# Final report

## Eating quality in Merino breeding programs

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# Abstract

To achieve a balance between improved lean meat yield (LMY), eating quality and wool production from Merino dual purpose production systems, genetic information is needed on LMY and eating quality traits of Merinos, including relationships with ewe lifetime wool production and reproduction. This would enable breeders and commercial producers to consider how best to include eating quality in their breeding programs.

Using the available eating quality data from resource flocks (the Sheep CRC's Information Nucleus, MLA Resource Flock and AWI's Merino Lifetime Productivity project), genetic parameters were estimated for the sensory eating quality traits of 3 lamb cuts (loin, topside and knuckle), including genetic and phenotypic correlations with objective eating quality, carcase composition, wool production and live animal carcase traits.

Low to moderate heritability estimates confirmed the potential to improve sensory eating quality traits of Merino lamb cuts. As genetic correlations among the sensory eating quality traits were all positive and high, both within and across cuts, selection on any one trait would improve other eating quality traits. Small, unfavourable decreases in overall liking of the cuts are expected to occur following selection for fleece weight and LMY (loins only) as well as fibre diameter (all cuts). Selection for muscling is expected to lead to small increases in the overall liking scores of all cuts, as well as small, favourable responses in intramuscular fat (yearling eye muscle depth only) and shear force values. As some of these genetic relationships differ from expected, analyses will be extended to identify if genetic group effects are influencing the results. Investment is warranted to further develop a breeding value and selection indexes that consider improvement of eating quality of Merino lamb.

# Executive summary

## Background

Dual purpose production systems are increasingly being implemented in commercial Merino flocks. Revenues are becoming increasingly important from both fleeces and potential breeding replacements, produced by ewes over their lifetime, as well as the carcases produced by surplus progeny, particularly wethers. To be able to achieve a balance between improved lean meat yield (LMY), eating quality and wool production from dual purpose production systems (Merino self-replacing flocks), accurate genetic parameter estimates are needed to develop breeding values for eating quality and LMY of Merino lambs. This would assist ram breeders and commercial producers in making selection decisions based on their target market requirements.

This report presents estimates of genetic parameters for sensory eating quality traits of 3 lamb cuts (loin, topside and knuckle), including genetic and phenotypic correlations with objective eating quality, carcase composition, wool production and live animal carcase traits. These genetic parameter estimates for eating quality and carcase composition traits of Merinos can be used to verify the appropriateness of the current genetic parameters used in Merino genetic evaluation and in the enhancement of MERINOSELECT indexes that include an emphasis on carcase traits.

## Objectives

This project, and consequently the final report, aimed to estimate genetic parameters for eating quality traits assessed on 3 Merino lamb cuts (loin, topside and knuckle), including genetic relationships with a range of Merino traits. The project also aimed to increase access to Australian Sheep Breeding Values (ASBVs) and comparative genotype information for eating quality traits of Merino sires by ram breeders and commercial producers. This aim had the intention to provide a selection index which could enable balanced selection for LMY, eating quality, wool production and reproduction in Merinos.

## Methodology

All available sensory eating quality data, as well as objective measures of eating quality and carcase composition traits, recorded on carcases produced by Merinos of the CRC for Sheep Industry Innovation's Information Nucleus flock, the MLA Resource Flock and AWI's Merino Lifetime Productivity were collated. Genetic parameters were estimated for the sensory eating quality traits of 3 lamb cuts (loin, topside and knuckle), including genetic and phenotypic correlations with objective eating quality, carcase composition, wool production and live animal carcase traits.

## Results/key findings

- Heritability estimates for sensory eating quality traits assessed on loin, topside and knuckle samples were low to moderate, confirming that selection to improve these traits assessed on a range of Merino lamb cuts is possible.
- As genetic correlations among the sensory eating quality traits were all positive and high, both within and across cuts, selection on any one trait would improve other eating quality traits.
- Irrespective of cut, better overall liking of the lamb meat would result from selection for increased intramuscular fat and lower shear force values, with responses similar in loin and topside cuts, but lower in the knuckle cut.

- Selection for fleece weight is expected to lead to small reductions in overall liking of loins (post-weaning fleece weight only) versus small improvements in overall liking of topsides and knuckles. In response to selection for reduced fibre diameter, overall liking scores of all cuts will tend to be reduced.
- Following selection for improved LMY, overall liking scores in loins are expected to decline, while scores in the topside and knuckle may be expected to increase. Unfavourable responses in intramuscular fat and shear force levels are confirmed to occur. However, too few records for LMY were available to accurately estimate these genetic correlations.
- Selection for muscling may lead to small favourable responses in overall liking scores of all cuts, as well as intramuscular fat (yearling eye muscle depth only) and shear force values. As some genetic relationships in this case differ from expected, analyses will be extended to identify if genetic group effects are influencing the results.
- While intramuscular fat and shear force values would be improved (yearling live weight only), negligible to small unfavourable responses in the overall liking scores would generally follow selection for live weight, particularly for scores of loin and topside cuts.
- Irrespective of assessed carcase fatness on live animals or on carcases, small favourable responses in intramuscular fat levels, meat tenderness and overall liking scores for loins and knuckles are expected to occur following selection for carcase fatness.
- Small, favourable responses in fleece weight (post-weaning assessment only) and mean fibre diameter are generally expected to follow selection on LMY, though coefficient of variation of diameter and staple length are expected to be altered unfavourably.

## Benefits to industry

This project, together with several other projects, has provided the data necessary to estimate genetic parameters for eating quality traits, assessed on a range of lamb cuts specifically for the Merino breed. These genetic parameter estimates will be useful in the development of a breeding value(s) for eating quality, allowing refinement of MERINOSELECT indexes to ensure that lamb produced by Merino dual purpose production systems are of acceptable quality, when eaten by consumers. For those Merino ewes mated to Terminal or Maternal sires to produce crossbred lambs, the genetic parameter estimates will provide confidence that the MERINOSELECT indexes used to generate those ewes are consistent with the eating quality objectives of the LAMBPLAN Terminal sire indexes.

## Future research and recommendations

Development of a breeding value for eating quality to include in MERINOSELECT indexes, such as the Dual Purpose+ and Dohne+ indexes, is warranted. Further investment should occur to support collaboration between geneticists and meat scientists to ensure that the appropriate information (genetic and phenotypic) and automated measurement technologies are available. This would facilitate having Merino breeding programs designed to be able to contribute to delivering lamb cuts of acceptable eating quality to consumers. This collaboration should include: 1) a framework for the effective management of eating quality data in a central database; 2) definition of the appropriate breeding objective trait; 3) development of an economic value(s) for eating quality of Merino cuts; 4) identification and evaluation of potential selection criteria traits (for the objective trait) based on automated measurements recorded on-farm and/or under the environments operating during processing of carcases in abattoirs; and 5) further recording of Merino eating quality and carcase composition data and genotyping to increase the accuracy of genetic parameters.

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# 1. Background

Incorporation of meat traits, together with traditional fine wool traits into sheep breeding programs, is being driven by continued demand for sheepmeat and changes in relative prices paid for wool and meat. Consequently, dual purpose production systems have been increasingly implemented in commercial Merino flocks, where revenues are important from fleeces. The breeding replacements produced by ewes over their lifetime and the carcases produced by surplus progeny, particularly wethers have become another potential area of revenue. In recent years, this trend has been supported by gross margin analyses, although recent wool markets have provided producers with incentives to keep finer wethers. Apart from 18 micron Merino based enterprises, a 20 micron Merino self-replacing enterprise selling trade Merino wether lambs continues to have a higher gross margin compared to other Merino based enterprises and most crossbred enterprises (Source: G. Casburn). As well as being able to identify Merino rams that suit these dual purpose production systems, commercial producers need to be able to source those rams from breeding programs that manage carcase 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” and be able to manage business risk through diversification, greater information on genetic relationships among traits is needed to use in estimating Australian Sheep Breeding Values (ASBVs) more accurately and for designing breeding programs that manage carcase fatness, reproduction and wool production in Merino based dual purpose systems, as well as eating quality and lean meat yield (LMY) traits. For Merinos, there has been very little information currently available to estimate the genetic correlations of wool and reproduction traits with sensory eating quality traits. To date, genetic correlations have been reported only for live weight, carcase and meat quality traits with wool traits in Merinos (Greeff et al. 2008; Mortimer et al. 2017a, b, c, 2018), including the objective measures of eating quality of intramuscular fat and shear force.

Continued lack of genetic information on LMY and eating quality traits of Merinos, including relationships with ewe lifetime wool production and reproduction, has prevented ram breeders and commercial producers being able to use comparative genetic information in their breeding programs (e.g. ASBVs, genotype differences). This has limited the ability to achieve a balance between improved LMY, eating quality of lamb and wool production from dual purpose production systems. To date the data collection protocols of current data sources, such as the MLA Resource Flock (RF) with its focus on meat traits, has had limited ability to provide this data.

Nevertheless, based on the current low to negligible genetic correlations estimated for Merinos, it does appear that there would be little impact on the objective eating quality traits of intramuscular fat and shear force based on selection for improved growth and wool production (Mortimer et al. 2017b, 2018). However, the low negative genetic correlation found between fleece weight and intramuscular fat suggested that Merino breeding programs should monitor intramuscular fat, where there is an emphasis on fleece weight. In addition, selection for increased LMY is expected to result in unfavourable changes in the eating quality of Merino lamb due to reductions in intramuscular fat and meat tenderness, as indicated by higher shear force values (Mortimer et al. 2018).

Recording of sensory eating quality traits on Merino wethers at several of AWI’s Merino Lifetime Productivity (MLP) sites through this project has provided data towards estimating genetic relationships of performances in reproduction, wool production and growth. Better information and tools will need quality data and the development of guidelines for collecting eating quality data on individuals in industry flocks to complement data from resource flocks. The data has also contributed to a range of studies needed for Merinos e.g. on-going support of genomic data available for genetic evaluation, particularly for hard-to-measure traits.

This final report addresses 'L.EQT.1908 Milestone 5' by collating the available sensory eating quality data, as well as objective measures, recorded on Merinos from all sources: the CRC for Sheep Industry Innovation's Information Nucleus flock; the MLA Resource Flock; and this project, which collected sensory eating quality information on 3 cuts from carcases of wethers produced at 2 sites of AWI's MLP project. The collation of the available Merino data, and subsequent analyses, have only been achieved because of the work of Dr Liselotte Pannier, Murdoch University, and Drs Andrew Swan and Sarita Guy, AGBU, in designing and establishing the lamb eating quality database as a component of the RF database.

Derived from the combined dataset, this report provides estimates of genetic parameters (heritability, genetic and phenotypic correlations) for sensory eating quality traits assessed on loin, topside and knuckle cuts. By extending the dataset to include the carcase composition and objective eating quality, wool production and live animal carcase traits recorded in these flocks, estimates of genetic parameters among and between the different trait groups are also reported.

## 2. Objectives

The final report's objective is to report genetic parameters estimated for the sensory eating quality traits of Merinos. The project's specific objectives were:

**Outcome 1:**

Provide ram breeders and commercial producers with increased access to ASBVs and comparative genotype information for eating quality traits of Merino sires by 2025.

Output 1a:

Provide phenotypic and genomic data for lamb eating quality from a minimum of 30 sires delivered to the MERINOSELECT database, for estimation of genetic parameters and inclusion in genetic evaluations by 2020.

***Achieved: Sensory eating quality data on 31 sires submitted to AGBU for entry to the lamb eating quality database under development by Drs Andrew Swan and Sarita Guy, AGBU (August 2021). Genotype data provided to the MERINOSELECT database (June 2020). Delivery of the lamb eating quality data was delayed due to its collection not being completed until 2021 (covid-19 restrictions impacting conduct of sample preparation for and conduct of tasting sessions). The data expands on the sensory and objective eating quality data generated from a range of MLA-funded projects based on the Information Nucleus/ Resource Flocks (e.g. L.GEN.1811 and L.EQT.1911).***

Output 1b:

Develop a framework and guidelines to support the collection of quality data on eating quality for the sheep industry by 2020.

***Achieved outside of this project: This is being delivered through activities such as: development of an eating quality database as part of the Sheep Genetics database redevelopment program;***

***Expression of Interest rounds to breeders to participate in the program, "MLA Resource Flock: Satellite flocks for eating quality and carcase traits"; activities under the MSA framework for sheep meat; and activities of the data quality metrics project relevant to genetic evaluation of sheep.***

**Outcome 2**:

Ram breeders and commercial producers are provided with a selection index that enables balanced selection for LMY, eating quality, wool production and reproduction in Merinos by 2025.

Output 2a:

Data on LMY, eating quality, wool production and reproduction traits is used to estimate the genetic relationships among these traits and submitted to the MerinoSelect database by 2020.

***Achieved in part: Data on sensory and objective eating quality, carcase composition and meat quality, wool production and growth traits used to estimate the genetic parameters presented in this report. Submission of data delayed due to the impacts of covid-19 on the project's data collection activities and development of the lamb eating quality database and its pipeline.***

Output 2b:

MerinoSelect reports an index value for a Merino eating quality index by 2021.

***Not achieved: Outside of this project, however, AGBU (Drs Andrew Swan and Daniel Brown) as a start to this work have examined the correlated responses in eating quality (defined as MSA grade) following selection over 10 years to a range of the current MERINOSELECT indexes (Dual Purpose+, Merino Production+, Fibre Production+ and Dohne+).***

**Outcome 3:**

Ram breeders and commercial producers have access to ASBVs for DEXA-derived and novel automated measures of carcase and meat quality traits of Merino sires by 2025.

