FEED INTAKE AND ITS GENETIC RELATIONSHIP WITH GROWTH TRAITS IN MERINO SHEEP

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SUMMARY

The feed cost for maintenance of the ewe flock is a major cost in lamb production systems and a reduction in these feed requirements could have an effect on carrying capacity and both biological and economic efficiency in sheep flocks. However information on the genetic variation of feed intake and its association with other production traits are scarce. This study reports on the variation in relative digestible dry matter intake (rDDMI), defined as the ratio of the digestible dry matter intake of each ewe divided by the group mean and its relationship with growth traits measured in 1279 Merino ewes. DDMI was estimated by faecal marker dilution method. Significant genetic variation was observed in intake with a heritability of 0.33 ± 0.09, suggesting scope for effective genetic selection. Genetic correlation between rDDMI with growth traits were generally low with the highest correlation (0.18 ± 0.09) observed with hogget weight.

INTRODUCTION

The feed cost for maintenance of the ewe flock and replacements accounts for about 60% of the total feed required for production of lamb carcass weight (Fogarty *et al.* 2003). Any reduction in these feed requirements through genetic improvement of maintenance requirement could have a dramatic impact on carrying capacity and both biological and economic efficiency in sheep flocks. Inclusion of feed intake in breeding programs requires knowledge of its genetic variation and relationship with other production traits. Information on the genetic variation of feed intake and its association with other production traits is scarce (Lee *et al.* 2002, Fogarty *et al.* 2006). This study reports on the relationship of feed intake of mature Merino ewes at maintenance (non-lactating, non-growing) and growth traits as young ewes.

MATERIALS & METHODS

Feed intake at maintenance was estimated in 1279 mature non-lactating, non-growing Merino ewes under grazing by faecal marker dilution method. Rumen controlled-release devices (CRDs) containing chromium sesquioxide capsules were used to estimate feed intake (Lee *et al.* 1995). The CRDs were administered 7-10 days prior to the first faecal sample being collected. Faecal samples were collected on 3 occasions from the ewes over a 7-10 day period and the faecal dry matter was analysed by atomic absorption spectrometry to determine chromium concentration. The daily release rate of chromium as supplied by manufacturer was divided by the concentration of chromium to estimate the daily faecal dry matter output. Pasture samples were analysed and average digestibility of dry matter was estimated and then used to calculate digestible dry matter intake. The ewes had full

pedigree and were from the QPLU$ flock at Trangie, NSW and the selection flock at Katanning, WA (Safari *et al*. 2007a). Intake data were collected at Trangie from 93 of the ewes in 2003 and 566 of the ewes in 2004 and from 620 ewes at Katanning in 2005 (Table 1). The birth weight, weaning weight and hogget weight for the ewes and their relatives was available for estimation of genetic correlations between feed intake and growth traits with the number of animals and means shown in Table 2.

   As there were large differences in mean digestible dry matter intake (DDMI), partially due to pasture digestibility differences and their variances across the groups, the relative DDMI (rDDMI) for each ewe was expressed as the ratio of the mean for each group. A mixed linear model was used for the analysis of rDDMI. Fixed effects for rDDMI were group, reproduction status of ewes at their previous lambing, bloodline and liveweight as covariate. The fixed effects for growth traits were: dam age, birth-rearing type, sex, bloodline, and flock/year as management group. Weaning age was included as a covariate for weaning weight and hogget weight. The only random effect for rDDMI was direct genetic while for growth traits both direct and maternal genetic effects were included in the model. The variance components were estimated by restricted maximum likelihood procedure using ASReml (Gilmour *et al*. 2006). An animal model with the corresponding significant fixed effects as described above was used. Three models were used to estimate genetic correlations between rDDMI and growth traits by inclusion or not of the liveweight (LW) as covariate for rDDMI and inclusion or not of maternal genetic effect (m^2) for the growth traits. Model 3 was included only for the purpose of comparison of the results of this study with the estimates published in meat sheep by Fogarty *et al*. (2006).

