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Genetic parameter estimation for meat traits in Merinos

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Abstract

Reviews of genetic parameters for sheep production traits show significant variation and potential for genetic improvement of most production traits. These reviews however show a lack of information on the inheritance of carcase traits in Merino sheep. There are several reports of estimates of genetic parameters for carcase and meat quality traits in Merino rams, but these are based on limited data sets and did not account for maternal effects which can inflate heritability estimates. This project was designed to address this need so more accurate genetic parameters could be produced and then made available to industry through bodies such as SGA. The scope of the project was significantly enhanced by a combined approach to the analysis of similar data sets in three states. The data were from 5870 Merino hogget rams that were the progeny of 543 sires from 3 research resource flocks (QPLU$, Trangie NSW; Katanning WA; SASDF, Turretfield SA) born over 7 years. Within one of the flocks (QPLU$) it was possible to examine the implications of selecting for either wool weight or fibre diameter on carcase traits and this suggested that some subtle changes do occur in carcase and meat quality traits when selection focuses solely on wool weight and fibre diameter. The propensity of the Merino to produce high pH meat was studied in some detail at the muscle level and this has provided insight essential if this issue is to be addressed across the industry.

Executive Summary

Reviews of genetic parameters for sheep production traits show significant variation and potential for genetic improvement of most production traits. These reviews however show a lack of information on the inheritance of carcase traits in Merino sheep. There are several reports of estimates of genetic parameters for carcase and meat quality traits in Merino rams, but these are based on limited data sets and they did not in particular account for maternal effects which can inflate heritability estimates.

Accurate estimates of genetic parameters are required for genetic evaluation and to design effective breeding programs. Genetic parameters for carcase and meat quality traits in Merino hogget rams were estimated using an animal model. The data were from 5870 Merino hogget rams that were the progeny of 543 sires from 3 research resource flocks (QPLU$, Trangie NSW; Katanning WA; SASDF, Turretfield SA) born over 7 years. Traits analysed included ultrasound scan fat (Scanfat) and eye muscle depth (Scanmus) on live animals, hot carcase weight (HCW), dressing percent (DP), fat depth at the GR (FatGR) and C sites (FatC), eye muscle depth (EMD), width (EMW) and area (EMA), meat colour (*L**, *a**, *b**) and pH. Live weights at various ages from weaning to slaughter at 18 months and the hogget wool traits, clean fleece weight (CFW), average fibre diameter (FD), clean yield (YLD), coefficient of variation of FD (CVFD) and staple strength (SS) were also analysed.

The heritability estimates for the ultrasound scan measures of fat and muscle together with the estimates for the carcase fat and muscle dimensions are moderate and range from 0.20 to 0.29 with low standard errors of 0.04 or less. The lightness of the meat colour (*L**) and meat pH also had moderate estimates of heritability (0.18 ± 0.03 and 0.22 ± 0.03), although redness and yellowness of the meat had low estimates (*b**; 0.10 ± 0.03). The heritability estimates were generally lower for the carcase traits than previous estimates, but the estimates for the meat quality traits were higher than previous estimates and this reflects the fact that previous estimates for meat quality traits were based on small numbers of observations. The genetic correlations for fat and muscle measurements with meat colour and pH traits exhibited marked variation and all the muscle dimensions were negatively correlated with meat lightness and yellowness, but the correlations were generally close to zero or negative between fat measurements and meat colour. Meat pH was positively correlated with muscle measures and negatively with fat measures. All colour measures were strongly negatively correlated with pH.

The genetic correlations between CFW and FatGR and between CFW and FatC were negative consistent with previous studies and the genetic correlations between CFW and EMD and FD and EMD were effectively zero. pH was positively correlated with CFW and negatively correlated with FD and the correlations between the wool traits (CFW and FD) and meat colour measures were close to zero. These relationships imply that selection for increased CFW will lead to leaner carcases and selection for decreased FD will have little impact on carcase composition. Decreasing FD will lead to an unfavourable increase in meat pH as will increasing CFW. A rise in meat pH is undesirable as the Merino is already known to be susceptible to producing high pH meat and understanding this aspect was the focus of another phase of this project.

This work has provided genetic parameter estimates that are necessary to design breeding programs to breed for both wool and meat traits in Merino sheep. These parameters can be used to

update the genetic parameters in the national genetic evaluation program SGA to provide more accurate breeding values in multiple trait sheep breeding programs. The effects from selecting for wool weight and fibre diameter on carcase and meat quality traits showed that subtle changes can occur and these need to be considered in multiple trait sheep breeding programs.

Recently, evidence emerged that the pH effect observed in Merinos varied between strains of Merinos with a higher pH in the meat of broad wool hogget rams compared with fine and medium wool hogget rams. The biological basis of this effect is not clear, although a propensity to stress may be part of the explanation. To examine this effect in more detail an experiment was undertaken to study the carcase and meat quality traits in a group of Merino wether hoggets representing differing strains from superfine through to broad wool types. Particular attention was given to the use of enzyme markers for characterising muscle in terms of aerobic and anaerobic potential as a means of understanding the biological basis of the pH effect. To avoid potential confounding due to sub-optimal nutrition the wethers were fed high protein, energy pellets for 5 weeks before slaughter and pre-slaughter stress minimised.

The carcase characteristics, meat quality and specific muscle enzyme activity was studied in 342 Merino wether hoggets representing 7 bloodlines comprising 2 superfine lines, 2 fine wool lines, 2 medium wool lines and 1 broad wool line over 2 years. All animals were supplemented at pasture for 5 weeks before slaughter with high energy pellets.

Fat levels in the superfine bloodlines based on GR were much greater than in other lines. This also applied to FATC for one of the superfine bloodlines when adjusted to the same carcase weight. Differences in loin muscle dimensions were minor, although the broad wool bloodline had a lower depth which translated into a smaller EMA. Significant differences were detected between bloodlines for muscle pH with superfine animals having the highest values for the loin. In the second year, muscle samples were taken from 2 bloodlines to determine the activity of fructose 1,6-bis-phosphatase, lactate dehydrogenase (LDH), isocitrate dehydrogenase (ICDH) and the concentration of myoglobin, indicators of anaerobic and aerobic metabolism. Of the enzymes, only ICDH activity was different between the 2 bloodlines, with muscle from the medium wool bloodline having a significantly higher activity than muscle from the superfine bloodline. This indicates a greater aerobic capacity in the muscle of the medium wool bloodline. The significantly lower muscle pH for medium wool bloodline was mirrored by a lower glycolytic capacity expressed as the LDH/ICDH ratio with a correlation of 0.46. Thus in this dataset, a high pH is related to a change in energy metabolism as reflected by the aerobic/anaerobic capacity of the muscle and this may be a reflection of a change in fibre type frequency, but this remains to be validated.

Superfine bloodlines produced the fattest carcases with the differences between bloodlines reflecting differing mature weights. Given the high pH of Merino hogget meat, shelf life will be compromised and it appears that lowered aerobic metabolism in muscle may be the cause of this propensity for a high pH. Given the positive genetic correlation between pH and EMD this indicates the need for the application of appropriate selection indices by industry and without this project this would not have been possible. The sheep industry will benefit directly as the genetic parameters are incorporated into SGA.

Contents

1 Background

Until recently there were no published estimates of heritabilities or genetic correlations for Australian Merinos for carcase or meat quality traits. Initial estimates of genetic parameters for these traits and their relationships with wool traits, namely clean fleece weight and fibre diameter, have been derived (see Fogarty *et al.* 2003).

For the ongoing development of genetic evaluation programs like SGA, improved precision of these estimates, as well as expansion of the genetic parameter estimates to include additional wool quality and reproduction traits, is needed. There is growing interest by some Merino breeders in improving the genetic merit of their flocks for meat traits, but the impact of this must be established on other measured and visually assessed traits associated with production of quality wool over an animal's lifetime. This project was established to derive the genetic parameters for meat traits in Merino sheep by utilising rams from the QPLU$ project run by NSW DPI at Trangie AR&AS. With the emergence of the Australian Sheep Industry Cooperative Research Centre it was decided to replicate a similar project at Katanning, WA under the supervision of DAFWA and running parallel to this SARDI successfully obtained MLA support to collect carcase measures on sheep bred as part of the Selection Demonstration flock (SASDF). To provide more accurate genetic estimates it was decided to conduct a joint analysis of the data sets and the results of this are presented here.

Previous work has shown that the Merino tends to produce meat with a higher pH, which has implications for colour, keeping quality and sometimes tenderness. This higher pH has recently been observed in the Sheep Meat Eating Quality project (see Hopkins *et al.* 2005). From preliminary work it was also identified that within Merinos there are differences between strains with broad wool strains having a higher meat pH. Variation even appeared to exist across the finer wool Merinos, but this required validation. The second purpose of this project was to clarify these findings by measuring muscle pH on weaner wethers bred by NSW DPI at Condobolin AR&AS. These sheep represented a number of different Merino strains.

2 Project Objectives

1. Enhanced precision of genetic parameters for meat quality and carcase traits, for incorporation into genetic evaluation systems used by Merino ram breeders by 31 December 2006.
2. Demonstration of the responses in carcase and meat quality traits and meat value to selection on a range of Merino wool breeding objectives in a range of Merino strains by 31 December 2006.
3. Determination of the effect of Merino strain on muscle pH with a decision as to whether examination of the keeping quality is required by 31 December 2003.

