# Technical Report

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# Abstract

This study investigated the genetic relationship between eye muscle width and depth recorded via ultrasound on live animals and on carcases (measured with callipers and computer tomography) in two populations of Australian and New Zealand sheep. Genetic correlations between ultrasound and carcase muscle dimensions were estimated within populations. Carcase eye muscle dimensions have sufficient genetic variation to be included in sheep breeding programs. Genetic correlations between carcase eye muscle depth (CEMD, CTEMD) and width (CEMW, CTEMW), and between CEMW-CTEMW and ultrasound eye muscle depth (PEMD) in Australian sheep were lower than expected. On the other hand, high genetic correlations were observed between ultrasound depth and width recorded in different ages on New Zealand Merinos. These differences indicate further research about CEMW is required and the implications of current selection practises has on carcase eye muscle dimensions.



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# Executive summary


1. Lean meat yield is an important driver of profit for producers, processors and retailers of sheep meat. There is a strong genetic correlation between ultrasound scanned eye muscle depth with eye muscle depth in the carcase which means genetic gain in the depth of the eye muscle and lean meat yield has been achieved by selecting upon the ultrasound trait in the live animal.
2. The study aimed to update understanding of the relationship between different measurements and determine the impact selection decisions may have on the dimensions of the eye muscle in the carcase.
3. Three different data sets were used to determine the genetic relationship between eye muscle dimensions in sheep. Data set 1 included ~26,000 Australian Merino and Merino cross sheep with post weaning measured ultrasound eye muscle depth (PEMD) and carcase measured eye muscle depth and width (CEMD and CEMW respectively). Data set 2 included New Zealand Merino ultrasound eye muscle with and depth measured at weaning (PEMD, PEMW), yearling (YEMD, YEMW) and hogget ages (HEMD, HEMW). Data set 3 consisted of animals with computer tomography (CT) measured carcase eye muscle depth and width (CTEMD, CTEMW).
4. Heritability estimates for ultrasound, carcase and CT traits were low to moderate ranging from 0.19 to 0.45.
5. The high genetic correlation has been observed between ultrasound PEMD and CEMD, and PEMD and CTEMD which means that ultrasound should continue to be used as a selection trait to improve eye muscle depth.
6. Although ultrasound measures of eye muscle depth and width are strongly correlated, correlations with carcase (CEMD and CEMW) and CT (CTEMD and CTEMW) measurements are weaker.
7. Further research is required to determine if current selection practices are changing the dimensions of the eye muscle within the carcase and increase the need for a CEMW breeding value.




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# Contents





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# 1 Introduction

Lean meat yield is an important driver of profit for producers, processors and retailers of sheep meat. Ultrasound scanned eye muscle depth is moderately heritable and strongly correlated genetically with eye muscle depth in the carcase. Consequently, the majority of genetic gain in the depth of the eye muscle and in turn lean meat yield has been achieved by seed stock breeders selecting upon the ultrasound trait in the live animal (Brown & Swan 2016). The strong genetic correlations between ultrasound scanned eye muscle depth and width, previously observed in several studies (Safari *et al.* 2005), has meant that Sheep Genetics (Brown *et al.* 2007) has provided breeding values only for muscle depth. This is in part also due to the greater difficulty in measuring eye muscle width via ultrasound.

There are several studies that have reported on the genetic relationship between ultrasound muscle dimensions (Brito *et al.* 2017) and ultrasound and carcase measurements (Safari *et al.* 2005; Greeff *et al.* 2008; Mortimer *et al.* 2010), but often on small numbers of records. In the following study the genetic relationship between ultrasound and carcase eye muscle measurements was investigated in three different data sets: > 25,000 Australian Merino and Merino-cross sheep where eye muscle dimensions were measured both with ultrasound post weaning and on the carcase; 826 Australian Merino and cross Merino measured on the carcase with computer tomography; and >30,000 New Zealand Merinos with ultrasound measurements at different ages. The objective of this study was to update the understanding of the relationship between these measurements and determine the impact selection decisions may have on the dimensions of the eye muscle in the carcase.

# 2 Methodology

## 2.1 Data

Three different data sets were used to determine the genetic relationships between different eye muscle dimensions in lamb (Data sets 1, 2 and 3).