Output 3:

As the opportunities arise, deliver to the MerinoSelect database phenotypic and genomic data on carcase composition and meat quality traits measured online in the abattoir from DEXA technology and novel technologies developed through the ALMTech project by 2020.

***Achieved in part: For this project, data on traits measured using DEXA technology were not recorded by the P.PSH.1908 project, as a processing plant with DEXA technology installed was unavailable at the time of slaughter of the progeny. Additional data collected by Dr Steph Fowler (NSW DPI), under MLA and Australian Livestock Measurement Technologies (ALMTech) funding, has been combined with project data to evaluate the ability of Near Infrared (NIR) spectroscopy to predict intramuscular fat in lamb loin cuts. The sensory eating quality will also be used to evaluate the potential of Raman spectroscopy to predict lamb meat quality and sensory properties.***

# 3. Methodology

The data used to estimate genetic parameters was derived from the Merino matings of 3 sources: the Information Nucleus flock (IN), with the design described in detail by van der Werf et al. (2010); the MLA Resource Flock (RF), details available at https://www.sheepgenetics.org.au/resources/mla-resource-flock/; and 2 sites of AWI's Merino Lifetime Productivity (MLP) project (the Macquarie and New England sites), the design is described by Ramsay et al (2019). All activities and procedures involving the animals were approved by the Animal Ethics Committee for each of the sites of the IN, RF and the MLP flocks.

## 3.1 Sensory eating quality traits

Merino eating quality data was available from sensory samples collected from the loin (l prefix in trait abbreviations), topside (t) and knuckle (k) cuts from carcases produced at the Kirby (26IN01) and Katanning (26IN08) sites of the IN (2009- and 2010-born progeny of 59 and 49 sires respectively) and the RF (2017- and 2018-born progeny of 51 and 50 sires respectively), and from the Macquarie (509312, Trangie) and New England (509313, Armidale) sites of the MLP project (2018-born progeny of 16 and 15 sires respectively). The RF data also included eating quality records collected on 2018-born progeny of 6 sires of a Merino stud (265006), where the loin cut only was sampled.

The sample collection and preparation, cooking procedures and sensory testing protocols applied to the grilled loin, topside and knuckle samples and tasted by panels of untrained consumers have been described by Pannier et al. (2014). The sensory testing protocols, which used untrained consumers, were based on those described by Thompson et al. (2005) and Watson et al. (2008) which underpin the Meat Standards Australia system and is endorsed by the UNECE.

Briefly, 5 sub-samples were prepared from each sensory sample and grilled under standardised conditions during each consumer tasting session and provided to 10 consumer. The eating quality traits were assessed by the consumers using a 0-100 scale (100 being most preferred) and included tenderness (ltend, ttend, ktend), juiciness (ljuice, tjuice, kjuice), liking of flavour (lflav, tflav, kflav) and overall liking (llike, tlike, klike) of loin, topside and knuckle samples respectively. The consumers also rated each sample according to a satisfaction score (lstar, tstar and kstar respectively). The satisfaction categories were: 2, unsatisfactory; 3, good every day quality; 4, better than every day quality; and 5, premium quality. The eating quality record for each sample was then based on the mean of the 10 consumer responses, with outliers clipped for accuracy. Table 1 summarises the data available from each flock for llike, tlike and klike, while Table 2 shows descriptive statistics for each trait.

## 3.2 Carcase composition and objective eating quality traits

Based on linkage to the sires represented in the sensory eating quality data, carcase composition and objective eating quality data for the sites/flocks were extracted from the IN/RF database. The data was extracted as adjusted trait values based on OVIS adjustment factors (AA Swan, personal communication). As appropriate, traits were pre-adjusted for the fixed effects of birth type, rearing type, age of the dam and age at measurement. The data for each trait included a contemporary group effect (defined as flock, management group, year of measurement and sex), which was modified to include the animal's date of slaughter.

Procedures used to measure the carcase composition traits in the abattoirs have been described by Gardner et al. (2010), Mortimer et al. (2017b) and Mortimer and Hopkins (2021), while measurement of the objective eating quality traits has been described by Mortimer et al. (2017c) and Mortimer and Hopkins (2021). The carcase composition traits included hot carcase weight (cwt, kg), dressing percentage (dress), carcase eye muscle depth (cemd, mm), total tissue depth at the 12th rib, 110 mm from the midline (cfat, mm), carcase fat depth at the C site measured on the cut surface between the 12th and 13th ribs over the maximum depth of the eye muscle (ccfat, mm) and predicted lean meat yield (lmy, %).

**Table 1. Number of records (n), mean, standard deviation (SD) and range for overall liking scores of the loin (llike), topside (tlike) and knuckle (klike) cuts collected from carcases from each flock[1]**

| Trait/flock | n | Mean | SD | Range |
|---|---|---|---|---|
| *llike* | | | | |
| 265006 | 71 | 64.5 | 9.484 | 46.3 - 83.0 |
| 26IN01 | 453 | 71.9 | 8.280 | 42.3 - 88.7 |
| 26IN08 | 412 | 68.5 | 8.757 | 36.9 - 86.6 |
| 509312 | 490 | 68.9 | 8.381 | 42.3 - 88.8 |
| 509313 | 183 | 69.9 | 7.850 | 49.0 - 87.6 |
| *tlike* | | | | |
| 26IN01 | 491 | 54.8 | 9.687 | 27.6 - 77.6 |
| 26IN08 | 411 | 50.3 | 9.963 | 20.8 - 79.4 |
| 509312 | 485 | 53.5 | 9.542 | 19.8 - 75.5 |
| 509313 | 189 | 51.9 | 9.023 | 28.1 - 74.3 |
| *klike* | | | | |
| 26IN01 | 217 | 62.1 | 8.073 | 40.5 - 81.9 |
| 26IN08 | 252 | 64.1 | 8.351 | 43.9 - 85.6 |
| 509312 | 491 | 65.1 | 6.985 | 40.4 - 84.2 |
| 509313 | 187 | 66.0 | 6.734 | 43.3 - 88.0 |

[1] 265006, a Merino stud; 26IN01, IN Kirby site; 26IN08, IN Katanning site; 509312, MLP Macquarie site; 509313, MLP New England site.

The objective eating quality traits were intramuscular fat (imf, %) and shear force (shearf5, N) of the loin after 5 days of ageing. The average age at slaughter of animals was 327.9 days (range of 169-440 days) with records greater than 440 days excluded from the data. A summary of the data for the carcase composition and objective eating quality traits is shown in Table 3. The number of sires represented in the data ranged between 232 (lmy) and 589 (cwt) sires.

## 3.3 Wool and live animal carcase traits

The process used to extract data for wool and live animal carcase traits from the MERINOSELECT database was similar to that used to generate the carcase composition and objective eating quality dataset, except that records were selected based on sites/flocks present in that dataset. Pre-adjusted data for fixed effects, for the standard traits used in the MERINOSELECT genetic evaluation system, were retrieved (Brown et al. 2007), as well as the contemporary group effects relevant to each trait record. The wool traits were recorded at post-weaning (p prefix) and yearling stages (y prefix) and included greasy fleece weight (pgfw and ygfw, kg), clean fleece weight (pcfw and ycfw, kg), mean fibre diameter (pfd and yfd, µm), coefficient of variation of fibre diameter (pdcv and ydcv, %), staple length (psl and ysl, mm) and staple strength (pss and yss, N/ktex). For animals with carcase composition and sensory eating quality records, post-weaning wool traits were only recorded at the 2 sites of the MLP flock. Otherwise, the post-weaning and yearling wool traits were recorded on the female siblings of those animals.

The live animal carcase traits, recorded at post-weaning and yearling stages, included body weight (pwt and ywt, kg) and ultrasound measurements at the C site (over the 12th rib, 45 mm from the midline) of eye muscle depth (pemd and yemd, mm) and subcutaneous fat depth (pcf and ycf, mm). Standard procedures were used to measure all traits, described by Mortimer et al. (2017a). Descriptive statistics for the fleece and live animal carcase traits are shown in Table 4. For pgfw and yfgw, the numbers of sires represented in the data were 287 and 363 sires, respectively.

## 3.4 Statistical methods

Variance and covariance components were estimated using ASReml (Gilmour et al. 2015). For each trait, univariate analyses were used to estimate phenotypic variances and heritability's with an animal model. Initially for each of the sensory eating quality traits, the significance of the fixed effects of birth-rearing type (single-single, multiple-single, multiple-multiple), age of dam, age at measurement and contemporary group (as defined for carcase traits in the MLA Resource Flock database, modified for slaughter group) was determined, with contemporary group only being retained in models of subsequent analyses. This was consistent with contemporary group being the only fixed effect fitted in the models to the carcase composition, meat quality, fleece and live animal carcase traits. For all traits, a direct genetic effect of animal was fitted as the random effect, with the random effects of maternal permanent environment and sire X flock interaction also evaluated for their significance in determining variation in each trait. For these analyses, the pedigree included all known ancestors, consisting of 45,766 animals across 21 generations. Genetic and phenotypic correlations among the traits were estimated from bivariate analyses.

While this report focuses on reporting estimates of genetic parameters for eating quality traits (both sensory and objective), for completeness Section 10.2 of the Appendix tabulates genetic and phenotypic correlation estimates among and between the carcase composition traits, post-weaning and yearling wool traits, and post-weaning and yearling live animal carcase traits.

# 4. Results and discussion

## 4.1 Heritability

### 4.1.1 Sensory eating quality traits

Within each cut, the sensory eating quality traits were of low to moderate heritability (Table 2). Overall liking (like) and liking of flavour (flav) of both loin and topside samples were of lower heritability (30-35% lower for like, 44-50% lower for flav) than in knuckle (0.17 ± 0.07, klike; 0.16 ± 0.07, kflav) samples. Tenderness across all cuts was moderately heritable (about 0.19). Juiciness was of low heritability in all cuts, with estimates not significantly different from zero (0.05 ± 0.04 to 0.09 ± 0.05). Heritability of consumer satisfaction score was identical in loin and topside (0.17 ± 0.06), but lower in knuckle cuts (0.13 ± 0.06). For the loin cut, heritability estimates were similar to multi-breed estimates from the IN flock (Mortimer et al. 2015; Swan et al. 2015), except for juiciness where the earlier estimate was 0.18 ± 0.07. For the topside cut, heritability estimates for all eating quality traits were much lower than the IN flock estimates. This report's estimates were lower than the estimates reported by Mortimer et al. (2015) by 47% for tflav (0.09 ± 0.05), 79% for tjuice (0.05 ± 0.04), 63% for tlike (0.11 ± 0.05) and 50% for ttend (0.18 ± 0.06). Irrespective of cut, the eating quality traits were not influenced by maternal permanent environmental effects, nor a sire X flock interaction effect.

### 4.1.2 Carcase composition and objective eating quality traits

For the carcase composition and objective eating quality traits reported herein, the heritability estimates shown in Table 3 confirm that improvement of these traits in Merinos is possible through selection. Heritability estimates for the carcase composition traits were moderate (cemd, 0.23 ± 0.04) to high (lmy, 0.56 ± 0.15). For the carcase yield (cwt, dress) and fatness (cfat, ccfat) traits, estimates were of the order of 0.40. Intramuscular fat was highly heritable (0.61 ± 0.05), while shear force was lowly heritable (0.16 ± 0.04). Heritabilities of cwt and cemd tended to be similar to Merino estimates published by Greeff et al. (2008; 0.37 ± 0.04 and 0.22 ± 0.03, respectively) and Mortimer et al. (2017b; 0.35 ± 0.10 and 0.12 ± 0.08, respectively). However, published Merino estimates for dress, cfat and ccfat were lower than those presented herein, ranging between 0.20 ± 0.03 and 0.28 ± 0.04 (Greeff et al. 2008) and 0.21 ± 0.11 and 0.29 ± 0.10 (Mortimer et al. 2017b). Predicted lmy has been reported to be of more moderate heritability by Mortimer at al. (2010, 0.34 ± 0.05 from a multi-breed population; 2017b, 0.29 ± 0.11 from a Merino population).

Though the heritability of 0.61 ± 0.05 for imf (Table 3) was consistent with published Merino estimates (0.53 ± 0.04, Mortimer et al., 2015; 0.58 ± 0.11, Mortimer et al. 2017c), it tended to be slightly higher than published multi-breed estimates (0.39 ± 0.05, Mortimer et al. 2010; 0.48 ± 0.05, Mortimer et al. 2014; 0.53 ± 0.04, Mortimer et al. 2015). In contrast, the multi-breed estimates for sf5 (0.38 ± 0.08, Mortimer et al. 2010; 0.27 ± 0.04, Mortimer et al. 2014; 0.24 ± 0.03, Mortimer et al. 2015) tended to be higher than the Merino estimates of this report (0.16 ± 0.04) and Mortimer et al. (2017c; 0.10 ± 0.09).