3 Methodology

3.1 Objective 1

3.1.1 Flock structure

The data were collected on 5870 Merino hogget rams that were slaughtered at approximately 18 months of age. The rams were the progeny of 543 sires and 4284 dams and were born over several years in 3 research resource flocks (Table 1). The average number of progeny per sire was 10.8 (range 1 – 56) and average number of progeny per dam was 1.37. The 3 flocks (QPLU$, SASDF and WA) are representative of the major bloodlines and strains in the Australian Merino population and have been described in detail by Safari *et al*. (2007a). The QPLU$ flock is located at Trangie in central western NSW and was established to demonstrate simultaneous improvement in wool weight and reduction in fibre diameter using a range of indexes in fine, medium and broad wool strains (Taylor and Atkins 1997). The WA flock is located at Katanning WA and was established to examine genetic variation in wool traits (Lewer *et al.* 1992). The SASDF flock is located at Turretfield SA and was established to demonstrate outcomes from alternative breeding strategies, technology transfer and generate diverse lines (Ponzoni *et al.* 1999). The 3 flocks were not genetically linked. The rams were surplus to the requirements for selected rams in the various flocks with approximately 25% of rams not slaughtered. All flocks had a control line as well as different selected lines. The rams that were kept for breeding and for replacements were selected on indexes using estimated breeding values from multiple trait analysis. The rams that were slaughtered were surplus rams from the control as well as from the different selection lines at each site.

This project capitalised on a research program already under way with the QPLU$ Merino selection lines run by NSW DPI at Trangie Agricultural Research and Advisory Station and funded initially by AWI~~L~~ Pty Ltd. The QPLU$ flock is described in Appendix 1.

For the QPLU$ flock each year ~60-70 Merino sires (8 sires per selection line) were single sire mated to Merino ewes within each of the 9 selection lines across Fine, Medium and Broad wool types of Merino. The scope of the work reported here was to collect data on male progeny born in 2001–2004, but data from male progeny born in 1997 and 1998 have also been included in the analysis to increase the database and the reliability of the estimates. The management and results for the progeny born in 1997 and 1998 have been reported previously (Safari *et al.* 2001; Fogarty *et al.* 2003) and will not be outlined here.

Table 1. Number of sires and rams slaughtered by year of birth in QPLU$, WA and SASDF flocks.

Year	QPLU$		WA		SASDF		Total	
	Sires	Rams	Sires	Rams	Sires	Rams	Sires	Rams
1997	72	678					72	678
1998	53	370					53	370
2000			41	370			41	370
2001	47	484	22	466			69	950
2002	54	503	16	380	36	403	106	1286
2003	62	509	21	287	16	228	99	1024
2004	48	411	21	395	34	386	103	1192

Total	336	2955	121	1898	86	1017	543	5870

3.1.2 Management

Lambs were identified to their sire and dam at lambing and birth type recorded at each site. QPLU$ lambs were weaned at 2.5 months and run separately in gender groups. The traits that have been examined in the joint analysis and their units of measurement are outlined in Table 2. The rams at each site were ultrasound scanned by industry accredited operators to obtain subcutaneous fat depth (Scanfat) and eye muscle depth (Scanmus, 45 mm from the midline over the 12th rib) on live animals. The QPLU$ rams were scanned at approximately 10 months of age and those in the other flocks at approximately 14 months of age. This meant that the QPLU$ rams were lighter at scanning and had lower FATUS and EMDUS than rams in the other flocks (Table 3). Scanning data were not available for the QPLU$ rams born in 1997 and 1998.

QPLU$ hogget rams were allocated to 2 slaughter groups in November of each year, balanced for sire. Rams were introduced to grain and then supplementary fed at pasture (a mixture of nature grasses and lucerne) for 5 weeks with pellets at 1kg/head.day every second day. In 2002 due to drought the animals were fed grain from July until pellet feeding commenced in December. The pellets were made on site at Trangie and consisted of 30% lucerne, 20% lupins, 30% wheat and 20% oats with bentonite, salt and lime added. These pellets had an average crude protein level of 19.7%, a ME of 12.1 MJ/kg DM and a digestibility of 77.4%.

Table 2. Traits names and abbreviations measured across different resource flocks.

Trait	Abbreviation	Unit
Body weight at weaning	Weanwt	kg
Age of weaning	Wean age	days
Body weight at shearing	Shearwt	kg
Body weight at scanning	Scanwt	kg
Body weight at slaughter	Slauwt	kg
Eye muscle depth	EMD	mm
Eye muscle width	EMW	mm
Eye muscle area	EMA	mm
Ultrasound eye muscle depth	Scanmus	mm
Ultrasound fat depth	Scanfat	mm
Fat depth 110 mm off the midline at 12th rib (GR-site)	FatGR	mm
Fat depth over eye muscle at 12th rib (C-site)	FatC	mm
Hot carcase weight	HCW	kg
Dressing percentage	Dress	%
Colour *L**	*L**	
Colour *a**	*a**	
Colour *b**	*b**	
pH *Longissimus*[1]	pHL[1]	
Clean Fleece Weight	CFW	kg
Fibre diameter	FD	micron
Coefficient of variation of fibre diameter	CVFD	%
Staple strength	SS	N/Ktex

[1] pH of *Longissimus thoracis et lumborum* muscle

Table 3. Means (s.d.) and numbers of rams measured for various traits in QPLU$, WA and SASDF flocks.

Trait	n*	QPLUS$	n	SASDF	n	WA
Weanwt	12530	20.48 (4.63)	7917	26.37 (5.72)	7561	27.00 (5.50)
Wean age	12530	81.7 (13.47)	7917	87.17 (5.72)	7561	93.00 (11.00)
Shearwt	11590	53.61 (10.49)	6652	59.74 (11.17)	5712	51.69 (9.24)
Scanwt	1844	59.06 (6.25)	1871	41.80 (8.05)	1016	63.10 (8.23)
Slauwt	2857	67.37 (10.49)	927	63.43 (8.00)	1474	61.00 (6.61)
EMD	2878	29.08 (3.76)	1015	27.86 (4.02)	1858	28.50 (3.60)
EMW	2878	63.89 (5.36)	1015	63.71 (5.38)	1858	63.68 (5.09)
EMA	2878	18.67 (3.40)	1015	17.85 (3.53)	1858	18.18 (2.93)
Scanmus	1845	20.95 (3.30)	1016	26.60 (2.36)	1845	25.43 (2.71)
Scanfat	1845	1.27 (0.48)	1016	2.65 (0.91)	1845	2.38 (0.85)
FatGR	2773	8.62 (3.77)	606	3.69 (2.28)	1850	4.67 (3.77)
FatC	2616	2.42 (1.31)	776	1.42 (0.72)	1849	2.10 (1.17)
HCW	2806	26.55 (4.94)	930	25.2 (4.06)	1868	23.63 (3.20)
Dress	2746	39.47 (3.32)	927	39.60 (2.48)	1474	38.36 (4.42)
*L**	2683	33.85 (3.18)	1015	32.12 (2.38)	1409	35.17 (3.71)
*a**	2658	19.29 (3.23)	1014	16.11 (1.98)	1408	20.86 (4.08)
*b**	2652	8.93 (1.94)	631	4.25 (1.49)	1410	9.72 (2.47)
pHL	2825	5.98 (0.33)	1016	6.10 (0.32)	1859	6.14 (0.33)
CFW	11682	4.64 (0.94)	6644	4.73 (0.98)	5808	3.15 (0.54)
Yield	11682	72.03 (5.80)	6644	71.82 (5.60)	5808	70.62 (5.14)
FD	11692	20.69 (2.20)	6654	20.09 (1.87)	6675	19.13 (1.70)
CVFD	11692	22.34 (3.20)	1016	22.23 (2.85)	6675	23.35 (3.00)
SS	2847	31.2 (10.27)	1016	30.85 (10.08)	6675	26.82 (9.91)

*The additional numbers for the wool traits are because data from female cohorts and parents of the rams have been used.

3.1.3 Slaughter procedures and measurements

Across sites the rams were slaughtered at approximately 18 months of age in commercial abattoirs. The rams were transported to the abattoirs and kept in lairage overnight and slaughtered the next day. The carcases were subject to standard AUS-MEAT trim, which involved removal of kidneys and internal fats. Hot carcase weight (HCW) was recorded and fat depth at the GR site (FatGR, soft tissue depth at the 12th rib 110 mm from the midline) was measured using a GR knife on the hot carcase. Dressing percentage (Dress) was calculated as the ratio of HCW to fasted liveweight (Slauwt) prior to transport to the abattoirs. The carcases were held in chillers at <5°C and 24h after slaughter they were cut between the 12th and 13th rib and eye muscle (*m. longissimus thoracis et lumborum*) depth (EMD), width (EMW) and fat depth over the eye muscle (FatC) were measured. The cross-sectional area of the eye muscle (EMA) was estimated as 80% of the product of EMD and EMW. Meat colour was measured on the cut surface of the eye muscle after at least 30 minutes exposure to the air using a Minolta Chromameter set on the *L**, *a**, *b** system (where *L** measures relative lightness, *a** relative redness, and *b** relative yellowness), except for the 2003 born rams in WA which only had about 10 minutes exposure. The pH of the eye muscle was also measured at this time. For the QPLU$ animals (2001-2004) the pH of the semitendinosus muscle (eye round) was also measured. Carcases from the QPLU$ (2002-2004 birth years) and WA flocks were subject to electrical stimulation as part of the commercial slaughtering process. For QPLU$ rams born in 1998-2001 and SASDF rams the abattoirs did not have electrical stimulation facilities and in the case of the latter group of carcases they were chilled for 48 hours to reach ultimate pH before they were cut and the carcase and meat measurements recorded. For the 2004 born QPLU$ animals muscle samples were also collected and held for 3 days and measured again for pH. The pH at 24 h in stimulated muscle explained a large proportion of the variation (R^2 = 0.71) at 72 h (Hopkins *et al.* 2007). The number of rams measured in each flock and their means for the various traits are shown in Table 3.

