Final report

Genetics of Merino meat value and lifetime performance

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Prepared by: Drs Sue Mortimer and David Hopkins
NSW Department of Primary Industries

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Meat & Livestock Australia Limited
PO Box 1961
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Abstract

Sheep producers managing dual-purpose Merino enterprises aim to diversify their businesses by producing both meat and wool. However, to achieve that through selection there is a need for more information on the 'right genetics' for components of meat and wool production, and reproduction. Using data from several Merino Lifetime Productivity Project sites, performance for a range of key meat production and quality traits was recorded and genetic parameters estimated for carcass value, its component traits and meat quality traits. Carcass value of individual sires was evaluated. Carcass composition and meat quality data from more than 1400 wethers was submitted to MERINOSELECT. Heritability estimates confirmed the potential of selection to improve performance in many carcass composition and meat quality traits of lamb meat from Merinos. Selection to improve lean meat yield will need to be balanced with improving meat quality traits due to unfavourable genetic relationships with intramuscular fat, shear force and iron content. The impact of selection to improve intramuscular fat and meat tenderness on retail colour stability should be monitored. Preliminary analyses demonstrated that carcass value among Merino sires had a range of $31.33/hd under a mixed farming system while the range under a fine wool production system was $62.48/hd.

Executive summary

Background

Incorporation of meat production traits together with traditional fine wool traits into sheep breeding programs is being driven by increased demand for sheep meat and changes in relative prices paid for wool and meat. Consequently, dual-purpose production systems are increasingly being implemented in commercial Merino flocks, where revenues are important from both fleeces and potential breeding replacements produced by ewes over their lifetime as well as the carcasses produced by surplus progeny, particularly wethers. As well as being able to identify Merino rams that suit these dual-purpose production systems, commercial producers need to be able to source these rams from breeding programs that manage carcass fatness, reproduction and wool production. Better information on genetic relationships among traits is needed to estimate Australian Sheep Breeding Values (ASBVs) more accurately and design breeding programs that manage carcass fatness, reproduction and wool production in dual-purpose systems based on Merinos, as well as meat and eating quality traits. Providing more accurate estimates of genetic parameters and increasing the number of Merino sheep with ASBVs for lean meat yield and meat quality traits will enable ram breeders and sheep producers to have more confidence in using these ASBVs in their selection decisions. Selection accuracy of these traits will be increased, leading to increased rates of genetic gain from dual-purpose selection indexes.

Objectives

This project aimed to provide more data to improve the accuracy of genetic parameters estimates and increase the number of Merino sheep with ASBVs for meat yield and meat quality traits. With this data contributing to analyses across resource flock data sets, design of selection indexes for dual-purpose production systems in Merinos would be able to be revisited and predicted rates of gain reviewed. The project also aimed to calculate carcass value for a range of Merino sires.

Methodology

A range of carcass composition and meat quality traits were recorded on carcasses from F1 wethers generated by AWI's Merino Lifetime Productivity (MLP) Project after finishing under different systems at the Trangie and Armidale sites. Genetic parameters were estimated for carcass yield, muscling and fatness traits and intramuscular fat, shear force, fresh meat colour, retail colour stability, pH and mineral traits. Sire adjusted means were estimated for hot carcass weight, total tissue depth at the 12th rib, dressing percentage and carcass value.

Results/key findings

- Heritability estimates confirmed that genetic variation for many carcass composition and meat quality traits of Merinos is available to be exploited through selection to improve these traits.
- There is scope to improve intramuscular fat, retail colour stability (defined as retoxy/met) and iron and zinc contents of Merino lamb loins and pH of the topside in order to meet consumer preferences for eating quality and freshness and recommended dietary guidelines.
- Selection to improve lean meat yield in Merinos will need to be balanced with improving meat quality traits due to unfavourable genetic relationships with intramuscular fat, shear

force and iron content. Carcass fatness, based on its association with higher reproduction, would also need attention.

- Selection to improve either intramuscular fat or tenderness of Merino lamb will result in redder fresh meat and less dark meat after 2 days of retail display, but the meat will be less red and discolour more after 2 days of retail display. Selection to increase fresh meat lightness would have little impact on meat redness and yellowness, but would increase the rate of discolouration after 2 days of retail display.
- Carcass value was found to be heritable. Increasing carcass value was associated with increases in dressing percentage and carcass fatness, favourable changes in pH and meat redness under retail display, but darker and more discoloured meat after 2 days of retail display. This pattern of responses would also follow selection for increased hot carcass weight.
- Preliminary economic analyses demonstrated that carcass value among Merino sires had a range of $31.33/hd under a mixed farming system while the range under a fine wool production system was $62.48/hd.

Benefits to industry

This project has increased the number of records within the MERINOSELECT database for carcass composition and meat quality traits from Merino carcasses and increased the number of Merino sires with ASBVs for these traits reported by Sheep Genetics. The data is now available to be combined with Merino data from other carcass reference populations to enable more accurate estimation of genetic parameters for meat production and quality, including relationships with wool production, reproduction and growth traits, across breeds and specific to the Merino breed. Subsequently, ASBVs of higher accuracy will be reported by Sheep Genetics, which will increase the accuracy of selection and lead to increased rates of genetic gain from dual-purpose selection indexes applied in Merino breeding programs.

Future research and recommendations

Combined analyses of Merino data across resource flocks (Information Nucleus flock, MLA Resource Flock, MLP Flock) are planned in collaboration with the Animal Genetics and Breeding Unit to improve the accuracy of genetic parameters for carcass composition, meat quality and eating quality, including genetic correlations with wool production, reproduction and growth traits. Further development of Merino breeding objectives and selection indexes for dual-purpose production systems should be undertaken to ensure that appropriate traits and selection strategies are provided to Merino breeders and producers to assist in better designing breeding programs to improve meat and wool production. Future research will involve more rigorous economic analyses using the GrassGro™ software, where both returns and costs are considered for both finishing systems, the sensitivity of income from carcasses to changes in the relative value of component traits is examined, wool value is included, the impacts of reproduction are evaluated and relationships with breeding values are estimated.

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1. Background

Sheep producers managing dual-purpose Merino enterprises aim to diversify their businesses by producing both meat and wool. However, to achieve that through selection they need more information on the 'right genetics' for components of meat and wool production, and reproduction. Incorporation of meat production traits together with traditional fine wool traits into sheep breeding programs is being driven by increased demand for sheep meat and changes in relative prices paid for wool and meat. Consequently, dual-purpose production systems are increasingly being implemented in commercial Merino flocks, where revenues are important from both fleeces and potential breeding replacements produced by ewes over their lifetime as well as the carcasses produced by surplus progeny, particularly wethers.

In recent years, this trend has been supported by gross margin analyses. For example, gross margin analyses of sheep enterprises conducted by the NSW Department of Primary Industries) NSW DPI in 2016 highlighted the impact of selling trade Merino wethers on profitability. A 20 micron Merino self-replacing enterprise selling trade Merino wether lambs had the highest gross margin compared to other Merino based enterprises and most crossbred enterprises, with a 10% increase in weaning rate translating to a further 10% increase in the gross margin when the change in weaning rate occurs with no additional costs to the enterprise (https://www.dpi.nsw.gov.au/about-us/media-centre/releases/2016/2016-sheep-peak, accessed 28 June 2021). As well as being able to identify Merino rams that suit these dual-purpose production systems, commercial producers need to be able to source these rams from breeding programs that manage carcass fatness, reproduction and wool production. This is supported by producer feedback from a focus group conducted as part of the Merino ewe displacement project (Source: G. Casburn), where one producer said, "I believe we can have a diversified business model by running the one species, if you have got the right genes".

In order to get 'the right genes', greater information on genetic relationships among traits is needed to estimate Australian Sheep Breeding Values (ASBVs) more accurately and design breeding programs that manage carcass fatness, reproduction and wool production in dual-purpose systems based on Merinos, as well as meat quality traits (e.g. intramuscular fat, tenderness, meat colour and iron levels). For Merinos, there has been little information available to estimate the genetic correlations between reproduction traits and meat quality traits, such as intramuscular fat and tenderness. For example in the case of lean meat yield, information is needed on its relationships with: reproduction traits (one available estimate of a negative relationship with lamb survival as a trait of the lamb; Brien *et al.* 2013); wool traits (where the positive relationship seems to be stronger for fleece weight in adults); and meat traits (strongly negative with carcass fat measurements, though GR fat depth was positively correlated to lamb survival). A previous study (Safari *et al.* 2008) reported no antagonism between reproduction traits (number of lambs born per ewe lambed, and number of lambs born and weaned per ewe joined) and carcass (fat depths at GR and C sites, eye muscle dimensions) and meat quality indicator traits (pH, fresh meat colour).

Genetic parameters for Merinos born in the Information Nucleus indicated that many of the meat production and quality traits would be expected to be improved through selection and that there were no major unfavourable genetic relationships between the key wool and meat traits (Mortimer *et al.* 2017a, b). Nonetheless, unfavourable changes in intramuscular fat, tenderness, colour and iron levels of lamb meat were expected to occur following selection emphasising either one of the key traits currently used in dual-purpose breeding programs i.e. live weight, and ultrasound fat and muscle depths. Adverse effects on meat quality and carcass fatness also were expected following selection for increased lean meat yield. However, the estimates of the genetic correlations involving

the carcass and meat quality traits were based on low numbers of records and with high standard errors. Further data is needed to validate and improve the accuracy of these estimates, as well as increase the number of records for these traits available to the MERINOSELECT database. Based on revised estimates, design of selection indexes for dual-purpose production systems in Merinos would be able to be revisited and predicted rates of gain reviewed.

The opportunity arose to obtain carcass and meat quality measurements on F1 wethers at several sites of the AWI-funded Merino Lifetime Productivity (MLP) Project, to increase the amount of carcass and meat quality data submitted to MERINOSELECT and estimate genetic relationships between lifetime performances in reproduction and wool production and the carcass and meat quality traits of Merinos. This phenotypic data, together with collection of genomic information, will also provide information on carcass and meat quality traits in Merinos needed for a range of studies e.g. on-going support of genomic data being available for genetic evaluation of Merinos, particularly for hard-to-measure traits. As the MLP Project used sires that were industry relevant and representative of a range of the main genetic groups in the MERINOSELECT database, data from this project would demonstrate the impact of ASBVs for key selection traits on meat yield and meat quality traits in Merinos to ram breeders and commercial producers. An earlier project, using performance data from three Merino Producer Demonstration Sites and a limited number of Merino sires, was unable to identify relationships among research breeding values for lean meat yield, intramuscular fat and shear force (Hocking Edwards 2014).

