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Variation in Grazing Intake of Prime Lamb Dam Genotypes

Abstract

A reduction in feed requirements for maintenance of sheep would have a dramatic impact on carrying capacity and both biological and economic efficiency in flocks. Estimates of genetic parameters are required to assess the potential for genetic improvement of feed efficiency and allow Estimated Breeding Values (EBVs) to be calculated and included in breeding programs. The results have demonstrated considerable genetic variation for intake for maintenance among maternal meatsheep genotypes. The high estimated heritability (0.41 ± 0.07) for intake together with the large range in sire progeny means indicates potential for rapid progress from direct selection. However intake at maintenance, especially under grazing, is very difficult and expensive to measure with current technology and requires large numbers of progeny per sire to be tested to provide accurate EBVs. The genetic correlations with a range of production traits were all close to zero, which precludes using these traits for indirect selection, although it means that breeding programs aimed at improving growth, carcass or reproduction traits, will not be antagonistic and will have little effect on intake or feed requirements for maintenance. The outcomes stress the importance of pursuing new technologies for measuring feed intake directly and/or determining the relationships with underlying physiological traits and use of genomic technologies.

Executive Summary

The feed cost for maintenance of the ewe flock and replacements accounts for over 65% of the feed required for production of lamb carcass weight. A reduction in this feed requirement through genetic improvement of efficiency of feed utilisation would have a dramatic impact on carrying capacity and both biological and economic efficiency in sheep flocks. There is currently no information on the genetic variation in feed requirements for maintenance or the relative feed efficiency among meat sheep. To include feed intake or efficiency in the breeding objective for meat sheep, reliable estimates of its heritability and genetic correlations with other production traits are required. These genetic parameters would allow estimated breeding values (EBVs) for feed intake to be calculated by Sheep Genetics Australia (SGA) and included in breeding programs.

The project aimed to estimate feed intake at grazing pasture for mature ewes in the MCPT project (LAMB.325A) and estimate heritability and genetic correlations between feed intake and production (growth, carcass, meat quality, wool and reproduction) traits for maternal genotypes. These genetic parameters are required to allow breeders to include reduction in feed requirements for maintenance as an objective in their breeding programs.

The project has demonstrated there is considerable genetic variation for intake for maintenance among maternal meatsheep genotypes. The high estimated heritability (0.41 ± 0.07) for intake together with the large range in sire progeny means indicates potential for rapid progress from selection. However intake at maintenance, especially under grazing, is very difficult and expensive to measure with current technology and requires large numbers of progeny per sire to provide accurate EBVs.

The genetic correlations with a range of production traits were all close to zero. Hence the use of other production traits for indirect selection to reduce maintenance requirements is not feasible. However on the positive side it also means that breeding programs aimed at improving production traits such as liveweight, carcass or reproduction, will not be antagonistic and will have little effect on intake, other than through the direct effect of increasing liveweight.

The project has established the potential for genetic improvement of feed efficiency and other modelling research has shown it can have a high impact on sheep enterprise profitability. The outcomes stress the importance of pursuing new technologies for measuring feed intake directly and/or determining the relationships with underlying physiological traits and use of genomic technologies.

Recommendations include:

- The genetic parameter information obtained from the project be made available to SGA.
- The proposed studies to investigate the relationship between IGF-1 and intake among a sample of the MCPT ewes should be pursued.
- The development of alternative technology for measuring feed intake of grazing animals be supported as well as the pursuit of physiological and genomic markers.

Contents

1 Background

The feed cost for maintenance of the ewe flock and replacements accounts for over 65% of the feed required for production of lamb carcass weight. A reduction in this feed requirement through genetic improvement of efficiency of feed utilisation would have a dramatic impact on carrying capacity and both biological and economic efficiency in sheep flocks. The Maternal Central Progeny Test (MCPT) (LAMB.325) has demonstrated a range in returns of over $40/ewe/year from 1stX ewes by different maternal sires, mainly due to differences in lambing rate of the ewes and carcass weight and fat level of the 2ndX lambs (Fogarty et al. 2005a). There is a range of over 10kg in mature weight of these 1stX ewe sire groups. This affects the maintenance feed requirements and relative carrying capacity of the groups. Taking account of the standard feed requirements to estimate feed requirements for ewe maintenance, gestation, lactation and lamb growth (SCA 1990) showed there was still considerable variation in productivity and gross margins of ewe groups of over $15/DSE/year, although little change in rankings of sire groups (Fogarty et al. 2003). There is currently no information on the genetic variation in feed requirements for maintenance or the relative feed efficiency among meat sheep.

Beef cattle studies have indicated cow/calf units with heavier mature weight cows convert feed energy to saleable calf with a 16% greater efficiency than do breeding units where the cows have low mature weights (Herd 1992). There is considerable genetic variation for residual feed intake in beef cattle (Archer et al. 1998) and significant response to selection has been demonstrated (Arthur et al. 2001). Net feed efficiency is a measure of the difference between an animal's actual feed intake over a given test period and its expected feed intake relative to its weight and growth. An animal consuming less feed than expected (based on its weight and physiological status) over a period will have a lower (negative) feed intake. Lee et al. (1995b, 2001) has reported estimates of heritability of 0.12 for feed intake of Merino sheep under grazing conditions.

To include feed intake or efficiency in the breeding objective for meat sheep, reliable estimates of its heritability and genetic correlations with other production traits are required. These genetic parameters would allow estimated breeding values (EBVs) for feed intake to be calculated by Sheep Genetics Australia (SGA) and included in breeding programs. The 1stX ewes in the MCPT, which are progeny of 91 maternal sires, have extensive performance data, including lambing rate over 3 years, lamb growth and carcass performance, wool production as well as faecal egg count (FEC) and milk production, with stored DNA samples. Collection of intake data from these ewes will quantify the genetic variation in meat sheep and provide estimates of heritability and genetic correlations with the other production traits in the data.

Results from the MCPT have highlighted the very large range in performance between ewe groups from different sires. For example the range among sire groups of 1stX ewes within breeds was up to 45% for lambs weaned per ewe joined, 4kg for 2ndX lamb weight and 2.2mm GR (at 24 kg carcass weight) for 2ndX carcass fat (Fogarty et al. 2005a). It is likely that there are large differences in the biological efficiency of these groups of ewes both overall and at various stages throughout the yearly production cycle, over and above that due to the range of 10kg in the average mature weight of the ewe genotypes. Quantifying the feed efficiency of selected groups of these ewes at the various stages (dry, pregnant, lactating) and levels of performance (number of lambs, growth rate, carcass composition) will allow more accurate decisions to be made about the overall merits of the various genotypes.

It will also provide actual data for developing decision support models for evaluating sustainable production systems more systematically.

2 Project Objectives

To allow breeders to reduce the feed requirements for maintenance and improve the overall efficiency of utilisation of feed in their LAMBPLAN breeding programs and lamb production systems.

Specific aims:
1. Estimate feed intake at grazing pasture for mature ewes in the MCPT project
2. Calculate maintenance requirements of ewes
3. Calculate heritability and genetic correlations between feed intake and production (growth, carcass, meat quality, wool and reproduction) traits for maternal genotypes.

3 Methodology

3.1 Measurements and Animals

Feed intake for all mature 1stX ewes in the Maternal Sire Central Progeny Test (MCPT) was estimated by faecal marker dilution and the feed requirements for maintenance calculated. Chromium sesquioxide capsules (Lee et al. 1995a), delivered intraruminally by Captec Chrome (Nufarm Ltd, New Zealand) controlled release devices (CRD), were used to estimate feed intake. The CRD were administered 7 – 10 days prior to the first faecal sample being collected. On average 3 rectal faecal samples were collected from the ewes over a 7 – 10 day period (with a minimum of 3 days between sampling). The faecal organic matter was analysed by atomic absorption spectrometry (Costigan and Ellis 1987) to determine the chromium concentration. The daily release rate of chromium, as indicated by the supplier, was divided by the concentration of chromium in the faecal organic matter to estimate the daily faecal organic matter output. At the beginning and end of each measurement period, 16 pasture quadrats (0.25 m^2) were cut to determine the availability of green and dead material and the proportion of legume in the pasture. Pasture samples were analysed for acid detergent fibre (ADF) and nitrogen (N) content by NSW Department of Primary Industries and FEEDTEST®, from which dry matter (DM) digestibility of the dry and green components were estimated (Oddy *et al.* 1983). The average availability and digestibility of green and dead material and proportion of legume was used in the “GRAZFEED” model (Horizon Agriculture, North Ryde, NSW 2113, Australia) to estimate the diet digestibility. The estimated diet digestibility was used to calculate digestible dry matter intake (DDMI). Ultrasound eye muscle depth and fat depth at the C site of the ewes were measured by a LAMBPLAN accredited scanner, and live weight of the ewes was recorded pre and post faecal sampling.