Data set 1 included data from Australian Merino and Merino-cross sheep. This data was collected between 2007 and 2019 from 35 commercial seed stock flocks, the Information Nucleus Flock and the MLA Resource Flock (van der Werf *et al.* 2010). Ultrasound muscle scanners accredited through Sheep Genetics (MLA) scanned eye muscle depth (PEMD) at the C site over the 12th rib, 45 mm from the midline at post weaning age (mean age 213 ±45 days). Carcase traits were measured using the procedures described in Mortimer et al. (2017b). The carcases were cut between the 12th and 13th ribs and eye muscle (*M. longissimus thoracis et lumborum*, LL) depth (CEMD) and eye muscle width (CEMW) were measured with vernier callipers. Mean animal age for carcase traits was 263 (±76) days. A summary of the Data set 1 records for each trait, number of sires, dams and contemporary groups, can be seen on Table 1.

Data set 2 included records from New Zealand Merinos which were collected between 2009 and 2019. Animals were ultrasound scanned at the C site over the 12th rib and measured for eye muscle depth and width at post weaning (7 – 10 months, PEMD, PEMW), yearling (10 – 13 months, YEMD, YEMW) and hogget age (13 – 18 months, HEMD, HEMW). For both data



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sets live weight was recorded at the time of scanning and was used to adjust the ultrasound measurements for weight. A summary of Data set 2 is presented on Table 2.

Data set 3 included computer tomography (CT) data collected from 826 animals from the MLA Resource Flock between 2018 and 2019. Carcases were CT scanned within 72 hours after slaughter according to the procedure described by Anderson *et al.* (2015). Prior to scanning, carcases were split into three primal components: fore-section, saddle and hind section to enable more rapid post scanning processing of the CT images. The method used for determination of muscle, fat and bone in the cut sections was similar to that described by Gardner *et al.* (2010), with the discrimination between fat, lean and bone adapted from the work by Alston *et al.* (2005). Lamb carcasses were transported to Murdoch University at 24 hours post slaughter. CT scanning was performed using Siemens Emotion 16 (16-slice) scanner according to the settings described by Anderson *et al.* (2022). The eye muscle area was measured at a site on the CT image where the eye muscle was perpendicular to the scanner and this was at either the caudal aspect of the 11$^{th}$ rib or the cranial aspect of the 12$^{th}$ rib. At the chosen CT slice (Figure 1), the measure tool was used in Image J to record the eye muscle width (CTEMW), depth (CTEMD) and the free hand tool to record the eye muscle area (CTEMA). The eye muscle depth and width measurements were taken at the widest part of the eye muscle. Not all carcasses were able to be evaluated due to carcass orientation. To check calibration of the measurement tool used in Image J, a phantom of know dimensions was included in the CT scans and measured using the measurement tool in Image J. Summaries for each CT trait, for each year of birth and for the total data set are shown on Table 3.

**Table 1. Number of records, mean values (standard deviation), coefficient of variation (CV), mean (standard deviation) weight (live weight for ultrasound and hot carcase weight for carcase traits), number of sires and dams and number of contemporary groups (Ncg_) for carcase and ultrasound traits in Data set 1. CEMD: carcase eye muscle depth (mm), CEMW carcase eye muscle width (mm), PEMD: post weaning ultrasound eye muscle depth (mm).**

| Data set | Trait | Records | Mean (SD) | CV | Mean Weight | Sires | Dams | Ncg |
|---|---|---|---|---|---|---|---|---|
| 1 | **PEMD** | 25,628 | 25.4 (4.8) | 18.8 | 41.99 (8.1) | 1,651 | 12,799 | 580 |
| | **CEMD** | 26,284 | 31.0 (4.7) | 15.3 | 23.21 (3.7) | 1,874 | 12,747 | 1,146 |
| | **CEMW** | 26,282 | 60.6 (5.5) | 9.0 | | 1,874 | 12,747 | |



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**Figure 1. An example of computed tomography image showing the eye muscle where depth (mm), width (mm) and area (cm) were measured** *(image credit: Dr Fiona Anderson)*.