Previously, genetic benchmarking of Merinos has been focussed on sire performance in measured and visually assessed traits relevant to wool production at yearling, hogget and a first adult shearing through central test sire evaluation. Benchmarking of Merino bloodlines through wether trials has also been conducted. A limited number of wether trials (conducted as a Peter Westblade Memorial Merino Challenge) have compared commercial flock performances for some carcass and meat quality traits and calculated carcass values (Martin and Wilson 2016), though this information as yet has not been presented in terms of comparisons of Merino bloodlines or types. More recently, Clarke *et al.* (2019) have reported variation between sires in value of production (wool and meat), based on live animal data being used to assign animals to market segments and therefore estimate the sale value for each animal.

The current project proposed to obtain this information, using the F1 wethers of the MLP project at several sites, Trangie and Armidale, following finishing at pasture and in a commercial feedlot. The sires represented at these sites were drawn from a range of Merino types, with the sites themselves being managed within mixed farming (Trangie) and fine wool production (Armidale) systems. Wethers born at the Trangie site were the progeny of two different ewe bloodlines, where one bloodline was being selected for increased wool production and body size while the other bloodline's breeding program was aimed at improving wool, fertility and growth traits. Estimates of the variation in enterprise profitability will be calculated, and association of profitability with variation in lean meat yield and meat quality evaluated, of Merino sires and Merino types when mated to ewes of differing genetic background. The existence of any trade-offs between carcass and wool values will be evaluated. The current project will complement the data generated by the MLP Project and its AWI-funded overlay projects and is designed to generate data for analyses conducted across projects.

Overall, by providing more accurate estimates of genetic parameters and increasing the number of Merino sheep with ASBVs for meat yield and eating quality traits the project will meet the objectives of industry strategic plans. Availability of ASBVs of higher accuracy will provide ram breeders and

sheep producers with confidence to use the ASBVs in their selection decisions and increase the accuracy of selection, leading to increased rates of genetic gain from dual purpose selection indexes.

2. Objectives

1. Measure 1500 progeny for carcass traits and overall carcass value by 31 December 2019.

Achieved: Measurements completed on 1454 progeny by February 2020.

2. As data is collected, provide 1500 records into the MERINOSELECT database and to AWI for inclusion in the AMSEA database to enhance the estimation of genetic correlations for a wide range of key carcass composition and meat quality traits in Merinos with reproduction, wool production and growth traits, particularly when combined with data collected at other MLP sites.

Achieved: Carcass composition and meat quality data submitted for entry to the MERINOSELECT database via the MLA Resource Flock database (June 2020) and live animal (growth and ultrasound fat scanning) data submitted for entry to the AMSEA and MERINOSELECT databases (May 2020). Genotype data provided to the MERINOSELECT database (June 2020).

3. Estimate the genetic correlations for a wider range of carcass composition and meat quality traits in Merinos with reproduction, wool production and growth traits, particularly when combined with data collected at other MLP sites, by March 2020.

Achieved in part: This report focussed on estimating heritabilities for and genetic correlations among Merino carcass composition and meat quality traits based on the data generated by the project. Planned work under Project L.EQT.1908 (Eating quality in Merino breeding programs), in collaboration with the Animal Genetics and Breeding Unit (AGBU), and analyses of the MLP data by AGBU will jointly achieve this objective by including estimation of genetic correlations across the fuller range of Merino trait groups and across resource flock data sets. As well, lifetime wool and reproduction data on the female sibs of the wethers to date have been collected only at a maximum of 2 lambing opportunities for both drops.

4. Demonstrate to commercial producers the variation in enterprise profitability, lean meat yield and meat quality of Merino sires and Merino types when mated to ewes of differing genetic backgrounds, and if any trade-offs between carcass and wool values exist.

Achieved in part: Preliminary analyses demonstrated that carcass value among Merino sires had a range of $31.33 per head under a mixed farming system while the range under a fine wool production system was $62.48 per head. From analyses conducted under the MLP Project, sire X ewe genotype interactions were unimportant, indicating that sire rankings for these traits were consistent and that ASBVs for these traits will reliably predict performance when sires are mated to ewes from different genetic backgrounds.

5. Provide data potentially on meat yield traits from carcasses assessed using the DEXA technology during processing (if possible) to test suitability of the technology to use as a measurement source in future carcass evaluation and genetic benchmarking.

Not achieved: A processing plant with DEXA technology installed was unavailable at the time of slaughter of the progeny.

6. Provide additional project for potential additional data on eating quality of Merino types and sires through consumer taste panel assessments for use in genetic benchmarking.

Achieved: Eating quality data for Merinos provided by L.EQT.1908 Eating quality in Merino breeding programs'.

3. Methodology

3.1 Experimental design and methods

3.1.1 Animals

Data was recorded on the carcasses produced from F1 wethers at 2 sites of AWI's MLP project managed within mixed farming (Trangie, Macquarie site hosted at NSW Department of Primary Industries' Trangie Agricultural Research Centre) and fine wool production (Armidale, New England site hosted at CSIRO's FD McMaster Laboratory, "Chiswick") systems. The design of the MLP project has been described by Ramsay *et al.* (2019), with the protocols that produced the F1 progeny at the Trangie site described by Egerton-Warburton *et al.* (2019). These protocols were implemented also at the Armidale site.

At both sites the F1 wethers were born in 2017 and 2018 following AI mating of industry sires in each of two years to foundation ewes. The MLP project web site provides details on the sources of sires and foundation ewes at each site (https://merinosuperiorsires.com.au/mlp-project). The wethers were the progeny of 30 (Trangie) and 28 (Armidale) sires at each site, with 2 link sires used across both sites. In terms of the MERINOSELECT wool types, the sires represented at Trangie were predominantly fine/fine medium types, while the sires represented at Armidale were mainly ultra/super fine types. The foundation ewes used at Trangie were sourced from 2 bloodline sources within the fine/fine medium type, differing in their breeding objectives and selection approaches. The Armidale flock's foundation ewes were derived from an ultrafine source.

3.1.2 Management

A timeline of key management events relevant to this project for each drop at Trangie and Armidale is presented in Table 1. For wethers managed at Trangie, generally drier seasonal conditions were experienced from lambing of the 2017 drop wethers. These conditions continued into 2018 and 2019, becoming drier from mid 2018. With the pastures consisting of limited dry, standing feed for both drops once weaned, feeding of the wethers was undertaken. Wethers were imprinted to supplementary feeding while on their dams. For the 2017 drop, feeding in the one management group occurred from January 2018, using self-feeders holding a mix of 70% barley and 30% field peas, plus lucerne hay was made available. Production feeding of the 2018 drop wethers commenced once weaned and continued through to slaughter, using self-feeders holding a mix of 80% barley and 20% lupins, with 20 kg of limestone and 10 kg of a commercially available lot fed lamb concentrate added per tonne of grain. Three months after weaning, these wethers were allocated to 2 management groups balanced for sire and weight. Barley straw was always available to the wethers. For both drops, feeding continued until slaughter. As a target body weight of 48 kg was achieved, the wethers were allocated to slaughter groups balanced for sire.

Table 1. Timeline of key management events from lambing for each site-drop combination (average age at an event in brackets)

	Lambing	Weaning	Shearing	Fat scanning	Feedlot entry	Slaughter
Trangie						
2017	May	September	February (9 months)	March (10 months)		March-May (11.6 months)
2018	May	August	January (8 months)	February (9 months)		February-May (11 months)
Armidale						
2017	September	January	June (9 months)	June (9 months)	June, July	August-September (11.7 months)
2018	September	January	April (7 months)	April (7.5 months)	May, June	July-August (10.8 months)

Similarly for the Armidale wethers, dry seasonal conditions occurred during the latter part of 2017 and into 2018, with drier conditions experienced in the second half of 2018 and into 2019. Limited carry-over of dry, standing feed was available to the lambs post-weaning for both drops and production feeding of the wethers commenced once weaned, using lick feeders. Before weaning, the wethers were imprinted to supplementary feeding. The wethers were fed 100% barley supplemented with buffer/mineral pellets. Three months after weaning, the wethers were allocated to 2 slaughter groups balanced as far as possible for body weight, sire and rearing type. To prepare the animals for finishing in a commercial feedlot, the wethers then were transitioned onto a ration similar to that used at the feedlot, being 80% barley and 20% cracked faba beans supplemented with buffer/mineral pellets self-feeders. Lambs were also trail fed faba beans/field peas (depending on availability) in the paddock at a rate of 1kg/hd/wk. Following the departure to the feedlot of wethers allocated to the first slaughter group, the ration for the remaining wethers was modified to contain 30% cracked faba beans until feedlot entry. Trail feeding of faba beans at 1kg/hd/wk also continued throughout this period. Once at the feedlot, lambs were feed a standard feedlot ration of 80% barley and 20% high protein grain (lupins, faba beans, etc. depending on availability) supplemented with custom buffers and mineral mixes. The slaughters were scheduled to have the wethers at a target body weight of 48 kg.

3.1.3 Live animal measurements

Body weights were monitored from post weaning at approximately monthly intervals. Ultrasound scanning traits (fat and eye muscle depth, as well as body weight) were recorded using an accredited scanner. Prior to slaughter in 13 groups (6 in 2018 and 7 in 2019, respectively; 4 and 5 from Trangie and 2 from Chiswick, respectively per year), the lambs were weighed and transported 80 and 500 km respectively, and held overnight in lairage with water before slaughter the next day.