3.1.4 Wool data

The wool data were extracted from the corresponding resource flocks data set and combined with carcase data. At the hogget shearing, greasy fleece weight was recorded and a midside wool sample collected for determination of clean yield that was used to calculate the clean fleece weight (CFW). The sample was also tested for average fibre diameter (FD), coefficient of variation of fibre diameter (CVFD) and staple strength (SS). The QPLU$ rams were shorn at 9 months of age and again at 15 months of age. Midside samples were taken at each shearing and tested for the above traits. The measurements at the 2 shearings for CFW were added together and were averaged for the other traits. The WA rams had low CFW, FD and SS which may indicate they were exposed to a harsher environment than the rams in the other flocks (Table 2).

3.1.5 Statistical analysis

The data were analysed with a linear mixed animal model using ASREML (Gilmour *et al.* 2006). Fixed effects were fitted for management group (based on flock, year, and slaughter group where applicable), age of the dam, birth type and rearing type. HCW were fitted as covariates for all the carcase traits except DP. For the ultrasound scan measurements (Scanfat and Scanmus) liveweight at scanning (Scanwt) was fitted as a covariate. Age at weaning was fitted as covariate for weaning

weight (Weanwt). For the wool traits, a combination of flock and year were defined as management group. For all traits line within flock was included as a fixed effect. Two way interactions were included in the model, although they were generally not significant and were deleted from the final model. Variance components were estimated by REML procedures fitting an animal model. The full linear mixed model was;

$y = Xb + Z_a a + Z_m m + e$

where *y* is the observation with the vectors of fixed effects (*b*), direct genetic effects (*a*), permanent maternal environmental effects (*m*) and random residual effects (*e*). The design matrices, Z_a and Z_m relate the effects to the observation. The fixed effects in the model included: age of dam (6 levels; 2 - ≥7 years), birth type (3 levels (single, twin and triplet), rearing type (3 levels; single-single, multiple-single, multiple-multiple) and management group (23). The variance-covariance structure for the effects was;

$$V\begin{vmatrix} a \\ m \\ e \end{vmatrix} = \begin{vmatrix} A\sigma_a^2 & 0 & 0 \\ 0 & I_m\sigma_m^2 & 0 \\ 0 & 0 & I_n\sigma_e^2 \end{vmatrix}$$

where A is the numerator relationship matrix, I_n and I_m are the identity matrices for animals and dams, σ^2_a, σ^2_m and σ^2_e are variance components for direct genetic, permanent maternal environmental and residual effects, respectively. Maternal genetic effects were not fitted because of lack of depth of pedigrees in this dataset, small number of offspring per dam and because no carcase records were available on the dams. Two random models were fitted. Model 1 only included the direct genetic effects and the permanent maternal environmental effect was added in Model 2. Log likelihood ratio tests were carried out to determine whether the permanent environmental effect contributed significantly to each trait.

Univariate analyses were used to estimate heritabilities for the carcase and meat traits as well as live weights and wool traits. Bivariate analyses were used to estimate the genetic and phenotypic correlations between the various carcase and meat traits and between these traits and live weights and wool traits.

3.2 Objective 2

3.2.1 Flock structure and management and data analysis

To met this objective data from the QPLU$ flock as already described was used. To examine selection response effects amongst traits genetic parameters were estimated using ASREML (Gilmour *et al.* 2006). An animal model was fitted to all traits which accounted for sire and dam pedigree. The models fitted also accounted for non-genetic sources of variation including birth status (single or multiple), rearing status (single or multiple), age at slaughter, age of dam (maiden or

adult), year of birth and slaughter group. Carcase weight was fitted as a covariate for estimating variance components and the heritability of carcase traits, but not for the fleece traits and their covariance with carcase traits.

3.3 Objective 3

3.3.1 Flock structure and management

The wethers used in this study were born in 2001 and 2002 at the Condobolin Agricultural Research and Advisory Station in central western New South Wales. The wethers represented 7 bloodlines comprising 2 superfine lines, 2 fine wool lines (2 only for 2002 drop animals, with 1 for 2001 drop animals), 2 medium wool lines and 1 broad wool line (only for 2001 drop animals). Each year, the ewes of each bloodline were joined to 2 rams of the same bloodline for the first cycle and a third sire added for the second cycle. Both drops of wethers were transported to the Orange Agricultural Institute (OAI) in the spring of 2002 and 2003 respectively at 15–16 months of age. The wethers were between 17–18 months old at slaughter and all had fully erupted permanent incisors classifying them as hoggets (Anon. 1998).

The wethers grazed pasture at OAI that consisted primarily of cocksfoot (*Dactylis glomerata*), Yorkshire fog (*Holcus lanatus*), phalaris (*Phalaris aquatica*) and tall fescue (*Festuca arundinacea*) grasses along with subterranean clover (*Trifolium subterraneum*). In 2002 the pasture had an average crude protein level of 7.1%, a ME of 6.5 MJ/kg DM and a digestibility of 46.7%. In 2003 the average crude protein level was 11.4%, the ME 8.2 MJ/kg DM and the digestibility 57.4%. The amount of available dry matter was determined to be about 2.5 t/ha in 2002 and up to 11 t/ha in 2003. In both years, the wethers were fed oats and lupins as an introductory feed to a formulated pellet which they were fed at pasture for 5 weeks before slaughter. The pellets comprised 30% lucerne, 20% lupins, 30% wheat and 20% oats with bentonite added. These pellets had an average crude protein level of 18.8%, a ME of 11.4 MJ/kg DM and a digestibility of 75.8%. The wethers were fed 1kg/head.day 3 times a week.

3.3.2 Slaughter procedures and measurements

The animals were yarded and held for 1.5–2 h before weighing the day before slaughter, then allowed to drink and graze pasture for 2–4 h before trucking to the abattoir, a trip of 100 km. At the abattoir the animals were held in yards overnight with access to water. Animals born in 2002 were randomly divided by bloodline into 2 slaughter groups and slaughtered within 1.5 h of each other. This was done to facilitate the collection of muscle samples soon after slaughter. A total of 123 wethers were slaughtered in 2002 and 219 in 2003 with the number per bloodline per year shown in Table 4.

Samples (about 5 g) of (loin muscle) were taken on all carcases (in 2003) below the 12th rib on entry to the chiller. Samples were taken within 1 h of death and frozen in liquid nitrogen and held at -80°C until assayed for selected enzyme activity. The same measures as for Trangie rams were also taken. The carcases were not electrically stimulated.

Table 4. Number of wether hoggets slaughtered over 2 years according to bloodline and strain.

Bloodline	Strain	Numbers slaughtered	
		2002	2003
A	Broad	14	—
B	Medium	30	52
C	Medium	10	24
D	Fine	36	43
E	Fine	—	24
F	Superfine	27	50
G	Superfine	6	26

For assay of muscle enzymes, samples from 50 carcases (2002 drop) were selected from the B (medium) and F (superfine) bloodlines (2 × 25) based on loin muscle pH values so as to cover the entire range in values. Before homogenisation, the muscle was pulverised at the temperature of liquid nitrogen and then homogenised using a Polytron at full speed in 20mM triethanolamine, 280mM sucrose, 1mM ethylenediamine tetra acetic acid, 1mM dithiothretiol, 100 μM phenylmethanesulphonylfluoride inhibitor, 2% Triton at pH 7.4. Samples were homogenised for 30 s, except those used for the determination of fructose 1,6-bis-phosphatase which were homogenised for 2.5 min in the same solution minus the Triton. The activity (μmoles/min.mg protein) of fructose 1,6-bis-phosphatase was determined using the procedure of Opie and Newsholme (1967) with the addition of a dialysis step to remove an inhibitor from the final homogenisation buffer. Lactate dehydrogenase (LDH) activity (μmoles/min.mg protein) was determined according to the procedure of Ansay (1974) and isocitrate dehydrogenase (ICDH) activity by the method described by Briand *et al.* (1981). Myoglobin concentration was determined using the method of Trout (1991).

3.3.3 Statistical analysis

Data were analysed using a REML procedure (Genstat 2004), which contained the fixed bloodline effect (1–7), with year of birth included as a random term. For carcase traits, hot carcase weight was included as a covariate and for colour traits; muscle pH was used as a covariate.

4 Results

4.1 Objective 1

4.1.1 Overall effects

The significance of fixed effects for the carcase traits is shown in Table 5. HCW was highly significant for all carcase and meat quality traits ($P < 0.001$), while for Scanfat and Scanmus, weight at scanning (Scanwt) was highly significant ($P < 0.001$). Birth type was significant for most of the carcase traits, while rearing type was only significant for FatGR ($P<0.001$) and FatC ($P<0.05$) and there was an effect of dam age for weight related traits. Birth type and rearing type ($P < 0.001$) significantly affected live weight at scanning (Table 5).

Table 5. Level of significance (P-values) of environmental factors affecting carcase traits.

Trait	Dam age	Birth type	Rear type	Hot carcase weight
Scanwt	<0.001	<0.001	<0.001	Not fitted
EMD	ns	ns	ns	<0.001
EMW	ns	<0.01	ns	<0.001
EMA	ns	<0.001	ns	<0.001
Scanmus[1]	ns	ns	ns	<0.001
Scanfat[1]	ns	ns	ns	<0.001
FatGR	ns	<0.001	<0.001	<0.001
FatC	ns	<0.001	<0.01	<0.001
HCW	<0.01	<0.001	ns	Not fitted
Dress	<0.01	ns	ns	Not fitted
*L**	ns	ns	ns	<0.001
*a**	ns	ns	ns	<0.001
*b**	ns	ns	ns	<0.001
pHL	ns	ns	ns	<0.001

[1]Scanwt used as covariate for Scanmus and Scanfat

4.1.2 Estimates of heritability

The estimates of the standard deviation and heritability for the carcase and meat traits are shown in Table 6 for the 3 different flocks. These show that carcases from the WA flock exhibited on average greater variation for the measured traits and lower heritabilities for the meat quality traits and that estimates based on the QPLU$ flock had the lowest standard errors.