All 1stX ewes in the MCPT were faecal sampled after they had completed their 3 years of evaluation of production. The ewes were non pregnant and grazing at pasture. Some 2528 ewes were sampled with approximate numbers of ewes involved at the various sites and time scale shown below. These 1stX ewes were the progeny of 91 maternal sires with LAMBPLAN EBVs that were nominated by seedstock breeders. The 1stX ewes were generated by artificial insemination of randomly assigned Merino (and Corriedale at

Hamilton) ewes in all years and sites, with 3 common sires used to provide genetic linkage (Fogarty et al. 2005b). The general design of MCPT is shown in Appendix 1.

Timetable for measurements by location – approximate number of ewes (groups)

Location		***2001/02***	***2002/03***	***2003/04***	***2004/05***
Cowra	*Spring*		*600 (3)*	*200(1)*	
	Autumn/Winter	*200 (1)*	*200(1)*		
Hamilton	*Summer/Autumn*	*305(1)*	*406 (2)*		
Rutherglen	*Spring*		*290(1)*	*280(1)*	*290(1)*

3.2 Protocols

3.2.1 Sheep measurements and sampling

Day	**Activity**
0	Ewes onto the test pasture
7-10	Weighed – overnight fast Fat depth / fat scored CRD's inserted
8-10days after CRD's inserted	1st faecal sample* Pasture sampled
3-4 days later	2nd faecal sample*
3-4 days later	3rd faecal sample* Pasture sampled
Following day or later	Weighed – overnight fast Remove from test pasture

Faecal sampling commenced immediately after the ewes were brought into the yards.

3.3 Pasture

Pasture paddocks were selected to have greater than 1.5 tDM/ha, be as uniform as possible and be large enough and have sufficient growth to maintain the ewes for at least 4 weeks. At least 12 quadrat cuts randomly across the paddock were taken at each pasture sampling. Each quadrat was sorted to determine the amount of green, dead and legume (on a DM basis) and dried after sorting. The dried dead and green material (including the respective legume components of each) was weighed to determine pasture availability. The dried samples were ground and then sent for analyses for acid digestible fibre (ADF) and nitrogen (N) content.

Diet digestibility was estimated using *Grazfeed* from the predicted digestibilities of the dead and green components (based on ADF and N – Oddy *et al.*, 1983) and the proportion of legume in the pasture. This procedure has been used successfully in previous studies to estimate intake with this type of CRD (Lee *et al.*, 1995a).

3.4 Faecal samples

Faecal samples were dried immediately after collection, or frozen until they could be dried. Dried samples were ground and the 3 samples from each animal pooled on an equal weight basis. The Cr analyses.of samples from all sites were carried out at the NSW Department of Primary Industries, Wollongbar laboratory.

3.5 Statistical analysis

A total of 2528 mature first cross ewe progeny of 91 sires were analysed. A mixed linear model was used to analyse the relative digestible dry matter intake (rDDMI) of the first cross ewes. Relative digestible dry matter intake (rDDMI) was calculated as the ratio of individual DDMI and the group average DDMI. Fixed effects included in the basic model were site (Cowra, Hamilton, Rutherglen), group (1 – 12), sire breed (1 – 8), and reproductive status of the ewe (Dry, lambed & lost (single, twins or triplets died), single born & raised, multiple born & single raised, multiple born & raised, at the previous lambing). Live weight gain (LWg, LW post faecal sampling minus LW pre faecal sampling), average live weight (aLW), fat depth at the C site (Cfat) and eye muscle depth (EMD) were included as linear covariates. All 2 and 3 way interactions were included in the initial model; interactions that were not significant ($P>0.05$) were removed from the model. The final model for rDDMI included the interactions site × group × LWg, site × group × aLW, site × Cfat, breed × Cfat (Table 2). Sire was fitted as a random term. Sire means were estimated using the basic model (without covariates) and included the interaction group × breed. The variance components were estimated by restricted maximum likelihood procedure using ASReml (Gilmour *et al.* 2002). An animal model with fixed effects and linear covariates the same as the basic model described above was used to account for as much variation as possible.

4 Results and Discussion

4.1 Variation among sites and crossbred ewes

Base data on the number of ewes sampled at each site, their liveweight, ultrasound muscle and fat depth are shown in Table 1. There was little difference in the liveweight, muscle and fat depth of the crossbred ewes at Cowra and Rutherglen, with those at Hamilton being lower. This reflects both the genetics of the base ewes, being fine wool Merino and Corriedale at Hamilton and the lower feed availability at the site. There was also a greater liveweight gain over the test sampling period among the ewes at Cowra and Rutherglen (2.0 – 2.6 kg) than Hamilton (0.6 kg) although there was considerable variation among the cohort groups at each location (Table 1).

There was a trend for the estimates of DDMI to increase over the 3 years the samples were collected from the various cohort groups. The increase was from 1.3-1.4kg DDMI in early 2002 to 2.64 in September 2004. The suspicion is that the release rate of the CRDs declined over that period (Keith Ellis pers. com.). The quality control data supplied with the CRDs indicates the release rates were evaluated in November 1999, with the capsules manufactured in November 1994. It may be possible to retest the release rate on some of the remaining capsules for recalibration, but it has not been possible to have this done to date.

Table 1 Number of ewes (n) and means (standard deviation) for digestible dry matter intake (DDMI), live weight gain (LW gain), average live weight (average LW), eye muscle depth (EMD) and C fat for the various sites and breed cross ewes

Site	Group	n	DDMI (kg/day)	LW gain (kg)	Average LW (kg)	EMD (mm)	C fat (mm)
Cowra		*1091*	*1.83 (0.51)*	*2.6 (2.9)*	*71.1 (9.1)*	*29.1 (3.4)*	*4.5 (1.9)*
	1	194	1.39 (0.23)	0.0 (1.4)	67.2 (7.4)	27.6 (2.7)	3.8 (1.4)
	2	196	1.46 (0.30)	1.1 (1.6)	79.6 (8.3)	31.0 (2.9)	5.8 (2.5)
	3	180	1.70 (0.35)	1.2 (2.3)	68.8 (7.9)	28.4 (3.4)	3.8 (1.3)
	4	182	2.00 (0.42)	3.1 (2.7)	69.0 (9.0)	27.8 (3.5)	3.7 (1.5)
	5	176	2.28 (0.37)	4.8 (1.4)	70.1 (7.6)	29.8 (3.0)	4.9 (1.5)
	6	163	2.30 (0.45)	6.3 (2.2)	71.6 (8.5)	30.2 (3.1)	5.0 (1.8)
Hamilton		*658*	*1.75 (0.53)*	*0.6 (3.1)*	*59.3 (8.2)*	*26.1 (3.5)*	*3.8 (2.4)*
	1	294	1.38 (0.30)	-0.1 (3.7)	61.1 (7.6)	27.4 (2.9)	4.5 (2.4)
	2	158	1.70 (0.41)	1.8 (2.3)	62.6 (7.9)	26.6 (3.9)	3.8 (2.6)
	3	206	2.32 (0.35)	0.7 (2.1)	54.0 (6.7)	23.8 (2.8)	2.6 (1.8)
Rutherglen		*779*	*2.69 (0.74)*	*2.0 (2.7)*	*69.1 (8.4)*	*27.5 (3.4)*	*5.3 (2.2)*
	1	279	2.67 (0.60)	3.4 (2.0)	65.8 (7.6)	25.6 (3.2)	4.2 (1.6)
	2	241	2.54 (0.75)	0.2 (2.8)	71.0 (8.8)	27.3 (3.2)	6.1 (2.4)
	3	259	2.84 (0.84)	2.2 (2.3)	70.6 (7.9)	29.8 (2.4)	5.9 (2.1)
Breed [A]							
BL		545	2.26 (0.70)	2.4 (3.2)	70.9 (10.0)	28.9 (3.3)	5.3 (2.4)
EF		211	2.07 (0.70)	1.8 (3.1)	65.9 (9.8)	25.5 (3.7)	3.3 (1.8)
Finnsheep		503	1.86 (0.59)	1.2 (2.7)	64.4 (8.6)	26.7 (3.4)	3.9 (1.6)
Coopworth		387	2.00 (0.75)	1.4 (3.1)	68.1 (9.9)	28.2 (3.2)	5.0 (2.4)
WS		150	2.30 (0.78)	2.8 (2.9)	72.0 (8.5)	29.7 (3.2)	4.9 (2.3)
Corriedale		148	1.88 (0.56)	2.2 (2.6)	59.3 (8.7)	26.1 (3.4)	3.3 (1.3)
BoL		145	1.70 (0.54)	1.9 (3.8)	67.6 (10.7)	29.2 (3.8)	5.0 (2.3)
Other		439	2.27 (0.80)	2.3 (2.7)	67.9 (9.3)	28.3 (3.6)	4.9 (2.1)

[A] BL=Border Leicester, EF=East Friesian, WS=White Suffolk, BoL=Booroola Leicester

To overcome this time trend and heterogeneity of variance across groups for DDMI, values were expressed as a ratio of the mean for each cohort group and relative DDMI was the trait analysed (rDDMI). The significant fixed effects in the final model are shown in Table 2. As expected, average liveweight of the ewes was highly significant (P<0.01), as well as liveweight gain over the sampling period, reproductive status at the previous lambing, fat depth and site (P<0.01). Sire breed of the crossbred ewes was not significant.