3.1.4 Slaughter procedure and chilling

The lambs were slaughtered commercially with electric stunning followed by exsanguination through severing of the jugular veins and carotid arteries. Immediately following exsanguination, animals were immobilized (2000 Hz, 150 µs pulse width at 4-6 Amps) to prevent excess kicking during carcass dressing procedures. Immediately afterwards, the carcasses (skin on) were subjected on the moving

chain to an electrical current via a unit designed to increase the removal of blood (15 Hz, 500 µs pulse width, 68 pulse interval (mS), 600 mA, 350 V, for 50 secs). Medium voltage electrical stimulation was applied to fully dressed carcasses just before chiller entry (15 Hz, 1000 µs pulse width, 68 pulse interval (mS), 600 mA, 350 V, for 50 secs). The carcasses were chilled at a mean (± s.d.) temperature 6.1 ± 2.7 ºC for 24 h.

3.1.5 pH decline and pH measures

Once carcasses entered the chillers, pH and temperature were measured in the caudal section of the *longissimus lumborum* (LL). Measurements were taken at regular intervals from approximately 35 ºC to 18 ºC using hand held pH meters with temperature compensation (WP-80, TPS Pty. Ltd., Brisbane, AUS), a polypropylene spear-type gel electrode (Ionode IJ 44) and cylindrical stainless steel probe attachment. The meters were calibrated intermittently at ambient temperature using pH buffers 4.01 and 6.86 (TPS Pty Ltd., Brisbane, AUS). The pH at 24 h post slaughter in the LL (pH24ll) and *semitendinosus* (ST; pHh24st) was measured after calibrating the meters at chiller temperature in 2019. In 2018, the pH was measured at 24h only in the ST. In both years, the pH of the LL (left side) was measured at the 12th rib during boning (see below) and then in LL aged for 5 days (ultimate). Ultimate pH was analysed as outlined by de Brito *et al.* (2016). Approximately 1 g of frozen aged sample was homogenised in an iodoacetate buffer and suspended in a water bath at 5 ºC. Ultimate pH was determined as the average of duplicate measures using a temperature and pH meter (Model smartCHEMC-CP, TPS Ltd., Queensland, AUS) calibrated at 5 ºC in pH 4.01 and 6.86 buffers. Duplicate pH measures were recorded and a third was taken if 2 readings differed by more than ±0.02.

The pH decline data were modelled following a spline approach of van de Ven *et al.* (2014), within the software package ASReml (VSN International, Hemel Hempstead, UK) under R (R Core Team, 2015). Temperature at pH 6 (splpH6tmp) and the pH at 18 °C (splpH18) were estimated.

3.1.6 Carcass measures

The carcasses were weighed hot (hcwt, kg) as per AUS-MEAT standards (Anon. 2005) and tissue depth (grfat, total tissue depth of fat and muscle in mm) was also measured at the 12th rib 110 mm from the backbone using a GR knife. Dressing percentage (dp) was calculated as the ratio of hcwt to preslaughter weight. The subcutaneous fat depth (mm) at the 5th rib 110 mm from the backbone was measured with a steel ruler on all carcasses in 2019. After 24 h, the carcasses in 2019 were weighed cold prior to boning. In both years, the forequarter (HAM No. 4971) was removed between the 4th and 5th ribs and discarded. Then the saddle (HAM No. 4910) was cut in half at the 12th rib and the rack saddle (HAM No. 4928) discarded and the shortloin saddle (HAM No. 4883) retained after removal of the flank and ribs with a cut 25 mm from the lateral edge of the LL. The hindlegs (HAM No. 5060) were retained in 2019.

Measures of subcutaneous fat depth (cfat, mm) and muscle depth and width (cemd and cemw in mm; LL right side) were taken at the 12th rib by experienced personnel using a metal ruler and these values were multiplied and the product then multiplied by 0.008 as a three component vector to give a cross sectional area estimate (cema, cm^2; Hopkins *et al.* 1992).

3.1.7 Instrumental colour measurement

The cut surface of the LL (12th rib, left side) was bloomed at ambient temperature for 30-40 min and fresh meat colour measured using a Minolta Chroma meter (Model CR-400) set on the CIE *L**, *a**, *b** system (whereby *L** measures relative lightness (cfl), *a** relative redness (cfa) and *b** relative yellowness (cfb)), and having an aperture size of 8mm, using the D65 illuminant and 10° standard observer. This colorimeter was calibrated with a white tile (Y = 84.7, x = 0.3182, y = 0.3353) and three replicate measurements were taken at different positions on the measured surface and their average recorded.

3.1.8 Partial boning

In 2019, the shortloin saddle (HAM No. 4883) was weighed and then the subcutaneous fat removed and weighed, then both eye of shortloins (HAM No. 5150) were excised from the bone and weighed and finally the bone was weighed. From the hindlegs (HAM No. 5060) one side was removed (left side) by boning leaving the pelvic bone in the other side (right). The right side was then boned producing the topside (HAM No. 5073) and the knuckle (HAM No. 5072) and these were each weighed. All the leg bones were weighed along with the pelvic bone, then the remaining meat and fat were weighed. All weights were recorded in grams.

3.1.9 Sample preparation for meat and eating quality testing

The silver skin (epimysium) was removed from both LL and the right side was vacuum packaged to be aged for 5 days and then used for sensory testing. The left side LL was sub-sampled, with a 25-30 g sample taken from the cranial end, diced and stored in 50 ml tubes for subsequent measurement of intramuscular fat (imf, %) and iron and zinc contents (mg/100 g fresh tissue). A 3-4cm slice of LL was then removed for later measurement of colour stability under simulated retail display and vacuum packed. From the caudal portion of the LL a sample (mean 67.9 ± 5.38 g) was sub-sectioned and vacuum packaged for subsequent measurement of shear force (shearf5). The cap muscle (*m. gracilis*) was removed from the topside and this cut and the knuckle were vacuum packed and aged for 5 days and then used for subsequent sensory testing. All samples were transported chilled on ice to the Centre for Red Meat and Sheep Development, (NSW DPI, Cowra) for further processing. Samples held vacuum packed for 5 days were stored at a mean (s.d.) temperature of 3.2°C ± 1.53 and then frozen at – 20 ºC until subsequent analysis.

3.1.10 Shear force and cooking loss

Samples of LL were prepared and cooked for shear force analysis as described by Hopkins and Thompson (2001). Shear force blocks from kill days within years were randomly allocated to cook batches, on an individual muscle basis. Shear force was measured as the average of 6 peak force recordings across each muscle block using a Lloyd (Model LRX, Lloyd instruments, Hampshire UK) fitted with a Warner Bratzler shear v blade. Cooking loss was calculated as a percentage of the pre-cook weight on all shear force blocks, using the pre-cook frozen weight and post cook weight as outlined by Hopkins and Thompson (2001).

3.1.11 Intramuscular fat, iron and zinc concentration

The moisture content of all LL sub-samples to be used for determination of imf and iron and zinc levels was measured by weighing samples prior to and post freeze drying at -50°C (ScanVac CoolSafeTM (LaboGene ApS., Lynge., Denmark) then recording the difference as a percentage. These same freeze-dried samples were stored at -20°C until determination of imf, iron and zinc contents. This entailed grinding the samples using a FOSS Knifetech™ 1095 sample mill (FOSS Pacific, Unit 2, 112-118 Talavera Road, North Ryde, NSW, 2113) and then imf determination using the FOSS Soxtec 2050 protocol as described by Hopkins *et al.* (2014) using 2.5 g samples. Selected mineral contents were determined using a microwave digestion and inductively coupled plasma-optical emission spectroscopy (ICP-OES) detection method.

3.1.12 Retail colour stability

Following their prescribed ageing period, a cutting guide was used to section the LL samples to a uniform 3 cm thickness with the myofibrils perpendicular on the measured surface. These sections were then individually placed on black foam trays and overwrapped with PVC food film wrap (15 µm) and permitted to bloom for 45 min before colorimetric analysis. Colorimetric measurements *L** (retl), *a** (reta) and *b** (retb) were taken over four display time intervals (0, 24, 48, and 72 h) between which all samples were displayed under simulated retail lighting (mean: 917 lx) and refrigeration (mean: 2.6°C ± 0.50.). A HunterLab spectrophotometer (Miniscan Model 45/0-L: Reston, VA, USA) with a 25 mm aperture was calibrated as per manufacturer guidelines (X = 80.4, Y = 85.3, Z = 91.5). This was set to illuminant D-65 and viewing angle 10°. At each reading, measurements were replicated after rotating the spectrophotometer 90° in the horizontal plane. The oxymyoglobin/metmyoglobin ratio (retoxy/met) was estimated by dividing the captured light reflectance at wavelength 630 nm, by that at wavelength 580 nm (AMSA, 2012).

3.1.13 Prediction of lean meat yield and carcass value

Estimated lean meat yield (elmy, %) was predicted using a variant of an equation developed for the Merino breed by Dr Graham Gardner (personal communication December 2019; see Table A4 for the terms of the equation). The equations used records on the 2018 drop for carcass measures (hcwt,

Table 2. Descriptive statistics (standard deviation in brackets) for carcass composition traits (hcwt, hot carcass weight, kg; dp, dressing percentage; grfat, total tissue depth in mm at the 12th rib, 110 mm from the backbone) rib used to calculate carcass value (cval, $/hd)

Birth year		Trangie		Armidale	
		Mean (SD)	Range	Mean (SD)	Range
2017	hcwt	24.4 (1.87)	19.3 - 33.7	23.8 (2.64)	16.7 - 33.0
	dp	45.0 (2.31)	38.5 - 61.9	46.7 (2.11)	35.6 - 51.8
	grfat	10.8 (4.04)	2 - 25	13.8 (3.81)	3 - 25
	cval	153.21 (15.16)	110.01 - 215.68	174.90 (26.24)	113.56 - 254.10
2018	hcwt	25.9 (1.86)	21.4 - 32.3	29.5 (3.38)	21.4 - 40.1
	dp	46.7 (1.94)	38.8 - 52.0	47.9 (2.18)	35.3 - 54.5
	grfat	14.4 (3.32)	7 - 31	21.7 (5.13)	11 - 42
	cval	164.64 (12.76)	128.40 - 206.72	224.20 (29.11)	149.80 - 308.77

cfat and cema) and weights from the partial boning process (trimmed loin, topside and round muscle weights; trimmed loin fat weight; leg and aitch bone weights). For both drops, carcass value

(cval, AUD$ per head) was calculated for each carcass using its hcwt, grfat and over the hook (OTH) price information from the abattoir feedback reports for the slaughters. As a means of accounting for differences in fat levels between carcasses, grfat was used to adjust for carcasses being outside specifications i.e. deductions of $0.30 per kg for carcasses with fat score 1 (≤5 mm) or of fat score 5 (≥21 mm). Table 2 presents descriptive statistics for each site.