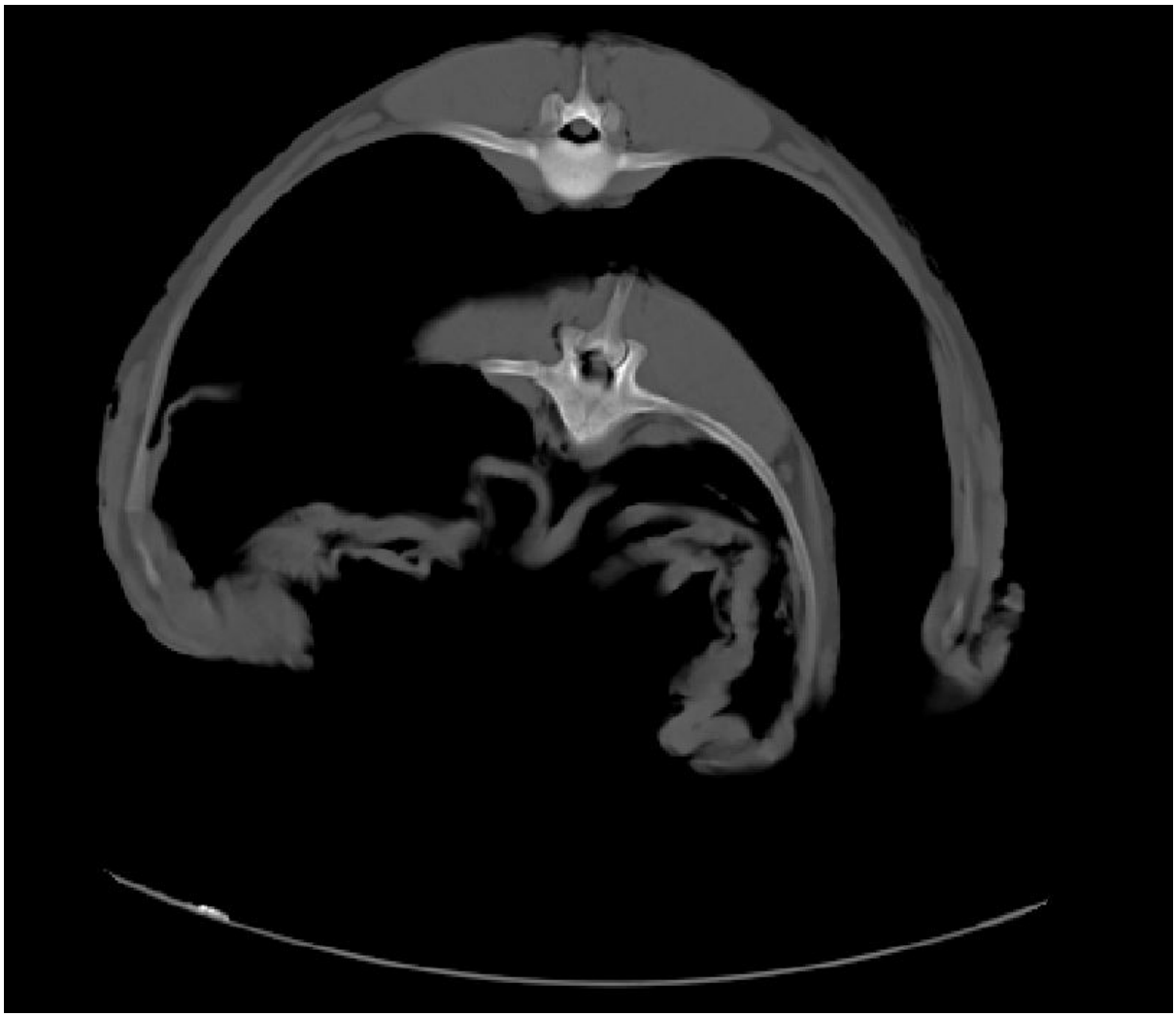

**Table 2. Number of records, trait mean values (standard deviation) and coefficient of variation (CV), mean live weight (standard deviation), number of sires and dams and number of contemporary groups (Ncg) for Data set 2. PEMD and PEMW: post weaning ultrasound eye muscle depth (mm) and width (mm), YEMD and YEMW: yearling ultrasound eye muscle depth (mm) and width (mm), and HEMD and HEMW: hogget ultrasound eye muscle depth (mm) and width (mm).**

| Data set | Trait | Records | Mean (SD) | CV | Live Weight (SD) | Sires | Dams | Ncg |
|---|---|---|---|---|---|---|---|---|
| 2 | **PEMD** | 3,251 | 26.1 (2.8) | 10.7 | 46.63 (7.8) | 169 | 3,251 | 85 |
| | **PEMW** | 5,616 | 68.8 (6.0) | 8.8 | | 144 | 2,760 | |
| | **YEMD** | 6,591 | 27.9 (3.6) | 12.8 | 51.86 (10.9) | 339 | 4,038 | 951 |
| | **YEMW** | 6,596 | 71.6 (6.2) | 8.7 | | 342 | 4,040 | |
| | **HEMD** | 21,616 | 27.8 (3.8) | 13.5 | 52.99 (12.1) | 752 | 11,118 | 403 |
| | **HEMW** | 21,087 | 71.1 (6.9) | 9.7 | | 733 | 10,629 | |



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**Table 3. Number of records, mean values (standard deviation) for computer tomography (CT) traits, mean values (standard deviation) for carcase (calliper measured) traits for the same animals, mean hot carcase weight (standard deviation) number of sires, number of dams, and number of contemporary groups (Ncg) for each birth year all animals in Data set 3. CTEMD: eye muscle depth (mm), CTEMW: eye muscle width (mm), CTEMA: eye muscle area ($cm^2$).**

| Data set | Birth Year | Trait | Records | Mean CT (SD) | Mean carcase (SD) | Mean Weight (SD) | Sires | Dams | Ncg |
|---|---|---|---|---|---|---|---|---|---|
| 3 | 2017 | CTEMD | 410 | 30.87 (3.5) | 31.48 (4.1) | 24.28 (3.3) | 76 | 203 | 16 |
| | | CTEMW | 410 | 64.29 (4.1) | 60.59 (4.2) | | | | |
| | | CTEMA | 410 | 16.02 (2.3) | 15.29 (2.5) | | | | |
| | 2018 | CTEMD | 416 | 32.10 (3.8) | 30.62 (4.3) | 25.11 (4.0) | 59 | 355 | 15 |
| | | CTEMW | 416 | 65.70 (4.3) | 59.57 (4.4) | | | | |
| | | CTEMA | 416 | 16.72 (2.8) | 14.63 (2.6) | | | | |
| | All | CTEMD | 826 | 31.49 (3.7) | 31.04 (4.2) | 24.7 (3.7) | 133 | 520 | 31 |
| | | CTEMW | 826 | 65.00 (4.3) | 60.07 (4.3) | | | | |
| | | CTEMA | 826 | 16.38 (2.6) | 14.96 (2.5) | | | | |

## 2.2 Statistical analysis

For all data sets, variance components and genetic parameters for each trait were estimated using a linear mixed model and REML methods using ASReml software (Gilmour *et al.* 2015). Fixed effects included type of birth (coded 1, 2, 3 or 4 for singles, twins, triplets and quadruplets respectively), contemporary group, sex (male or female) and the age of dam. Maternal effects were not fitted in any of the models since preliminary analysis showed they were non-significant. For all analyses, the animal effect represented the additive genetic variance and contemporary group was defined by breed, flock, management group, sex and date of measurement.

For Data set 1, models used for the analysis of the ultrasound and carcase traits included the random effects of animal, genetic group (Swan et al. 2016) and sire × flock interaction. The quadratic function of live weight at scanning (post weaning) and hot carcase weight was used to adjust the ultrasound and calliper measured carcase traits respectively. Phenotypic variance was calculated as the sum of additive genetic, residual and sire × site variance.

Similarly, for Data set 2, random effects of animal and sire × flock × year interaction were included in the analysis. Ultrasound traits were adjusted using the quadratic function of live weight at scanning (post weaning, yearling and hogget). In this case phenotypic variance was calculated as the sum of additive genetic and sire × site × year variance.

Genetic groups and sire x flock interactions were not fitted for Data set 3 since it was not possible for the analysis to converge and obtain genetic parameter estimates due to the small number of records. For this data, phenotypic variance was calculated as the sum of additive genetic and residual variance.



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For each dataset, phenotypic and genetic covariance for all traits and correlations between traits were estimated using bivariate analysis in ASReml.

# 3 Results and Discussion

## 3.1 Variance components

Variance components and heritability estimates for ultrasound and carcase traits for each of the data sets are shown in Tables 4, 5 and 6. For Data set 1, heritability estimates were moderate for carcase traits ranging from 0.19 (±0.02) for CEMD to 0.27 (±0.02) for CEMW; higher heritability (0.32±0.02) was observed for PEMD. Similar heritabilities for CEMD and CEMW have been observed in previous studies (Greeff *et al.* 2008; Huisman *et al.* 2016; Mortimer *et al.* 2017b).

Heritability for PEMD for both Data set 1 and 2 was higher than previously reported (Safari *et al.* 2005; Greeff *et al.* 2008; Mortimer *et al.* 2017a). Higher heritabilities were observed for the New Zealand Merino ultrasound traits: ranging from 0.23 (±0.03, YEMW) to 0.45 (±0.04, PEMD) (Table 3). Increased heritabilities have been observed in the past when live weight was used to adjust measurements (Mortimer *et al.* 2014).

**Table 4. Estimates of phenotypic ($\hat{\sigma}_p$), additive ($\hat{\sigma}_a$) residual ($\hat{\sigma}_\varepsilon$) and sire x flock ($\hat{\sigma}_{sire\ x\ flock}$) variance and heritability ($h^2$) for ultrasound and carcase eye muscle traits. Standard error in parentheses. CEMD: carcase eye muscle depth (mm), CEMW carcase eye muscle width (mm), PEMD and PEMW: post weaning ultrasound eye muscle depth (mm).**

| Data set | Trait | $h^2$ | $\hat{\sigma}_p$ | $\hat{\sigma}_a$ | $\hat{\sigma}_\varepsilon$ | $\hat{\sigma}_{sire\ x\ flock}$ |
|---|---|---|---|---|---|---|
| 1 | PEMD | 0.32 (0.02) | 4.95 (0.46) | 1.59 (0.1) | 3.28 (0.08) | 0.08 (0.02) |
| | CEMD | 0.19 (0.02) | 10.12 (0.09) | 1.92 (0.18) | 8.06 (0.16) | 0.14 (0.05) |
| | CEMW | 0.27 (0.02) | 14.81 (0.14) | 3.93 (0.3) | 10.55 (0.25) | 0.33 (0.08) |

**Table 5. Estimates of phenotypic ($\hat{\sigma}_p$), additive ($\hat{\sigma}_a$) residual ($\hat{\sigma}_\varepsilon$) and sire × flock × year ($\hat{\sigma}_{sire\ x\ flock\ x\ year}$) variance, and heritability ($h^2$) for ultrasound traits in Data set 2. Standard error in parentheses. PEMD and PEMW: post weaning ultrasound eye muscle depth (mm) and width (mm), YEMD and YEMW: yearling ultrasound eye muscle depth (mm) and width (mm), and HEMD and HEMW: hogget ultrasound eye muscle depth (mm) and width (mm).**

| Data set | Trait | $h^2$ | $\hat{\sigma}_p$ | $\hat{\sigma}_a$ | $\hat{\sigma}_\varepsilon$ | $\hat{\sigma}_{sire\ x\ flock\ x\ year}$ |
|---|---|---|---|---|---|---|
| 2 | PEMD | 0.45 (0.04) | 3.15 (0.07) | 1.35 (0.14) | 1.76 (0.10) | 0.03 (0.02) |
| | YEMD | 0.34 (0.04) | 3.42 (0.07) | 1.13 (0.18) | 2.16 (0.13) | 0.13 (0.04) |
| | HEMD | 0.31 (0.02) | 3.78 (0.04) | 1.16 (0.10) | 2.49 (0.07) | 0.13 (0.02) |
| | PEMW | 0.29 (0.03) | 10.01 (0.22) | 2.86 (0.40) | 7.09 (0.32) | 0.06 (0.04) |
| | YEMW | 0.23 (0.03) | 9.48 (0.19) | 2.20 (0.42) | 7.01 (0.33) | 0.27 (0.11) |
| | HEMW | 0.27 (0.02) | 10.56 (0.12) | 2.82 (0.26) | 7.46 (0.20) | 0.27 (0.06) |



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When CT traits were compared with carcase calliper measured eye muscle dimensions for the same animals in Data set 3, genetic variance is lower (2.59 for CTEMD and 3.38 for CEMD, Table 6) or similar (5.00 for CTEMW and 5.57 for CEMW, Table 6). Similarly, heritability estimates were lower than calliper traits for Dataset 3 (0.22 for CTEMD vs 0.32 for CEMD, 0.29 for CTEMW vs 0.35 for CEMW). These estimates were lower than previously reported heritabilities for CT traits for different terminal sheep breeds, when live animals where scanned. McLaren *et al.* (2021) estimated moderate to high heritability values using higher numbers of records for Texel (0.33 for CTEMD and 0.30 for CTEMA, ~3000 records), Suffolk (0.27 for CTEMD and 0.34 for CTEMA, ~1800 records) and Charolais (0.53 for CTEMD and 0.47 for CTEMA, ~1500 records). Lower heritability values for the CT traits measured in Data set 3 compared with previous studies indicates more data is needed to determine the potential for selection for CT traits without affecting current breeding goals.

**Table 6. Estimates of phenotypic ($\hat{\sigma}_p$), additive ($\hat{\sigma}_a$) and residual ($\hat{\sigma}_\varepsilon$) variance and heritability ($h^2$) for the Computer Tomography traits in Data set 3. Standard error in parentheses. Variance components for ultrasound and calliper measured muscle dimensions for the same animals are also presented. CTEMD: CT eye muscle depth (mm), CTEMW: CT eye muscle width (mm), CTEMA: CT eye muscle area (cm$^2$), PEMD: post weaning ultrasound eye muscle depth, CEMD: calliper measured carcase eye muscle depth, CEMW: calliper measured carcase eye muscle width.**

| Data set | Recording | Trait | $h^2$ | $\hat{\sigma}_p$ | $\hat{\sigma}_a$ | $\hat{\sigma}_\varepsilon$ |
|---|---|---|---|---|---|---|
| 3 | Computer Tomography | CTEMD | 0.22 (0.09) | 11.59 (1.90) | 2.59 (0.90) | 4.99 (0.81) |
| | | CTEMW | 0.29 (0.11) | 17.23 (2.39) | 5.00 (1.72) | 8.18 (1.53) |
| | | CTEMA | 0.27 (0.09) | 6.14 (1.16) | 1.63 (0.47) | 1.98 (0.41) |
| | Ultrasound | PEMD | 0.45 (0.02) | 5.25 (0.05) | 2.35 (0.10) | 2.90 (0.08) |
| | Calliper | CEMD | 0.32 (0.02) | 10.55 (0.01) | 3.38 (0.20) | 7.17 (0.2) |
| | | CEMW | 0.35 (0.02) | 15.67 (0.13) | 5.57 (0.27) | 10.19 (0.22) |

## 3.2 Correlations between traits

Estimates of genetic and phenotypic correlations between carcase calliper traits and post weaning ultrasound eye muscle depth for Data set 1, which included Australian Merino and Merino-cross sheep, are shown in Table 7. The genetic correlation between PEMD and CEMD was strong (0.77±0.04), but for the same animals CEMD was only moderately correlated with CEMW (0.38±0.05). Moreover, the correlation between CEMW and PEMD was low (0.17±0.04).



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**Table 7. Estimates of genetic (below diagonal) and phenotypic (above diagonal) correlations and their standard errors (parentheses) between carcase traits and ultrasound post weaning eye muscle depth for Data set 1. PEMD: post weaning ultrasound eye muscle depth, CEMD: carcase eye muscle depth, CEMW: carcase eye muscle width.**

| | PEMD | CEMD | CEMW |
|---|---|---|---|
| **PEMD** | | 0.23 (0.01) | 0.06 (0.01) |
| **CEMD** | 0.77 (0.04) | | 0.09 (0.01) |
| **CEMW** | 0.17 (0.04) | 0.38 (0.05) | |

In contrast, for Data set 2 which included only New Zealand Merino sheep, the correlations between ultrasound traits exhibited high genetic correlations between muscle depth and width at the same age (0.92 ±0.03 to 0.99 ±0.02) as well as between traits recorded at different ages (0.78 ±0.15 to 0.90 ±0.07, Table 8).

**Table 8. Estimates of genetic and phenotypic correlations between ultrasound eye muscle depth and width for different ages (post weaning, yearling and hogget) for Data set 2 (standard error in parentheses). PEMD and PEMW: post weaning ultrasound eye muscle depth and width, YEMD and YEMW: yearling ultrasound eye muscle depth and width, and HEMD and HEMW: hogget ultrasound eye muscle depth and width**

| | *Genetic* | | | *Phenotypic* | | |
|---|---|---|---|---|---|---|
| | **PEMD** | **YEMD** | **HEMD** | **PEMD** | **YEMD** | **HEMD** |
| **PEMW** | 0.92 (0.03) | 0.84 (0.16) | 0.88 (0.09) | 0.61 (0.01) | 0.15 (0.94) | 0.64 (0.23) |
| **YEMW** | 0.78 (0.15) | 0.99 (0.02) | 0.87 (0.07) | 0.57 (0.46) | 0.68 (0.01) | 0.49 (0.03) |
| **HEMW** | 0.90 (0.07) | 0.80 (0.07) | 0.95 (0.01) | 0.60 (0.21) | 0.48 (0.03) | 0.70 (0.01) |

Data set 3 included 826 animals with eye muscle dimensions measured with ultrasound at post weaning age and computer tomography (CT) and callipers on the carcase. Analysis of this data showed high genetic correlations between CTEMA and CTEMD (0.97 ±0.04) and CTEMA and CTEMW (0.76 ±0.08, Table 7). Genetic correlation between CTEMD and CTEMW was higher than the one estimated between CEMD and CEMW for Data set 1 (0.57 ±0.16 for CTEMD-CTEMW, 0.38 ±0.05 for CEMD-CEMW). However, Data set 3 included only a small number of animals recorded for CT traits (826) compared to ~26,000 animals present in Data set 1. Correlations between CT, ultrasound and calliper measured eye muscle dimensions ranged from 0.23 ±0.14 (CTEMD and CEMW) to 0.97 ±0.11 (CTEMA and PEMD, Table 10). Higher standard errors observed in the correlations between CT and ultrasound and calliper traits also reflect the lower number of records available for CT traits.



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**Table 9. Estimates of genetic (below diagonal) and phenotypic (above diagonal) correlations and their standard errors (parentheses) between CT traits. CTEMA: CT eye muscle area, CTEMD: CT eye muscle depth, CTEMW: CT eye muscle width.**

| | CTEMA | CTEMD | CTEMW |
|---|---|---|---|
| **CTEMA** | | 0.75 (0.02) | 0.48 (0.03) |
| **CTEMD** | 0.97 (0.04) | | 0.05 (0.04) |
| **CTEMW** | 0.76 (0.08) | 0.57 (0.16) | |

**Table 10. Genetic and phenotypic correlations between CT traits and post weaning ultrasound measured eye muscle depth (PEMD), calliper measured carcase eye muscle depth (CEMD) and width (CEMW).**

| | Genetic | | | Phenotypic | | |
|---|---|---|---|---|---|---|
| | **CTEMA** | **CTEMD** | **CTEMW** | **CTEMA** | **CTEMD** | **CTEMW** |
| **PEMD** | 0.82 (0.07) | 0.97 (0.11) | 0.53 (0.11) | 0.67 (0.03) | 0.28 (0.03) | 0.15 (0.04) |
| **CEMD** | 0.79 (0.07) | 0.84 (0.11) | 0.58 (0.12) | 0.52 (0.03) | 0.44 (0.03) | 0.23 (0.04) |
| **CEMW** | 0.46 (0.09) | 0.23 (0.14) | 0.88 (0.07) | 0.39 (0.03) | 0.14 (0.04) | 0.57 (0.02) |

High correlations between PEMD and CEMD have previously been reported by Greeff *et al.* (2008) (0.77) and Mortimer *et al.* (2010) (0.82). Similarly to the present report, high genetic correlations between CTEMD and PEMD have been observed in different sheep breeds ranging from 0.80 to 0.84 (McLaren *et al.* 2021). Moderate positive genetic correlations between CEMD and CEMW, and between CTEMD and CTEMW found in this study were similar to Safari *et al.* (2005) (0.23) and Greeff *et al.* (2008) (0.41). Based on these results, carcase eye muscle depth appears to be a genetically different trait to carcase eye muscle width. These low correlations in carcase measures contradict the New Zealand ultrasound results for corresponding traits as well as previous studies using ultrasound eye muscle dimensions at post weaning age, where correlations between eye muscle depth and width ranged between 0.78 in Australia (Safari *et al.* 2005) and 0.82 in New Zealand (Brito *et al.* 2017). Lower genetic correlations between ultrasound and carcase measurements could be a result of ultrasound limitations to accurately predict muscle dimensions. Hopkins *et al.* (2007) showed that ultrasound muscle depth measurements are subject to more errors in heavier sheep. Moreover, it would be beneficial for future investigations to include accurate animal age records since limitations might also include potential failure to properly account for age variation.



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# 4 Conclusions

The high genetic correlation between ultrasound PEMD and CEMD, and PEMD and CTEMD means that ultrasound should continue to be used as a selection trait to improve CEMD. However, whilst ultrasound measures of EMD and EMW are strongly correlated with each other, their correlations with carcase calliper and CT measurements are weaker. In particular, further research is required to determine if current selection practices are changing the dimensions of the eye muscle within the carcase and increase the need for a CEMW breeding value.

# 5 References


Alston C.L., Mengersen K.L., Thompson J.M., Littlefield P.J., Perry D. & Ball A.J. (2005) Extending the Bayesian mixture model to incorporate spatial information in analysing sheep CAT scan images. *Australian Journal of Agricultural Research* **56**, 373-88.

Anderson F., Williams A., Gardner G.E. & Brown D.J. (2022) Determination of eye muscle measures using computed tomography in lamb.

Anderson F., Williams A., Pannier L., Pethick D.W. & Gardner G.E. (2015) Sire carcass breeding values affect body composition in lambs — 1. Effects on lean weight and its distribution within the carcass as measured by computed tomography. *Meat Science* **108**, 145-54.

Brito L.F., McEwan J.C., Miller S., Bain W., Lee M., Dodds K., Newman S.-A., Pickering N., Schenkel F.S. & Clarke S. (2017) Genetic parameters for various growth, carcass and meat quality traits in a New Zealand sheep population. *Small Ruminant Research* **154**, 81-91.

Brown D.J., Huisman A.E., Swan A.A., U. G.H., Woolaston R.R.B., A. J., Atkins K.D. & Banks R.G. (2007) Genetic evaluation for the Australian sheep industry. In: *18th Conference of the Association for the Advancement of Animal Breeding and Genetics* (eds. by Donoghue K, Pattie B & Restall B), pp. 187 - 94, Armidale, Australia.

Brown D.J. & Swan A.A. (2016) Genetic importance of fat and eye muscle depth in Merino breeding programs. *Animal Production Science* **56**, 690-7.

Gardner G.E., Williams A., Siddell J., Ball A.J., Mortimer S., Jacob R.H., Pearce K.L., Hocking Edwards J.E., Rowe J.B. & Pethick D.W. (2010) Using Australian Sheep Breeding Values to increase lean meat yield percentage. *Animal Production Science* **50**, 1098-106.

Gilmour A.R., Gogel B.J., Cullis B.R., Welham S.J. & Thompson R. (2015) ASReml User Guide Release 4.1. In: *VSN International Ltd, Hemel Hempstead, UK*

Greeff J.C., Safari E., Fogarty N.M., Hopkins D.L., Brien F.D., Atkins K.D., Mortimer S.I. & van der Werf J.H. (2008) Genetic parameters for carcass and meat quality traits and their relationships to liveweight and wool production in hogget Merino rams. *J Anim Breed Genet* **125**, 205-15.

Hopkins D.L., Stanley D.F. & Ponnampalam E.N. (2007) Relationship between real-time ultrasound and carcass measures and composition in heavy sheep. *Australian Journal of Experimental Agriculture* **47**, 1304-8.

Huisman A.E., Brown D.J. & Fogarty N.M. (2016) Ability of sire breeding values to predict progeny bodyweight, fat and muscle using various transformations across environments in terminal sire sheep breeds. *Animal Production Science* **56**, 95.




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McLaren A., Kaseja K., McLean K.A., Boon S. & Lambe N.R. (2021) Genetic analyses of novel traits derived from CT scanning for implementation in terminal sire sheep breeding programmes. *Livestock Science* **250**, 104555.

Mortimer S.I., Hatcher S., Fogarty N.M., van der Werf J.H.J., Brown D.J., Swan A.A., Greeff J.C., Refshauge G., Edwards J.E.H. & Gaunt G.M. (2017a) Genetic parameters for wool traits, live weight, and ultrasound carcass traits in Merino sheep. *Journal of Animal Science* **95**, 1879-91.

Mortimer S.I., Hatcher S., Fogarty N.M., van der Werf J.H.J., Brown D.J., Swan A.A., Jacob R.H., Geesink G.H., Hopkins D.L., Edwards J.E.H., Ponnampalam E.N., Pearce K.L. & Pethick D.W. (2017b) