GENETIC AND PHENOTYPIC COMPONENTS OF FEED INTAKE BY GRAZING EWES

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SUMMARY

Estimates of pasture intake were made on 500 Merino ewes using chromic oxide
controlled release devices. There was evidence that genetic effects on intake
existed independently of liveweight, although both liveweight and fatness also
influenced intake. The heritabilities of faecal organic matter (OM) output (and
hence intake) and faecal OM adjusted for liveweight were estimated to be 0.26
(+0.16) and 0.21 (+0.16) respectively.

INTRODUCTION

Feed is a major cost in maintaining a breeding flock. Although the methods
used to calculate feed costs can be debated, extensive grazing involves a high
capital cost. The feed requirement of the breeding flock determines the stocking
rate and hence the production achieved per hectare. The choice of breeding stock
and breeding strategies in the Merino wool enterprise should aim to maximise
profit. To date, the emphasis has focussed on returns with little emphasis on
costs.

An optimum selection index should include feed intake as a breeding objective
(not necessarily as a trait for selection) with an appropriate economic value
(James, 1982). This requires good estimates of the genetic variance of intake and
the genetic correlations between intake and all other traits (both those in the
objective and those used for selection). These estimates are not available in any
sheep population and so the optimum procedure cannot be used.

Recently, controlled release devices (CRD) have allowed faecal output, and
hence pasture intake, to be estimated reliably (Ellis and Rodden, 1987). The
procedure is both precise and unbiased (Lee et al., 1988). Using CRDs, we are
determining (i) the extent of genetic variation in pasture intake both between
and within Merino flocks and (ii) whether this genetic variation is completely
explained by body size differences or whether variation exists independently of
weight. Intake is being estimated on four occasions in the reproductive cycle.
This report is based on estimates from early pregnancy.

METHODS

Faecal output (and hence pasture intake) was estimated in approximately 300
ewes in each of two years (1988 and 1989). The ewes were subsamples from a
multiple bloodline flock which was established to estimate between- and
within-flock genetic parameters for traits of economic importance in Merino sheep
(Atkins and McGuirk, 1979). The flock consists of 15 separate randomly-bred
subflocks sampled from strains and bloodlines within the Australian Merino
population. The design closely follows the optimum for jointly estimating genetic
variation within and between breeds/flocks (Taylor, 1976). Three sires were
represented in each flock within each age group, with 3-4 ewes/sire. In 1988, ewes
born in 1983 and 1984 were measured while in 1989 the 1983 born ewes were replaced
with ewes born in 1985, and approximately 100 ewes born in 1984 were replaced by
an equivalent number of half sisters. In total approximately 500 individual ewes
were sampled over two years of measurement.

Faecal samples were collected from the ewes over a 2-3 week period, commencing 2 weeks after the completion of a 6 week mating period. During the measurement period ewes grazed an irrigated pasture, which included white clover, rye grass and phalaris. Liveweights were recorded at the start and end of each collection period, and ultrasonic fat depths (approximately 50mm from the midline between the 12-13th ribs) were measured at the start of each period.

Least squares methods were used to analyse measures of faecal organic matter (OM) output. The estimates of repeatability within-ewe and analyses of the interactions of year of measurement with flock, sire and ewe were based on individual sampling days. The model included age group, flock, sire, ewe, year of measurement, flock x year, sire x year, ewe x year, and day of sampling. Because only 1 estimate of fat depth and 2 estimates of liveweight (meaned) were available per ewe per sampling period, estimates of faecal OM were reduced to a single meaned measure for further analyses to examine the relationships with liveweight and fatness. Genetic parameters and their standard errors were calculated from the estimated variance components according to Becker (1984).

RESULTS

Both year and day of sampling were significant sources of variation. The repeatability of estimates of faecal output between samplings within a period (or device) was 0.39 (±0.02). Neither of the interactions of flock or sire with year were significant. However, both ewe and the ewe x year interaction were significant sources of variation.

Figure 1 Relationship between faecal organic matter output and liveweight both within- and between-flock

Between-flock variation in faecal OM output was strongly related to variation in liveweight (Figure 1), although flock differences independent of liveweight were still a significant source of variation.
Estimates of within-flock genetic and phenotypic correlations, and heritability are shown in Table 1. Including liveweight and fat depth as covariates in the analysis of faecal OM output reduced variation between sires by a small amount. The regression of faecal OM output on liveweight within-flocks was lower than that between-flocks (Figure 1).

