the heritability and genetic correlations was large. The objective of this paper is to provide some combined estimate of genetic parameters that may be of use in estimating likely responses to selection and may assist in genetic evaluation of Merinos for intake related traits. Combining the estimates should improve the precision of the genetic parameter estimates.
METHODS
Estimates of the heritability of pasture intake (as DOMI), DOMI/kg liveweight, liveweight, wool growth and wool growth efficiency (g clean wool/kg DOMI), and their genetic correlations, were available for reproducing ewes (Lee et al. 1995). Pasture intake was estimated in the ewes using chromic oxide delivered using intraruminal controlled release devices. These parameter estimates were derived by pooling estimates based on 553-583 records (but only 431-462 records for wool growth and efficiency) collected in each of four seasons.

Parameters for the same traits plus fibre diameter were also available for young mixed-sex sheep and adult wethers (Lee 2000), in which pasture intake had been estimated using the alkane technique (Dove and Mayes 1991). These parameter estimates were based on 1729 and 1292 records in the young sheep and adult wethers, respectively. These sheep were part of CSIRO Livestock Industries’ Fine Wool Project flock (Swan et al. 2000).

All parameter sets were obtained from multiple bloodline flocks of Merino sheep, and although two were derived from the same genotypes, the estimates were treated as independent for pooling purposes. Using the sampling variance for parameters as a suitable weighting, differences among estimates for each trait were tested for significance and a weighted (combined) estimate obtained where differences were not apparent. For example, the weighted heritability estimate (\( h_w^2 \)) was calculated from the individual estimates as:

\[
h_w^2 = \frac{h_1^2 \times \frac{1}{\text{se}(h_1^2)^2} + \ldots + h_n^2 \times \frac{1}{\text{se}(h_n^2)^2}}{\frac{1}{\text{se}(h_1^2)^2} + \ldots + \frac{1}{\text{se}(h_n^2)^2}}
\]

and the standard error of that weighted estimate (se\(_w\)) as:

\[
\text{se}_w = \frac{1}{\frac{1}{\text{se}(h_1^2)^2} + \ldots + \frac{1}{\text{se}(h_n^2)^2}}
\]

The weighted genetic correlations and respective standard errors were similarly estimated.

RESULTS AND DISCUSSION
The combined heritability and genetic correlation estimates are presented in Table 1. The combined heritability estimate for liveweight is based only on the two estimates of Lee (2000), as that from the

Table 1. Weighted heritability estimates and genetic correlations (± s.e.) of feed intake, liveweight, wool growth, wool growth efficiency and fibre diameter

<table>
<thead>
<tr>
<th>Trait</th>
<th>DOMI</th>
<th>DOMI/LW</th>
<th>Liveweight</th>
<th>Wool growth</th>
<th>Efficiency</th>
<th>Fibre diameter</th>
</tr>
</thead>
<tbody>
<tr>
<td>DOMI(^1)</td>
<td>0.12 ± 0.04</td>
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<tr>
<td>DOMI/LW(^1)</td>
<td>ne(^3)</td>
<td>0.10 ± 0.04</td>
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<td></td>
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<tr>
<td>Liveweight(^1)</td>
<td>0.57 ± 0.14</td>
<td>-0.29 ± 0.15</td>
<td>0.36 ± 0.06(^2)</td>
<td></td>
<td></td>
<td></td>
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<tr>
<td>Wool growth(^1)</td>
<td>-0.02 ± 0.17</td>
<td>-0.23 ± 0.17</td>
<td>0.24 ± 0.09</td>
<td>0.37 ± 0.05</td>
<td></td>
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<tr>
<td>Efficiency(^1)</td>
<td>-0.63 ± 0.12</td>
<td>-0.63 ± 0.12</td>
<td>0.02 ± 0.12</td>
<td>0.84 ± 0.20</td>
<td>0.25 ± 0.05</td>
<td></td>
</tr>
<tr>
<td>Fibre diameter(^1)</td>
<td>0.40 ± 0.15</td>
<td>0.31 ± 0.16</td>
<td>0.20 ± 0.11</td>
<td>0.18 ± 0.11</td>
<td>-0.03 ± 0.12</td>
<td>0.66 ± 0.08</td>
</tr>
</tbody>
</table>

\(^1\) Weighted estimates from all 3 data sets; \(^2\) Weighted estimates from young mixed-sex sheep and adult wethers only; \(^3\) Not estimated.
study of Lee et al. (1995) was significantly higher. Similarly, the estimate for fibre diameter was based only on results from the study of Lee (2000), as no previous estimates of the genetic relationships between fibre diameter and feed intake were available.

The combined heritabilities for intake, wool growth and its efficiency are similar to those of the individual estimates, but the standard error of the estimates was almost halved. There was a considerable improvement in the precision of the combined estimates of the genetic correlations between feed intake, liveweight, wool growth and wool growth efficiency over that of the individual estimates. No combined estimate for the genetic relationship of feed intake and intake expressed per unit liveweight was possible due to significant heterogeneity among the individual estimates.

The strong genetic relationship between wool growth and the efficiency of its production is confirmed in the combined estimates and supports the conclusions of earlier pen studies on sheep from flocks selected for increased fleece weight (Williams 1979). Although increasing liveweight is likely to lead to lower intakes per unit of liveweight, the efficiency of wool production would not be expected to change. Increasing wool growth through selection will thus lead to improved efficiency, but have little effect on intake, other than indirectly through possible changes in liveweight. Reducing fibre diameter should not affect wool production efficiency, but feed intake may decline.

Given the strong genetic relationship between wool growth and efficiency, little would be gained by including feed intake in the selection criteria, although intake may still be included in the breeding objectives. However, if the breeding objective included reducing fibre diameter (which has a poor genetic relationship with efficiency and a weak relationship with intake), with no or little change in wool growth, then measurement of intake, perhaps in progeny groups, may assist in ranking progeny tested sires.

The ability to accurately estimate breeding values is related to both the heritability of the trait and number of progeny tested. Figure 1 indicates the effect of the number of progeny tested on the correlation between estimated and true breeding values for intake, wool growth and fibre diameter. An equivalent accuracy for estimated breeding values for feed intake will require much larger progeny groups than that needed for traits such as wool growth and fibre diameter. However, given the current size of progeny groups in Central Test Sire Evaluation is 30-40, a correlation of 0.65 would still be possible for pasture intake of sires.

Currently, account is taken of feed intake in breeding objectives by including the costs within the economic value of the traits, based on generic relationships with production. For example, in OBJECT (software widely used to establish personalised breeding objectives for Merino Ram breeders), feed costs are included in the economic values for liveweight and reproductive performance (Semple et al. 1994). The genetic relationships established within this study now allow feed costs to be included in the economic value for wool traits included in the breeding objective. Alternatively, the availability of the genetic parameters for feed intake now allows it to be incorporated as an additional trait in the breeding objective. This will have a negative economic value (or cost) and the genetic correlations with the production traits will be accounted for in the expected responses to selection on the index. Under these circumstances, of course, no allowance is made for the consequences of feed intake changes in the economic values for the production traits.
Estimation of breeding values for feed intake in central test or on-farm genetic evaluations is also possible using these parameters.

**Figure 1.** The relationship between the correlation of the estimated breeding value with true breeding value (infinite progeny) and the number of progeny tested (MacLeod 1992).

**REFERENCES**