Table 6. Phenotypic standard deviation (σ_p) and heritabilities (h^2) for different resource flocks.

	QPLU$[1]		SASDF[2]		WA[3]	
Trait	σ_p	h^2	σ_p	h^2	σ_p	h^2
EMD (mm)	2.73	0.33	3.19	0.19	3.2	0.20
EMW (mm)	3.92	0.28	3.97	0.24	4.41	0.33
EMA (mm^2)	3.93	0.28	3.93	0.24	4.40	0.32
FatGR	2.70	0.27	2.08	0.37	2.15	0.22
FatC	0.39	0.16	0.26	0.20	0.33	0.26
*L**	1.75	0.18	2.30	0.33	2.80	0.12
*a**	2.87	0.12	1.57	0.26	3.30	0.07
*b**	1.75	0.09	1.20	0.26	2.15	0.07
pHL	0.30	0.28	0.31	0.29	0.41	0.23

[1]s.e of h^2 = 0.05; [2]s.e of h^2 = 0.09; [3]s.e. of h^2 = 0.07

The estimates of heritability for HCW and the various fat and muscle dimension measurements were moderate and ranged from 0.22 to 0.37 with low standard errors of 0.04 or less when the analysis was combined across flocks (Table 7). Dress had a moderate heritability of 0.25 ± 0.04. The brightness of the meat colour (*L**) and meat pH also had moderate estimates of heritability (0.18 ± 0.03 and 0.22 ± 0.03 respectively), although redness (a*; 0.10 ± 0.03) and yellowness (b*; 0.10 ±

0.03) of the meat had low estimates. The heritability estimate for live weight at scanning was moderate (0.32 ± 0.05) with a significant permanent maternal environmental effect (0.13 ± 0.03) which was less for HCW (Table 7).

Table 7. Additive (V_a) and residual (V_e) variance, heritability (h^2_a ± s.e), permanent maternal environmental effect (c^2_{pm} ± s.e) and phenotypic standard deviation (σ_p) of carcase traits.

Trait	V_a	V_e	h^2_a	c^2_{pm}	σ_p
Scanwt (kg)	12.14	20.41	0.32 ± 0.05	0.13 ± 0.03	
EMD (mm)	1.91	6.93	0.22 ± 0.03	-	2.97
EMW (mm)	4. 84	11.97	0.29 ± 0.03	--	4.1
EMA (mm^2)	1.56	4.27	0.26 ± 0.04	--	2.41
Scanmus (mm)	0.93	3.19	0.22 ± 0.04	-	2.03
Scanfat (mm)	0.06	0.18	0.25 ± 0.04	--	0.49
FatGR	1.62	4.27	0.28 ± 0.04	-	2.43
FatC	0.26	0.98	0.20 ± 0.03	--	1.11
HCW	3.75	5.59	0.37 ± 0.04	0.07 ± 0.03	3.17
Dress	1.50	4.51	0.25 ± 0.04	--	2.45
*L**	1.24	5.65	0.18 ± 0.03	--	2.62
*a**	0.78	7.00	0.10 ± 0.03	--	2.79
*b**	0.32	3.05	0.10 ± 0.03	--	1.84
pHL	0.025	0.090	0.22 ± 0.03	--	0.16

4.1.3 Correlations between carcase traits and live weight

The genetic correlations between HCW and the various liveweights were high with Weanwt being 0.60 ± 0.04, Scanwt 0.89 ± 0.03 and Slauwt 0.94 ± 0.01 (Table 8). The genetic correlations for Scanwt were moderate with FatGR (0.33 ± 0.09) and muscle dimensions (EMA 0.39 ± 0.08), although close to zero for meat colour and pH, with the exception of muscle redness (a*) at -0.19 ± 0.14. The correlations for FatC with the various live weights were much lower than those for FatGR. The correlations for weaning weight (Weanwt) were lower than those for weights at older ages. The phenotypic correlations were generally much lower than the corresponding genetic correlations.

The ultrasound measurements on the live animals were highly genetically correlated with the corresponding carcase measurements (0.69 ± 0.09 FatC and 0.77 ± 0.07 EMD; Table 8), but the phenotypic correlations were much smaller (Table 9). There was a moderate negative correlation (-0.39 ± 0.14) between scan muscle depth and meat lightness (*L**) and a positive correlation with meat pH (0.26 ± 0.10).

Table 8. Genetic correlations (± se) between body weight traits and carcase traits in Merino rams adjusted to covariates[1].

Traits	Weanwt	Scanwt	Scanmus	Scanfat	Slauwt
EMD	0.38 ± 0.06	0.41 ± 0.08	**0.77 ± 0.07**	0.26 ± 0.10	0.38 ± 0.08
EMW	0.33 ± 0.06	0.23 ± 0.09	0.25 ± 0.09	0.27 ± 0.10	0.29 ± 0.08
EMA	0.33 ± 0.06	0.39 ± 0.08	0.63 ± 0.08	0.15 ± 0.10	0.38 ± 0.07
FatGR	0.04 ± 0.07	0.33 ± 0.09	0.32 ± 0.09	0.55 ± 0.09	0.35 ± 0.07
FatC	-0.03 ± 0.07	-0.02 ± 0.10	0.09 ± 0.11	**0.69 ± 0.09**	0.05 ± 0.09
HCW	**0.60 ± 0.04**	**0.89 ± 0.03**	0.70 ± 0.06	0.37 ± 0.09	**0.94 ± 0.01**
Dress	-0.07 ± 0.07	0.28 ± 0.10	0.47 ± 0.17	0.45 ± 0.08	0.16 ± 0.09
*L**	0.10 ± 0.08	0.00 ± 0.11	-0.39 ± 0.14	-0.04 ± 0.12	0.01 ± 0.10
*a**	-0.02 ± 0.10	-0.19 ± 0.14	-0.06 ± 0.14	0.02 ± 0.15	-0.15 ± 0.13
*b**	-0.07 ± 0.13	0.00 ± 0.17	-0.23 ± 0.16	0.12 ± 0.17	0.03 ± 0.16
pHL	0.00 ± 0.07	0.10 ± 0.10	**0.26 ± 0.10**	0.07 ± 0.10	0.05 ± 0.09

[1]Covariates: Hot carcase weight for carcase traits: Scanwt weight for Scanmus and Scanfat

Table 9. Phenotypic correlations (± se) between body weight traits and carcase traits in Merino rams adjusted to covariates[1].

Traits	Weanwt	Scanwt	Scanmus	Scanfat	Slauwt
EMD	0.14 ± 0.01	0.35 ± 0.01	0.27 ± 0.01	0.03 ± 0.02	0.38 ± 0.01
EMW	0.17± 0.01	0.33 ± 0.01	0.15 ± 0.02	-0.07 ± 0.02	0.35 ± 0.01
EMA	0.17 ± 0.01	0.40 ± 0.01	0.27 ± 0.01	-0.01 ± 0.02	0.42 ± 0.01
FatGR	-0.03 ± 0.01	0.26 ± 0.02	0.12 ± 0.02	0.19 ± 0.02	0.38 ± 0.01
FatC	-0.02 ± 0.01	0.14 ± 0.02	0.02 ± 0.02	0.19 ± 0.01	0.18 ± 0.01
HCW	0.38 ± 0.01	0.74 ± 0.01	0.49 ± 0.01	0.29 ± 0.01	0.82 ± 0.01
Dress	-0.11 ± 0.02	0.12 ± 0.02	0.19 ± 0.02	0.12 ± 0.02	0.03 ± 0.02
*L**	0.02 ± 0.02	-0.05 ± 0.02	-0.14 ± 0.02	0.01 ± 0.02	-0.03 ± 0.02
*a**	-0.0 ± 0.02	-0.01 ± 0.02	-0.04 ± 0.02	-0.01 ± 0.02	-0.01 ± 0.01
*b**	-0.00 ± 0.02	0.00 ± 0.02	-0.06 ± 0.02	-0.02 ± 0.02	-0.01 ± 0.02
pHL	0.01 ± 0.01	0.06 ± 0.02	0.09 ± 0.02	0.02 ± 0.01	0.03 ± 0.02

[1]Covariates: Hot carcase weight for carcase traits: Scanwt weight for Scanmus and Scanfat

4.1.4 Correlations between wool traits and liveweight

In general the genetic correlations between the live animal traits at scanning and the wool traits were greater than the corresponding phenotypic correlations (Table 10). The genetic correlation between Slauwt and fleece weight was positive (CFW; 0.23 ± 0.05) and also with FD (0.22 ± 0.05), while those for the other wool traits were generally smaller. The genetic correlations between muscle depth and fat depth at scanning and the wool traits were low and close to zero apart from for CFW and Scanfat (-0.17 ± 0.07).

Table 10. Phenotypic and genetic correlations (± se) between the wool traits and ultrasound muscle and fat depth on live Merino rams adjusted to a common live weight[1].

	Genetic correlations			Phenotypic correlations		
Traits	Scanmus	Scanfat	Slauwt	Scanmus	Scanfat	Slauwt
CFW	-0.13 ± 0.07	**-0.17 ± 0.07**	**0.23 ± 0.05**	0.02 ± 0.02	-0.04 ± 0.02	0.38 ± 0.01
FD	0.09 ± 0.06	0.07 ± 0.06	**0.22 ± 0.05**	0.07 ± 0.02	0.08 ± 0.02	0.19 ± 0.01
CVFD	-0.17 ± 0.07	-0.04 ± 0.07	-0.30 ± 0.05	-0.08 ± 0.02	0.01 ± 0.02	-0.17 ± 0.02
SS	0.08 ± 0.09	-0.02 ± 0.09	0.17 ± 0.08	0.07 ± 0.02	-0.00 ± 0.02	0.09 ± 0.03
Yield	0.14 ± 0.07	-0.15 ± 0.11	0.02 ± 0.05	0.06 ± 0.02	0.01 ± 0.02	0.02 ± 0.01

[1]Covariates: Live weight at ultrasound scanning for muscle and fat

4.1.5 Correlations between carcase traits

Carcase FatGR had moderate genetic correlations with muscle dimensions (Table 11), but in opposite directions (0.18 ± 0.10 EMD and -0.17 ± 0.10 EMW), while the correlation of FatC with muscle depth was low and negative, but moderate with muscle width (-0.08 ± 0.11 EMD and -0.21 ± 0.10 EMW). EMA was more highly correlated with EMD (0.89 ± 0.00) than EMW (0.78 ± 0.04). The genetic correlation between EMD and the lightness and yellowness of the muscle was negative and moderate (Table 11), but with muscle pH was positive and low with a large standard error (0.14 ± 0.10).