Table 1 Estimates (+s.e.) of heritability (diagonal), genetic correlations (above diagonal) and phenotypic correlations (below diagonal)

<table>
<thead>
<tr>
<th></th>
<th>Fat Depth</th>
<th>Liveweight</th>
<th>Faecal OM</th>
<th>Faecal OM/LW</th>
</tr>
</thead>
<tbody>
<tr>
<td>Fat Depth</td>
<td>0.43 ±0.17</td>
<td>0.49 ±0.19</td>
<td>0.27 ±0.38</td>
<td>-0.14 ±0.38</td>
</tr>
<tr>
<td>Liveweight</td>
<td>0.50 ±0.09</td>
<td>0.63 ±0.18</td>
<td>0.39 ±0.29</td>
<td>-0.34 ±0.31</td>
</tr>
<tr>
<td>Faecal OM</td>
<td>-0.10 ±0.11</td>
<td>0.22 ±0.11</td>
<td>0.26 ±0.16</td>
<td>0.70 ±0.21</td>
</tr>
<tr>
<td>Faecal OM/LW</td>
<td>-0.34 ±0.10</td>
<td>-0.28 ±0.11</td>
<td>0.87 ±0.03</td>
<td>0.21 ±0.16</td>
</tr>
<tr>
<td>Mean</td>
<td>3.34 mm</td>
<td>48.57 kg</td>
<td>308.04 g/d</td>
<td>6.40 g/kg/d</td>
</tr>
<tr>
<td>S.D.</td>
<td>0.86</td>
<td>5.61</td>
<td>70.29</td>
<td>1.48</td>
</tr>
<tr>
<td>No. estimates</td>
<td>1.00</td>
<td>1.98</td>
<td>4.51</td>
<td>4.51</td>
</tr>
<tr>
<td>per ewe per year</td>
<td></td>
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Table 2 Estimates of the partial correlations and multiple regressions (+s.e.) of fat depth and liveweight with faecal organic matter output

<table>
<thead>
<tr>
<th></th>
<th>Faecal OM q/d</th>
<th>Faecal OM/LW q/kg/d</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>r</td>
<td>b</td>
</tr>
<tr>
<td>Genetic level</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Fat mm</td>
<td>0.09</td>
<td>6.03 ±6.36</td>
</tr>
<tr>
<td>Liveweight kg</td>
<td>0.31</td>
<td>2.76 ±0.81</td>
</tr>
<tr>
<td>Phenotypic level</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Fat mm</td>
<td>-0.25</td>
<td>-22.70 ±4.29</td>
</tr>
<tr>
<td>Liveweight kg</td>
<td>0.31</td>
<td>4.44 ±0.66</td>
</tr>
</tbody>
</table>

Discussion

In general, these early estimates of genetic correlations of liveweight and fatness with faecal OM estimates were imprecise. Liveweight had a moderate positive correlation with faecal OM at both the genetic (0.39) and phenotypic (0.22) levels, and a negative correlation with faecal OM adjusted for liveweight (-0.34 and -0.28 respectively). Fat depth was also moderately correlated with faecal OM/kg liveweight at the phenotypic level (-0.34) and faecal OM at the genetic level (0.27). However, the partial correlations (Table 2) indicate that the effects of fat level per se on pasture intake operate mainly at the phenotypic level. Liveweight effects on faecal OM adjusted for liveweight are evident at the genetic level.

The DM digestibility of available pasture was the same in both years (0.56) and, if no differences in herbage selection are assumed between genotypes, the parameters estimated for faecal output will be virtually identical to those for pasture intake. The year effect on mean faecal output/intake is likely to be directly attributable to the higher total DM availability in the second year (Hodgson, 1982).

Between ewe effects include variation in herbage selection and digestibility, differences between devices in release rate of marker and true differences in intake. All but the latter are assumed to be random effects. The ewe x year interaction possibly indicates between device effects and/or within ewe variation in liveweight and fatness between years.
The relatively low repeatability of faecal OM (intake) estimates is not surprising given the nature of the trait and the factors operating at the within-ewe level (Lee et al., 1990). It does highlight the need for repeated sampling to ensure a reliable estimate of at least medium term intake is obtained, overcoming short term fluctuations. As expected, the estimate of faecal OM (intake) heritability based on the mean of up to 5 measures (0.26±0.16) was higher than those based on individual measures (0.14±0.09).

Simply dividing faecal OM by liveweight did not fully remove the effects of liveweight. The change in sign and the magnitude of simple correlations between liveweight and faecal OM after adjustment for liveweight indicate that the exponent for liveweight should be less than unity. It is apparent from the partial correlations that fatness had virtually no effect at the genetic level. The main effect of fatness was at the phenotypic level, possibly of a metabolic nature (Forbes, 1980).

We can conclude that selection for increased liveweight in adult Merinos will lead to increased food intake, although intake per unit liveweight may decline. Selection for reduced subcutaneous fat depth in adults is likely to have little effect on feed costs other than those associated with correlated changes in liveweight. Inferences on the likely intakes of genotypes (in our case flocks) based simply on a knowledge of liveweight and fat depth would seem less predictable.

ACKNOWLEDGEMENT

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REFERENCES