Table 2. Model and significance of fixed effects for rDOMI

Source	DF	F Incremental	F Adjusted	Significance
Site	2	0.69	12.38	< 0.001
Group	9	1.86	2.83	0.004
LWgain	1	60.59	36.92	< 0.001
averageLW	1	54.17	110.40	< 0.001
Reproduction	4	36.78	25.92	< 0.001
FatC	1	19.08	15.10	< 0.001
EMD	1	8.19	5.84	0.016
Sire breed	7	0.95	1.01	ns
Site.group.LWg	11	5.64	5.63	< 0.001
Site.group.aLW	11	2.79	2.79	0.003
Site.FatC	2	8.44	7.05	0.001
Breed.FatC	7	2.68	2.50	0.018

There were significant interactions for liveweight gain and average liveweight with site.group (P<0.01). The relationships between rDDMI and average liveweight of the crossbred ewes at each site are shown in Figure 1. The regressions were 0.0068 ± 0.0010 rDDMI/kg for Cowra, 0.0082 ± 0.0015 rDDMI/kg for Hamilton and 0.0081 ± 0.0012 rDDMI/kg for Rutherglen, with the equations as follows:

Cowra: $\text{rDDMI} = 0.48 + 0.0068\ \text{aLW}$

Hamilton: $\text{rDDMI} = 0.47 + 0.0082\ \text{aLW}$

Rutherglen: $\text{rDDMI} = 0.42 + 0.0081\ \text{aLW}$

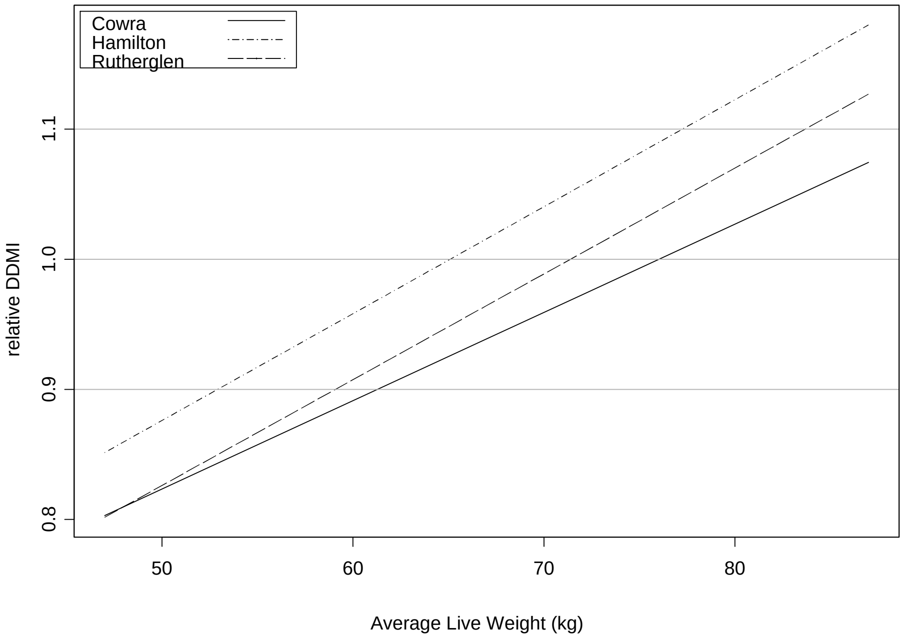

Figure 1. The relationship between rDDMI and average live weight of crossbred ewes

The relationships between rDDMI and liveweight gain over the approximately 10 day sampling period of the crossbred ewes at each site are shown in Figure 2. The regressions were 0.008 ± 0.003 rDDMI/kg for Cowra, 0.0003 ± 0.003 rDDMI/kg for Hamilton and 0.026 ± 0.003 rDDMI/kg for Rutherglen. There was no effect of liveweight gain at Hamilton where there was little average gain in ewe liveweight over the period (Table 1), whereas rDDMI increased with liveweight gain at Cowra and more so at Rutherglen, where there was an average gain of over 2 kg during the sampling period at both sites.

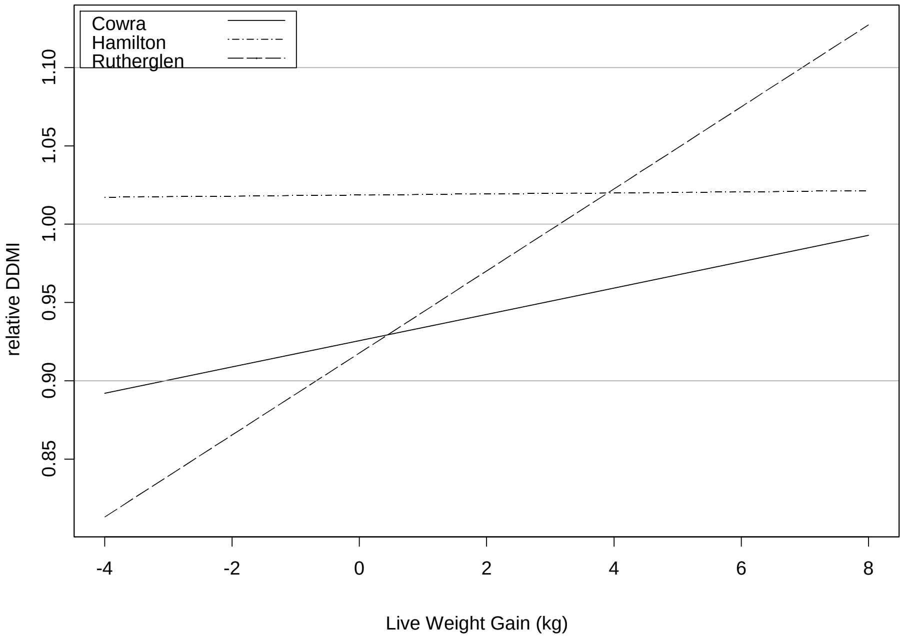

Figure 2. The relationship between rDDMI and live weight gain of crossbred ewes

Reproductive status of the ewes at the previous lambing had a significant effect on rDDMI (P<0.01). Ewes that were dry or lambed and lost had lower rDDMI than ewes that had single lambs which were lower than those ewes that had multiples, regardless of whether they were reared as multiples or singles (Table 3). The ewes that previously reared multiples had 7-9% higher feed intake than the ewes that were dry or lambed and lost.

Sire breed of the crossbred ewes was not significant for rDDMI (P>0.05), with the predicted means for the sire breeds shown in Table 3. The Finnsheep cross ewes had a low mean (0.91) with all the other breed crosses being close to 1.0.

There were significant associations between rDDMI and both ultrasound fat depth at the C site (FatC) (P<0.01) and eye muscle depth (EMD) (P<0.05). The overall regressions were negative for both traits (-0.013 ± 0.003 rDDMI/mm for FatC and -0.005 ± 0.002 rDDMI/mm for EMD). There were significant interactions of FatC with site (P<0.01) and sire breed (P<0.05), with the former illustrated in Figure 3. There was a stronger negative regression for FatC at Cowra (-0.026 ± 0.005 rDDMI/mm) than at Hamilton (-0.010 ± 0.005 rDDMI/mm) or Rutherglen (-0.006 ± 0.005 rDDMI/mm). The significant sire breed by FatC interaction was largely due to strong negative regressions for the Finnsheep (-0.030 ± 0.007 rDDMI/mm) and Corriedale (-0.025 ± 0.013 rDDMI/mm) breeds with the Border Leicester showing little relationship (-0.001 ± 0.004 rDDMI/mm).

Table 3. Predicted means (±standard error) of rDOMI for sire breed and reproduction status of crossbred ewes and regressions for FatC and eye muscle depth (EMD)

Sire breed	**rDDMI**	**Reproduction status**	**rDDMI**
Border Leicester	0.98 ± 0.02	Dry	0.93 ± 0.02^{c}
East Friesian	0.98 ± 0.03	Lamb & lost	0.91 ± 0.02^{c}
Finnsheep	0.91 ± 0.03	Single	0.97 ± 0.01^{b}
Coopworth	0.97 ± 0.03	Multiple/single	1.03 ± 0.02^{a}
White Suffolk	1.02 ± 0.04	Multiple	1.04 ± 0.01^{a}
Corriedale	0.99 ± 0.04	**Regression**	
Booroola Leicester	0.99 ± 0.04	FatC (rDDMI/mm)	-0.013 ± 0.003
Other	0.98 ± 0.02	EMD (rDDMI/mm)	-0.005 ± 0.002

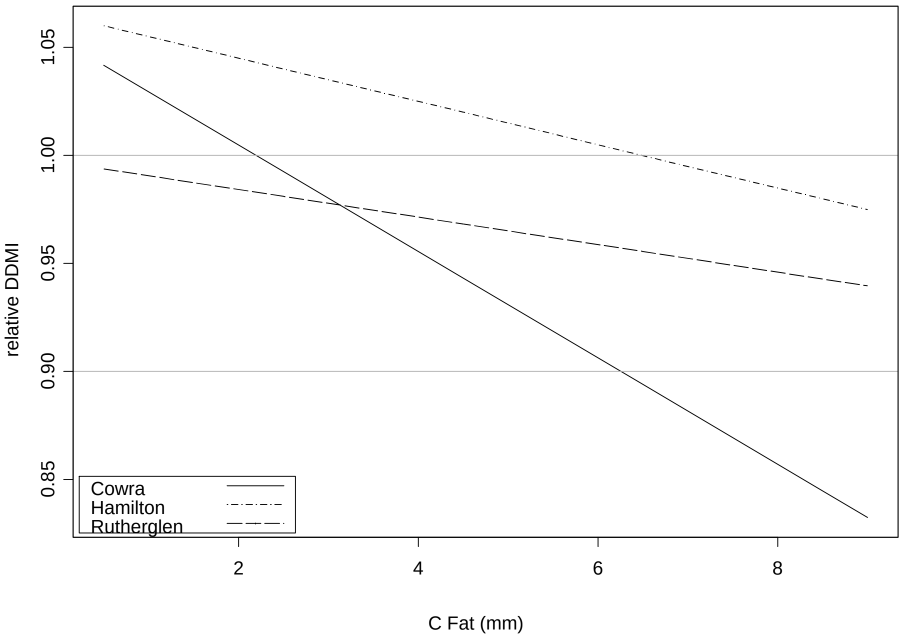

Figure 3. The relationship between rDDMI and fat depth of crossbred ewes

4.2 Genetic parameters

There was considerable genetic variation for rDDMI of the ewes sampled at maintenance, resulting in an estimated heritability of 0.41 ± 0.07 (Table 4). Removal of breed of sire from the model did not change the genetic variance or estimate of heritability. The BLUP sire means showed a considerable range for rDDMI within the various sire breeds (Table 5) as well as across all 91 sires (Table 6). There was a range of over 20% in rDDMI across sire progeny groups within all sire breeds, with the range for the East Friesian being 43%, Coopworth 34% and Border Leicester 30%. Ten of the 12 Finnsheep sire groups were below 1.0. The sire means for rDDMI of crossbred ewe progeny within each of the breeds are illustrated in Figures 4 to 11. The 3 link sires, Border Leicester 12, Finnsheep 7 and Coopworth 5 had 178, 239 and 200 respectively ewe progeny per sire sampled. The other 88 sires had an average of 21.7 crossbred ewe progeny per sire ranging from 8 to 40.

Table 4. Genetic variance, heritability (± s.e.) and phenotypic standard deviation for rDDMI of crossbred ewes

Component	Parameter
Genetic variance	0.0176 ± 0.0032
Residual variance	0.0253 ± 0.0026
Heritability	0.41 ± 0.07
Phenotypic standard deviation	0.207

Table 5. Range of predicted sire means (±s.e.) within sire breed for rDDMI of crossbred ewes and number of sires

Sire breed	**Sires (n)**	**Range of sire means for rDDMI** **Minimum**	 **Maximum**
Border Leicester	18	0.90 ± 0.04	1.20 ± 0.05
East Friesian	12	0.75 ± 0.05	1.18 ± 0.06
Finnsheep	12	0.83 ± 0.04	1.03 ± 0.03
Coopworth	9	0.77 ± 0.04	1.11 ± 0.04
White Suffolk	7	0.94 ± 0.04	1.14 ± 0.06
Corriedale	6	0.92 ± 0.04	1.03 ± 0.03
Booroola Leicester	6	0.86 ± 0.04	1.12 ± 0.07
Other	21	0.87 ± 0.04	1.29 ± 0.06

Table 6 Predicted means (±s.e.) for rDDMI of sires from the various breeds and the number of crossbred ewe progeny sampled

Sire breed	Sire id	Progeny	Mean
Border Leicester	2	23	1.06 ± 0.04
	8	26	1.00 ± 0.04
	*12**	*178*	*1.06 ± 0.02*
	13	23	1.00 ± 0.04
	24	20	0.93 ± 0.04
	25	20	1.05 ± 0.04
	32	9	1.07 ± 0.06
	35	40	1.03 ± 0.03
	52	33	0.98 ± 0.03
	53	25	0.93 ± 0.04
	54	34	1.05 ± 0.03
	61	8	0.93 ± 0.06
	62	12	0.91 ± 0.05
	70	23	0.90 ± 0.04
	71	20	0.98 ± 0.04
	81	22	1.08 ± 0.04
	82	11	1.20 ± 0.05
	83	18	0.92 ± 0.04
East Friesian	6	32	0.94 ± 0.04
	19	15	1.14 ± 0.05
	28	16	1.06 ± 0.05
	39	29	0.96 ± 0.04
	44	12	0.97 ± 0.05
	45	13	1.00 ± 0.05
	47	8	1.18 ± 0.06
	59	25	1.00 ± 0.04
	68	15	0.94 ± 0.05
	69	15	0.97 ± 0.05
	77	14	0.75 ± 0.05
	89	17	1.11 ± 0.05
Finnsheep	3	31	1.03 ± 0.03
	*7**	*239*	*0.87 ± 0.01*
	9	38	0.96 ± 0.03
	17	27	0.91 ± 0.04
	21	23	1.02 ± 0.04
	22	17	0.84 ± 0.04
	23	17	0.86 ± 0.04
	40	38	0.98 ± 0.03
	48	14	0.91 ± 0.05
	67	12	0.92 ± 0.05
	76	28	0.93 ± 0.04
	88	19	0.83 ± 0.04
Coopworth	*5**	*200*	*0.98 ± 0.02*
	16	22	1.01 ± 0.04
	18	21	1.00 ± 0.04
	26	23	1.11 ± 0.04
	36	37	0.98 ± 0.03
	37	29	0.88 ± 0.04
	65	23	1.00 ± 0.04
	74	13	1.01 ± 0.05
	85	19	0.77 ± 0.04
White Suffolk	10	29	0.94 ± 0.04
	33	23	1.05 ± 0.04
	42	25	1.01 ± 0.04
	51	11	1.02 ± 0.06
	60	36	1.09 ± 0.03
	80	12	1.14 ± 0.06
	90	14	1.10 ± 0.05
Corriedale	4	40	1.03 ± 0.03
	11	28	0.92 ± 0.04
	20	27	0.99 ± 0.04
	27	15	0.98 ± 0.05
	46	17	0.95 ± 0.05
	64	21	0.95 ± 0.04
Booroola L	1	32	0.86 ± 0.04
	15	33	0.97 ± 0.04
	34	36	0.99 ± 0.03
	43	9	1.12 ± 0.07
	55	20	0.96 ± 0.05
	63	15	0.92 ± 0.05
Others	14	27	0.89 ± 0.04
	29	22	0.92 ± 0.04
	30	26	0.92 ± 0.04
	31	26	0.98 ± 0.04
	38	27	1.00 ± 0.04
	41	30	0.99 ± 0.04
	49	15	0.89 ± 0.05
	50	16	0.95 ± 0.05
	56	31	0.99 ± 0.03
	57	24	0.92 ± 0.04
	58	23	0.96 ± 0.04
	66	20	0.90 ± 0.05
	72	12	1.01 ± 0.05
	73	21	1.00 ± 0.04
	75	22	0.91 ± 0.04
	78	13	1.13 ± 0.05
	79	8	1.29 ± 0.06
	84	16	0.99 ± 0.05
	86	24	1.17 ± 0.04
	87	22	0.87 ± 0.04
	91	14	1.02 ± 0.05

* Link Sires

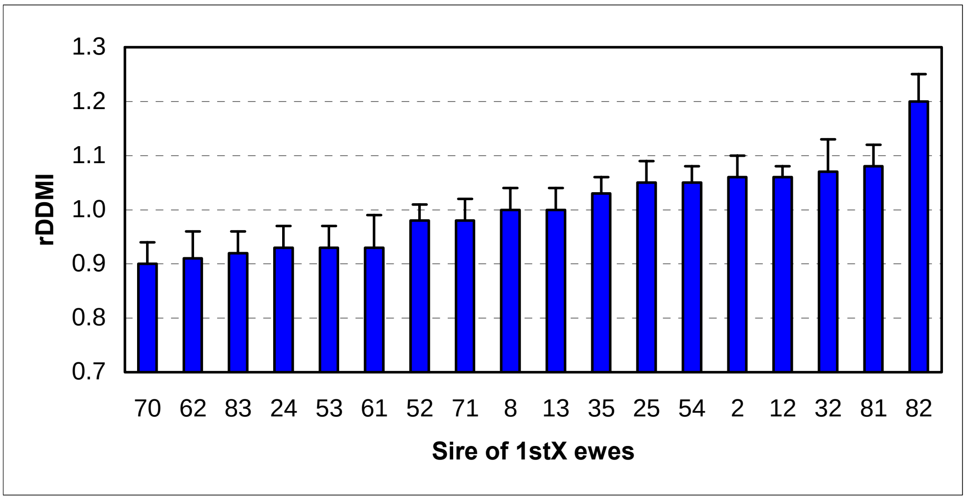

Figure 4. Predicted Border Leicester sire means (T=s.e.) for rDDMI of crossbred ewe progeny

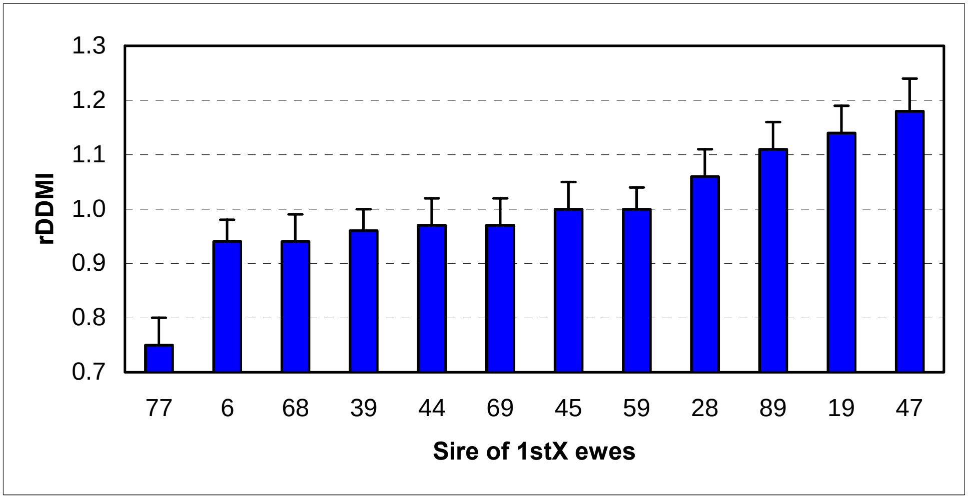

Figure 5. Predicted East Friesian sire means (T=s.e.) for rDDMI of crossbred ewe progeny

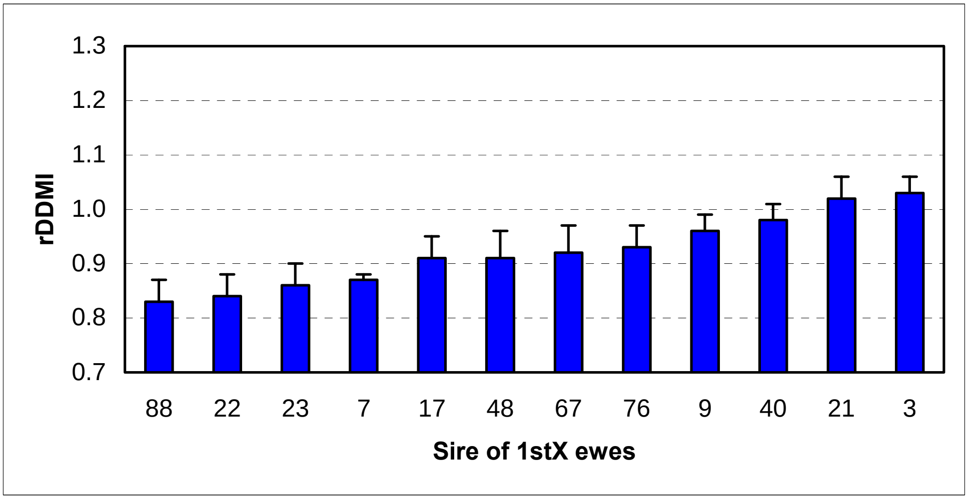

Figure 6. Predicted Finnsheep sire means (T=s.e.) for rDDMI of crossbred ewe progeny

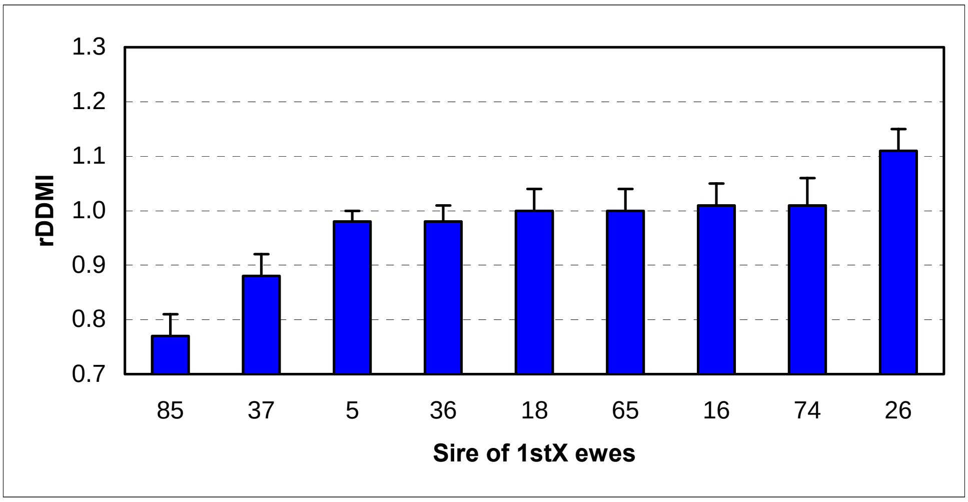

Figure 7. Predicted Coopworth sire means (T=s.e.) for rDDMI of crossbred ewe progeny

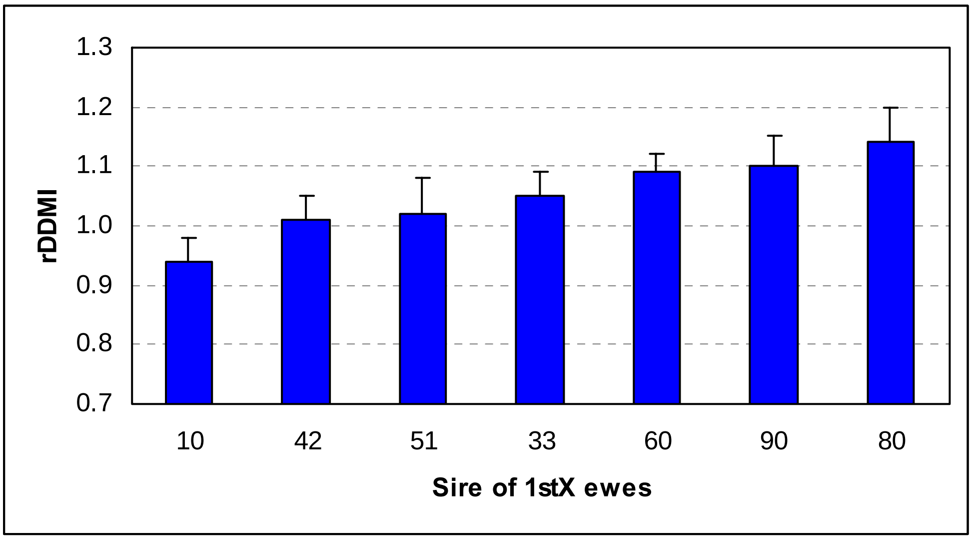

Figure 8. Predicted White Suffolk sire means (T=s.e.) for rDDMI of crossbred ewe progeny

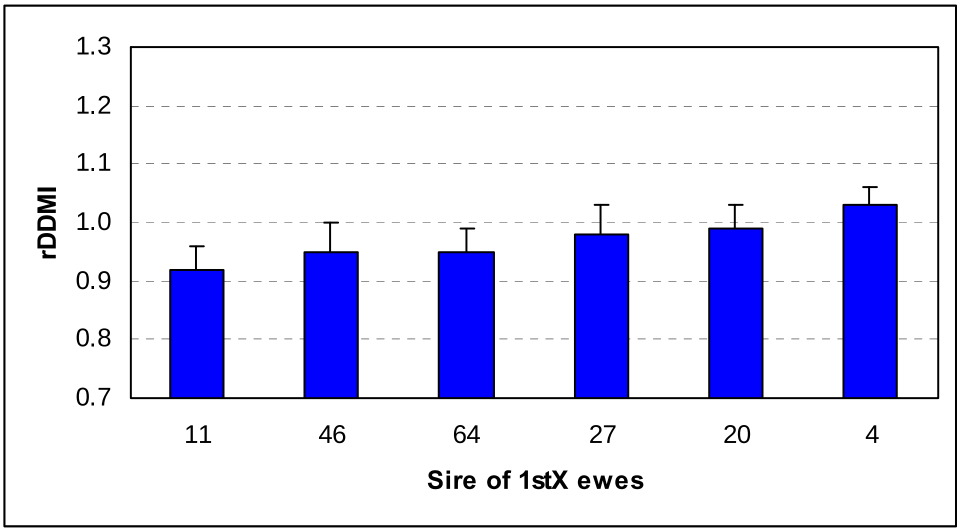

Figure 9. Predicted Corriedale sire means (T=s.e.) for rDDMI of crossbred ewe progeny

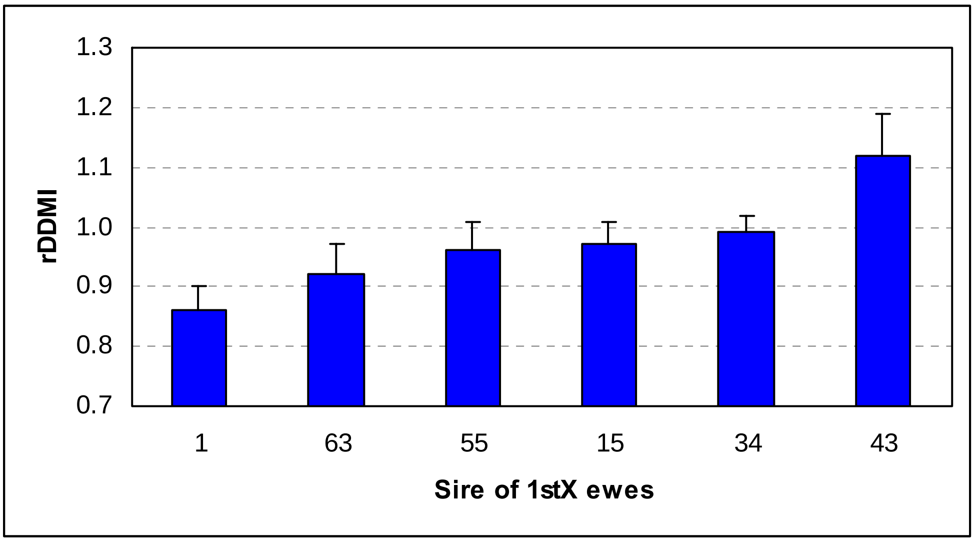

Figure 10. Predicted Booroola Leicester sire means (T=s.e.) for rDDMI of crossbred ewe progeny

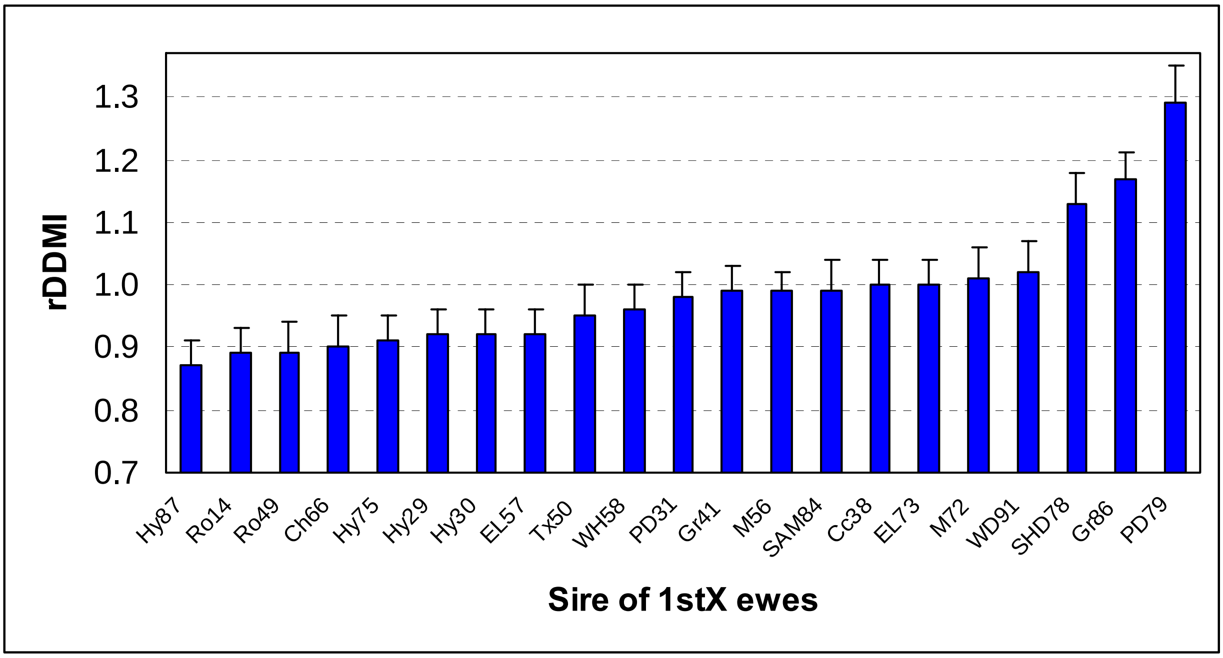

Figure 11. Predicted sire means for other breeds (T=s.e.) for rDDMI of crossbred ewe progeny

Breed codes: Hy=Hyfer, Ro=Romney, Ch=Cheviot, EL=English Leicester, Tx=Texel, WH=Wiltshire Horn, PD=Poll Dorset, Gr=Gromark, M=Merino, SAM=SAMM, Cc=Coringa composite, WD=White Dorper, SHD=South Hampshire Down

The genetic and phenotypic correlations for rDDMI with various growth, carcass, wool and reproduction traits of 1stX progeny are shown in Table 7. The estimates using Model 1 (final model) included covariates for aLW, LWg, Cfat and EMD whereas Model 2 had these covariates deleted. The crossbred progeny for the growth traits include both the 1stX ewes and their half sib wethers. The carcass traits involve the carcass measurements on the half sib wether progeny. The wool traits were measured at hogget shearing on the 1stX ewes and lambing records over their first 3 joinings were used for reproduction. All of the genetic correlations are low and smaller than their standard error. The phenotypic correlations are generally smaller than the corresponding genetic correlation and close to zero. The estimates of correlations from Model 1 and Model 2 were very similar, except for some increase for growth traits, especially post weaning and carcass weight. There was also a small increase from negative to positive for fleece weight although they were still not significantly different from zero.

Table 7. Phenotypic (r_p) and genetic (r_g) correlations (± s.e.) for rDDMI of crossbred ewes with growth, carcass, wool and reproduction traits for model 1 and model 2 ^{A}

	Model 1		Model 2	
Traits	r_p	r_g	r_p	r_g
Growth (1stX ewes + wethers)				
Birth weight	0.02 ± 0.03	-0.04 ± 0.14	0.08 ± 0.03	0.07 ± 0.13
Weaning weight	0.07 ± 0.03	0.01 ± 0.10	0.12 ± 0.02	0.10 ± 0.10
Post weaning weight	0.08 ± 0.03	0.09 ± 0.10	0.15 ± 0.02	0.23 ± 0.10
Carcass (1stX wethers)				
Hot carcass weight	0.01 ± 0.06	0.01 ± 0.12	0.10 ± 0.06	0.19 ± 0.11
Dressing %	-0.04 ± 0.06	-0.09 ± 0.13	-0.04 ± 0.06	-0.09 ± 0.12
Fat GR site	-0.02 ± 0.06	-0.05 ± 0.12	-0.05 ± 0.06	-0.10 ± 0.12
Fat C site	-0.02 ± 0.06	-0.03 ± 0.13	-0.05 ± 0.06	-0.10 ± 0.13
Eye muscle depth	0.03 ± 0.06	0.08 ± 0.14	0.04 ± 0.06	0.09 ± 0.14
Eye muscle width	0.04 ± 0.06	0.09 ± 0.15	0.04 ± 0.06	0.09 ± 0.14
Eye muscle area	0.04 ± 0.06	0.10 ± 0.13	0.04 ± 0.06	0.10 ± 0.13
Wool (1stX ewe hoggets)				
Greasy fleece weight	0.03 ± 0.03	-0.04 ± 0.10	0.08 ± 0.02	0.05 ± 0.10
Clean fleece weight	0.02 ± 0.03	-0.02 ± 0.10	0.07 ± 0.03	0.06 ± 0.10
Yield %	-0.01 ± 0.02	-0.02 ± 0.12	-0.01 ± 0.02	0.02 ± 0.12
Fibre diameter	0.01 ± 0.03	-0.01 ± 0.10	0.02 ± 0.03	0.04 ± 0.09
Reproduction (1stX ewes 3 joinings)				
Number of lambs born	0.05 ± 0.03	0.08 ± 0.13	0.07 ± 0.02	0.07 ± 0.13
Number of lambs weaned	0.06 ± 0.03	0.03 ± 0.15	0.07 ± 0.02	0.01 ± 0.15

^{A} Model 1 is final model and includes covariates for aLW, LWg, Cfat and EMD; Model 2 has all covariates deleted

4.3 Discussion

As expected there was an increase in rDDMI with average liveweight of the crossbred ewes. If we assume a mean intake of 1.4 kg DDM / day (for the 70 kg crossbred ewes) our regression of approximately 0.007 rDDMI / kg liveweight is equivalent to 9.8 g DDMI / day / kg. This is within the range of 9.6 to 10.8 g DDMI / day / kg reported for Merino ewes at various seasons by Lee et al. (1995a).

The significantly higher intakes for the crossbred ewes that had reared multiples compared to singles (+7%) and for singles compared to dry and lambed and lost ewes (+5%) were consistent with differences found by Lee et al. (1995a) for Merino ewes in the summer after their lambs had been weaned. Similarly the reduced intake among fatter crossbred ewes was also reported by Lee et al. (1995a) for Merino ewes.

The sire breed effect was not significant for crossbred ewe intake when liveweight was included in the model. This is consistent with two different studies by Lee et al. (1995a, 2002) in which differences in intake between bloodlines of Merinos were removed when intake was adjusted for liveweight. While overall the sire breed effect was not significant, the Finnsheep cross ewes were lower than all the other breed crosses and a majority of their sire means were below average for intake.

There was considerable genetic variation for intake which resulted in a high estimate of heritability (0.41 ± 0.07). This is much higher than the only other estimates of heritability for intake in sheep of 0.10 to 0.12 for pooled estimates with similarly low standard errors in Merinos (Lee et al. 1995b, 2002). There is a greater diversity of genotypes among the sires in MCPT than across the bloodlines in the Merino experiments which could be contributing to greater genetic variation in the MCPT data. The phenotypic variance as expressed by the coefficient of variation was similar (approximately 20%) in the various studies. The other major contributor to the difference in genetic variance was the accuracy achieved through the number of progeny per sire sampled. There was an average of 27.8 progeny per sire (21.7 progeny per sire for the 88 non link sires and 206 progeny per sire for the 3 link sires) in the MCPT. In contrast the Merino studies had approximately 4 progeny per sire (Lee et al. 1995b) and 9-12 progeny per sire (Lee et al. 2002). The reduced accuracy of EBVs with small numbers of progeny tested was highlighted by Lee et al. (2001). The range of intakes among the sire progeny groups of ewes was over 20% among all breeds which illustrates the considerable variation found and potential for exploitation through selection.

The genetic correlations of intake with all the production traits analysed; growth, carcass, wool and reproduction were low and not significantly different from zero. Lee (1995b, 2002) reported genetic correlations of intake in Merinos with liveweight and wool traits that had slightly higher absolute values, although with similar standard errors that also rendered them not significantly different from zero. The low genetic correlations for intake and efficiency with production traits indicate that investigating underlying physiological and genomic relationships may be more fruitful. IGF-1 is one such parameter that has been reported to be genetically related to efficiency in both beef cattle (Moore et al. 2003) and pigs (Bunter et al. 2005). The opportunity to investigate the relationship between IGF-1 and intake among a sample of the MCPT ewes should be pursued.

4.4 Implications

Selection of a particular maternal sire breed for crossbred ewes will not have an effect on intake, feed requirements and therefore the stocking rate of the ewes, providing any liveweight differences are taken into account. The possible exception to this is the Finnsheep breed in which the Finnsheep cross ewes on average had intakes 7% lower than the average of all breed cross ewes after accounting for differences in liveweight, previous reproduction and fat depth. Other factors such as net reproduction rate, growth of lambs and overall profitability (Fogarty et al. 2005a) also need to be taken into account when choosing a particular maternal sire breed.

The considerable genetic variation for intake for maintenance as demonstrated by the large range in sire progeny means and the high estimated heritability, together with a coefficient of variation of about 20% indicates potential for rapid progress from selection. However intake at maintenance, especially under grazing, is very difficult and expensive to measure with current technology using chromium sesquioxide marker dilution or alkane techniques and requires large numbers (at least 20) of progeny per sire to provide accurate EBVs.

The genetic correlations with a range of production traits were all close to zero. Hence the use of other production traits for indirect selection to reduce maintenance requirements is not feasible. However on the positive side it also means that breeding programs aimed at improving production traits such as liveweight, carcass or reproduction, will not be antagonistic and will have little effect on intake or feed requirements for maintenance, other than through any direct effect of increasing liveweight.

5 Success in Achieving Objectives

The project successfully achieved the specific aims of estimating feed intake at grazing pasture for the mature ewes in the MCPT project and estimating genetic parameters, heritability for grazing intake and genetic correlations between feed intake and production (growth, carcass, meat quality, wool and reproduction) traits for maternal genotypes. The project provides the first estimates of genetic parameters for intake in meat sheep and is the largest sheep experiment undertaken with over 2,500 ewes measured for grazing intake.

The genetic parameters estimated from the project will be made available through this report and the scientific paper being prepared to Sheep Genetics Australia (SGA) for use in genetic evaluation. Incorporation of the parameters into the SGA parameter matrix and procedures would allow calculation of EBVs if appropriate data were available. This would allow breeders to reduce the feed requirements for maintenance and improve the overall efficiency of utilisation of feed in their breeding programs and production systems.

6 Impact on Meat and Livestock Industry – now & in five years time

The project has provided a better understanding of the genetic variation that exists among meatsheep and the potential for genetically reducing ewe maintenance feed requirements. The genetic parameters estimated from the project provide SGA with the basis for calculating EBVs to allow breeders to include reduced feed requirements in their breeding programs. However because of the difficulty and expense of directly measuring feed intake in grazing animals with current technology it is unlikely to be taken up in the immediate future.

The project has established the potential for genetic improvement of feed efficiency and other modelling research shows it can have a high impact on sheep enterprise profitability (W Pitchford pers. comm.). The outcomes stress the importance of pursuing new technologies for measuring feed intake directly and/or underlying physiological traits and genomic technologies.

7 Conclusions and Recommendations

In a lamb production enterprise around 65% of the total feed needed to produce lamb carcass weight is required to maintain the ewe flock throughout the year and grow out replacement ewes. This feed, at critical times of the year, largely determines stocking rate. Improvement in feed efficiency or intake for maintenance of the ewe flock could have a major impact on carrying capacity of enterprises. The importance of reducing maintenance feed requirements by selecting ewes that eat less per unit body weight was reaffirmed at the recent MLA Workshop on genetic improvement (W Pitchford, pers. comm.).

The project has demonstrated there is considerable genetic variation for intake for maintenance among maternal meatsheep genotypes. The high estimated heritability (0.41 ± 0.07) for intake together with the large range in sire progeny means indicates potential for rapid progress from selection. However intake at maintenance, especially under grazing, is very difficult and expensive to measure with current technology and requires large numbers of progeny per sire to provide accurate EBVs.

The genetic correlations with a range of production traits were all close to zero. Hence the use of other production traits for indirect selection to reduce maintenance requirements is not feasible. However on the positive side it also means that breeding programs aimed at improving production traits such as liveweight, carcass or reproduction, will not be antagonistic and will have little effect on intake, other than through any direct effect of increasing liveweight.

7.1 Recommendations

a) The genetic parameter information obtained from the project be made available to SGA.
b) The proposed studies to investigate the relationship between IGF-1 and intake among a sample of the MCPT ewes should be pursued.
c) The development of alternative technology for measuring feed intake of grazing animals be supported as well as the pursuit of physiological and genomic markers.

8 Bibliography

Archer, JA, Arthur, PF, Herd, RM and Richardson, EC (1998) Genetic variation in feed efficiency and its component traits. *Proceedings of the 6th World Congress on Genetics Applied to Livestock Production* **25:** 81-84.

Arthur, PF, Archer, JA, Herd, RM and Melville, GJ. (2001) Response to selection for net feed intake in beef cattle. *Proceedings of the Association for the Advancement of Animal Breeding and Genetics* **14:**135-138.

Bunter, K. L. Hermesch, S. Luxford, B. G. Graser H.-U., Crump, RE (2005) Insulin-like growth factor-i (igf-i) measured in juvenile pigs is genetically correlated with economically important performance traits. *Proceedings of the Association for the Advancement of Animal Breeding and Genetics* **16**, 90.

Costigan, P and Ellis, KJ (1987) Analysis of faecal chromium derived from controlled release marker devices. *New Zealand Journal of Technology* **3:** 89-92.

Fogarty, N.M., McLeod, L.J. and Morgan, J.E. (2003). Variation among crossbred ewes in lamb productivity and profit on a feed unit basis. *Proceedings of the Association for the Advancement of Animal Breeding and Genetics* **15**: 314-317.

Fogarty, N.M., Ingham, V., McLeod, L., Morgan, J.E. and Gaunt, G. (2005a). Dynamic Dams for Lamb Production: More $$$s from crossbred ewes with the right genetics. Technical Bulletin 50, NSW Department of Primary Industries, Orange. 57pp. Also available at: http://www.agric.nsw.gov.au/reader/sheep-meat/dynamic-dams.html

Fogarty, N.M., Ingham, V.M., Gilmour, A.R., Cummins, L.P., Gaunt, G.M., Stafford, J., Hocking Edwards, J.E. and Banks, R.G. (2005b). Genetic evaluation of crossbred lamb production. 1. Breed and fixed effects for birth and weaning weight of first cross lambs, gestation length and reproduction of base ewes. *Australian Journal of Agricultural Research* **56**: 443-453.

Gilmour, AR, Gogel, BJ, Cullis, BR, Welham, SJ, Thompson, R (2002) 'ASReml user guide release 1.0' (VSN International Ltd: Hemel Hempstead, UK)

Herd, RM (1992) Changing the size of beef cattle – implications for cow feed requirements. *Proceedings of the Australian Association of Animal Breeding and Genetics* **10:** 334-337.

Lee, GJ, Atkins, KD, Mortimer, SI (1995a). Variation between Merino ewes in pasture intake. 1. Between flock differences and some environmental sources of variation. *Livestock Production Science* **41**, 133-142.

Lee, GJ, Atkins, KD, Mortimer, SI (1995b) Variation between Merino ewes in pasture intake. 2. Within-flock genetic parameters for intake and some production traits. *Livestock Production Science* **41:** 143-150.

Lee, GJ, Atkins, KD and Swan AA (2001) Genetic parameters for pasture intake and wool growth efficiency in Merino sheep. *Proceedings of the Association for the Advancement of Animal Breeding and Genetics* **14:**505-508.

Lee, GJ, Atkins, KD and Swan AA (2002) Pasture intake and digestibility by young and non-breeding adult sheep: the extent of genetic variation and relationships with productivity. *Livestock Production Science* **73**, 185-198.

Moore, KL, Johnston, DL, Herd, RM, Graser, H-U (2003) Genetic and non-genetic effects on plasma insulin-like growth factor-1 (IGF-1) concentration and production traits in Angus cattle. *Proceedings of the Association for the Advancement of Animal Breeding and Genetics* **15:** 222-226.

Oddy VH, Robards GE, Low SG (1983) Prediction of *in vivo* dry matter digestibility from the fibre and nitrogen content of a feed. In 'Feed Information and Animal Production'. pp. 395-398. (Commonwealth Agricultural Bureaux: Farnham Royal, U.K.)

SCA (1990) ‘Feeding standards for Australian livestock Ruminants’ CSIRO, Melbourne

9 Appendices

9.1 Appendix 1 – Design of MCPT

General design of Maternal Sire Central Progeny Test (MCPT) Evaluations

Maternal Sires X Merino Ewes

Matings of maternal sires at Cowra, Hamilton and Struan* - 1997, 1998, 1999 (2000)
eg. Border Leicester, Booroola Leicester, Coopworth, Corriedale,
East Friesian, Finnsheep

1stX ewes ***- grown out***

- survival
- growth
- breeding season
- wool wt, yield, fibre diam
- faecal egg count

1stX wethers ***- slaughtered***

- survival
- growth
- carcass wt, fat, ema, pH, colour

Terminal sires X 1stX ewes (x 3 years)

- breeding season
- lambing rate
- wool wt

2ndX lambs ***- slaughtered***

- survival
- growth
- carcass wt, fat, ema, pH, colour
- pelts

* 1stX ewes born at Struan were transferred to Rutherglen for evaluation

9.2 Appendix 2 – Communications and publications

Media

MLA Media Release (28/10/04) prepared: *Genetic variation established for feed efficiency in ewes.*

ABC Radio interview (NF) Bruce Reynolds, Orange, NSW

ABC Radio interview (NF) Brooke Carrington, Longreach, Qld

The Land – interview and article

Advisory

Anon (2002). Feed efficiency EBVs determined for sheep. *FEEDBACK* Nov/Dec p.10.

Thatcher, Laurie. (2003) Improving efficiency of feed use. *Australian Farm Journal* April p58.

Fogarty, N.M. (2003).Profitable crossbred ewes – Genetics counts. *Cowra AR&AS Centenary Field Day Notes* Cowra, 6 November, 4 pp.

Anon (2005). Genetic variation in feed efficiency. *FEEDBACK* Jan/Feb p.2.

Anon (2005) Genetic variation in feed efficiency of ewes. *SA Lamb Newsletter* No. 32. March, p10.

Anon (2005) Breeding ewes with feed efficiency. *The Muster* No. **63** May, p 31.

Scientific

Fogarty, N.M., McLeod, L.J. and Morgan, J.E. (2003). Variation among crossbred ewes in lamb productivity and profit on a feed unit basis. *Proceedings of the Association for the Advancement of Animal Breeding and Genetics* **15**: 314-317.

Lee, G.J. (2004) Comparison of physical separation and alkane concentrations to estimate the species composition of herbage samples from a pastoral environment. *Proceedings of the Australian Society of Animal Production* **25**: 116-119. CD-ROM *Animal Production in Australia* **25:** 116-119.

Lee, G.J. and MacGregor, C.M. (2004). Comparison of a microbial analysis of faeces and alkane concentrations of faeces to estimate the botanical composition of the diet of grazing sheep. *Proceedings of the Australian Society of Animal Production* **25**: 108-111. CD-ROM *Animal Production in Australia* **25:** 108-111.

Fogarty, N.M., Lee, G., Ingham, V., Gaunt, G. and Cummins, L. (2006). Variation in feed intake of grazing crossbred ewes and genetic correlations with production traits. *Australian Journal of Agricultural Research* (in preparation)

9.3 Appendix 3 – Acknowledgements

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Primary Industries Research Victoria (PIRVic), Department of Primary Industries, Rutherglen Centre - Greg Seymour, Paul Curran, Taffy Phillips and Max Daniel have provided technical support, together with other staff at Rutherglen.

Primary Industries South Australia and the South Australian Research and Development Institute ran a site during the first phase of the MCPT project at Struan (1998 – 2001). This site was managed initially by John Stafford until his retirement in August 2000 and subsequently by Dr Janelle Hocking Edwards and Dr Nick Edwards.

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