The fat measurements had generally close to zero or negative correlations with muscle colour traits, apart from the redness (*a**) of the muscle with which the genetic correlations were moderate (Table 11). FatC had a negative correlation with pH (-0.18 ± 0.11). Muscle pH was negatively correlated (genetic and phenotypic) with colour traits.

Table 11. Phenotypic (above diagonal) and genetic (below diagonal) correlations (± se) between carcase traits in Merino rams adjusted to a weight[1].

Traits	EMD	EMW	EMA	FatGR	FatC	*L**	*a**	*b**	pHL
EMD		0.23 ± 0.00	0.88 ± 0.00	0.13 ± 0.01	0.02 ± 0.01	-0.10 ± 0.01	-0.05 ± 0.01	-0.04 ± 0.02	0.06 ± 0.01
EMW	0.41 ± 0.08		0.64 ± 0.01	-0.04 ± 0.01	-0.10 ± 0.01	-0.13 ± 0.01	-0.05 ± 0.01	-0.09 ± 0.01	0.07 ± 0.01
EMA	0.89 ± 0.00	0.78 ± 0.04		0.09 ± 0.01	-0.03 ± 0.01	-0.13 ± 0.01	-0.06 ± 0.01	-0.07 ± 0.02	0.07 ± 0.01
FatGR	**0.18 ± 0.10**	**-0.17 ± 0.10**	0.05 ± 0.10		0.33 ± 0.01	-0.02 ± 0.02	-0.02 ± 0.01	-0.01 ± 0.02	-0.02 ± 0.01
FatC	-0.08 ± 0.11	**-0.21 ± 0.10**	**-0.17 ± 0.10**	0.67 ± 0.08		0.00 ± 0.01	-0.03 ± 0.02	-0.00 ± 0.01	-0.02 ± 0.01
*L**	**-0.37 ± 0.11**	**-0.37 ± 0.10**	**-0.44 ± 0.10**	-0.07 ± 0.12	0.01 ± 0.12		0.58 ± 0.01	0.67 ± 0.01	-0.50 ± 0.01
*a**	-0.07 ± 0.14	-0.19 ± 0.12	-0.13 ± 0.13	**-0.18 ± 0.14**	**-0.17 ± 0.15**	0.45 ± 0.11		0.80 ± 0.01	-0.47 ± 0.01
b*	**-0.27 ± 0.16**	**-0.47 ± 0.14**	**-0.39 ± 0.15**	-0.02 ± 0.17	-0.08 ± 0.15	0.81 ± 0.07	0.86 ± 0.06		-0.55 ± 0.01
pHL	**0.14 ± 0.10**	**0.15 ± 0.10**	**0.17 ± 0.10**	-0.06 ± 0.11	**-0.18 ± 0.11**	**-0.57 ± 0.08**	**-0.78 ± 0.08**	**-0.94 ± 0.07**	

[1]Covariates: Hot carcase weight

4.1.6 Correlations between carcase and wool traits

There were generally small to moderate genetic correlations between carcase fat traits and CFW, while those with and FD, CVFD and SS were low (Table 12). The genetic correlation between FatC and Yield was moderate and negative. The correlations for eye muscle traits with the wool traits were generally close to zero and much smaller than those for fat traits.

The correlations for meat colour lightness (*L**) with the wool traits were mostly all less than their standard error, but the redness (*a**) and yellowness (*b**) of the muscle was moderately positively correlated with SS and the latter negatively correlated with Yield (Table 12). The genetic correlations for meat pH with the wool traits were positive for CFW (0.19 ± 0.07) and CVFD (0.16 ± 0.07). The phenotypic correlations between the carcase and wool traits varied to some extent from the corresponding genetic correlations, although they were generally close to zero with very small standard errors (Table 13).

Table 12. Genetic correlations (± se) between wool and carcase quality traits in Merino rams adjusted to a constant weight[1]

	CFW	FD	CVFD	SS	Yield
EMD	-0.03 ± 0.08	0.04 ± 0.06	-0.03 ± 0.07	-0.04 ± 0.10	0.10 ± 0.06
EMW	-0.02 ± 0.07	-0.00 ± 0.05	-0.10 ± 0.06	0.02 ± 0.09	0.07 ± 0.06
EMA	0.04 ± 0.06	0.03 ± 0.06	-0.06 ± 0.07	-0.01 ± 0.09	0.07 ± 0.10
FatGR	**-0.22 ± 0.07**	0.05 ± 0.06	-0.10 ± 0.07	-0.02 ± 0.09	-0.04 ± 0.06
FatC	**-0.11 ± 0.07**	0.04 ± 0.06	-0.04 ± 0.07	-0.18 ± 0.09	**-0.21 ± 0.06**
Dress	-0.33 ± 0.06	-0.04 ± 0.05	-0.04 ± 0.07	-0.05 ± 0.09	0.11 ± 0.06
*a**	-0.09 ± 0.09	0.03 ± 0.08	-0.13 ± 0.09	**0.28 ± 0.12**	-0.10 ± 0.08
*b**	-0.08 ± 0.13	-0.05 ± 0.10	-0.15 ± 0.12	**0.25 ± 0.14**	**-0.22 ± 0.16**
*L**	0.01 ± 0.07	-0.04 ± 0.07	-0.04 ± 0.08	0.06 ± 0.10	-0.07 ± 0.07
pHL	**0.19 ± 0.07**	-0.07 ± 0.08	**0.16 ± 0.07**	-0.01 ± 0.09	0.05 ± 0.06

[1]Covariates: Hot carcase weight for carcase traits

Table 13. Phenotypic correlations (± se) between wool and carcase quality traits in Merino rams adjusted to a constant weight[1].

	CFW	FD	CVFD	SS	Yield
EMD	0.02 ± 0.01	0.04 ± 0.01	-0.02 ± 0.02	0.00 ± 0.02	0.04 ± 0.01
EMW	0.02 ± 0.01	0.02 ± 0.01	-0.05 ± 0.02	0.04 ± 0.02	0.02 ± 0.01
EMA	0.04 ± 0.01	0.04 ± 0.01	-0.04 ± 0.02	0.02 ± 0.02	0.04 ± 0.01
FatGR	-0.05 ± 0.02	0.04 ± 0.02	-0.05 ± 0.02	0.01 ± 0.03	0.03 ± 0.01
FatC	-0.06 ± 0.01	0.04 ± 0.01	-0.02 ± 0.02	0.01 ± 0.02	0.00 ± 0.01
Dress	-0.22 ± 0.01	-0.05 ± 0.02	-0.00 ± 0.02	0.03 ± 0.03	0.10 ± 0.02
*a**	0.03 ± 0.02	0.01 ± 0.01	-0.01 ± 0.02	0.03 ± 0.02	-0.01 ± 0.01
*b**	0.03 ± 0.02	0.00 ± 0.02	0.01 ± 0.02	-0.01 ± 0.02	-0.01 ± 0.02
*L**	0.00 ± 0.02	-0.03 ± 0.02	0.00 ± 0.02	-0.04 ± 0.03	-0.02 ± 0.02
pHL	0.03 ± 0.01	-0.02 ± 0.02	0.03 ± 0.02	-0.03 ± 0.02	-0.00 ± 0.01

[1]Covariates: Hot carcase weight for carcase traits

4.2 Objective 2

Estimates of the heritability of carcase traits (Table 6) and the genetic correlations between these and clean fleece weight and mean fibre diameter are given in Table 14. Heritabilities of the carcase and meat traits range from moderate (EMD 0.33) to weak (*b** 0.09) indicating that all should respond to single trait selection although the rate of response will vary between traits. The magnitude of the heritabilities was similar across the carcase traits to those generated by the larger data set (Table 6), except for EMD which was higher for the QPLU$ animals.

The genetic correlations between CFW and the carcase traits are generally negligible (Table 14), although between FatGR and CFW the correlation was negative consistent with the results for the larger data set (Table 12). There was moderate antagonism between the CFW and pH (irrespective of muscle), which was similar to that found for the larger data set (rg 0.19; Table 12).

The genetic correlations were positive for FatGR and FD and FatC and FD (Table 14) and higher than for the larger data set (Table 12), but also had larger standard errors. The dimensions of the eye muscle appear to be unrelated to FD as found for the larger data set, while the meat colour traits are all negatively correlated with FD, but with large standard errors. In the larger data set the correlation between pH and FD was negative and low and this was similar for the QPLU$ data (Table 14) and thus favourable, although the standard error was high.

Although the standard errors are large, the estimates suggest that selection to increase fleece weight should result in a decline in FatGR, an increase in muscle pH (in both muscles) and a reduction in muscle yellowness and redness.

Table 14. Genetic and phenotypic correlations (± se) between wool and carcase quality traits in QPLU$ Merino rams adjusted to a constant weight[1].

	Genetic correlation		Phenotypic correlation	
	CFW	FD	CFW	FD
EMD	-0.03 ± 0.08	0.03 ± 0.08	-0.00 ± 0.02	0.06 ± 0.02
EMW	-0.00 ± 0.08	-0.05 ± 0.08	0.01 ± 0.02	0.02 ± 0.02
EMA	-0.00 ± 0.08	0.01 ± 0.08	0.01 ± 0.02	0.05 ± 0.02
FatGR	**-0.21 ± 0.09**	0.14 ± 0.08	-0.08 ± 0.02	0.04 ± 0.02
FatC	-0.07 ± 0.10	0.13 ± 0.09	-0.08 ± 0.01	0.02 ± 0.02
Dress	-0.36 ± 0.07	-0.06 ± 0.06	-0.25 ± 0.02	-0.04 ± 0.02
*a**	-0.17 ± 0.12	-0.12 ± 0.11	0.02 ± 0.02	-0.01 ± 0.02
*b**	-0.20 ± 0.13	-0.13 ± 0.12	0.03 ± 0.02	-0.00 ± 0.02
*L**	-0.02 ± 0.10	-0.10 ± 0.09	0.02 ± 0.02	-0.02 ± 0.02
pHL	**0.26 ± 0.09**	-0.10 ± 0.09	0.04 ± 0.02	-0.02 ± 0.02
pHST*	**0.17 ± 0.09**	0.01 ± 0.09	-0.00 ± 0.02	0.00 ± 0.02

[1]Covariates: Hot carcase weight for carcase traits; *pH of the semitendinosus muscle

The genetic parameters in Table 14 were estimated from a population of rams bred within lines that have either been randomly selected or selected for various weightings of fleece weight and fibre diameter since 1995 (see Appendix). The net effect of this selection on the carcase traits should be evident in selected line deviations from the averages of the control line of each strain. These are presented for some of the carcase traits in Table 15.

Table 15. Line averages for body weight and carcase traits of 2001 - 2004 drop rams.

Trait	Fine wool			Medium-Peppin				Broad wool	
	Selection method								
	8%	Control	Industry	3%	8%	15%	Control	8%	Control
LWT (kg)	2.1	62.1	3.1*	0.5	0.3	-0.2	68.1	-0.6	78.5
HCW(kg)	0	25.2	1.0	-0.3	0.3	-0.4	26.5	-1.4*	31.6
DP (%)	-1.2*	40.1	-0.1	-0.6*	0	-0.4	38.6	-1.3*	39.9
GR (mm)	-1.3*	9.4	-0.8	-0.6	-0.6	-0.4	9.1	-1.6*	10.5
EMA (cm^2)	-0.5	14.0	1.0*	-0.3	0.8*	-0.1	14.6	-0.8	16.1
*L**	-0.4	34.6	-0.6	0	-0.3	-0.4	33.8	0.9*	33.5
*a**	0.1	19.5	-0.4	-0.8*	-0.2	-0.5	19.9	0.6	19.4
pH Loin	0.1*	5.9	0.1*	0.1*	0.1*	0.1*	5.9	0	5.9

*denotes a significant difference from the Control line of that strain ($P < 0.05$)

The breeding objectives of each line are signified by C (randomly selected control), 8% (equal selection for CFW and FD), 3% (increase CFW, maintain FD), 15% (reduce FD, maintain CFW) and Industry-classer (selection for CFW, FD and fleece quality, body size and conformation).

In accord with the moderate antagonism between CFW and pH Loin (rg = 0.26) the majority of selection lines show significant increases in loin pH. The exception is the selected broad wool line whose pH did not deviate from that of the control line of that strain. Another consistent observation was that of a reduction in FatGR in all lines although these were only significant in the fine and broad wool strains. This observation is consistent with the unfavourable genetic correlations between CFW and FD and FatGR (rgs of -0.21 and 0.14 respectively). With the exception of two selected medium wool lines (Industry and 8%) consistent reductions in EMA across all three strains were observed. One of the exceptions, the Industry line is understandable given that selection was also imposed on body size and conformation which resulted in a significant 3.1kg and 1.0 cm^2 increase in slaughter weight and EMA respectively. The other exception, the 8% medium wool line, contradicted the expectation of a decrease in EMA with a significant 0.8cm^2 increase compared to the control line even though neither slaughter weight nor carcase weight increased significantly. The reason for this line's departure from expectation is uncertain at this time.

In terms of muscle colour there were variable responses. Muscle redness tended to decrease in all medium wool lines although only significantly in the 3% line, while within the fine and broad wool selection lines redness (*a**) tended to increase. Muscle lightness tended to decrease or not change in the medium wool and fine selected lines while lightness (*L**) increased significantly in the broad selected line. This may reflect a genuine departure of the broad wool strain in terms of the genetic relationship between muscle physiology and fleece traits given its contradictory response in pH, muscle lightness and to a lesser extent redness.

4.3 Objective 3

A summary of differences between bloodlines for carcase traits is shown in Table 16. The notable finding was the much greater ($P < 0.001$) fat levels in the superfine bloodlines based on GR, with this also true for FatC measures in the superfine bloodline F ($P < 0.001$). Differences in loin muscle dimensions were minor, although bloodline A had a lower depth which translated into a smaller loin cross sectional area ($P < 0.05$).

Significant differences ($P < 0.001$) were detected between bloodlines for muscle pH with superfine animals having the highest values for the loin (Table 17). The differences for the ST were less consistent between bloodlines, but of the bloodlines the broad wool line had the lowest levels in both muscles. There were few differences between bloodlines for the meat colour traits measured on the loin muscle (Table 17). The correlation coefficients between colour the parameters *L**, *a**, *b** and pH were –0.23, –0.40 and –0.34, respectively.

Table 16. Predicted means (av. s.e.d.) of liveweight, carcase weight, GR, fat depth over the loin (FatC) and LL muscle depth, width and cross sectional area adjusted to a hot carcase weight of 21.6 kg, for animals according bloodlines.

Bloodline	Pre-slaughter liveweight (kg)	Hot carcase weight (kg)	GR (mm)	FatC (mm)	LL depth (mm)	LL width (mm)	LL area (cm^2)
A	53.8b	23.3a	7.4d	1.9b	25.0b	61.9b	12.3b
B	56.5a	24.5a	7.0d	1.8b	26.7a	61.2ab	13.1a
C	48.6c	20.9bc	8.3cd	1.9b	26.7a	61.0ab	13.1a
D	45.3de	19.9cd	9.5bc	2.0b	27.7a	61.2ab	13.6a
E	44.6e	19.5d	9.4bc	2.3b	27.6a	60.7ab	13.4a
F	45.5de	20.4bcd	11.7a	3.6a	27.2a	59.6a	13.0ab
G	47.4ce	21.5b	11.2a	2.3b	27.6a	60.2ab	13.3a
Av s.e.d.	1.12	0.60	0.66	0.27	0.57	0.83	0.36

Means followed by a different letter in a column (a, b, c, d, e) are significantly different ($P < 0.05$).

Table 17. Predicted means (av. s.e.d.) of colour parameters (*L, *a**, *b**) for m. *longissimus thoracis et lumborum* (LL) and ultimate pH of the LL and m. *semitendinosus* (ST) for animals according to bloodlines.**

Bloodline	*L**	*a**	*b**	pH (LL)	pH (ST)
A	33.1a	21.0a	8.7a	5.76c	5.88c
B	33.6a	20.3abc	8.5a	5.76c	5.99bc
C	33.4a	19.6c	8.0ab	5.82bc	6.03ab
D	34.0ab	20.6ab	8.6a	5.80bc	6.00bc
E	33.0a	19.8bc	7.9b	5.86ab	6.00bc
F	33.6a	19.6c	8.4ab	5.90a	6.15a
G	34.7b	20.2ac	8.5a	5.88a	6.03ab
Av s.e.d.	*0.51*	*0.48*	*0.27*	*0.04*	*0.06*

Means followed by a different letter in a column (a, b, c) are significantly different ($P < 0.05$).

Of the muscle enzymes examined, only ICDH was different between the 2 bloodlines (Table 18), with muscle from bloodline B animals (medium) having significantly higher ($P < 0.05$) activity than muscle from bloodline F animals (superfine). The activities of LDH and ICDH were expressed on a per gram muscle basis and a per milligram protein basis to enable comparison with published studies (e.g. Juire *et al.* 1998).

Table 18. Predicted means (av. s.e.d.) of enzyme activities (LDH, ICDH, fructose 1,6-bis-phosphatase), ratio of LDH/ICDH, and myoglobin content for m. *longissimus thoracis et lumborum* (LL) from animals of 2 bloodlines.

Bloodline	B	F	Av s.e.d
LDH μmol/min/g muscle	857a	886a	*37.0*
LDH μmol/min/mg protein	12.3a	12.5a	*0.41*
ICDH μmol/min/mg protein	0.065a	0.057b	*0.003*
ICDH nmol/min/g muscle	5500a	4920b	*280*
LDH/ICDH μmol/nmol (muscle)	0.16a	0.19b	*0.01*
LDH/ICDH μmol/μmol (protein)	197a	226b	*15.0*
Fructose μmol/min/mg protein	0.0043a	0.0057a	*0.0008*
Myoglobin	0.27a	0.28a	*0.01*
pH	5.79a	5.95b	*0.05*

Means followed by a different letter in a row (a, b) are significantly different ($P < 0.05$)

5 Discussion

5.1 Objective 1

5.1.1 Heritability estimates

The heritability estimates for the ultrasound scan measures of fat and muscle together with the estimates for the carcase fat and muscle dimensions are moderate and range from 0.20 to 0.29. This level of genetic variation indicates that genetic improvement in carcase traits could be achieved in the Merino by selection.