3.2 Statistical analysis

3.2.1 Genetic parameters

Variance and covariance estimations were performed using ASReml (Gilmour *et al.* 2015). For each trait, univariate analyses were used to estimate phenotypic variances and heritabilities with an animal model. Models included fixed effects of birth-rearing type (single-single, multiple-single, multiple-multiple), age of dam, age at measurement, Merino wool type (ultra/superfine, fine/fine-medium, medium/strong) and contemporary group (as defined in the MERINOSELECT data base, modified for slaughter group). For models fitted to the carcass fat and eye muscle measures and the meat quality traits, hcwt was included as a covariate. A direct genetic effect of animal was fitted as the random effect. A maternal permanent environmental effect was also included as a random effect, but it was found to be not significant for all traits, as was also the case for a sire by site interaction. For these analyses, sire and dam pedigree only were used. When these data are combined with other data sets (e.g. MERINOSELECT, MLA Resource Flocks), greater depth of pedigree information, as well as fitting of a wider range of random effects (e.g. genetic group), will be used in planned analyses.

Genetic and phenotypic correlations among the traits were estimated from bivariate analyses.

3.2.2 Carcass value

For the data from each site, separate analyses to calculate adjusted sire means for hcwt, grfat, dp and cval were performed using ASReml (Gilmour et al. 2015). The fixed effects of sire, ewe bloodline and their interaction were first tested, with non-significant effects then excluded from the model. Random effects fitted in the model were birth type (single, twin, triplet (Trangie data only)), rearing type (single, twin) and dam age (2 (Armidale data only), 3, 4, 5, 6 and 7 year old at mating), as well as a contemporary group effect (accounting for management and slaughter group effects).

4. Results and discussion

4.1 Genetic parameters

4.1.1 Descriptive statistics

Descriptive statistics for the carcass composition and meat quality traits are presented in Table 3. The wethers were managed to achieve a target liveweight of 48 kg at slaughter, however the mean hcwt (25.7 kg) was heavier than the target and mean value (21.1 kg) for Merinos from the Information Nucleus flock reported by Mortimer *et al.* (2017a), where animals were managed to be slaughtered at an average target carcass weight of 22 kg for wethers and 21 kg for ewes. The mean

value for imf of the loin samples was 4.3%, with 52% of samples greater than 4%. However, only 27% of samples were in the range of 4-5% recommended by Pannier *et al.* (2018) for lamb to avoid unfavourable responses in imf and eating quality of lamb from selection for elmy, as well as sensory eating quality scores being reduced as imf declines. The mean value for shearf5 (25.4 N, 66% of samples) was less than 27 N found for acceptable eating quality (Hopkins *et al.* 2006).

Table 3. Descriptive statistics and estimates of phenotypic variance and heritability (standard error in brackets) for carcass composition and meat quality traits[1] assessed on Merino carcasses

	n	Mean	SD	Range	Phenotypic variance	Heritability
Carcass composition						
hcwt	1447	25.7	3.0	16.7 – 40.1	4.99 (0.26)	0.82 (0.11)
dp	1446	46.4	2.4	35.3 – 61.9	4.07 (0.19)	0.47 (0.10)
grfat	1447	14.4	5.4	2.0 – 42.0	10.42 (0.49)	0.44 (0.10)
cval	1447	172.80	31.3	110.00 – 308.80	368.78 (19.70)	0.85 (0.11)
cemd	1448	28.1	3.1	19.0 – 40.0	6.53 (0.31)	0.49 (0.10)
cemw	1448	58.9	3.8	46.0 – 71.0	12.49 (0.59)	0.49 (0.10)
cema	1448	13.3	1.8	8.0 – 21.1	2.33 (0.12)	0.64 (0.11)
cfat	1448	4.9	2.1	1.0 – 14.0	3.26 (0.16)	0.57 (0.11)
elmy	683	57.6	2.6	46.8 - 64.4	4.60 (0.34)	0.47 (0.17)
Meat quality						
imf	1437	4.28	1.33	0.81 - 10.75	1.34 (0.07)	0.87 (0.10)
shearf5	1438	25.4	5.6	13.0 - 58.4	27.28 (1.33)	0.52 (0.11)
iron	1438	2.00	0.253	1.30 - 3.10	0.048 (0.002)	0.61 (0.12)
zinc	1438	2.30	0.268	1.52 - 3.27	5.60 (0.27)	0.48 (0.11)
cfa	1446	20.5	1.4	14.2 - 25.2	1.89 (0.08)	0.23 (0.08)
cfb	1446	3.2	1.1	-1.0 - 7.1	0.78 (0.04)	0.52 (0.10)
cfl	1446	35.2	2.2	28.9 - 44.1	3.69 (0.17)	0.45 (0.10)
reta	1437	16.5	1.8	10.2 - 22.7	2.98 (0.12)	0.09 (0.05)
retb	1437	15.9	1.6	8.9 - 22.1	2.31 (0.10)	0.11 (0.06)
retl	1437	39.2	2.9	30.6 - 48.8	5.56 (0.28)	0.59 (0.12)
retoxy/met	1437	3.3	0.6	1.9 - 5.6	0.26 (0.01)	0.11 (0.06)
pH24ll	1273	5.58	0.13	5.31 - 6.97	0.015 (0.001)	0.18 (0.08)
pH24st	1447	5.81	0.23	5.13 - 6.84	0.042 (0.002)	0.05 (0.05)
splpH18	1448	5.92	0.13	5.62 - 6.75	0.012 (0.001)	0.30 (0.09)
splpH6tmp	1379	22.87	6.458	6.0 - 39.4	28.58 (1.32)	0.36(0.09)

[1] hcwt, hot carcass weight, kg; dp, dressing percentage; grfat, total tissue depth in mm at the 12th rib, 110mm from the backline; cval, carcass value, $/hd; cemd, eye muscle depth, mm; cemw, eye muscle width, mm; cema, eye muscle area, cm^2; cfat, carcass fat depth in mm at the 12th rib; elmy, estimated lean meat yield, %; imf, intramuscular fat, %; shearf5, shear force after 5 days of ageing, N; iron, iron content, mg/100 g fresh tissue; zinc, zinc content, mg/100 g fresh tissue ; cfa, fresh meat redness; cfb, fresh meat yellowness; cfl, fresh meat lightness; reta, retail display redness; retb, retail display yellowness; retl, retail display lightness; retoxy/met, retail display oxy/met value; ph24ll, pH at 24 h after slaughter in LL muscle; pH24st, pH at 24 h after slaughter in ST muscle; splpH18, pH at 18 °C predicted using a spline model; splpH6tmp, temperature at pH 6 predicted using a spline model.

With all samples having cfa values greater than 9.5 (redder) and almost 70% of samples with cfl values greater than 34 (lighter), on average consumers would find the fresh meat colour of these samples acceptable (Khliji *et al.* 2010). However, the mean retoxy/met value after 2 days of retail

display was 3.3 (48% of samples greater than 3.3), below which average consumers consider lamb to be discoloured (Khliji *et al.* 2010). A mean pH value at the threshold of acceptability (44% of samples) was seen for mean pHst (values should be less than 5.8, Warner *et al.* 2010), while 95% of loin samples had a pH lower than 5.8. The mean values for iron and zinc contents (2.00 mg/100 g and 2.30 mg/100 g respectively) were slightly lower than those reported by Mortimer *et al.* (2017b) for Merino loins, Pannier *et al.* (2010, 2014) for lamb loins produced from a multi-breed population and Fowler *et al.* (2018) for lamb loins produced under extensive conditions. These values indicate that the samples of Merino lamb (from the loin) can be claimed only as "good sources" of iron for women over 50 yr old and men, and of zinc for women of all ages, according to recommended dietary guidelines used by dieticians (NHMRC 2003).

As 73% of loin samples were predicted to have reached a pH of 6 between 18 and 35°C, modelled here using a spline approach, a majority of samples were deemed to have met pH decline requirements and acceptable muscle shortening had occurred during rigour development. Meeting this requirement for pH decline is expected to contribute to optimal eating quality of lamb available to domestic and some overseas markets (Thompson *et al.* 2005).

4.1.2 Heritability

Heritability estimates for the carcass composition traits were all high (Table 3), ranging between 0.44 ± 0.10 for grfat and 0.82 ± 0.11 for hcwt. Most heritability estimates for the meat quality traits were also high (greater than 0.30 in value), though estimates were moderate for cfa (0.23 ± 0.08) and pH24ll (0.18 ± 0.08) and low for reta (0.09 ± 0.05), retb (0.11± 0.06), ret oxy/met (0.11 ± 0.06) and pHst (0.05± 0.05). Carcass value (0.85 ± 11) and the pH decline criteria (0.30 ± 0.09, splpH18; 0.39 ± 0.11, splpH6tmp) were highly heritable. All estimates were associated with relatively large standard errors.

The heritabilities for most traits were higher than estimates published previously for Merinos (Greeff *et al.* 2008; Mortimer *et al.* 2017a, b), though estimates for the meat quality traits of low to moderate heritability (retail colour stability and pH traits) were similar to the published values. For the carcass composition traits, published estimates in Merinos range between 0.20 ± 0.03 (cfat) and 0.37 ± 0.04 (hcwt) from Greeff *et al.* (2008) and between 0.12 ± 0.08 (cemd) and 0.35 ± 0.10 (hcwt) from Mortimer *et al.* (2017a). The published estimates for meat quality traits range from 0.10 ± 0.03 (cfa, cfb) to 0.22 ± 0.03 (pH) (Greeff *et al.* 2008) and between 0.00 ± 0.00 (reta) and 0.58 ± 0.11 (imf) (Mortimer *et al.* 2017a).