**Table 2. Descriptive statistics (unadjusted data) and estimates of phenotypic and additive genetic variances and heritability (standard error in brackets) for sensory eating quality traits[1] assessed on loin, topside and knuckle cuts from Merino carcases**

| | n | Mean | SD | Range | Phenotypic variance | Additive variance | Heritability |
|---|---|---|---|---|---|---|---|
| *Loin* | | | | | | | |
| ltend | 1609 | 71.9 | 9.587 | 34.4 - 92.9 | 81.65 (2.30) | 15.70 (5.23) | 0.19 (0.06) |
| ljuice | 1609 | 64.3 | 9.735 | 32.9 - 89.3 | 80.75 (2.92) | 7.33 (3.80) | 0.09 (0.05) |
| lflav | 1609 | 68.8 | 8.215 | 37.1 - 87.8 | 62.04 (2.24) | 4.74 (2.89) | 0.08 (0.05) |
| llike | 1609 | 69.6 | 8.617 | 36.9 - 88.8 | 66.11 (2.40) | 8.08 (3.48) | 0.12 (0.05) |
| lstar | 1553 | 3.7 | 0.364 | 2.6 - 4.7 | 0.12 (0.00) | 0.02 (0.01) | 0.17 (0.06) |
| *Topside* | | | | | | | |
| ttend | 1576 | 47.4 | 11.73 | 9.9 - 80.3 | 123.90 (4.59) | 22.90 (7.68) | 0.18 (0.06) |
| tjuice | 1576 | 52.9 | 10.07 | 20.2 - 85.8 | 86.61 (3.15) | 4.52 (3.65) | 0.05 (0.04) |
| tflav | 1576 | 55.6 | 8.798 | 27.4 - 79.3 | 71.70 (2.62) | 6.14 (3.51) | 0.09 (0.05) |
| tlike | 1576 | 52.9 | 9.795 | 19.8 - 79.4 | 87.25 (3.19) | 9.29 (4.49) | 0.11 (0.05) |
| tstar | 1520 | 3.0 | 0.353 | 2.1 - 4.2 | 0.12 (0.00) | 0.02 (0.01) | 0.17 (0.06) |
| *Knuckle* | | | | | | | |
| ktend | 1147 | 63.5 | 8.709 | 33.4 - 89.5 | 71.93 (3.13) | 13.53 (5.35) | 0.19 (0.07) |
| kjuice | 1147 | 64.4 | 9.210 | 25.6 - 86.6 | 68.24 (2.91) | 4.38 (3.65) | 0.06 (0.05) |
| kflav | 1147 | 63.5 | 7.321 | 40.4 - 86.9 | 50.18 (2.17) | 7.94 (3.53) | 0.16 (0.07) |
| klike | 1147 | 64.5 | 7.579 | 40.4 – 88.0 | 53.84 (2.34) | 9.22 (3.91) | 0.17 (0.07) |
| kstar | 1147 | 3.5 | 0.319 | 2.6 - 4.6 | 0.09 (0.00) | 0.01 (0.01) | 0.13 (0.06) |

[1] Sensory eating quality traits assessed on a 0-100 scale (100 being most preferred) assessed on loin ('l' prefix), topside ('t' prefix) and knuckle ('k' prefix) cuts: tend, tenderness; juice, juiciness; flav, liking of flavour; like, overall liking, Star, consumer satisfaction score : 2, unsatisfactory; 3, good everyday quality; 4, better than everyday quality; 5, premium quality.

**Table 3. Descriptive statistics (adjusted data) and estimates of phenotypic variance and heritability (standard error in brackets) for carcase composition and objective eating quality traits[1] assessed on Merino carcases**

| | n | Mean | SD | Range | Phenotypic variance | Additive variance | Heritability |
|---|---|---|---|---|---|---|---|
| cwt | 6438 | 22.01 | 3.67 | 11.0 – 40.1 | 4.97 (0.10) | 2.15 (0.27) | 0.43 (0.05) |
| dress | 3755 | 42.98 | 3.36 | 28.4 –85.9 | 6.41 (0.16) | 2.80 (0.37) | 0.44 (0.05) |
| cemd | 6170 | 27.85 | 3.81 | 16.0 – 46.0 | 10.23 (0.20) | 2.34 (0.44) | 0.23 (0.04) |
| cfat | 6373 | 12.08 | 5.28 | 0.5 – 42.0 | 11.99 (0.24) | 4.94 (0.60) | 0.41 (0.05) |
| ccfat | 6157 | 3.872 | 2.17 | 0.08 – 16.0 | 3.14 (0.06) | 1.27 (0.14) | 0.41 (0.04) |
| imf | 6109 | 4.883 | 1.38 | 0.8 – 13.7 | 1.23 (0.03) | 0.75 (0.07) | 0.61 (0.05) |
| sf5 | 5920 | 31.48 | 12.30 | 12.3 – 105.1 | 72.82 (1.44) | 11.48 (3.09) | 0.16 (0.04) |
| lmy | 730 | 58.32 | 3.10 | 49.2 - 67.1 | 5.33 (0.30) | 2.98 (0.88) | 0.56 (0.15) |

[1] cwt, hot carcass weight, kg; dress, dressing percentage; cemd, carcass eye muscle depth, mm; cfat, total tissue depth in mm at the 12th rib, 110mm from the backline; ccfat, carcass fat depth in mm at the 12th rib; imf, intramuscular fat of the loin, %; sf5, shear force after 5 days of ageing of the loin, N; lmy, predicted lean meat yield, %.

### 4.1.3 Wool and live animal carcase traits

For assessments at both the post-weaning and yearling stages, heritability was high for all wool, live weight and ultrasound traits (Table 4). There was a tendency for estimates to be higher for the fleece weights and live animal carcase traits recorded in yearlings. Compared with estimates reported by Swan et al. (2016) for yearling wool traits and post-weaning live animal carcase traits, this report’s estimates were higher than expected for the fleece weight and live animal carcase traits (0.32 ± 0.05 versus 0.56 ± 0.06 for ygfw; 0.38 ± 0.06 versus 0.55 ± 0.08 for ycfw; 0.22 ± 0.06 versus 0.32 ± 0.05 for pwt; 0.21 ± 0.05 versus 0.40 ± 0.04 for pemd; and 0.19 ± 0.04 versus 0.33 ± 0.04 for pcf, respectively). Heritability estimates for the yearling wool quality traits (yfd, ydcv, ysl and yss) tended to be more similar between the studies. Consequently, the estimates reported herein were only consistent in part with an overview of trends across published estimates for Australian Merinos by Swan et al. (2016): fibre diameter traits and staple length of high heritability; fleece weight and staple strength of moderate heritability; and live weight and ultrasound traits of low to moderate heritability. For this report’s analyses, a genetic group effect was not fitted in the model. Consequently, estimates of additive genetic variance of many of the traits would be biased, as first shown for Merino fleece weights, fibre diameter and live weight by Atkins et al. (1999).

**Table 4. Descriptive statistics (adjusted data) and estimates of phenotypic variance and heritability (standard error in brackets) for post weaning (p prefix) and yearling (y prefix) fleece and live animal carcase traits[1] assessed on Merinos**

| | n | Mean | SD | Range | Phenotypic variance | Additive variance | Heritability |
|---|---|---|---|---|---|---|---|
| pgfw | 7573 | 2.947 | 0.941 | 0.7 – 6.7 | 0.284 (0.006) | 0.12 (0.01) | 0.43 (0.04) |
| ygfw | 6544 | 3.107 | 0.867 | 0.8 – 6.6 | 0.322 (0.007) | 0.18 (0.02) | 0.56 (0.06) |
| pcfw | 7538 | 2.00 | 0.674 | 0.5 – 4.9 | 0.153 (0.003) | 0.06 (0.01) | 0.41 (0.05) |
| ycfw | 6492 | 2.198 | 0.587 | 0.6 – 5.0 | 0.186 (0.004) | 0.10 (0.02) | 0.55 (0.08) |
| pfd | 7982 | 16.42 | 1.599 | 12.2 – 22.9 | 1.35 (0.03) | 1.23 (0.07) | 0.91 (0.04) |
| yfd | 6516 | 15.88 | 1.757 | 11.4 – 33.7 | 1.67 (0.05) | 1.30 (0.10) | 0.78 (0.06) |
| pdcv | 7958 | 18.64 | 2.659 | 11.7 – 31.3 | 5.65 (0.11) | 2.01 (0.28) | 0.36 (0.05) |
| ydcv | 6522 | 18.06 | 2.501 | 11.8 – 29.6 | 5.33 (0.11) | 2.30 (0.26) | 0.43 (0.04) |
| psl | 7203 | 73.80 | 13.52 | 32.0 – 123.0 | 83.31 (1.82) | 59.60 (4.31) | 0.72 (0.04) |
| ysl | 6029 | 88.52 | 13.52 | 44.0 -163.0 | 123.04 (3.44) | 89.86 (8.34) | 0.73 (0.06) |
| pss | 7184 | 31.76 | 12.73 | 4.0 – 77.0 | 91.83 (1.92) | 44.91 (4.98) | 0.49 (0.05) |
| yss | 6012 | 32.27 | 13.17 | 4.0 – 75.0 | 80.52 (1.63) | 24.88 (3.35) | 0.31 (0.04) |
| pwt | 8659 | 35.39 | 9.691 | 10.0 – 74.60 | 22.60 (0.42) | 7.23 (1.13) | 0.32 (0.05) |
| ywt | 16052 | 40.79 | 9.281 | 14.8 – 81.0 | 23.56 (0.35) | 13.31 (1.04) | 0.57 (0.04) |
| pemd | 8825 | 22.38 | 3.858 | 10.0 – 38.0 | 6.87 (0.12) | 2.73 (0.28) | 0.40 (0.04) |
| yemd | 4852 | 22.43 | 3.476 | 12.0 – 37.0 | 4.86 (0.12) | 2.15 (0.35) | 0.44 (0.07) |
| pcf | 8820 | 2.52 | 0.932 | 0.5- 9.0 | 0.416 (0.01) | 0.14 (0.02) | 0.33 (0.04) |
| ycf | 4848 | 2.572 | 0.923 | 0.5 – 9.0 | 0.356 (0.01) | 0.14 (0.02) | 0.40 (0.05) |

[1] gfw, greasy fleece weight, kg; cfw, clean fleece weight, kg; fd, mean fibre diameter, µm; dcv, fd coefficient of variation, %; ss, staple strength, N/ktex; sl, staple length, mm; wt, live weight, kg; emd, ultrasound eye muscle depth, mm; cf, ultrasound fat depth, mm.

## 4.2 Correlations

### 4.2.1 Sensory eating quality traits

Genetic correlations within cuts were highly positive among the sensory eating quality traits (Table 5), ranging between 0.90 ± 0.08 and 0.99 ± 0.06 for loins, 0.88 ± 0.16 and 1.00 ± 0.08 for topsides and 0.80 ± 0.23 and 1.00 ± 0.06 for knuckles. The genetic correlations were consistent with those for loin and topside cuts from a multi-breed population, reported by Mortimer et al. (2015), where estimates were greater than 0.90. For both reports, phenotypic correlations were high, but slightly lower than the genetic correlations. Among traits, within a cut, phenotypic correlations were 0.75 to 0.93 for loins, 0.75 to 0.91 for topsides and 0.69 to 0.91 for knuckles (Table 5).

Genetic correlations between sensory eating quality traits of different cuts were high and positive (Table 6). Estimates within combinations of the cuts ranged between 0.66 ± 0.40 and 1.00 ± 0.14 (between traits of loins and topside), 0.55 ± 0.52 and 0.98 ± 0.31 (between traits of loins and knuckles) and 0.67 ± 0.32 and 1.00 ± 0.42 (between traits of topsides and knuckles). Many estimates were not significantly different from zero (relatively large standard errors, particularly for estimates involving juiciness), however, the estimates were generally consistent with the corresponding estimates reported by Mortimer et al. (2015). Also consistent with Mortimer et al. (2015), phenotypic correlations between sensory eating quality traits of different cuts were weak to lowly positive (see Appendix, Table A1), ranging between 0.20 and 0.30 (between traits of loins and topside), 0.16 and 0.23 (between traits of loins and knuckles) and 0.14 and 0.26 (between traits of topsides and knuckles).

Selecting Merinos for improved overall liking score in any one cut will improve overall liking of other cuts (all genetic correlation estimates ≥ 0.86), as well as other eating quality traits within that cut and in other cuts. This result is consistent with the relationships reported by Mortimer et al. (2015; e.g. llike X tlike genetic correlation of 0.93), though Swan et al. (2015) reported a genetic correlation of 0.55 between llike and tlike.

**Table 5. Genetic (below diagonal) and phenotypic (above diagonal) correlation estimates (standard errors in brackets) for sensory eating quality traits[1] assessed on loin, topside and knuckle cuts from Merino carcases**

| | tend | Juice | flav | like | star |
|---|---|---|---|---|---|
| *Loin* | | | | | |
| ltend | | 0.77 (0.01) | 0.75 (0.01) | 0.83 (0.01) | 0.77 (0.01) |
| ljuice | 0.95 (0.08) | | 0.78 (0.01) | 0.84 (0.01) | 0.76 (0.01) |
| lflav | 0.92 (0.15) | 0.92 (0.11) | | 0.93 (0.00) | 0.80 (0.01) |
| llike | 0.92 (0.12) | 0.90 (0.08) | 0.92 (0.10) | | 0.85 (0.01) |
| lstar | 0.97 (0.09) | 0.99 (0.06) | 0.91 (0.16) | 0.99 (0.06) | |
| *Topside* | | | | | |
| ttend | | 0.78 (0.01) | 0.75 (0.01) | 0.87 (0.01) | 0.81 (0.01) |
| tjuice | 0.90 (0.16) | | 0.78 (0.01) | 0.83 (0.01) | 0.76 (0.01) |
| tflav | 0.89 (0.11) | 0.96 (0.13) | | 0.91 (0.00) | 0.80 (0.01) |
| tlike | 0.98 (0.05) | 0.88 (0.16) | 0.99 (0.04) | | 0.87 (0.01) |
| tstar | 0.89 (0.06) | 0.97 (0.15) | 1.00 (0.08) | 0.99 (0.04) | |
| *Knuckle* | | | | | |
| ktend | | 0.71 (0.01) | 0.70 (0.02) | 0.82 (0.01) | 0.79 (0.01) |
| kjuice | 0.93 (0.19) | | 0.70 (0.02) | 0.79 (0.01) | 0.69 (0.02) |
| kflav | 0.89 (0.10) | 0.91 (0.21) | | 0.91 (0.01) | 0.76 (0.01) |
| klike | 0.97 (0.05) | 0.85 (0.21) | 0.95 (0.04) | | 0.84 (0.01) |
| kstar | 1.00 (0.06) | 0.80 (0.23) | 0.98 (0.06) | 0.96 (0.05) | |

[1] See Table 2 for abbreviations.