Our heritability estimates for the scan traits are the same as the means from the literature reviewed by (Safari *et al.* 2005), although the carcase fat and muscle traits are somewhat lower (see Table 6). These analyses included permanent environmental effects if significant and these have generally not been included in other analyses. Also our data are from Merino ram hoggets that were relatively lean at slaughter which may have reduced the variation that could be expressed especially for carcase fat. The brightness of muscle colour (*L**) and meat ultimate pH showed moderate heritability (0.18 and 0.22 respectively), although the other colour measurements, redness (*a**) and yellowness (*b**) were much lower. Our estimates for brightness and pH were slightly higher than the mean estimates reported by (Safari *et al.* 2005), which was based on 2 earlier reports from limited subsets of our data (Fogarty *et al.* 2003; Greeff *et al.* 2003). Despite the moderate heritabilities genetic progress is likely to be slow for fat depth and especially meat pH as the phenotypic variance is low. Additionally pH can not be measured directly and has a coefficient of variation of less than 10%. Improvements in pH in the Merino may be better achieved by improved nutrition and pre-slaughter management to avoid stress (Gardner *et al.* 1999).

5.1.2 Correlations

Fogarty *et al.* (2003) and Greeff *et al.* (2005) published genetic parameters between carcase traits and wool traits. They, however, estimated the genetic parameters at a constant age and at a constant live weight/hot carcase weight for the carcase traits only. Wool traits were not adjusted to a constant live weight although it is well known that significant phenotypic and genetic relationships exist between wool traits and live weight. This study estimated the phenotypic and genetic correlations between wool, live weight and carcase traits at a constant live weight or carcase weight as appropriate.

Fogarty *et al.* (2003) reported a negative genetic correlation between CFW and FatGR as did Greeff *et al.* (2005), similar to the findings from the much larger data set presented here. Further to this Fogarty *et al.* (2003) reported a positive genetic correlation between FD and FatGR, whereas the correlation was effectively zero in the report of Greeff *et al.* (2005) and in the present study it was close to zero. These results illustrate the need for the correlations to be updated in SGA. Correlations presented here suggest that selection for either increased CFW or reduced FD will not impact unfavourably on muscle traits, but obviously given the effects reported for fat measures such selection could produce fatter carcases.

Live weight traits at different ages and ultrasound measurements of muscle and subcutaneous fat are important indicator traits of meat yield and fat content. However, relatively poor genetic relationships with low accuracy were found between pH and the live weight and ultrasound scanning traits, apart from the positive correlation between meat pH and scanned muscle depth. Another exception was the negative correlation between scanned muscle depth (Scanmus) and meat colour lightness (*L**) implying that selection for increased muscle depth will lead to darker meat. This effect was confirmed with the carcase measure of muscle depth, an effect not reported by Fogarty *et al.* (2003). The genetic relationships between the colour traits and the wool traits were inconclusive due to the low accuracy of the estimates.

Merino breeding programs normally place greater emphasis on breeding for higher wool production and lower fibre diameter. The poor genetic relationships between the wool and carcase traits implies that selection for increased CFW and reduced FD may not change body composition, but pH may increase. This is undesirable as the Merino is already known to be susceptible of producing high pH meat (Gardner *et al.* 1999). It is interesting that muscle depth whether measured by scanning on the live animal (Scanmus) or on the carcase (EMD) was positively genetically correlated to pH implying that selection for increased muscling will not serve to overcome the tendency for high pH. This would appear consistent with the data of Gardner *et al.* (2006) which showed that as the muscling estimated breeding value of a terminal sire increased the muscle in cross-bred progeny became more glycolytic, although Martin *et al.* (2004) showed this response was mediated by nutrition.

As the Merino is a major contributor of genes to slaughter lamb production in Australia, it is clear that this characteristic should be considered to improve meat quality of Australian lamb in general. It is thus essential that breeding programs consider the potential to make the Merino less susceptible to the production of high pH meat.

This study provides genetic parameter estimates that are necessary to design breeding programs to breed for both wool and meat traits in Merino sheep. These parameters can be used to update the genetic parameters in the national genetic evaluation program (Brown *et al.* 2006) to provide more accurate breeding values in multiple trait sheep breeding programs.

5.2 Objective 2

The net change in the carcase and meat traits under long-term simultaneous selection for increased fleece weight and finer fibre diameter will depend on the relative magnitude of the correlations between each fleece and carcase or meat trait and the relative selection emphasis applied to fleece weight versus fibre diameter in the breeding objective. The challenge remaining is to consider the implications of the genetic parameters and correlated responses presented here in light of contemporary and future breeding strategies to increase the carcase value of predominantly wool producing flocks. There may be a need to counter the predicted and observed increases in pH in terms of tenderness and shelf life of mutton product. Similarly the anticipated and observed decline in GR in all lines including the Industry line needs to be considered in terms of carcase quality and consumer requirements for optimal leanness of product. The predicted reduction in EMA under joint selection for fleece weight and fibre diameter is of less concern given that most industry flocks also impose selection on body weight and conformation which should halt or reverse any decline in EMA as observed in the Industry line (Table 15). If it was considered economic to reverse these changes and increase EMA and GR and reduce pH through selective breeding, the trade offs in terms of foregone improvements in fleece weight, fibre diameter and fleece value would need to be carefully considered. Experience suggests that carcase price premiums/discounts will need to be demonstrated to entice breeders to refine existing breeding objectives and/or adopt novel selection criteria to remedy deterioration in these carcase traits.

5.3 Objective 3

5.3.1 Carcase and meat quality measures

Fogarty *et al.* (2003) sampled fine wool Merino hogget rams and found these were fatter than medium and broad wool types. Similar results were obtained in the current study using wethers. Similarly, Fogarty *et al.* (2003) found that there was no difference for LL muscle dimensions between strains. Our results are consistent with this result when differences in carcase weight are taken into account. Hopkins (1996) found that for the LL, lightness (L^*) values below 34 indicate dark meat as determined by consumers. In the present study differences between bloodlines were minimal and showed no particular pattern, whereas Fogarty *et al.* (2003) found that the fine wool strain produced lighter coloured LL than other strains. Muscle pH values measured by Fogarty *et al.* (2003) indicated animals with low levels of muscle glycogen (Gardner *et al.* 1999). To counter any tendency for low muscle glycogen, animals in the current work were supplemented with high energy pellets for 5 weeks before slaughter. To achieve an ultimate pH of 5.5, muscle needs to contain at least 50–60 µmol/g of glucose as glycogen immediately pre-slaughter to form sufficient lactic acid (Tarrant 1989). The absolute pH values in the LL of the hoggets in the current study were however higher than found in previous reports for Merino lambs (Hopkins and Fogarty 1998; Gardner *et al.* 1999; Hopkins

et al. 2005) but the overall higher level in the ST is consistent with previous work Gardner *et al.* 1999; Hopkins *et al.* 2005). Across muscles it was apparent that animals with finer wool had higher muscle pH than stronger wool bloodlines, a result contrary to that of Fogarty *et al.* (2003) In this regard it should be stressed that Fogarty *et al.* (2003) did not test superfine bloodlines and the fine and medium wool strains had similar values in their work and we did not test many broad wool animals.

The observed difference in muscle pH in our study may reflect a higher intake of the supplement in the medium wool lines and thus a higher glycogen concentration, or a difference between bloodlines in the response of muscle glycogen under the same level of intake (Martin *et al.* 2004). Alternatively the response of the bloodlines to the stress of slaughter may differ having an impact on muscle metabolism. The tendency for the finer wool strains to produce higher pH meat does indicate a greater likelihood of a reduced shelf life (Egan and Bray 1988), but it was not considered fruitful to pursue this aspect of the work given that Sheep CRC work running in parallel at the time had objectives to understand the physiological/stress response in Merinos and to better understand the propensity for production of high pH meat (Warner *et al.* 2006). Although some of the findings were inconclusive it did emerge that meat from Merinos does discolor under retail display at a faster rate than meat from crossbred lambs particularly for leg cuts (Warner *et al.* 2006). It appears that the use of more highly muscled Merino rams can reduce the pH effect in progeny (Martin *et al.* 2004), but there are still some fundamental work to be undertaken to fully understand the physiological mechanism.

5.3.2 Muscle enzyme activity

The activity of LDH and ICDH have been used as indicators of the anaerobic and aerobic metabolism of muscle respectively (Juire *et al.* 1998), but the use of fructose 1,6-bis-phosphatase as an anaerobic indicator is new. Previous work in other mammalian species has shown expression exclusive to type IIB muscle fibres (Opie and Newsholme 1967). Myoglobin levels tend to be higher in more aerobic muscle (Swatland 1994) and were also measured for this reason. For comparison with other results in the literature the activities have been defined in terms of min./per. muscle (Juire *et al.* 1998; Serra *et al*. 2004). Activity can also be defined in terms of the amount of protein and the results in Table 16 indicate that the significance of the differences between bloodlines were the same irrespective of how activity was defined. The ratio of LDH to ICDH has been used as an indication of muscle glycolytic capacity (Serra *et al*. 2004). The activity of ICDH was higher in the loin muscle from animals of bloodline B indicating greater aerobic capacity irrespective of how activity is defined; however there was no difference in myoglobin level. The myoglobin level was higher in the loin of the Merino hoggets in the current study than the Merino lambs studied by Hopkins *et al*. (2005). This is in agreement with the concept that pigment increases as animal's age (Ledward and Shorthose 1971). The significantly lower muscle pH for bloodline B was mirrored by a lower glycolytic capacity expressed as the LDH/ICDH ratio with a correlation of 0.46 and a negative correlation of 0.41 with ICDH activity. This indicates the loin of bloodline B animals was relatively more oxidative.

Jurie *et al*. (1998) found that the ST muscle has lower ICDH activity than the loin in cattle and it has been reported many times that the ST in lambs has a higher ultimate pH than the LL (e.g. Gardner *et al*. 1999; Hopkins *et al*. 2005). Therefore, the fact that the loin muscle from B bloodline animals had a lower mean pH and higher ICDH activity appears consistent with previous observations.