The analyses of the earlier studies were based on data sets with greater numbers of sires, made greater use of the available pedigree data and appropriately accounted for genetic groups in the data. Additionally, hcwt was not included as a covariate in models fitted to the carcass eye muscle and fat measures and meat quality data reported by Mortimer *et al.* (2017a, b). For several of the traits, phenotypic variances were higher than earlier estimates for Merinos and inflation of the additive genetic variances was evident from comparisons of estimates from the current project with genetic variances derived by the earlier Merino studies (results not shown). Nonetheless, the estimates from the current project confirm that genetic variation is available to be exploited through selection for many of the carcass composition and meat quality traits of Merinos.

4.1.3 Correlations

Estimates of genetic and phenotypic correlations among the carcass composition traits are shown in Table 4. Most genetic correlations among the carcass component traits were positive. Selection for heavier hcwt will increase dp (0.49), carcass fatness (grfat, 0.59; cfat, 0.50) and carcass muscling (cemd, 0.31). Hot carcass weight had a very high genetic correlation with cval (0.99) and a negative genetic correlation with elmy which was not significantly different to zero (-0.37). Dressing percentage had a similar pattern of genetic correlation, though the genetic correlation of dp with elmy was negative and stronger (-0.68). Lean meat yield had negative genetic correlations with carcass fatness (-0.96, grfat; -0.81, cfat) and positive genetic correlations with carcass muscling (0.43, cemw). The estimates reported herein were consistent with those reported for Merinos by Greeff *et al.* (2008) and Mortimer *et al.* (2017a) shown in Table A1.

Table 4. Genetic (below diagonal) and phenotypic (above diagonal) correlation estimates (standard error in brackets) for carcass composition traits[1] assessed on Merino carcasses

	hcwt	dp	grfat	cval	cemd	cemw	cema	cfat	elmy
hcwt		0.48	0.43	0.98	0.26	0.15	0.30	0.29	-0.26
dp	0.49 (0.11)		0.18	0.45	0.09	-0.06	0.04	0.11	-0.29
grfat	0.59 (0.11)	0.56 (0.14)		-0.03	0.15	-0.14	0.05	0.34	-0.63
cval	0.99 (0.00)	0.47 (0.12)	0.03 (0.16)		0.11	0.17	0.19	0.12	-0.21
cemd	0.31 (0.13)	0.43 (0.15)	0.40 (0.16)	0.11 (0.15)		0.12	0.85	0.00	0.13
cemw	-0.02 (0.15)	-0.07 (0.17)	-0.20 (0.17)	0.00 (0.15)	0.46 (0.14)		0.62	-0.11	0.45
cema	0.25 (0.13)	0.27 (0.15)	0.15 (0.16)	0.10 (0.14)	0.91 (0.03)	0.78 (0.07)		-0.06	0.34
cfat	0.50 (0.11)	0.49 (0.14)	0.74 (0.11)	0.30 (0.13)	-0.13 (0.16)	-0.25 (0.16)	-0.21 (0.15)		-0.50
elmy	-0.37 (0.19)	-0.68 (0.18)	-0.96 (0.06)	-0.36 (0.20)	0.03 (0.25)	0.43 (0.20)	0.22 (0.23)	-0.81 (0.12)	

[1] See Table 3 for trait abbreviations.

Carcass value had positive genetic correlations with dp (0.47) and cfat (0.30) and a negative genetic correlation with elmy (-0.36). Due to the assumptions used in its calculation, cval was essentially determined by price for carcass weight with deductions for grfat based on equivalence to fat score 1 and fat score 5. This simple estimate of carcass value does not take into account that as fatness within fat scores 2-4 increases, there is a decrease in lean meat yield at a constant weight. Both at the genetic (0.03) and phenotypic (-0.03) levels, cval and grfat are uncorrelated.

The high negative genetic correlation between imf and shearf5 (-0.79, Table 5) confirms the favourable association between these traits in Merinos reported by Mortimer *et al.* (2017b; see Table A2). Improvements in imf (higher) will increase both fresh meat colour traits (0.73, cfb; 0.74, cfl) and meat lightness after 2 days of retail display (0.69, retl), but will reduce redness (-0.49, reta)

Table 5. Genetic (below diagonal) and phenotypic (above diagonal) correlation estimates (standard error in brackets) for meat quality traits assessed on Merino carcasses (see Table 3 for trait abbreviations)

	imf	shearf5	iron	zinc	cfa	cfb	cfl	reta	retb	retl	retoxy/met	pH24ll	pH24st	splph18	splph6tmp
imf		-0.38	0.02	-0.11	0.08	0.41	0.35	-0.17	0.03	0.34	-0.23	-0.04	-0.05	-0.03	0.01
shearf5	-0.79 (0.08)		-0.11	0.10	-0.16	-0.30	-0.19	0.00	-0.05	-0.17	0.03	0.16	0.23	0.07	-0.06
iron	-0.02 (0.14)	-0.13 (0.17)		0.17	0.31	-0.06	-0.41	-0.07	-0.27	-0.53	-0.07	-0.10	-0.07	-0.11	0.12
zinc	-0.20 (0.14)	0.15 (0.17)	0.11 (0.17)		-0.01	-0.08	-0.06	0.01	-0.04	-0.09	0.02	0.06	0.05	-0.03	0.01
cfa	0.24 (0.17)	-0.32 (0.19)	0.25 (0.19)	0.24 (0.21)		0.55	-0.44	0.19	-0.02	-0.10	0.13	-0.36	-0.30	-0.27	0.19
cfb	0.73 (0.08)	-0.69 (0.10)	-0.21 (0.16)	0.00 (0.17)	0.57 (0.14)		0.43	0.13	0.14	0.33	0.04	-0.37	-0.34	-0.22	0.12
cfl	0.74 (0.09)	-0.69 (0.12)	-0.55 (0.12)	-0.18 (0.18)	-0.03 (0.22)	-0.06 (0.24)		-0.05	0.17	0.50	-0.09	-0.10	-0.10	0.00	-0.02
reta	-0.49 (0.21)	0.53 (0.24)	-0.24 (0.26)	0.29 (0.26)	0.36 (0.30)	-0.19 (0.25)	-0.47 (0.24)		0.67	-0.21	0.95	-0.19	-0.22	-0.14	0.09
retb	0.28 (0.23)	-0.30 (0.26)	-0.92 (0.14)	-0.07 (0.27)	0.12 (0.31)	0.58 (0.23)	0.68 (0.22)	0.13 (0.38)		n.c.	0.60	0.01	-0.03	0.05	-0.09
retl	0.69 (0.08)	-0.51 (0.14)	- 0.78 (0.08)	-0.19 (0.17)	0.00 (0.21)	0.70 (0.11)	0.92 (0.05)	-0.17 (0.25)	n.c.		-0.29	0.04	-0.01	0.09	-0.11
retoxy/met	-0.71 (0.18)	0.66 (0.20)	-0.15 (0.25)	0.30 (0.24)	0.18 (0.30)	-0.43 (0.21)	-0.61 (0.20)	0.96 (0.03)	0.02 (0.37)	-0.34 (0.22)		-0.10	-0.16	-0.10	0.08
ph24ll	-0.31 (0.18)	0.26 (0.22)	-0.28 (0.22)	0.07 (0.24)	-0.71 (0.17)	-0.48 (0.18)	-0.06 (0.24)	-0.34 (0.33)	0.25 (0.33)	0.13 (0.22)	-0.06 (0.33)		n.c.	0.54	-0.35
ph24st	-0.32 (0.28)	0.33 (0.32)	-0.45 (0.32)	-0.33 (0.39)	-0.66 (0.35)	-0.48 (0.32)	-0.14 (0.37)	-0.21 (0.53)	0.31 (0.49)	0.09 (0.36)	-0.07 (0.50)	n.c		0.30	-0.20
splph18	-0.13 (0.16)	0.20 (0.19)	0.01 (0.19)	-0.10 (0.20)	-0.36 (0.20)	-0.19 (0.18)	-0.03 (0.20)	-0.65 (0.26)	-0.10 (0.29)	0.04 (0.19)	-0.48 (0.26)	0.66 (0.16)	0.72 (0.36)		-0.96
splph6tmp	0.12 (0.15)	-0.17 (0.19)	0.02 (0.18)	0.10 (0.19)	0.29 (0.21)	0.15 (0.17)	0.05 (0.19)	0.59 (0.26)	0.06 (0.28)	0.00 (0.18)	0.42 (0.26)	-0.60 (0.18)	-0.63 (0.37)	-0.99 (0.01)	

and increase the rate of browning (-0.71, retoxy/met) of lamb during retail display. Similar responses would be observed on selection for lower shearf5 (more tender lamb), given genetic correlations of -0.69,-0.69, 0.53, -0.51 and 0.66 with cfb, cfl, reta, retl and retoxy/met, respectively. These likely responses in fresh meat colour and retail colour stability traits from selection for improved intramuscular fat and tenderness are consistent with those expected from the genetic correlations reported by Mortimer *et al.* (2014).

Redness had a positive genetic correlation yellowness of fresh meat (0.57), which agreed with the high positive estimates published for Merino lamb (see Table A2). Among the retail colour stability traits, reta and retoxy/met had a high, positive genetic correlation (0.96), which is consistent with an estimate of 0.98 ± 0.01 (Mortimer *et al.* 2014) from a multibreed population. Fresh meat lightness and yellowness were genetically correlated with retb (0.68 and 0.58, respectively), retl (0.92 and 0.70, respectively) and retoxy/met (-0.61 and -0.43). Only genetic correlations of cfl with retl and retoxy/met were consistent with estimates reported by Mortimer *et al.* (2014).

Genetic correlations of fresh meat colour with loin pH tended to be negative (-0.71, cfa; -0.48, cfb), whereas genetic correlations with retail colour stability traits were not significantly different from zero. Increasing fresh meat lightness would be expected to reduce iron content of lamb loins (-0.55). Unfavourable changes in iron content would also be associated with selection to increase retl (-0.78) and retb (-0.92).

The pH decline traits had a very high negative genetic correlation (-0.99), with splpH18 positively correlated with pH24ll (0.66) and pH24st (0.72), and splpH6tmp negatively correlated with pH24ll (-0.60) and pH24st (-0.63).