Model 1: rDDMI (+LW) and growth (+m^2)
Model 2: rDDM (-LW) and growth (+m^2)
Model 3: rDDMI (-LW) and growth (-m^2)

Table 1. Number of ewes (n) and mean (s.d.) for digestible dry matter intake (DDMI, kg/day) and liveweight (LW, kg)

Group	n	DDMI	LW
Trangie_2003	93	2.88 (0.59)	59.4 (7.5)
Trangie _2004	566	2.00 (0.61)	66.9 (8.2)
Katanning	620	1.49 (0.27)	67.3 (7.7)

Table 2. Number of observations (n), mean (s.d.) and coefficient of variation (CV) for relative dry matter intake (rDDM) and growth traits

Traits	N	Mean (s.d.)	CV
rDDM	1279	1.0 (0.22)	22
Birth weight (kg)	24,850	4.3 (0.9)	21
Weaning weight (kg)	20,076	22.9 (5.1)	22
Hogget weight (kg)	19,609	53.0 (9.9)	19

RESULTS AND DISSSCUSSION

All the fixed effects were significant (P<0.01) for rDDMI and the growth traits with the exception of bloodline for rDDMI. The relationship between rDDMI and liveweight (LW) from model 1 was:

$$rDDMI = 0.53 + 0.0054 \, LW \quad (\pm 0.0008, \, rDDMI/kg)$$

This is similar to the relationship reported by Fogarty *et al*. (2006) for crossbreed ewes. The estimated heritability from initial analysis of data was 0.17 ± 0.08. After 20 outliers with high standard residuals were removed from the analysis, the heritability increased to 0.33 ± 0.09. All outliers had significant (P<0.001) impact on the variance components. The estimate of heritability for feed intake is close to the estimates of Fogarty *et al*. (2006) in crossbred ewes, but higher than the estimates by Lee *et al*. (2002). In beef cattle Koots *et al*. (1994) have estimated an average heritability of 0.34 for feed intake, while Pitchford (2004) reported an average across species heritability of 0.25 for net feed efficiency.

The genetic and phenotypic correlations between growth traits and rDDMI are presented in Table 3. Maternal genetic effect is significant for growth traits (Safari *et al*., 2005; Safari *et al*., 2007b). The first two models estimated the genetic and phenotypic correlations between growth and rDDMI with and without LW. The estimates from Model 3 are similar with the estimates from a corresponding Model 2 by Fogarty *et al*. (2006). These estimates of correlations were generally low and for the Model 3, highest (0.18) was observed with hogget weight.

The phenotypic correlations were generally lower than the genetic correlations. Given considerable genetic variance for feed intake it is possible to improve feed efficiency by reducing feed intake for ewe maintenance through selection. With low genetic correlation between growth traits and feed intake, feed intake can be included as a component of a selection index to improve both traits.

Feed intake is difficult and expensive to measure. In this study we measured feed intake rather than net or residual feed intake which is used mainly in other species. The live weight gain estimate would be subject to large errors if measured over the short feed intake period (*circa* 2 weeks) which is constrained by the life of the CRD. The coefficient of variation of feed intake using indirect measurements (marker) is approximately twice of the direct measurement (5-12% vs. 17-25%), however it is less expensive and only practical way to measure in large number of animals.

Table 3 Genetic (r_g) and phenotypic (r_p) correlations of feed intake (rDDMI) with growth (birth weight (BWT), weaning weight (WWT), Hogget weight (HWT)) traits

	Model 1		Model 2		Model 3	
	r_g	r_p	r_g	r_p	r_g	r_p
BWT	0.15 ± 0.12	0.06 ± 0.03	0.24 ± 0.12	0.09 ± 0.03	0.12 ± 0.08	0.09 ± 0.03
WWT	-0.08 ± 0.12	0.02 ± 0.03	0.09 ± 0.11	0.11 ± 0.03	0.10 ± 0.09	0.11 ± 0.03
HWT	0.02 ± 0.10	0.01 ± 0.03	0.20 ± 0.09	0.12 ± 0.03	0.18 ± 0.09	0.12 ± 0.03

CONCLUSIONS

Given considerable genetic variance for feed intake demonstrated by high heritability together with a coefficient of variation of 22% it is possible to improve feed efficiency by reducing feed intake for ewe maintenance through selection. With low genetic correlation between growth traits and feed intake, feed intake can be included as a component of a selection index to improve both traits.

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