Muscles consist of distinct fibre types that can be conveniently differentiated on the basis of their contractile and metabolic properties. They are: (i) slow-twitch oxidative fibres (type I); (ii) fast-twitch oxidative-glycolytic fibres (type IIa); and (iii) fast-twitch glycolytic fibres (type IIb) (Peter *et al*. 1972). Type I fibres have a low glycolytic capacity compared with type IIa fibres. Type IIb fibres have the highest glycolytic capacity (Lister 1989). With slow rates of glycogen synthesis type IIb fibres are the most susceptible to stress induced glycogen depletion (Monin 1981). These differences can be largely explained by the different enzyme compliment of each fibre type of mammals (Saltin and Gollnick 1983). Thus the very high activity of glycogen phosphorylase in combination with low activities of glycogen synthase and hexokinase mean that muscle groups with an increased ratio of anaerobic to aerobic capacity will more rapidly deplete and more slowly replete glycogen levels. Clear evidence for this effect was shown by Gardner *et al*. (2001) where the more aerobic *m. semimembranosus* showed a strong linear relationship between the extent of glycogen repletion during a 72 h period after exercise depletion whereas the more anaerobic ST muscle showed no significant repletion during the same time period. In the current study the differences between the 2 bloodlines in terms of enzyme activities are consistent with such a change in the ratio of anaerobic to aerobic capacity within the same muscle type. In fact, although not significant, the trend for a lower activity of fructose 1,6-bis-phosphatase in muscle from bloodline B supports this contention. These results tentatively suggest that there may be a difference in fibre type frequency in the loin muscle of the two bloodlines and this appears to impact on muscle pH. There is however strong evidence that the metabolic pattern of energy metabolism within muscle, pre-slaughter nutrition and stress interact to determine the final concentration of glycogen within muscle at slaughter (Pethick *et al*. 2005). As such an increased anaerobic energy metabolism of muscle is associated with a greater chance of low glycogen at slaughter, especially when nutrition is below that required for positive growth. It has also been shown that double-muscled cattle show a more anaerobic metabolism than normal muscle cattle (Sudre *et al.* 2005) and are more sensitive to stress. Similarly genetic lines of sheep which show increased muscle development need a higher nutritional input to achieve elevated glycogen stores within muscle (Martin *et al*. 2004). It is also possible that the pattern of energy metabolism as reflected by changes in enzyme activity may occur without changes in fibre type frequency.

Whether the activities of these enzymes explains the propensity for Merinos to produce higher muscle pH values (Hopkins and Fogarty 1998; Gardner *et al*. 1999; Hopkins *et al*. 2005) when slaughtered under commercial conditions is not completely clear as there are no comparative data for non Merinos. What is of interest is the absolute ICDH activity which is double that reported by Jurie *et al*. (1998) for loin muscle from young Saler and Limousin bulls. In contrast LDH activity was lower in the sheep loin of the current study than reported by Jurie *et al*. (1998) in loin from cattle. These differences are also apparent when the results of Serra *et al*. (2004) for young Brown Swiss bulls are compared with the results of the current study. In this regard it is worth noting that the pH of the loin reported by Serra *et al*. (2004) was 5.56, which is much lower than found in the current study.

6 Success in Achieving Objectives

This project has exceeded its original scope by the combining of data sets across three sites through co-operation between scientists funded by either the Australian Sheep Industry Cooperative Research Centre or Meat and Livestock Australia. This has produced the most comprehensive data set of genetic parameters for the Australian Merino allowing the interrelationships between wool and meat traits to be established. Further to this the intensive study of meat quality and enzyme activity has provided insight into a complex set of factors that leads the Merino to produce high pH meat. This will contribute to our understanding and help with the design of subsequent studies.

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

Given the importance of the Merino to the Australian sheep industry and the desire to produce high quality wool and meat the results of this project are essential for the establishment of more accurate and comprehensive breeding indices. In this sense the combined data set gives much greater confidence to the accuracy of the genetic parameters which will be used by groups such as SGA to service the industry. The usefulness of the work can not be understated and the data set will impact on the industry for many years.

Given the genetic correlations between traits and in particular those that impact on pH and the clear evidence that the Merino is susceptible to the production of high pH meat this work suggests the industry will have to address this issue to ensure the production of high quality meat.

8 Conclusions and Recommendations

8.1 Objectives 1 & 2

It is essential that breeding programs consider the potential to make the Merino less susceptible to produce high pH meat and this study provides genetic parameter estimates that are necessary to design breeding programs to breed for both wool and meat traits in Merino sheep. These parameters can be used to update the genetic parameters in the national genetic evaluation program SGA to provide more accurate breeding values in multiple trait sheep breeding programs.

8.2 Objective 3

Superfine bloodlines produced the fattest carcases with the differences between bloodlines reflecting differing mature weights. The loin muscle from hogget's is darker than lamb loins and this will significantly reduce the retail value of such meat, but in this study there was no apparent effect of bloodline on loin colour. Given the high pH of Merino hogget meat, shelf life will be compromised and it appears that lowered aerobic metabolism in muscle may be the cause of this propensity for a high pH. The issue of high pH meat in Merinos has been the subject of research in the Sheep CRC

and it appears there may be some scope to lower this by providing high levels of nutrition pre-slaughter.

9 Acknowledgements

9.1 Objectives 1 & 2

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9.2 Objective 3

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11 Appendices

11.1 Appendix 1

The Merino flock being studied within the QPLU$ project consists of 9 selection lines within the fine (based on Merryville bloodline), medium (based on Haddon Rig bloodline) and broad (based on East Bungaree bloodline) strains as described in Table 1. These lines were established in 1995, following matings within a fully pedigreed foundation flock during 1993 and 1994. Until 1998, all selection pressure applied was through the rams selected as sires with each line. Rams were selected across three age groups while ewes were selected across six age groups. In successive years, about 30% of ewes have been culled from each line. Selection continued for a total of 10 rounds, with the final drop born in 2004.

Table 1. The QPLU$ selection lines.

Strain	Selection Line	Description of Breeding Objective
Fine	***8% MP***	Equal emphasis on reduced fibre diameter and increased fleece weight
	Control	Randomly selected line that represents the original population
Medium	***3% MP***	Maintain fibre diameter and maximise increases in fleece weight
	8% MP	Equal emphasis on reduced fibre diameter and increased fleece weight
	15% MP	Maintain fleece weight and maximise reduction in fibre diameter
	Industry	Reduce fibre diameter by 0.5 microns, increase fleece weight and improve wool quality and conformation
	Control	Randomly selected line that represents the original population
Broad	***8% MP***	Equal emphasis on reduced fibre diameter and increased fleece weight
	Control	Randomly selected line that represents the original population

- The 5 selection lines that are named 3% MP, 8% MP and 15% MP are selected using an index of fleece weight and fibre diameter. The percentage figures refer to the micron premium on which they are based, which in turn reflect different emphases on fleece weight and fibre diameter. Micron premium is simply a measure of the relative increase in price per kg of wool that would result from a 1 micron reduction in fibre diameter (an 8% micron premium means that 1 micron finer wool would attract an 8% price premium).
- The Industry line is being bred to an objective set by the QPLU$ Industry Liaison Committee. This is a committee of ram breeders, classers and wool producers whose objective is to reduce fibre diameter by 0.5 micron, increase fleece weight and improve wool quality and conformation.

Selections are made by prominent stud classer, Mr John Williams. The Industry line sheep are ranked according to an index that has been developed to meet their objective and Mr Williams uses this ranking in combination with his own visual assessment to make selections.

- The Control lines are randomly mated to represent the foundation sheep from which the first selections were made. In addition, semen from the foundation sires was stored so that at the end of the project, the top sires produced by 10 years of selection can be compared with their starting point.

11.2 Appendix 2

Publications arising from project

Hopkins, D. (2003). Meat and wool traits, Feedback, MLA, Sept, p7.

Hopkins, D. (2003). pH effect on Merinos, Feedback, MLA, Oct, p14.

Hopkins, D. (2003). Correlations between meat and wool traits. A few selected lines, Newsletter of the Trangie QPLU$ project, No. 5, pp.5.

Hopkins, D.L., Hatcher, S., Pethick, D. W. and Thornberry, K.J. (2005). Carcass traits, meat quality and muscle enzyme activity in strains of Merino hoggets. *Australian Journal of Experimental Agriculture* **45,** No. 10, 1225-1230.

Hopkins, D. (2005). Are there differences between strains of Merinos? Feedback, Jan/Feb, MLA, p.2.

Hopkins, D. (2006). Establishing the relationship between meat and wool traits in Merinos. A few selected lines, Newsletter of the Trangie QPLU$ project, No. 5, pp.3.

Taylor, P., Mortimer, S., Bird-Gardiner, T., Hopkins, D., Hatcher, S. and Atkins, K. (2006). The Trangie QPLU$ selection lines: responses in other wool quality and production traits and fleece value. C E Pope (Ed.), Trangie QPLU$ Merinos – Open 2006, pp.12-18.

Mortimer, S.I., Hopkins, D.L., Stanley, D.F., McMillan, D.C. and Anderson, S.L. (2006). Strain differences in merinos for carcase and meat quality. *Australian Society of Animal Production 26th Biennial Conference*, (Short communication No. 2).

Planned future publications

Hopkins, D.L., Mortimer, S.I., Stanley, D.F., McMillan D.C., and Anderson S.L. (2007). Strain differences in Merinos for carcass and meat quality*. Proceedings of the New Zealand Society of Animal Production.* **67,** (in press).

Greeff, J.C., Fogarty, N.M., Hopkins, D.L., Brien, F.D. Atkins, K.D., Safari, E., Mortimer, S.I. and van der Werf, J.H.J (2007). Genetic parameters for carcass and meat quality traits and their relationships to liveweight and wool production in Merino rams. *Australian Journal of Agricultural Research.*