Table 6 presents estimates of genetic and phenotypic correlations of the carcass composition traits with meat quality traits. Only the genetic correlations between dp and imf (0.30), dp and zinc (-0.43) and cemw and imf (-0.30) were significantly different from zero. Similarly, genetic correlations between carcass composition and meat quality traits reported by Mortimer *et al.* (2018) tended to be less than 0.20 in size (see Table A3) and were not significantly different from zero. Consistent with the very high positive genetic correlation between hcwt and cval (0.99), genetic correlations of the meat quality traits with cval were similar to those with hcwt.

Genetic correlations of hcwt and cval with retail colour stability traits only were significantly different from zero among the estimates between the carcass composition and meat colour traits (Table 7). Hot carcass weight and cval had positive genetic correlations with reta (0.66, hcwt; 0.79, cval) and retoxy/met (0.67, hcwt; 0.79), while the genetic correlations with retl were negative (-0.35, hcwt; -0.35, cval). In a multibreed population, genetic correlations of hcwt with retail stability traits were not significantly different from zero (Mortimer *et al.* 2014). There was a trend for the carcass muscling traits to be negatively correlated with the fresh meat colour traits. Greeff *et al.* (2008) also observed negative genetic correlations between these traits (Table A3).

Very few of the genetic correlations between the pH traits and carcass composition traits were significantly different from zero (Table 8). Hot carcass weight was negatively correlated with splpH18 (-0.50) and positively correlated with splpH6tmp (0.37), while cval was negatively correlated with both pH24ll (-0.46) and splpH18 (-0.40). Low, positive genetic correlations of the carcass muscling traits with loin pH were also found by Greeff *et al.* (2008).

Table 6. Genetic and phenotypic correlation estimates (standard error in brackets) between carcass composition and meat quality traits[1] assessed on Merino carcasses

	hcwt	dp	grfat	cval	cemd	cemw	cema	cfat	elmy
Genetic correlations									
imf	-0.03	0.30	0.14	-0.07	0.09	-0.30	-0.11	0.22	-0.12
	(0.12)	(0.13)	(0.14)	(0.12)	(0.14)	(0.12)	(0.13)	(0.13)	(0.20)
shearf5	0.07	-0.20	0.01	0.07	-0.06	0.23	0.06	-0.15	-0.20
	(0.15)	(0.17)	(0.18)	(0.15)	(0.17)	(0.16)	(0.16)	(0.17)	(0.25)
iron	0.17	-0.03	0.18	0.09	0.05	-0.05	0.02	0.18	-0.36
	(0.14)	(0.17)	(0.17)	(0.14)	(0.16)	(0.16)	(0.15)	(0.16)	(0.23)
zinc	0.15	-0.43	0.02	0.16	0.09	-0.15	-0.02	-0.03	0.20
	(0.15)	(0.15)	(0.18)	(0.15)	(0.17)	(0.17)	(0.16)	(0.17)	(0.25)
Phenotypic correlations									
imf	0.05	0.11	0.10	0.02	-0.04	-0.19	-0.14	0.11	-0.17
shearf5	0.03	-0.02	-0.05	0.01	0.00	0.16	0.09	-0.10	0.08
iron	0.17	0.04	0.14	0.09	0.07	-0.03	0.04	0.07	-0.17
zinc	0.15	-0.15	0.05	0.16	0.01	-0.04	-0.01	0.00	-0.01

[1] See Table 3 for trait abbreviations.

Table 7. Genetic and phenotypic correlation estimates (standard error in brackets) between carcass composition and meat colour traits[1] assessed on Merino carcasses

	hcwt	dp	grfat	cval	cemd	cemw	cema	cfat	elmy
Genetic correlations									
cfa	0.16	0.00	-0.17	0.24	-0.04	-0.20	-0.13	-0.10	0.16
	(0.19)	(0.21)	(0.21)	(0.18)	(0.20)	(0.20)	(0.19)	(0.21)	(0.30)
cfb	-0.19	0.20	-0.06	-0.10	0.06	-0.27	-0.10	0.09	0.07
	(0.14)	(0.16)	(0.17)	(0.14)	(0.16)	(0.15)	(0.15)	(0.16)	(0.25)
cfl	-0.29	0.20	-0.09	-0.25	0.02	-0.24	-0.11	0.14	-0.03
	(0.14)	(0.17)	(0.18)	(0.14)	(0.17)	(0.16)	(0.16)	(0.17)	(0.26)
reta	0.66	0.12	-0.08	0.79	0.22	-0.17	0.05	-0.44	0.18
	(0.17)	(0.27)	(0.27)	(0.13)	(0.26)	(0.26)	(0.25)	(0.23)	(0.41)
retb	0.09	0.18	-0.16	0.29	0.00	-0.12	-0.07	-0.30	-0.16
	(0.24)	(0.25)	(0.26)	(0.23)	(0.25)	(0.25)	(0.24)	(0.24)	(0.39)
retl	-0.35	-0.01	-0.20	-0.35	-0.12	-0.13	-0.17	-0.07	0.28
	(0.13)	(0.16)	(0.17)	(0.13)	(0.16)	(0.16)	(0.15)	(0.16)	(0.24)
retoxy/met	0.67	0.10	-0.06	0.79	0.14	-0.12	0.02	-0.40	0.10
	(0.15)	(0.25)	(0.26)	(0.11)	(0.24)	(0.24)	(0.23)	(0.22)	(0.39)
Phenotypic correlations									
cfa	0.03	0.00	0.03	0.06	0.00	-0.06	-0.04	0.04	0.06
cfb	-0.16	0.04	0.04	-0.10	0.04	-0.14	-0.05	0.08	-0.05
cfl	-0.20	0.02	-0.04	-0.16	0.02	-0.09	-0.04	0.01	-0.05
reta	0.18	-0.01	-0.02	0.26	0.09	0.05	0.09	-0.02	0.17
retb	0.00	-0.01	-0.08	0.08	0.03	0.01	0.03	-0.05	0.16
retl	-0.20	-0.04	-0.08	-0.19	-0.05	-0.06	-0.08	-0.01	0.04
retoxy/met	0.20	-0.01	-0.01	0.27	0.10	0.07	0.12	-0.02	0.15

[1] See Table 3 for trait abbreviations.

Table 8. Genetic and phenotypic correlation estimates (standard error in brackets) between carcass composition and pH traits[1] assessed on Merino carcasses

	hcwt	dp	grfat	cval	cemd	cemw	cema	cfat	elmy
Genetic correlations									
pH24ll	-0.34	-0.16	-0.07	-0.46	0.19	0.34	0.31	-0.09	-0.06
	(0.21)	(0.23)	(0.24)	(0.20)	(0.22)	(0.22)	(0.21)	(0.23)	(0.36)
pH24st	0.10	-0.40	-0.69	-0.08	-0.27	0.65	0.09	-0.52	0.39
	(0.36)	(0.41)	(0.40)	(0.37)	(0.34)	(0.40)	(0.35)	(0.39)	(0.57)
splpH18	-0.50	-0.20	-0.07	-0.40	-0.29	0.18	-0.10	-0.10	-0.09
	(0.13)	(0.19)	(0.20)	(0.15)	(0.18)	(0.19)	(0.18)	(0.19)	(0.26)
splpH6tmp	0.37	0.08	-0.02	0.25	0.31	-0.16	0.14	0.06	0.22
	(0.14)	(0.18)	(0.19)	(0.16)	(0.17)	(0.18)	(0.17)	(0.18)	(0.24)
Phenotypic correlations									
pH24ll	-0.01	0.01	-0.01	-0.07	0.00	0.07	0.04	-0.06	0.00
pH24st	0.06	0.01	-0.03	0.01	0.01	0.08	0.05	-0.05	0.03
splpH18	-0.26	-0.04	-0.11	-0.21	-0.09	0.03	-0.05	-0.11	0.07
splpH6tmp	0.22	0.06	0.12	0.15	0.09	-0.03	0.05	0.10	-0.04

[1] See Table 3 for trait abbreviations.

However, Mortimer *et al.* (2018) noted that selection emphasising either one of the key traits currently used in dual purpose breeding programs may have detrimental effects on imf, meat tenderness, colour and iron content of lamb produced from Merinos. That study also identified that selection for increased elmy may have adverse effects on those meat quality traits.

4.2 Carcass value

Sire was significant for all traits at both sites ($P < 0.001$), while ewe bloodline was significant for hcwt ($P < 0.05$) and cval ($P < 0.05$) at the Trangie site only. The interaction between sire and ewe bloodline was not significant for any trait at either site.

At the Trangie site, sire adjusted means for hcwt, dp, grfat and cval ranged between 23.5±0.30 and 27.8±0.30 kg, 43.7±0.35 and 48.1±0.35%, 9.2±0.67 and 17.0±0.57 mm and $145.78±2.24 and $177.11±2.20 per head, respectively (Figure 1). Across both birth years, the averages were 25.2 kg, 45.9%, 12.5 mm and $159.06 per head for these traits, respectively. The ranges in sire adjusted means at the Armidale site, where the wethers were finished in a commercial feedlot, were 24.4±0.85 to 31.6±1.00 kg, 45.9±0.50 to 49.6±0.53%, 16.4±1.25 to 25.1±1.20 mm and $180.82±7.91 to $243.30±9.21 per head for hcwt, dp, grfat and cval, respectively (Figure 1). The average values across birth years for these traits were 28.2 kg, 47.5%, 19.7 mm and $212.49 per head, respectively. Among the sires of the 2017 born progeny at Trangie and Armidale, the ranges in cval means were $17.99 and $51.87 per head, respectively. The ranges in cval for the 2018 born progeny were $23.46 and $60.23 per head, respectively.

Due to the assumptions used in this study, carcass value was essentially determined by carcass weight (Figure 2a; unity correlation between CVAL and HCWT at both sites). However, for sires with similar adjusted means for carcass value, a range in mean carcass fat levels was evident (Figure 2b, correlations of hcwt with grfat of 0.81 at Trangie and 0.69 at Armidale).