**Table 6. Genetic correlation estimates (standard errors in brackets) among sensory eating quality traits[1] between loin, topside and knuckle cuts from Merino carcases**

| | Tend | juice | flav | like | star |
|---|---|---|---|---|---|
| *Loin[2] X topside* | | | | | |
| ltend | 0.91 (0.19) | 0.93 (0.32) | 0.92 (0.21) | 0.90 (0.23) | 0.87 (0.15) |
| ljuice | 0.81 (0.22) | 0.97 (0.32) | 0.75 (0.30) | 0.83 (0.26) | 0.72 (0.23) |
| lflav | 0.87 (0.30) | 0.72 (0.44) | 0.97 (0.32) | 0.66 (0.40) | 0.89 (0.28) |
| llike | 0.89 (0.22) | 0.67 (0.40) | 0.89 (0.28) | 0.97 (0.24) | 0.92 (0.18) |
| lstar | 0.86 (0.23) | 0.80 (0.45) | 0.95 (0.28) | 0.62 (0.31) | 1.00 (0.14) |
| *Loin X knuckle* | | | | | |
| ltend | 0.67 (0.23) | 0.93 (0.54) | 0.77 (0.25) | 0.76 (0.23) | 0.76 (0.24) |
| ljuice | 0.81 (0.25) | 0.66 (0.49) | 0.93 (0.27) | 0.91 (0.24) | 0.88 (0.26) |
| lflav | 0.75 (0.30) | 0.95 (0.49) | 0.98 (0.31) | 0.91 (0.28) | 0.93 (0.27) |
| llike | 0.71 (0.25) | 0.81 (0.46) | 0.89 (0.25) | 0.86 (0.23) | 0.84 (0.24) |
| lstar | 0.82 (0.22) | 0.55 (0.52) | 0.97 (0.23) | 0.96 (0.20) | 0.97 (0.20) |
| *Topside X knuckle* | | | | | |
| ttend | 0.78 (0.22) | 0.98 (0.49) | 0.71 (0.25) | 0.86 (0.23) | 0.71 (0.26) |
| tjuice | 0.99 (0.49) | 0.92 (0.55) | 1.00 (0.42) | 0.86 (0.42) | 0.79 (0.44) |
| tflav | 0.67 (0.32) | 0.98 (0.47) | 0.74 (0.31) | 0.77 (0.30) | 0.73 (0.34) |
| tlike | 0.82 (0.29) | 0.78 (0.46) | 0.82 (0.29) | 0.91 (0.27) | 0.88 (0.31) |
| tstar | 0.73 (0.25) | 0.98 (0.51) | 0.70 (0.27) | 0.84 (0.25) | 0.87 (0.27) |

[1] See Table 2 for abbreviations.

[2] Row headings indicate first cut's traits, column headings indicate second cut's traits.

### 4.2.2 Sensory eating quality traits with carcase composition traits

Table 7 presents genetic correlations between the sensory eating quality traits of each cut with carcase composition traits. All estimates were associated with relatively large standard errors, particularly those involving lmy, where there were much fewer records (n=730). For each cut, dress and cemd tended to have slight to low positive genetic correlations with the sensory eating quality traits, though estimates were not significantly different from zero. Genetic correlations tended to be slight to low positive (favourable) of cfat and ccfat with the eating quality traits of loins and knuckles, whereas these genetic correlations were slight and negative with eating quality traits of knuckles. Lean meat yield was negatively correlated with the eating quality traits of loins, but these genetic correlations tended to be positive and low for lmy with the traits assessed on topside and knuckles.

Phenotypic correlations between the sensory eating quality traits of each cut and carcase composition traits are presented in Table A2 of the Appendix. Phenotypic correlations were negligible (less than 0.10 in size). Within each cut, overall liking tended have a low negative correlation with lmy (-0.13, -0.0 2 and -0.08 for llike, tlike and klike, respectively).

### 4.2.3 Sensory eating quality traits with objective eating quality traits

For each cut, imf and sf5 were positively and negatively correlated, respectively, with the sensory eating quality traits (Table 7). Irrespective of cut, higher (better) eating quality scores would result from selection for increased imf and lower sf5, consistent with the results of Swan et al. (2015) and Mortimer et al. (2015). For imf, a tendency of genetic correlations with scores assessed on loins (range of 0.47 ± 0.14 to 0.87 ± 0.29) being higher than on topsides (range of 0.32 ± 0.15 to 0.78 ±

0.36) was also reported by Mortimer et al. (2015). For sf5, genetic correlations with the scores assessed on both cuts were high. Across the scores, the ranges were -0.87 ± 0.29 to -0.98 ± 0.23 on loins and -0.83 ± 0.30 to -0.92 ± 0.43 on topsides. Particularly for sf5, the genetic correlations were lower for scores assessed on knuckles (range of 0.10 ± 0.29 to -0.51 ± 0.35). The corresponding phenotypic correlations within each cut were weaker than the genetic correlations (Table A2 of the Appendix), though followed the same pattern of positive and negative relationships of imf and sf5 with the sensory eating quality traits.

### 4.2.4 Sensory eating quality traits with wool traits

Tables 8 and 9 present genetic correlations between the sensory eating quality traits of each cut with post-weaning and yearling wool traits, respectively. All estimates were associated with relatively large standard errors and were not significantly different from zero. The genetic correlations of the fleece weights with the sensory eating quality traits of all cuts tended to be at most low and positive at both stages, except for negative genetic correlations with the traits of loins. Low, positive genetic correlations tended to be also found between the fibre diameter traits and staple length with the eating quality traits. It seems that selection to increase fleece weight and staple length or reduce fibre diameter would, at best, improve slightly overall liking of lamb cuts. Corresponding phenotypic correlations between the sensory eating quality traits of each cut with post-weaning wool traits are presented in Table A3 of the Appendix. The phenotypic correlations were no larger than 0.12, 0.07 and 0.08 in size for loin, topside and knuckle cuts respectively.

### 4.2.5 Sensory eating quality traits with live animal carcase traits

Genetic correlations between the sensory eating quality traits of loin cuts and post-weaning live weight tended to be negligible, while the genetic correlations for topside cuts were lowly positive and for knuckle cuts were lowly negative (Table 8). At yearling stage, these genetic correlations tended to be lowly negative (Table 9). In general, the sensory eating quality traits tended to have low positive genetic correlations with ultrasound eye muscle and fat depths recorded post-weaning and on yearlings.

**Table 7. Genetic correlation estimates (standard errors in brackets) of sensory eating quality traits[1] assessed on loin, topside and knuckle cuts from Merino carcases with carcase composition and meat quality traits[2]**

| | cwt | dress | cemd | cfat | ccfat | lmy | imf | sf5 |
|---|---|---|---|---|---|---|---|---|
| *Loin* | | | | | | | | |
| ltend | 0.05 (0.18) | 0.35 (0.22) | 0.28 (0.20) | 0.24 (0.17) | 0.06 (0.17) | -0.28 (0.31) | 0.47 (0.14) | -0.96 (0.22) |
| ljuice | 0.31 (0.23) | 0.54 (0.31) | 0.53 (0.25) | 0.38 (0.22) | 0.03 (0.22) | -0.54 (0.40) | 0.66 (0.20) | -0.87 (0.29) |
| lflav | 0.02 (0.25) | 0.62 (0.38) | 0.28 (0.28) | 0.39 (0.24) | 0.11 (0.23) | -0.44 (0.46) | 0.87 (0.29) | -0.94 (0.33) |
| llike | 0.08 (0.21) | 0.49 (0.28) | 0.31 (0.23) | 0.37 (0.19) | 0.09 (0.20) | -0.39 (0.37) | 0.64 (0.17) | -0.88 (0.29) |
| lstar | 0.04 (0.19) | 0.30 (0.24) | 0.30 (0.21) | 0.29 (0.18) | 0.21 (0.18) | -0.34 (0.33) | 0.72 (0.16) | -0.98 (0.23) |
| *Topside* | | | | | | | | |
| ttend | -0.11 (0.18) | 0.03 (0.23) | 0.22 (0.20) | 0.05 (0.17) | -0.13 (0.17) | 0.33 (0.34) | 0.32 (0.15) | -0.88 (0.21) |
| tjuice | -0.28 (0.30) | -0.53 (0.42) | 0.13 (0.36) | -0.19 (0.29) | -0.13 (0.28) | 0.00 (0.56) | 0.78 (0.36) | -0.92 (0.43) |
| tflav | -0.13 (0.23) | 0.10 (0.31) | -0.01 (0.33) | -0.03 (0.23) | -0.09 (0.23) | 0.06 (0.45) | 0.55 (0.23) | -0.89 (0.31) |
| tlike | -0.12 (0.21) | 0.10 (0.28) | 0.19 (0.25) | -0.01 (0.21) | -0.09 (0.21) | 0.31 (0.40) | 0.55 (0.20) | -0.83 (0.30) |
| tstar | -0.08 (0.19) | -0.07 (0.24) | 0.17 (0.21) | 0.01 (0.18) | -0.03 (0.18) | 0.41 (0.35) | 0.42 (0.15) | -0.74 (0.22) |
| *Knuckle* | | | | | | | | |
| ktend | -0.08 (0.20) | 0.07 (0.29) | 0.21 (0.24) | 0.21 (0.20) | -0.02 (0.20) | 0.34 (0.39) | 0.24 (0.17) | -0.34 (0.33) |
| kjuice | 0.08 (0.32) | 0.13 (0.43) | 0.46 (0.34) | 0.23 (0.32) | 0.08 (0.30) | 0.34 (0.55) | 0.85 (0.65) | 0.10 (0.48) |
| kflav | -0.09 (0.21) | 0.04 (0.30) | 0.27 (0.26) | 0.32 (0.23) | 0.26 (0.22) | -0.04 (0.41) | 0.50 (0.20) | -0.16 (0.35) |
| klike | -0.04 (0.21) | 0.00 (0.29) | 0.27 (0.25) | 0.31 (0.22) | 0.13 (0.21) | 0.18 (0.39) | 0.40 (0.18) | -0.29 (0.34) |
| kstar | -0.23 (0.22) | -0.05 (0.30) | -0.04 (0.26) | 0.28 (0.23) | 0.27 (0.22) | -0.01 (0.43) | 0.48 (0.20) | -0.51 (0.35) |

[1] See Table 2 for abbreviations.

[2] See Table 3 for abbreviations.

**Table 8. Genetic correlation estimates (standard errors in brackets) of sensory eating quality traits[1] assessed on loin, topside and knuckle cuts from Merino carcases with post weaning fleece traits[2] and live animal carcase traits**

| | pgfw | pcfw | pfd | pdcv | psl | pss | pwt | pemd | pcf |
|---|---|---|---|---|---|---|---|---|---|
| *Loin* | | | | | | | | | |
| ltend | -0.04 (0.22) | -0.19 (0.22) | 0.21 (0.19) | -0.04 0.24) | 0.13 (0.21) | -0.02 (0.25) | 0.13 (0.21) | 0.17 (0.17) | 0.20 (0.17) |
| ljuice | -0.23 (0.26) | -0.41 (0.25) | 0.26 (0.24) | 0.21 (0.31) | 0.05 (0.27) | -0.06 (0.31) | 0.01 (0.27) | 0.33 (0.22) | 0.26 (0.22) |
| lflav | -0.24 (0.28) | -0.42 (0.28) | 0.28(0.27) | 0.18 (0.35) | 0.23 (0.30) | -0.19 (0.35) | -0.01 (0.30) | 0.28 (0.23) | 0.19 (0.23) |
| llike | -0.09 (0.25) | -0.27 (0.25) | 0.24 (0.22) | 0.08 (0.28) | 0.23 (0.25) | -0.04 (0.29) | -0.02 (0.25) | 0.32 (0.19) | 0.34 (0.20) |
| lstar | -0.18 (0.22) | -0.30 (0.22) | 0.09 (0.20) | -0.12 (0.25) | 0.24 (0.22) | -0.03 (0.26) | -0.09 (0.22) | 0.29 (0.18) | 0.41 (0.17) |
| *Topside* | | | | | | | | | |
| ttend | 0.14 (0.21) | 0.05 (0.22) | 0.14 (0.18) | 0.02 (0.24) | 0.10 (0.21) | 0.34 (0.24) | 0.05 (0.21) | 0.11 (0.18) | 0.19 (0.18) |
| tjuice | 0.25 (0.35) | 0.24 (0.38) | 0.08 (0.30) | 0.08 (0.38) | 0.18 (0.35) | 0.41 (0.38) | 0.27 (0.35) | 0.07 (0.29) | 0.07 (0.29) |
| tflav | 0.39 (0.27) | 0.50 (0.29) | 0.25 (0.26) | 0.05 (0.32) | 0.30 (0.28) | 0.57 (0.30) | 0.30 (0.29) | 0.22 (0.23) | 0.24 (0.24) |
| tlike | 0.26 (0.26) | 0.26 (0.28) | 0.17 (0.23) | 0.13 (0.29) | 0.16 (0.26) | 0.51 (0.27) | 0.25 (0.26) | 0.24 (0.22) | 0.23 (0.22) |
| tstar | 0.19 (0.22) | 0.14 (0.23) | 0.25 (0.19) | 0.18 (0.25) | 0.08 (0.22) | 0.51 (0.23) | 0.16 (0.22) | 0.13 (0.19) | 0.23 (0.19) |
| *Knuckle* | | | | | | | | | |
| ktend | 0.32 (0.25) | 0.13 (0.28) | 0.13 (0.22) | -0.08 (0.29) | -0.07 (0.26) | 0.39 (0.28) | -0.12 (0.25) | 0.16 (0.22) | 0.11 (0.21) |
| kjuice | 0.20 (0.40) | 0.04 (0.43) | 0.46 (0.38) | -0.23 (0.43) | 0.10 (0.41) | 0.53 (0.41) | 0.22 (0.37) | 0.42 (0.35) | 0.24 (0.33) |
| kflav | 0.22 (0.27) | 0.03 (0.30) | 0.14 (0.23) | -0.33 (0.29) | 0.22 (0.28) | 0.43 (0.30) | -0.31 (0.26) | 0.40 (0.23) | 0.36 (0.23) |
| klike | 0.27 (0.26) | 0.06 (0.29) | 0.25 (0.23) | -0.20 (0.30) | 0.05 (0.28) | 0.46 (0.28) | -0.11 (0.26) | 0.40 (0.23) | 0.33 (0.22) |
| kstar | 0.26 (0.28) | 0.12 (0.31) | 0.00 (0.25) | -0.05 (0.32) | 0.03 (0.30) | 0.34 (0.32) | -0.23 (0.28) | 0.24 (0.24) | 0.30 (0.23) |

[1] See Table 2 for abbreviations.