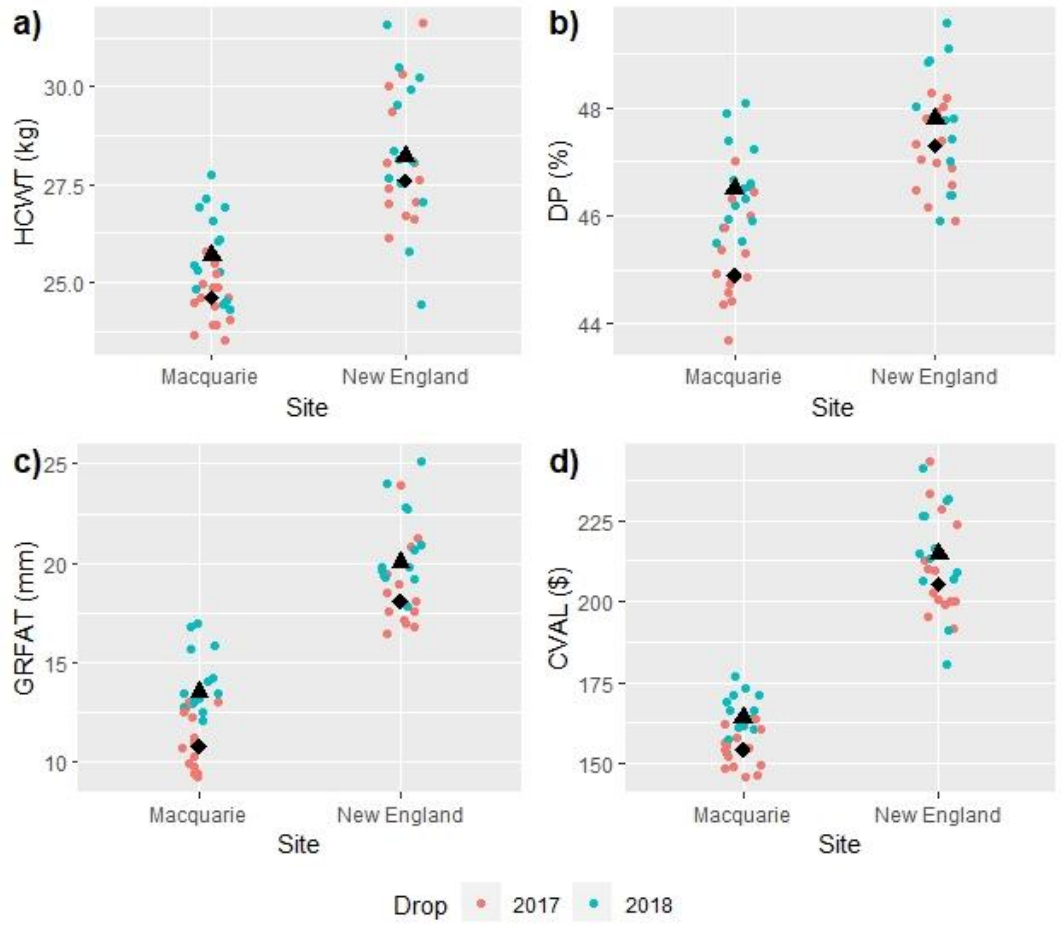

Figure 1. Adjusted sire means for a) hot carcass weight, b) dressing percentage, c) total tissue depth in mm at the 12th rib, 110mm from the backbone and d) carcass value at Trangie and Armidale sites, with black diamonds and triangles representing median values within site for 2017 and 2018 birth years respectively

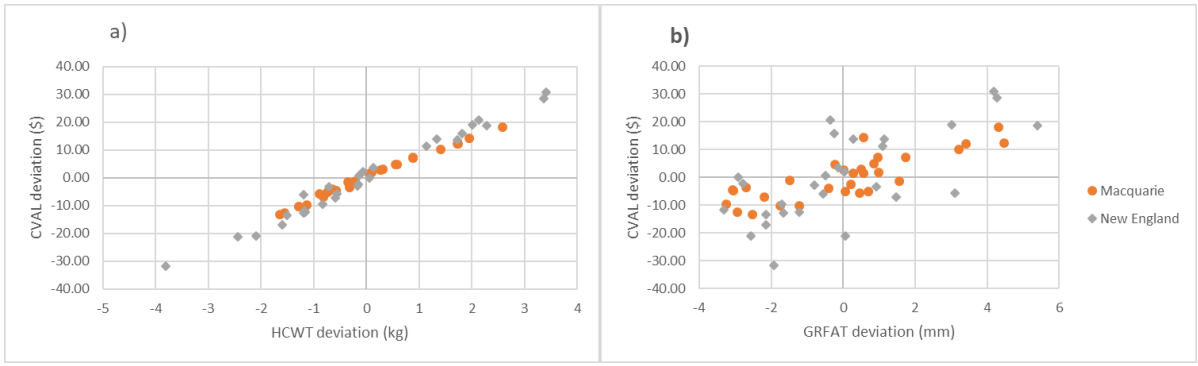

Figure 2. Deviations of adjusted sire means from the average at each site for carcass value relative to a) hot carcass weight and b) total tissue depth in mm at the 12th rib, 110mm from the backbone

Sires were only compared within site and consequently within their own finishing system, where both systems had a target liveweight of 48 kg at slaughter. This, together with the Armidale progeny

being finished under feedlot conditions, produced fatter carcasses from the Armidale wethers at the same weight and similar ages to carcasses from the Trangie wethers. Adjusted sire means for grfat were 21 mm and over for 29% of Armidale sires, versus none for Trangie sires. This contrasts with the perception that fine wool Merinos are late maturing (Hopkins *et al.* 2005) and suggests that the progeny of certain Armidale sires may not have been managed for best expression of their genetic potential for growth balanced with fat level, probably due to feedlot finishing. This was not apparent for progeny of sires at the Trangie site that were finished on pastures with supplementary feeding.

MLA market reports of OTH indicators for NSW show that during both 2018 and 2019 prices received at the time of slaughters of NE progeny were much higher than when Trangie wethers were processed (as for the feedback reports), hence their higher carcass values. Also, information was not readily available on the impact of price differentials for fat levels on carcass prices to use in predicting carcass value. In conclusion, this preliminary study has shown that considerable variation exists in carcass value of individual Merino sires when based on a simple economic model.

5. Conclusion

This project has been able to submit more than 1400 records for carcass composition and meat quality traits from Merino carcasses to the MERINOSELECT database, as well as providing live animal assessments of carcass traits to the AMSEA database. Genetic parameters were able to be estimated using the data generated by the project, which included the first significant estimates of genetic correlations for Merinos involving a range of retail colour stability traits. These estimates were associated with relatively large standard errors. However, combining the current project's data with data from the MLA Resource Flock and MLP databases will allow genetic analyses to be conducted that estimate more accurately the genetic correlations among key meat production and quality traits and other economically important traits determining profitability of Merino dual-purpose production systems. These genetic analyses will include eating quality data assessed on cuts taken from 2018 drop carcasses of the current project (under Project L.EQT.1908) and cuts taken from 2017 and 2018 drop carcasses of the MLA Resource Flock.

A simple economic model demonstrated the variation between Merino sires in carcass value, hot carcass weight, dressing percentage and GR tissue depth. Carcass value was essentially determined by hot carcass weight, as information on price differentials for fat levels of Merino lambs was not readily available to use in predicting carcass value.

5.1 Key findings

- Heritability estimates confirmed that genetic variation for many carcass composition and meat quality traits of Merinos is available to be exploited through selection to improve these traits.
- There is scope to improve intramuscular fat, retail colour stability (defined as retoxy/met) and iron and zinc contents of Merino lamb loins and pH of the topside in order to meet consumer preferences for eating quality and freshness and recommended dietary guidelines.
- Selection to improve lean meat yield will need to be balanced with improving meat quality traits due to unfavourable genetic relationships with intramuscular fat, shear force and iron content. Carcass fatness, based on its association with higher reproduction, would also need attention.

- Selection to improve either intramuscular fat or tenderness of Merino lamb will result in redder fresh meat and less dark meat after 2 days of retail display, but the meat will be less red and discolour more after 2 days of retail display. Selection to increase fresh meat lightness would have little impact on meat redness and yellowness but increase the rate of discolouration after 2 days of retail display.
- Carcass value was found to be heritable. Increasing carcass value was associated with increases in dressing percentage and carcass fatness, favourable changes in pH and meat redness under retail display, but darker and more discoloured meat after 2 days of retail display. This pattern of responses would also follow selection for increased hot carcass weight.
- Preliminary economic analyses demonstrated that carcass value among Merino sires had a range of $31.33 per head under a mixed farming system while the range under a fine wool production system was $62.48 per head.

5.2 Benefits to industry

This project has increased the number of records within the MERINOSELECT database for carcass composition and meat quality traits from Merino carcasses. By obtaining these records from the F1 wether progeny of the MLP Project at Trangie and Armidale sites, the project has increased the number of Merino sires with ASBVs for traits reported by Sheep Genetics such as intramuscular fat and shear force. These ASBVs are now available to breeders and sheep producers for use in their selection decisions aimed at improving meat and wool income from their flocks. The data are now available to be combined with Merino data from other resource flocks to enable more accurate estimation of genetic parameters for meat production and quality, including relationships with wool production, reproduction and growth traits. Subsequently, ASBVs of higher accuracy will be reported by Sheep Genetics, which will increase the accuracy of selection and lead to increased rates of genetic gain from dual purpose selection indexes applied in Merino breeding programs.

6. Future research and recommendations

Combined analyses of Merino data from across resource flocks (Information Nucleus flock, MLA Resource Flock, MLP Flock) are planned in collaboration with AGBU to improve the accuracy of genetic parameters for carcass composition and meat quality, including genetic correlations with wool production, reproduction and growth traits. These analyses will also include the eating quality data within the resource flock databases. Breed-specific and across breed analyses will be conducted to identify if the genetic parameters to be used in genetic evaluations differ across the Merino, maternal and terminal breeds. As happens now, review of the genetic parameters will occur in future due to the collection of more records. Additionally, the application of automated measurement technologies to assess lean meat yield, meat quality and eating quality in processing plants, and perhaps in live animals, will mean that genetic parameters will be needed for these new trait definitions to allow inclusion of those traits in genetic evaluations (Gardner *et al.* 2021).

Further development of Merino breeding objectives and selection indexes for dual purpose production systems should be undertaken to ensure that appropriate traits and selection strategies are provided to Merino breeders and producers to assist in better designing breeding programs to improve meat and wool production.

Future research will involve more rigorous economic analyses using the GrassGro™ software, where both returns and costs are considered for both finishing systems, wool value is included, the impacts of reproduction are evaluated and relationships with breeding values are estimated (following Hall *et al.* 1997). Furthermore, rather than relying on actual prices received at one point in time, the analyses will evaluate the sensitivity of income from carcasses to changes in the relative value of component traits.

Once the genetic parameters from this project are validated by combined genetic analyses and as breeding objectives and selection indexes for wool and meat production systems are further developed, industry application of the information should be enabled through the development and adoption activities of Sheep Genetics and activities funded by MLA and AWI.

7. Collaborations and publications arising from the project

1. Mortimer SI, Smith JL, Hine BC, Fowler SM, Holman BWB, Hopkins DL, Egerton-Warburton KL and Swan AA (Submitted for presentation at the 24th conference AAABG 2021) Variation between Merino sires in lamb carcass value. *Proceedings of the Association for the Advancement of Animal Breeding and Genetics.*

2. Comparison of colorimetric instruments for measuring lamb meat colour and their settings (loins sampled across 3 kills), led by Dr Ben Holman (NSW DPI):

> Holman BWB, Diffey SM, Logan BG, Mortimer SI and Hopkins DL (2020) Nix Pro Color Sensor Comparison to HunterLab MiniScan for Measuring Lamb Meat Colour and Investigation of Repeat Measures, Illuminant and Standard Observer Effects. *Food Analytical Methods* **14**, 697-705. https://doi.org/10.1007/s12161-020-01914-0

3. Evaluation of NIR spectroscopy to predict IMF (loins sampled across 3 kills), led by Dr Steph Fowler (NSW DPI):

> Fowler SM, Wheeler D, Morris S, Mortimer SI and Hopkins DL (2021) Partial Least Squares and Machine Learning for the prediction of intramuscular fat content of lamb loin. *Meat Science* 177, 108505 (pp. 6). https://doi.org/10.1016/j.meatsci.2021.108505

Evaluation of NIR spectroscopy will be extended to include more kills and an evaluation of Raman spectroscopy (RS) for measurement of meat quality.

4. Collection of disease information based on carcass and offal inspections on 2017 drop Armidale carcasses to link to resilience assessments under Project ON-00511 - Resilience in Merino Sheep, an AWI-funded project, led by Dr Brad Hine, CSIRO.

5. Investigation of effect of iron concentration on colour parameters and redox myoglobin fractional changes in lamb meat measured across a three day display period, led by Dr Ben Holman (NSW DPI).

6. Evaluation of the impact of kill order on pH measures, led by Dr Tharcilla Alvarenga (NSW DPI).

7. Evaluation of the significance of ewe bloodline sources and their interactions with sire effects on Merino fleece traits, visual traits, body composition and reproduction traits recorded on progeny under AWI's Merino Lifetime Productivity (MLP) 5th Site Macquarie and ON-00536 'MLPAO Macquarie wethers':

Egerton-Warburton KL, Mortimer SI and Swan AA (2019) Accounting for ewe source effects in genetic evaluation of Merino fleece traits. *Proceedings of the Association for the Advancement of Animal Breeding and Genetics* **23**, 520-523.

Mortimer SI, Egerton-Warburton KL and Swan AA (2019) Impact of ewe genotype on sire breeding values in genetic evaluation of Merino body composition and components of reproduction. *Animal Production in Australia* **33**, lxxix.

Mortimer SI, Egerton-Warburton KL and Swan AA (2019) Impact of ewe genotype on sire breeding values in genetic evaluation of Merino visual traits **33**, lxxx.

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10. Appendix

Table A1. Estimates of genetic (below diagonal) and phenotypic (above diagonal) correlations estimates for carcass composition traits[1] in Merinos reported by Mortimer *et al.* (2017a) and Greeff *et al.* (2008; second value where it occurs)

	hcwt	dp	grfat	cfat	cemw	cemd	cema	elmy
hcwt	-	0.58	0.58	0.40	0.34	0.35	0.43	-0.29
dp	0.78	-	0.43, 0.08	0.27, 0.07	0.20, 0.02	0.20, 0.06	0.24, 0.04	-0.37
grfat	0.57	0.96, 0.53	-	0.53, 0.33	0.07, -0.04	0.26, 0.13	0.24, 0.09	-0.56
cfat	0.47	0.88, 0.49	0.92, 0.67	-	-0.02, -0.10	0.15, 0.02	0.10, -0.03	-0.39
cemw	0.31	0.13, 0.26	-0.15, -0.17	-0.40, 0.21	-	0.23, 0.23	0.65, 0.64	0.26
cemd	0.39	0.42, 0.34	-0.04, 0.18	0.04, -0.08	0.38, 0.41	-	0.88, 0.88	0.12
cema	0.42	0.30, 0.36	-0.15, 0.05	-0.2, -0.17	0.83, 0.78	0.83, 0.89	-	0.22
elmy	-0.22	-0.66	-0.84	-0.80	0.58	0.46	0.63	

[1] See Table 3 for trait abbreviations.

Table A2. Estimates of genetic (below diagonal) and phenotypic (above diagonal) correlations estimates for meat quality traits[1] in Merinos reported by Mortimer *et al.* (2017a) and Greeff *et al.* (2008; second value where it occurs)

	imf	shearf5	pH24LL	pH24ST	cfa	cfb	cfl	iron	zinc
imf	-	-0.30	-0.09	-0.07	0.12	0.23	0.26	0.04	0.03
shearf5	-0.76	-	0.07	0.13	-0.14	-0.17	-0.15	-0.05	0.00
pH24LL	-0.01	-0.45	-	0.36	-0.21, -0.47	-0.18, -0.55	-0.02, -0.50	-0.09	0.03
pH24ST	-0.18	0.38	0.68	-	-0.12	-0.10	-0.07	-0.08	0.05
cfa	0.17	0.02	-0.25, -0.78	-0.19	-	0.58, 0.80	-0.06, 0.58	0.12	0.04
cfb	0.67	-0.97	-0.63, -0.94	-0.59	0.74, 0.86	-	0.33, 0.67	-0.03	0.04
cfl	0.50	-0.70	-0.23, -0.57	-0.37	0.14, 0.45	0.72, 0.81	-	-0.19	0.00
iron	0.16	-0.09	-0.21	-0.13	0.77	0.56	-0.33		0.26
zinc	0.41	-0.25	0.14	0.05	0.15	-0.24	0.07	0.10	

[1] See Table 3 for trait abbreviations.

Table A3. Genetic and phenotypic correlation estimates (standard error in brackets) between carcass composition and meat quality traits[1] reported by Mortimer *et al.* (2017b, 2018c) and Greeff *et al.* (2008; second value where it occurs)

	hcwt	dp	grfat	cfat	cemw	cemd	cema	elmy
Genetic correlations								
imf	0.04	0.15	0.16	0.10	-0.06	-0.13	-0.10	-0.27
shearf5	-0.09	-0.20	-0.53	-0.08	0.17	-0.02	0.00	0.53
iron	-0.27	0.08	-0.10	0.03	-0.25	-0.10	-0.19	-0.25
zinc	-0.04	-0.10	-0.21	0.03	-0.13	-0.12	-0.25	-0.12
pH24ll	-0.19	-0.33, -0.02	0.09, -0.06	-0.06, -0.18	-0.30, 0.15	-0.27, 0.14	-0.38, 0.17	-0.18
pH24st	-0.24	-0.03	-0.49	-0.05	-0.01	-0.27	-0.20	0.2
cfa	0.23	0.35, -0.13	0.48, -0.18	0.38, -0.17	0.03, -0.19	0.06, -0.07	0.11, -0.13	-0.69
cfb	0.27	0.27, -0.06	0.49, -0.02	0.13, -0.08	0.26, -0.47	-0.11, -0.27	0.14, -0.39	-0.32
cfl	-0.19	-0.30, -0.27	-0.16, -0.07	-0.51, 0.01	0.32, -0.37	-0.27, -0.37	0.02, -0.44	0.49
Phenotypic correlations								
imf	0.18	0.10	0.23	0.15	-0.03	0.01	-0.01	-0.25
shearf5	-0.15	-0.09	-0.18	-0.10	0.00	-0.05	-0.04	0.15
iron	0.03	0.05	0.09	0.07	0.02	0.03	0.04	-0.04
zinc	0.06	-0.02	0.02	0.03	0.06	0.01	0.04	0.00
pH24ll	-0.12	-0.03, 0.03	-0.11, -0.02	-0.11, -0.02	0.04, 0.07	-0.05, 0.06	-0.03, 0.07	0.03
pH24st	-0.08	0.05	-0.07	-0.10	-0.01	-0.03	-0.04	-0.14
cfa	0.07	0.05, -0.03	0.08, -0.02	0.04, -0.03	0.02, -0.05	0.06, -0.05	0.05, -0.06	-0.05
cfb	0.03	0.02, -0.02	0.06, -0.01	0.04, 0.00	-0.14, -0.09	0.00, -0.04	-0.17, -0.07	-0.05
cfl	-0.12	-0.13, -0.05	-0.14, -0.02	0.01, 0.00	-0.15, -0.13	-0.16, -0.10	-0.17, -0.13	0.01

[1] See Table 3 for trait abbreviations.

Table A4. Constant and regression coefficients for the terms of the prediction equation used to estimate lean meat yield (elmy, %) in Merinos (Source: GE Gardner, December 2019)

Term	Values and coefficients
Constant	60.16331799
Merino sire type	-1.28197621
Hot carcass weight (kg)	-0.75173028
Total tissue depth of fat and muscle (mm)	-0.24658775
Subcutaneous fat depth at the 12th rib (mm)	-0.09422474
Carcass eye muscle area (cm^2)	0.09863912
Weight of fat trim of the loin (g)	-0.00181367
Loin muscle weight (g)	0.01162464
Topside weight (g)	0.01085531
Round weight (g)	0.01814463
Sum of leg and aitch bone (g)	-0.00107521