[2] See Table 4 for abbreviations.

**Table 9. Genetic correlation estimates (standard errors in brackets) of sensory eating quality traits[1] assessed on loin, topside and knuckle cuts from Merino carcases with yearling fleece traits[2] and live animal carcase traits**

| | ygfw | ycfw | yfd | ydcv | ysl | yss | ywt | yemd | ycf |
|---|---|---|---|---|---|---|---|---|---|
| *Loin* | | | | | | | | | |
| ltend | 0.12 (0.20) | -0.09 (0.21) | 0.08 (0.20) | 0.26 (0.22) | 0.02 (0.20) | -0.10 (0.24) | -0.09 (0.16) | 0.17 (0.25) | 0.29 (0.23) |
| ljuice | 0.18 (0.26) | -0.03 (0.28) | 0.31 (0.27) | 0.12 (0.28) | 0.15 (0.27) | 0.17 (0.30) | 0.01 (0.22) | 0.26 (0.31) | 0.33 (0.27) |
| lflav | 0.05 (0.28) | -0.07 (0.30) | -0.04 (0.29) | 0.13 (0.31) | 0.08 (0.30) | 0.03 (0.33) | -0.19 (0.24) | 0.10 (0.34) | 0.34 (0.30) |
| llike | 0.16 (0.23) | 0.05 (0.25) | 0.01 (0.24) | 0.11 (0.25) | 0.13 (0.24) | 0.05 (0.28) | -0.14 (0.20) | 0.10 (0.29) | 0.29 (0.25) |
| lstar | -0.11 (0.21) | -0.18 (0.22) | -0.09 (0.21) | 0.19 90.23) | 0.11 (0.22) | 0.11 (0.26) | -0.15 (0.18) | 0.13 (0.26) | 0.29 (0.25) |
| *Topside* | | | | | | | | | |
| ttend | 0.13 (0.20) | 0.06 (0.21) | 0.31 (0.20) | 0.20 (0.21) | 0.06 (0.20) | -0.20 (0.22) | -0.29 (0.16) | -0.03 (0.25) | 0.16 (0.23) |
| tjuice | 0.60 (0.34) | 0.57 (0.38) | 0.21 (0.34) | 0.16 (0.34) | 0.12 (0.35) | 0.02 (0.38) | -0.26 (0.29) | -0.13 (0.40) | 0.08 (0.36) |
| tflav | 0.22 (0.28) | 0.13 (0.30) | 0.24 (0.29) | 0.24 (0.28) | 0.11 (0.29) | -0.05 (0.32) | -0.13 (0.23) | -0.15 (0.34) | -0.11 (0.31) |
| tlike | 0.29 (0.25) | 0.22 (0.27) | 0.34 (0.26) | 0.22 (0.26) | 0.17 (0.26) | -0.14 (0.28) | -0.14 (0.21) | -0.09 (0.30) | 0.07 (0.27) |
| tstar | 0.25 (0.21) | 0.14 (0.23) | 0.29 (0.21) | 0.25 (0.22) | 0.06 (0.22) | -0.05 (0.25) | -0.15 (0.17) | -0.18 (0.26) | 0.18 (0.25) |
| *Knuckle* | | | | | | | | | |
| ktend | 0.25 (0.23) | 0.16 (0.24) | 0.46 (0.21) | 0.37 (0.22) | -0.11 (0.23) | 0.10 (0.27) | -0.33 (0.19) | -0.14 (0.29) | 0.04 (0.27) |
| kjuice | 0.78 (0.35) | 0.62 (0.33) | 0.62 (0.37) | 0.41 (0.32) | 0.10 (0.36) | 0.36 (0.38) | -0.28 (0.30) | 0.04 (0.44) | 0.17 (0.40) |
| kflav | 0.40 (0.23) | 0.39 (0.24) | 0.40 (0.23) | 0.26 (0.24) | 0.03 (0.25) | 0.22 (0.27) | -0.11 (0.22) | 0.20 (0.32) | 0.31 (0.29) |
| klike | 0.40 (0.22) | 0.29 (0.25) | 0.43 (0.22) | 0.35 (0.23) | -0.09 (0.24) | 0.23 (0.27) | -0.25 (0.20) | 0.14 (0.32) | 0.21 (0.29) |
| kstar | 0.39 (0.25) | 0.42 (0.27) | 0.24 (0.26) | 0.40 (0.24) | -0.08 (0.27) | 0.19 (0.30) | -0.43 (0.22) | -0.09 (0.32) | 0.16 (0.30) |

[1] See Table 2 for abbreviations.

[2] See Table 4 for abbreviations.

### 4.2.6 Lean meat yield and eating quality traits with key production traits

Consistent with published estimates for Merinos (Mortimer et al. 2018), lmy had unfavourable negative (-0.32 ± 0.12) and positive (0.41 ± 0.22) genetic correlations with imf and sf5 (Table 10). As expected, a highly negative genetic correlation was estimated between imf and sf5 (-0.73 ± 0.09). It has been noted earlier (Section 4.2.3) that improved sensory eating quality scores would follow from selection to increase imf levels and lower sf5 values.

Predicted lean meat yield had unfavourable negative genetic correlations with all production traits (live weights, cwt, dress, eye muscle traits and carcase fat traits). For all production traits, there were low positive and negative genetic correlations with imf and sf5, respectively (Table 10) indicating that improvements in imf and sf5 would follow selection to increase these production traits. It appears that selection for growth and muscling in Merinos will lead to favourable responses in imf and meat tenderness. Except for estimates involving imf, overall the genetic correlations involving lmy and sf5 tended to be stronger than the previous Merino estimates Mortimer et al. (2017b, 2018), particularly for genetic correlations of lmy and sf5 with ywt and cwt and lmy with pemd and yemd. In the case of the genetic relationship between lmy and cemd, the estimate was low and negative (-0.09 ± 0.18) versus the previous estimate in Merinos of 0.46 ± 0.30 and an estimate of 0.10 from a multi-breed population (Swan et al. 2015).

**Table 10. Genetic correlation estimates (standard errors in brackets) of predicted lean meat yield (lmy), loin intramuscular fat (imf), loin shear force (sf5), loin overall liking (llike), topside overall liking (tlike) and knuckle overall liking (klike) with live animal and carcase composition traits**

| | lmy | imf | sf5 | llike | tlike | klike |
|---|---|---|---|---|---|---|
| imf | -0.32 (0.12) | | | | | |
| sf5 | 0.41 (0.22) | -0.73 (0.09) | | | | |
| llike | -0.39 (0.37) | 0.64 (0.17) | -0.88 (0.29) | | | |
| tlike | 0.31 (0.40) | 0.55 (0.20) | -0.83 (0.30) | 0.97 (0.24) | | |
| klike | 0.18 (0.39) | 0.40 (0.18) | -0.29 (0.34) | 0.86 (0.23) | 0.91 (0.27) | |
| pwt[1] | -0.21 (0.18) | 0.03 (0.09) | -0.10 (0.15) | -0.02 (0.25) | 0.25 (0.26) | -0.11 (0.26) |
| ywt | -0.51 (0.09) | 0.19 (0.04) | -0.26 (0.05) | -0.14 (0.20) | -0.14 (0.21) | -0.25 (0.20) |
| cwt | -0.35 (0.13) | 0.09 (0.07) | -0.25 (0.13) | 0.08 (0.21) | -0.12 (0.21) | -0.04 (0.21) |
| dress | -0.31 (0.15) | 0.22 (0.08) | -0.42 (0.13) | 0.49 (0.28) | 0.10 (0.28) | 0.00 (0.29) |
| pemd | -0.46 (0.14) | 0.05 (0.07) | -0.28 (0.12) | 0.32 (0.19) | 0.24 (0.22) | 0.40 (0.23) |
| yemd | -0.44 (0.17) | 0.15 (0.06) | -0.22 (0.13) | 0.10 (0.29) | -0.09 (0.30) | 0.14 (0.32) |
| cemd | -0.09 (0.18) | 0.02 (0.08) | -0.18 (0.16) | 0.31 (0.23) | 0.19 (0.25) | 0.27 (0.25) |
| pcf | -0.66 (0.13) | 0.17 (0.07) | -0.33 (0.13) | 0.34 (0.20) | 0.23 (0.22) | 0.33 (0.22) |
| ycf | -0.71 (0.14) | 0.17 (0.06) | -0.32 (0.12) | 0.29 (0.25) | 0.07 (0.27) | 0.21 (0.29) |
| cfat | -0.69 (0.10) | 0.22 (0.07) | -0.37 (0.12) | 0.37 (0.19) | -0.01 (0.21) | 0.31 (0.22) |
| ccfat | -0.70 (0.11) | 0.24 (0.06) | -0.44 (0.11) | 0.09 (0.20) | -0.09 (0.21) | 0.13 (0.21) |

[1] See Tables 3 and 4 for abbreviations.

Though standard errors are relatively large for the estimates involving the sensory eating quality traits in Table 10, it is evident from Table 10 that selection for lmy will result in in a deterioration of objective eating quality traits (lower levels of imf, less tender lamb), with the impact on sensory overall liking tending to vary with the cut. Overall liking scores in loins are expected to decline, but in contrast scores in the topside and knuckle are expected to increase. As well, improved overall liking scores for each cut seem likely to occur following selection for increased muscling in Merinos, versus the antagonistic relationship used when incorporating eating quality into terminal sire indexes (Swan et al. 2015). This report's estimate is also inconsistent with other studies where increased sire breeding values for pemd were associated with reduced eating quality scores of loins and topsides in a multi-breed population (Pannier et al. 2014) and of loins in progeny of Poll Dorset sires mated to Border Leicester X Merino ewes (Hopkins et al. 2005).

Irrespective of if carcase fatness is assessed on live animals or on carcases, favourable responses in imf levels, meat tenderness and overall liking scores for loins and knuckles are expected to occur following selection for carcase fatness. Positive associations between sire breeding values for pfat and tenderness scores of loins have been reported by Pannier et al. (2014) and Hopkins et al. (2007). In contrast, responses in overall liking score of topsides tend to be favourable from selection to increase ultrasound fatness but unfavourable from selection to increase carcase fatness. Negligible to small unfavourable responses in the overall liking scores would generally follow selection for live weight in Merinos (pwt, ywt), particularly for loin and topside cuts where genetic correlations ranged between -0.02 ± 0.25 and -0.25 ± 0.20. Sire breeding values for pwt have been reported to be negatively associated with eating quality scores (Pannier et al. 2014; Kirby site only of the IN) or not associated (Hopkins et al. 2005).

Small, favourable responses in fleece weight (post-weaning assessment only) and mean fibre diameter are expected to follow selection on lean meat yield, though coefficient of variation of diameter and staple length are expected to be altered unfavourably (Table 11). A similar pattern of responses was observed for these traits recorded on yearlings by Mortimer et al. (2017b). Selection for lmy is likely to have a detrimental impact on sl, based on the negative genetic correlations estimated by this study (-0.20 ± 0.17, psl; -0.43 ± 0.14) and the earlier Merino estimate (-0.22 ± 0.14, ysl; Mortimer et al 2017b).

**Table 11. Genetic correlation estimates (standard errors in brackets) of predicted lean meat yield (lmy), loin intramuscular fat (imf) and loin shear force (sf5), loin overall liking (llike), topside overall liking (tlike) and knuckle overall liking (klike) with post-weaning and yearling wool traits**

| | lmy | imf | sf5 | llike | tlike | klike |
|---|---|---|---|---|---|---|
| pgfw[1] | 0.25 (0.20) | -0.16 (0.09) | 0.04 (0.15) | -0.09 (0.25) | 0.26 (0.26) | 0.27 (0.26) |
| ygfw | -0.03 (0.15) | 0.00 (0.08) | -0.18 (0.12) | 0.16 (0.23) | 0.29 (0.25) | 0.40 (0.22) |
| pcfw | 0.26 (0.20) | -0.14 (0.10) | 0.05 (0.16) | -0.27 (0.25) | 0.26 (0.28) | 0.06 (0.29) |
| ycfw | -0.04 (0.16) | 0.07 (0.08) | -0.11 (0.14) | 0.05 (0.25) | 0.22 (0.27) | 0.29 (0.25) |
| pfd | -0.32 (0.17) | 0.04 (0.07) | 0.05 (0.12) | 0.24 (0.22) | 0.17 (0.23) | 0.25 (0.23) |
| yfd | -0.29 (0.14) | 0.03 (0.06) | -0.09 (0.12) | 0.01 (0.24) | 0.34 (0.26) | 0.43 (0.22) |
| pdcv | 0.30 (0.21) | -0.06 (0.10) | 0.09 (0.16) | 0.08 (0.28) | 0.13 (0.29) | -0.20 (0.30) |
| ydcv | 0.27 (0.17) | -0.07 (0.08) | 0.01 (0.13) | 0.11 (0.25) | 0.22 (0.26) | 0.35 (0.23) |
| psl | -0.20 (0.17) | 0.01 (0.08) | -0.13 (0.13) | 0.23 (0.25) | 0.16 (0.26) | 0.05 (0.28) |
| ysl | -0.43 (0.14) | 0.00 (0.07) | -0.19 (0.13) | 0.13 (0.24) | 0.17 (0.26) | -0.09 (0.24) |
| pss | 0.05 (0.22) | 0.07 (0.09) | -0.14 (0.16) | -0.04 (0.29) | 0.51 (0.27) | 0.46 (0.28) |
| yss | -0.09 (0.20) | -0.03 (0.09) | -0.09 (0.15) | 0.05 (0.28) | -0.14 (0.28) | 0.23 (0.27) |

[1] See Table 4 for abbreviations.

In general, selection to improve the wool production traits appears unlikely to alter imf and sf5 levels, though imf levels may be slightly reduced from selection for increased post-weaning fleece weight while sf5 levels would be improved following selection to improve yearling fleece weights.

The genetic correlations were less than 0.20 in size. Previously, Mortimer et al. (2017c) reported low to negligible genetic correlations between yearling wool production and the objective eating quality traits, concluding that wool breeding programs will have little or no effect on imf and sf5.

Across the Merino lamb cuts, there is a tendency for selection improving fleece weight to increase overall liking scores to a small extent. However, small, negative genetic correlations were found between post-weaning fleece weights and overall liking of loins. The fibre diameter distribution traits tended to have small, unfavourable genetic correlations with overall liking across the cuts, while staple length had small, favourable genetic correlations.

With few lmy records available for analyses and some genetic relationships different from those published, immediate analyses are planned to include more lmy records as they become available and the fitting of a genetic group effect in the model. As not accounting appropriately for genetic groups in models fitted to sheep data is known to bias estimates of additive genetic variances (e.g. Atkins et al. 1999), omitting a genetic group effect may have led to biases in estimates of heritability and genetic correlations. Additional modelling of the sensory eating quality data will also fit a repeatability model to the sensory eating quality traits based on the 10 individual consumer assessments for each sample of a cut, rather than defining each trait as the average of the 10 consumer responses.

# 5. Conclusion

By combining data on sensory and objective eating quality traits across available sources, this report has provided the first estimates specific to the Merino breed of heritability of sensory eating quality traits assessed on several cuts of lamb. As well, estimates are now available of genetic and phenotypic correlations of the sensory eating quality traits with carcase composition, wool production and growth traits.

## 5.1 Key findings

- Heritability estimates for sensory eating quality traits assessed on loin, topside and knuckle samples were low to moderate, confirming that selection to improve these traits assessed on a range of Merino lamb cuts is possible.
- Selection to improve any one sensory eating quality trait within a cut will improve other eating quality traits, due to highly positive genetic correlations (ranges of 0.90 to 0.99 for loins, 0.88 to 1.00 for topsides and 0.80 to 1.00 for knuckles).
- Selection on sensory eating quality traits assessed on any one meat cut can be expected to improve sensory traits of other meat cuts, due to high and positive genetic correlations.
- Irrespective of cut, better overall liking of the lamb meat would result from selection for increased intramuscular fat and lower shear force values, with responses similar in loin and topside cuts but lower in the knuckle cut.
- Selection for fleece weight is expected to lead to small reductions in overall liking of loins (pgfw and pcfw only) versus small improvements in overall liking of topsides and knuckles. In response to selection for reduced fibre diameter, overall liking scores of all cuts will tend to be reduced.
- Following selection for improved lean meat yield, overall liking scores in loins are expected to decline while scores in the topside and knuckle may be expected to increase. Unfavourable responses in intramuscular fat and shear force levels are confirmed to occur.

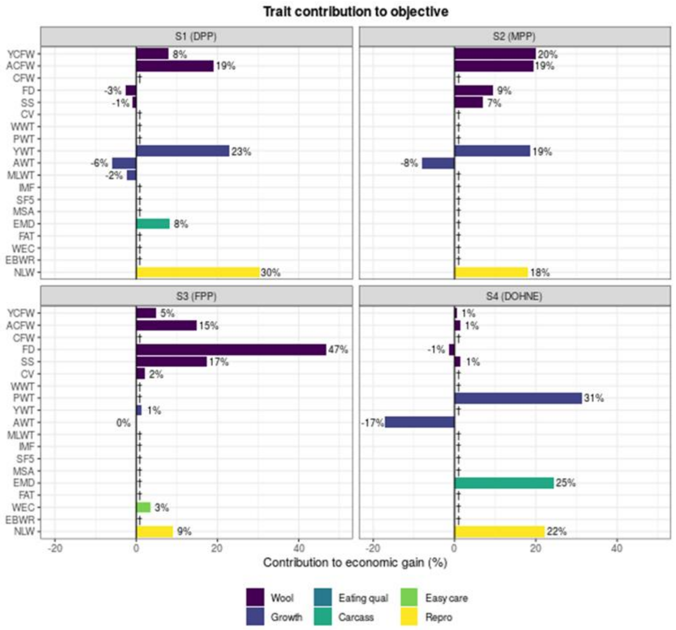
However, too few records for lean meat yield were available to estimate accurately these genetic correlations.

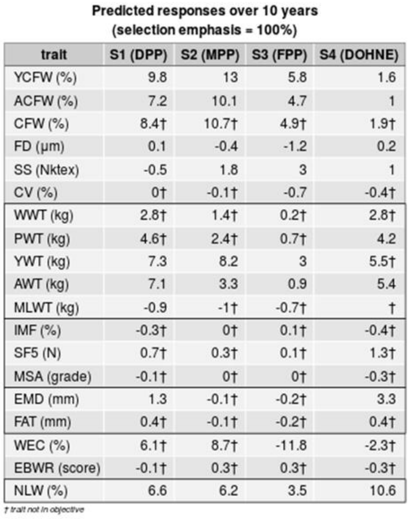
- Selection for muscling will lead to small favourable responses in overall liking scores of all cuts, as well as intramuscular fat (yemd only) and shear force values. As some genetic relationships such as in this case differ from expected, analyses will be extended to identify if genetic group effects are influencing the results.
- While intramuscular fat and shear force values would be improved (ywt only), negligible to small unfavourable responses in the overall liking scores would generally follow selection for live weight, particularly for scores of loin and topside cuts.
- Irrespective of if carcase fatness is assessed on live animals or on carcases, small favourable responses in imf levels, meat tenderness and overall liking scores for loins and knuckles are expected to occur following selection for carcase fatness.
- Small, favourable responses in fleece weight (post-weaning assessment only) and mean fibre diameter are generally expected to follow selection on lean meat yield, though coefficient of variation of diameter and staple are expected to be altered unfavourably.

## 5.2 Benefits to industry

The genetic parameters for eating quality and carcase composition traits of Merinos presented in this report can be used to verify the appropriateness of current genetic parameters used by OVIS to generate breeding values for these traits and used to design MERINOSELECT indexes. Using the current matrix of genetic parameters, the correlated responses over 10 years have been predicted for intramuscular fat, shear force and MSA grade (defined as topside overall liking) following selection on several MERINOSELECT indexes (AA Swan, personal communication; Figure 1).

**Figure 1. Predicted responses over 10 years in objective traits and correlated responses in non-objective traits of MERINOSELECT indexes (DPP, Dual Purpose+; MPP Merino Production+; FPP Fibre Production+, FPP; Dohne, Dohne+) (Source: AA Swan)**





Predicted responses over 10 years
(selection emphasis = 100%)

| trait | S1 (DPP) | S2 (MPP) | S3 (FPP) | S4 (DOHNE) |
|---|---|---|---|---|
| YCFW (%) | 9.8 | 13 | 5.8 | 1.6 |
| ACFW (%) | 7.2 | 10.1 | 4.7 | 1 |
| CFW (%) | 8.4† | 10.7† | 4.9† | 1.9† |
| FD (µm) | 0.1 | -0.4 | -1.2 | 0.2 |
| SS (Nktex) | -0.5 | 1.8 | 3 | 1 |
| CV (%) | 0† | -0.1† | -0.7 | -0.4† |
| WWT (kg) | 2.8† | 1.4† | 0.2† | 2.8† |
| PWT (kg) | 4.6† | 2.4† | 0.7† | 4.2 |
| YWT (kg) | 7.3 | 8.2 | 3 | 5.5† |
| AWT (kg) | 7.1 | 3.3 | 0.9 | 5.4 |
| MLWT (kg) | -0.9 | -1† | -0.7† | † |
| IMF (%) | -0.3† | 0† | 0.1† | -0.4† |
| SF5 (N) | 0.7† | 0.3† | 0.1† | 1.3† |
| MSA (grade) | -0.1† | 0† | 0† | -0.3† |
| EMD (mm) | 1.3 | -0.1† | -0.2† | 3.3 |
| FAT (mm) | 0.4† | -0.1† | -0.2† | 0.4† |
| WEC (%) | 6.1† | 8.7† | -11.8 | -2.3† |
| EBWR (score) | -0.1† | 0.3† | 0.3† | -0.3† |
| NLW (%) | 6.6 | 6.2 | 3.5 | 10.6 |

† trait not in objective

For the Dual Purpose+ and Dohne+ indexes, where the breeding objectives also include improvement of carcase traits, it is expected that small unfavourable decreases would occur in the eating quality traits. On the other hand, the indexes where carcase traits were not part of the breeding objective are expected to produce no detrimental changes in the eating quality traits.

With Merino breeding ewes currently making up 74% of the Australian flock, and of those 27% mated for crossbred lamb production (MLA and AWI 2021), these predicted responses in eating quality traits indicate that development of MERINOSELECT indexes that consider eating quality traits in the breeding objective is warranted. Similar to the lamb eating quality indexes for Terminal sires (Swan et al. 2015), refinement of these indexes would contribute to ensuring that lamb produced by Merino dual purpose production systems are of acceptable quality when eaten by consumers. For those Merino ewes mated to Terminal or Maternal sires to produce crossbred lambs, it would be prudent to understand if the MERINOSELECT objectives used to generate those ewes are consistent with the eating quality objectives of the LAMBPLAN Terminal sire indexes.

# 6. Future research and recommendations

Development of a breeding value for eating quality to include in MERINOSELECT indexes, such as the Dual Purpose+ and Dohne+ indexes, is warranted but requires accurate genetic parameters. While heritability estimates presented in this report have been estimated with reasonable accuracy for the consumer scores, the current and further data ( phenotypic and genomic) that are being accumulated on the sensory eating quality traits of Merino lamb, as well as data across the range of Merino production traits, should be analysed to obtain more accurate estimates of genetic correlations. Apart from contributing to a review of the Merino genetic parameters used in the OVIS software, more accurate genetic parameter estimates can be used to monitor expected responses in eating quality traits (sensory, plus intramuscular fat and shear force) from the current range of MERINOSELECT indexes.

Genetic parameters are also being estimated for the Terminal breeds (analyses conducted by Drs Sarita Guy and Andrew Swan, AGBU). More accurate genetic parameters for Merinos, would identify if different genetic parameter matrices are needed for LAMBPLAN versus MERINOSELECT genetic evaluations.

As there appears to be an impact of cut on the genetic correlations between eating quality traits and production traits, it is critical that collaboration between geneticists and meat scientists is supported to ensure that the appropriate information (genetic and phenotypic) and automated measurement technologies are available to have Merino breeding programs designed to be able to contribute to delivering lamb cuts with eating quality acceptable to consumers. This collaboration should include: a framework for the effective management of eating quality data in a central database; definition of the appropriate eating quality trait to include in the breeding objective (Swan et al. (2015) used overall liking of the topside); developing an economic value(s) for eating quality of Merino cuts; and identification and evaluation of potential selection criteria traits (for the objective trait) based on automated measurements recorded on-farm and/or under the environments operating during processing of carcases in abattoirs (intramuscular fat versus other measures such as shear force and pH decline).

With respect to the report’s parameter estimates, specific additional analyses will include estimating genetic correlations with reproduction traits. Additionally, there is an immediate need to examine the importance of genetic groups as a source of genetic variation influencing the genetic parameter estimates for the sensory eating quality traits, as well as carcase composition traits. Not including the genetic group effect in models may be impacting the analyses and leading to genetic parameter estimates that are not consistent with previous findings.

## 7. Collaborations and publications arising from the project

1. 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 and sensory eating quality.

2. Investigation of the potential of using Vis-NIR SRS to determine the eating quality of lamb, based on scans of loin, topside and knuckle cuts sampled from 50 lamb carcases, led by Dr Tharcilla Alvarenga (NSW DPI) and conducted as part of L.EQT.1905 Estimation of the age/maturity of beef and sheep using spatially resolved visible-near-infrared spectroscopy.

3. Collaboration with Drs Andrew Swan and Sarita Guy, AGBU, and Dr Liselotte Pannier, Murdoch University.

## 8. Acknowledgements

The genetic parameters reported in this final report are based on the available sensory eating quality data recorded on Merinos of several genetic resource flocks as young animals: 1) AWI's MLP flock under Project L.EQT.1908; 2) MLA's Resource Flock under Projects L.GEN.1811 and L.EQT.1911; and 3) the CRC for Sheep Industry Innovation's Information Nucleus flock. MLA are thanked for the opportunity to combine the data sets for analysis.

Dr Andrew Swan is particularly acknowledged for the discussions and guidance that have occurred in working with him on the genetics of eating quality in Merino sheep. Dr Swan extracted the phenotypic, fixed effect and pedigree data from a range of databases for each flock: the IN/RF and MERINOSELECT databases. These discussions have further benefited from inputs by Dr Sarita Guy and her work on the genetics of eating quality in Terminal breeds.

Dr David Hopkins (NSW DPI) provided key advice and information to develop the project. Dr Hopkins co-ordinated the collection of the sensory eating quality data and supervised sample collection in the abattoir.

Dr Liselotte Pannier (Murdoch University) is thanked for her advice on design of the picks for the tasting sessions, as well as preparation of the sensory eating quality for transfer to the eating quality database. As noted earlier, her work with Drs Swan and Guy on developing a data pipeline for the lamb eating quality data made possible the analyses reported herein.

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Tastepoint Pty Ltd and the University of New England Meat Science department conducted the tasting sessions. John and Janine Chalmers (Tastepoint) are very gratefully acknowledged for their high level of customer service and assistance in working to complete the tasting of the samples amid the impacts of covid-19 during 2020 and 2021.

## 8.1 L.EQT.1908 data

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## 8.2 MLA Resource Flock data

The MLA Resource Flock data were generated by projects L.GEN.1811 Sensory testing to underpin genomic prediction of lamb eating quality and L.EQT.1911. Resource Flock Sensory Evaluation and MSA Model Development (Murdoch) led by Professor David Pethick and Dr Liselotte Pannier. The contributions of staff and resources provided at the Kirby (University of New England) and Katanning (Department of Primary Industry & Regional Development (Sheep Industry Business Innovation) WA) sites are acknowledged, as well as the sensory testing conducted by Murdoch University, University of New England and Tastepoint Pty Ltd.

## 8.3 Information Nucleus flock data

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# 10. Appendix

## 10.1 Phenotypic correlations among sensory eating quality traits and with carcass composition, objective eating quality, wool and live animal carcass traits

**Table A1. Phenotypic correlation estimates among sensory eating quality traits[1] between loin, topside and knuckle cuts from Merino carcasses**

| | tend | juice | flav | like | star |
|---|---|---|---|---|---|
| *Loin[2] X topside* | | | | | |
| ltend | 0.31 | 0.25 | 0.27 | 0.30 | 0.27 |
| ljuice | 0.28 | 0.27 | 0.25 | 0.28 | 0.23 |
| lflav | 0.21 | 0.19 | 0.23 | 0.23 | 0.19 |
| llike | 0.27 | 0.24 | 0.26 | 0.29 | 0.23 |
| lstar | 0.26 | 0.22 | 0.26 | 0.27 | 0.26 |
| *Loin X knuckle* | | | | | |
| ltend | 0.23 | 0.18 | 0.18 | 0.20 | 0.18 |
| ljuice | 0.22 | 0.20 | 0.16 | 0.19 | 0.16 |
| lflav | 0.19 | 0.17 | 0.17 | 0.19 | 0.18 |
| llike | 0.22 | 0.19 | 0.19 | 0.21 | 0.20 |
| lstar | 0.20 | 0.16 | 0.17 | 0.20 | 0.20 |
| *Topside X knuckle* | | | | | |
| ttend | 0.26 | 0.16 | 0.16 | 0.19 | 0.21 |
| tjuice | 0.22 | 0.19 | 0.16 | 0.20 | 0.19 |
| tflav | 0.19 | 0.14 | 0.15 | 0.17 | 0.17 |
| tlike | 0.24 | 0.17 | 0.17 | 0.20 | 0.20 |
| tstar | 0.22 | 0.14 | 0.13 | 0.17 | 0.18 |

[1] See Table 2 for abbreviations.

[2] Row headings for first cut's traits, column headings for second cut's traits.

**Table A2. Phenotypic correlation estimates of sensory eating quality traits[1] assessed on loin, topside and knuckle cuts from Merino carcasses with carcass composition and objective eating quality traits[2]**

| | cwt | dress | cemd | cfat | ccfat | lmy | imf | sf5 |
|---|---|---|---|---|---|---|---|---|
| *Loin* | | | | | | | | |
| ltend | 0.04 (0.03) | 0.03 (0.04) | 0.01 (0.03) | 0.08 (0.03) | 0.02 (0.03) | -0.12 (0.06) | 0.21 (0.02) | -0.42 (0.02) |
| ljuice | 0.05 (0.03) | -0.03 (0.04) | 0.02 (0.03) | 0.06 (0.03) | 0.01 (0.03) | -0.09 (0.07) | 0.25 (0.02) | -0.31 (0.02) |
| lflav | 0.04 (0.03) | -0.02 (0.04) | 0.01 (0.03) | 0.08 (0.03) | 0.04 (0.03) | -0.09 (0.07) | 0.22 (0.02) | -0.29 (0.03) |
| llike | 0.05 (0.03) | -0.02 (0.04) | 0.02 (0.03) | 0.08 (0.03) | 0.04 (0.03) | -0.13 (0.06) | 0.24 (0.02) | -0.34 (0.02) |
| lstar | 0.05 (0.03) | -0.02 (0.04) | 0.02 (0.03) | 0.08 (0.03) | 0.03 (0.03) | -0.08 (0.07) | 0.26 (0.02) | -0.39 (0.02) |
| *Topside* | | | | | | | | |
| ttend | -0.07 (0.03) | 0.02 (0.04) | 0.03 (0.03) | 0.00 (0.03) | -0.01 (0.03) | -0.01 (0.07) | 0.09 (0.03) | -0.33 (0.02) |
| tjuice | -0.04 (0.03) | -0.03 (0.04) | 0.03 (0.03) | 0.00 (0.03) | -0.02 (0.03) | 0.00 (0.07) | 0.11 (0.02) | -0.23 (0.03) |
| tflav | -0.04 (0.03) | 0.00 (0.04) | 0.05 (0.03) | 0.01 (0.03) | -0.02 (0.03) | -0.03 (0.07) | 0.09 (0.02) | -0.25 (0.03) |
| tlike | -0.04 (0.03) | -0.01 (0.04) | 0.04 (0.03) | 0.01 (0.03) | -0.01 (0.03) | -0.02 (0.07) | 0.10 (0.02) | -0.29 (0.03) |
| tstar | -0.05 (0.03) | -0.04 (0.04) | 0.03 (0.03) | 0.01 (0.03) | -0.03 (0.03) | -0.04 (0.07) | 0.10 (0.03) | -0.28 (0.03) |
| *Knuckle* | | | | | | | | |
| ktend | -0.10 (0.03) | -0.07 (0.05) | -0.02 (0.03) | 0.03 (0.03) | -0.03 (0.03) | -0.08 (0.07) | 0.06 (0.03) | -0.12 (0.03) |
| kjuice | -0.03 (0.03) | -0.09 (0.05) | 0.00 (0.03) | 0.04 (0.03) | -0.04 (0.03) | -0.07 (0.06) | 0.09 (0.03) | -0.09 (0.03) |
| kflav | -0.06 (0.03) | -0.04 (0.05) | 0.00 (0.03) | 0.03 (0.03) | 0.00 (0.03) | -0.05 (0.07) | 0.07 (0.03) | -0.06 (0.03) |
| klike | -0.05 (0.03) | -0.07 (0.05) | 0.01 (0.03) | 0.06 (0.03) | -0.01 (0.03) | -0.08 (0.07) | 0.08 (0.03) | -0.07 (0.03) |
| kstar | -0.08 (0.03) | -0.08 (0.05) | -0.06 (0.03) | 0.03 (0.03) | -0.02 (0.03) | -0.08 (0.07) | 0.07 (0.03) | -0.12 (0.03) |

[1] See Table 2 for abbreviations.

[2] See Table 3 for abbreviations.

**Table A3. Phenotypic correlation estimates (standard errors in brackets) of sensory eating quality traits$^1$ assessed on loin, topside and knuckle cuts from Merino carcasses with post weaning fleece traits$^2$ and live animal carcass traits**

| | pgfw | pcfw | pfd | pdcv | psl | pss | pwt | pemd | pcf |
|---|---|---|---|---|---|---|---|---|---|
| *Loin* | | | | | | | | | |
| ltend | -0.10 (0.04) | -0.10 (0.04) | 0.05 (0.04) | 0.03 (0.04) | -0.04 (0.05) | 0.03 (0.05) | 0.02 (0.04) | 0.02 (0.03) | 0.07 (0.03) |
| ljuice | -0.10 (0.04) | -0.10 (0.04) | 0.01 (0.04) | 0.03 (0.04) | -0.09 (0.04) | 0.01 (0.05) | 0.04 (0.04) | 0.04 (0.03) | 0.06 (0.03) |
| lflav | -0.11 (0.04) | -0.11 (0.04) | 0.04 (0.04) | 0.07 (0.04) | -0.07 (0.05) | 0.02 (0.05) | 0.02 (0.04) | 0.03 (0.03) | 0.07 (0.03) |
| llike | -0.09 (0.04) | -0.09 (0.04) | 0.04 (0.04) | 0.05 (0.04) | -0.06 (0.05) | 0.04 (0.05) | 0.04 (0.04) | 0.04 (0.03) | 0.08 (0.03) |
| lstar | -0.11 (0.04) | -0.12 (0.04) | 0.06 (0.04) | 0.06 (0.04) | -0.04 (0.05) | 0.07 (0.05) | 0.03 (0.04) | 0.03 (0.03) | 0.07 (0.03) |
| *Topside* | | | | | | | | | |
| ttend | -0.01 (0.04) | -0.02 (0.04) | 0.02 (0.04) | 0.04 (0.04) | 0.04 (0.05) | -0.01 (0.05) | -0.03 (0.04) | -0.04 (0.03) | 0.00 (0.03) |
| tjuice | 0.00 (0.04) | 0.00 (0.04) | -0.02 (0.04) | -0.01 (0.04) | 0.04 (0.04) | 0.01 (0.05) | -0.02 (0.04) | -0.03 (0.03) | 0.01 (0.03) |
| tflav | 0.00 (0.04) | 0.00 (0.04) | 0.03 (0.04) | 0.02 (0.04) | 0.01 (0.05) | -0.02 (0.05) | -0.01 (0.04) | -0.04 (0.03) | 0.01 (0.03) |
| ltike | -0.02 (0.04) | -0.02 (0.04) | 0.01 (0.04) | 0.00 (0.04) | 0.03 (0.05) | -0.03 (0.05) | -0.02 (0.04) | -0.04 (0.03) | 0.00 (0.03) |
| tstar | -0.01 (0.04) | -0.02 (0.04) | 0.01 (0.04) | 0.07 (0.04) | 0.01 (0.05) | -0.03 (0.05) | -0.04 (0.04) | -0.06 (0.03) | -0.02 (0.03) |
| *Knuckle* | | | | | | | | | |
| ktend | -0.01 (0.04) | -0.03 (0.04) | 0.01 (0.04) | -0.03 (0.04) | -0.03 (0.05) | -0.01 (0.06) | -0.04 (0.05) | 0.01 (0.03) | 0.00 (0.03) |
| kjuice | -0.04 (0.04) | -0.05 (0.04) | 0.01 (0.04) | -0.10 (0.05) | -0.01 (0.05) | -0.03 (0.06) | 0.00 (0.04) | 0.04 (0.03) | 0.03 (0.03) |
| kflav | -0.04 (0.04) | -0.06 (0.04) | -0.01 (0.04) | -0.07(0.04) | -0.04 (0.05) | -0.03 (0.06) | -0.08 (0.05) | 0.01 (0.03) | 0.03 (0.03) |
| klike | -0.04 (0.04) | -0.06 (0.04) | 0.03 (0.04) | -0.07 (0.04) | -0.04 (0.05) | -0.02 (0.06) | -0.02 (0.05) | 0.03 (0.03) | 0.04 (0.03) |
| kstar | -0.03 (0.04) | -0.03 (0.04) | -0.01 (0.04) | 0.02 (0.04) | -0.03 (0.05) | -0.03 (0.06) | -0.05 (0.05) | 0.00 (0.03) | 0.01 (0.03) |

[1] See Table 2 for abbreviations.

[2] See Table 4 for abbreviations.

## 10.2 Genetic and phenotypic correlations among and between carcass composition, objective eating quality, wool and live animal carcass traits

**Table A4. Genetic (below diagonal, standard errors in brackets) and phenotypic (above diagonal) correlation estimates for carcass composition and objective eating quality traits[1] assessed on Merino carcasses**

| | cwt | dress | cemd | cfat | ccfat | lmy | imf | sf5 |
|---|---|---|---|---|---|---|---|---|
| cwt | | 0.60 (0.01) | 0.36 (0.01) | 0.52 (0.01) | 0.34 (0.01) | -0.39 (0.03) | 0.12 (0.01) | -0.11 (0.01) |
| dress | 0.80 (0.04) | | 0.22 (0.02) | 0.44 (0.01) | 0.32 (0.02) | -0.32 (0.04) | 0.13 (0.02) | -0.11 (0.02) |
| cemd | 0.57 (0.09) | 0.55 (0.10) | | 0.23 (0.01) | 0.10 (0.01) | -0.08 (0.04) | -0.01 (0.01) | -0.05 (0.01) |
| cfat | 0.55 (0.06) | 0.78 (0.06) | 0.33 (0.10) | | 0.44 (0.01) | -0.57 (0.02) | 0.19 (0.01) | -0.14 (0.01) |
| ccfat | 0.48 (0.06) | 0.75 (0.06) | 0.21 (0.09) | 0.83 (0.05) | | -0.52 (0.03) | 0.14 (0.01) | -0.11 (0.01) |
| lmy | -0.35 (0.13) | -0.31 (0.15) | -0.09 (0.18) | -0.69 (0.10) | -0.70 (0.11) | | -0.33 (0.03) | 0.18 (0.04) |
| imf | 0.09 (0.07) | 0.22 (0.08) | 0.02 (0.08) | 0.22 (0.07) | 0.24 (0.06) | -0.32 (0.12) | | -0.25 (0.01) |
| sf5 | -0.25 (0.13) | -0.42 (0.13) | -0.18 (0.16) | -0.37 (0.12) | -0.44 (0.11) | 0.41 (0.22) | -0.73 (0.09) | |

[1] See Table 3 for abbreviations.

**Table A5. Genetic (below diagonal, standard errors in brackets) and phenotypic (above diagonal) correlation estimates for post weaning fleece and live animal carcass traits[1]**

| | pgfw | pcfw | pfd | pdcv | psl | pss | pwt | pemd | pcf |
|---|---|---|---|---|---|---|---|---|---|
| pgfw | | 0.93 (0.00) | 0.18 (0.01) | 0.03 (0.01) | 0.31 (0.01) | 0.09 (0.01) | 0.43 (0.03) | 0.15 (0.02) | 0.07(0.02) |
| pcfw | 0.96 (0.01) | | 0.20 (0.01) | 0.00 (0.01) | 0.35 (0.01) | 0.14 (0.02) | 0.43 (0.03) | 0.15 (0.02) | 0.08 (0.02) |
| pfd | 0.34 (0.05) | 0.38 (0.05) | | -0.12 (0.01) | 0.35 (0.01) | 0.21 (0.01) | 0.27 (0.03) | 0.20 (0.02) | 0.20 (0.02) |
| pdcv | 0.25 (0.08) | 0.16 (0.09) | -0.17 (0.06) | | -0.17 (0.01) | -0.35 (0.01) | -0.13 (0.04) | -0.21 (0.02) | -0.10 (0.02) |
| psl | 0.43 (0.05) | 0.47 (0.05) | 0.42 (0.04) | -0.26 (0.07) | | 0.07 (0.02) | 0.18 (0.05) | 0.18 (0.02) | 0.14 (0.02) |
| pss | 0.09 (0.07) | 0.24 (0.08) | 0.27 (0.05) | -0.61 (0.06) | 0.08 (0.06) | | 0.10 (0.05) | 0.10 (0.02) | 0.05 (0.020 |
| pwt | 0.28 (0.09) | 0.25 (0.10) | 0.41 (0.08) | -0.24 (0.11) | 0.43 (0.09) | -0.26 (0.11) | | 0.52 (0.01) | 0.42 (0.02) |
| pemd | 0.14 (0.08) | 0.08 (0.09) | 0.29 (0.06) | -0.30 (0.09) | 0.32 (0.07) | 0.06 (0.09) | 0.68 (0.06) | | 0.53 (0.01) |
| pcf | 0.04 (0.08) | 0.02 (0.09) | 0.37 (0.07) | -0.34 (0.10) | 0.27 (0.08) | 0.07 (0.10) | 0.49 (0.08) | 0.79 (0.04) | |

[1] See Table 4 for abbreviations.

**Table A6. Genetic (below diagonal, standard errors in brackets) and phenotypic (above diagonal) correlation estimates for yearling fleece and live animal carcass traits[1]**

| | ygfw | ycfw | yfd | Ydcv | ysl | yss | ywt | yemd | ycf |
|---|---|---|---|---|---|---|---|---|---|
| ygfw | | 0.94 (0.00) | 0.15 (0.02) | 0.03 (0.02) | 0.31 (0.02) | 0.13 (0.02) | 0.49 (0.01) | 0.13 (0.03) | 0.06 (0.03) |
| ycfw | 0.94 (0.01) | | 0.16 (0.02) | -0.01 (0.02) | 0.36 (0.02) | 0.18 (0.02) | 0.48 (0.01) | 0.12 (0.03) | 0.06 (0.03) |
| yfd | 0.16 (0.06) | 0.16 (0.07) | | -0.05 (0.02) | 0.26 (0.02) | 0.16 (0.02) | 0.27 (0.02) | 0.20 (0.03) | 0.19(0.03) |
| ydcv | 0.22 (0.07) | 0.21 (0.08) | 0.08 (0.07) | | -0.18 (0.02) | -0.37 (0.01) | -0.10 (0.02) | -0.12 (0.03) | -0.10 (0.03) |
| ysl | 0.41 (0.06) | 0.46 (0.07) | 0.34 (0.06) | -0.10 (0.07) | | 0.10 (0.02) | 0.26 (0.02) | 0.17 (0.03) | 0.15 (0.03) |
| yss | 0.13 (0.08) | 0.20 (0.09) | 0.19 (0.08) | -0.59 (0.06) | 0.04 (0.08) | | 0.05 (0.08) | -0.02 (0.03) | -0.01 (0.03) |
| ywt | 0.47 (0.06) | 0.46 (0.07) | 0.40 (0.06) | -0.03 (0.07) | 0.28 (0.06) | -0.11 (0.08) | | 0.54 (0.01) | 0.47 (0.01) |
| yemd | 0.16 (0.11) | 0.11 (0.13) | 0.49 (0.12) | -0.23 (0.11) | 0.39 (0.12) | 0.08 (0.13) | 0.73 (0.05) | | 0.52 (0.01) |
| ycf | -0.03 (0.10) | 0.07 (0.11) | 0.54 (0.10) | -0.18 (0.11) | 0.53 (0.10) | -0.03 (0.13) | 0.65 (0.05) | 0.87 (0.05) | |

[1] See Table 4 for abbreviations.

**Table A7. Genetic correlation estimates (standard errors in brackets) of post weaning fleece and live animal carcass traits with carcass composition and objective eating quality traits[1]**

| | cwt | dress | cemd | cfat | ccfat | lmy | imf | sf5 |
|---|---|---|---|---|---|---|---|---|
| pgfw | 0.30 (0.09)nc | -0.19 (0.10) | 0.05 (0.12) | 0.01 (0.10)nc | 0.01 (0.09) | 0.25 (0.20) | -0.16 (0.09) | 0.04 (0.15) nc |
| pcfw | 0.31 (0.09) | -0.18 (0.10) | 0.12 (0.13) | -0.06 (0.10) | 0.00 (0.10) | 0.26 (0.20) | -0.14 (0.10) | 0.05 (0.16) |
| pfd | 0.48 (0.07) | 0.24 (0.08) | 0.47 (0.10) | 0.28 (0.08) | 0.14 (0.08) | -0.32 (0.17) | 0.04 (0.07) | 0.05 (0.12) |
| pdcv | -0.22 (0.10) | -0.43 (0.10) | -0.44 (0.10) | -0.34 (0.10) | -0.28 (0.10) | 0.30 (0.21) | -0.06 (0.10) | 0.09 (0.16) |
| psl | 0.49 (0.08) | 0.34 (0.09) | 0.27 (0.11) | 0.31 (0.08) | 0.28 (0.08) | -0.20 (0.17) | 0.01 (0.08) | -0.13 (0.13) |
| pss | -0.04 (0.10) | -0.02 (0.11) | 0.26 (0.13) | -0.14 (0.11) | -0.10 (0.11) | 0.05 (0.22) | 0.07 (0.09) | -0.14 (0.16) |
| pwt | 0.87 (0.04)nc | 0.45 (0.10) | 0.51 (0.11) | 0.39 (0.09) | 0.30 (0.09) | -0.21 (0.18) | 0.03 (0.09) | -0.10 (0.15) |
| pemd | 0.67 (0.06) | 0.64 (0.07) | 0.80 (0.08) | 0.65 (0.07) | 0.52 (0.07) | -0.46 (0.14) | 0.05 (0.07) | -0.28 (0.12) |
| pcf | 0.64 (0.07) | 0.77 (0.07) | 0.44 (0.11) | 0.81 (0.06) | 0.82 (0.06) | -0.66 (0.13) | 0.17 (0.07) | -0.33 (0.13) |

[1] See Tables 3 and 4 for abbreviations; nc, log likelihood not converged.

**Table A8. Phenotypic correlation estimates (standard errors in brackets) of post weaning fleece and live animal carcass traits with carcass composition and objective eating quality traits[1]**

| | cwt | dress | cemd | cfat | ccfat | lmy | imf | sf5 |
|---|---|---|---|---|---|---|---|---|
| pgfw | 0.15 (0.02)nc | -0.07 (0.05) | 0.09 (0.02) | 0.00 (0.02)nc | 0.02 (0.02) | -0.07 (0.13) | -0.05 (0.02) | 0.03 (0.03)nc |
| pcfw | 0.15 (0.02) | 0.02 (0.05) | 0.09 (0.03) | 0.00 (0.02) | 0.04 (0.02) | -0.06 (0.12) | -0.04 (0.02) | 0.01 (0.03) |
| pfd | 0.20 (0.02) | 0.19 (0.04) | 0.12 (0.02) | 0.16 (0.02) | 0.08 (0.02) | -0.08 (0.11) | 0.03 (0.02) | 0.02 (0.03) |
| pdcv | -0.11 (0.02) | -0.40 (0.04) | -0.40 (0.04) | -0.10 (0.02) | -0.09 (0.02) | 0.17 (0.13) | -0.03 (0.03) | 0.01 (0.03) |
| psl | 0.17 (0.03) | 0.17 (0.05) | 0.08 (0.03) | 0.14 (0.03) | 0.05 (0.03) | 0.04 (0.12) | 0.01 (0.03) | -0.02 (0.03) |
| pss | -0.02 (0.03) | 0.08 (0.05) | 0.13 (0.03) | -0.03 (0.03) | -0.03 (0.03) | -0.09 (0.11) | -0.04 (0.03) | 0.00 (0.04) |
| pwt | 0.68 (0.01)nc | 0.18 (0.03) | 0.22 (0.02) | 0.29 (0.02) | 0.20 (0.02) | -0.34 (0.05) | 0.11 (0.02) | -0.04 (0.02) |
| pemd | 0.41 (0.01) | 0.24 (0.02) | 0.29 (0.01) | 0.32 (0.01) | 0.19 (0.02) | -0.22 (0.04) | 0.06 (0.02) | -0.08 (0.02) |
| pcf | 0.33 (0.01) | 0.22 (0.02) | 0.14 (0.02) | 0.39 (0.01) | 0.33 (0.01) | -0.44 (0.04) | 0.13 (0.02) | -0.10 (0.02) |

[1] See Tables 3 and 4 for abbreviations; nc, log likelihood not converged.

**Table A9. Genetic correlation estimates (standard errors in brackets) of yearling fleece and live animal carcass traits with carcass composition and objective eating quality traits[1]**

| | cwt | dress | cemd | cfat | ccfat | lmy | imf | sf5 |
|---|---|---|---|---|---|---|---|---|
| ygfw | 0.29 (0.07) | -0.27 (0.09) | -0.01 (0.10) | 0.09 (0.08) | 0.15 (0.08) | -0.03 (0.15) | 0.00 (0.08) | -0.18 (0.12) |
| ycfw | 0.23 (0.08) | -0.21 (0.09) | 0.05 (0.12) | 0.09 (0.08) | 0.17 (0.09) | -0.04 (0.16) | 0.07 (0.08) | -0.11 (0.14) |
| yfd | 0.39 (0.07) | 0.27 (0.08) | 0.38 (0.11) | 0.37 (0.08) | 0.31 (0.08) | -0.29 (0.14) | 0.03 (0.06) | -0.09 (0.12) |
| ydcv | -0.21 (0.8) | -0.36 (0.09) | 0.01 (0.11) | -0.15 (0.09) | -0.22 (0.09) | 0.27 (0.17) | -0.07 (0.08) | 0.01 (0.13) |
| ysl | 0.40 (0.08) | 0.34 (0.09) | 0.18 (0.12) | 0.30 (0.09) | 0.27 (0.08) | -0.43 (0.14) | 0.00 (0.07) | -0.19 (0.13) |
| yss | 0.08 (0.09) | 0.09 (0.11) | -0.10 (0.13) | -0.01 (0.10) | 0.09 (0.10) | -0.09 (0.20) | -0.03 (0.09) | -0.09 (0.15) |
| ywt | 0.97 (0.01) | 0.42 (0.05) | 0.60 (0.04) | 0.61 (0.03) | 0.50 (0.04) | -0.51 (0.09) | 0.19 (0.04) | -0.26 (0.05) |
| yemd | 0.85 (008) | 0.75 (0.09) | 0.90 (0.11)nc | 0.77 (0.09) | 0.55 (0.08) | -0.44 (0.17) | 0.15 (0.06) | -0.22 (0.13) |
| ycf | 0.86 (0.06) | 0.74 (0.08) | 0.69 (0.10) | 0.98 (0.06) | 0.87 (0.06) | -0.71 (0.14) | 0.17 (0.06) | -0.32 (0.12) |

[1] See Tables 3 and 4 for abbreviations; nc, log likelihood not converged.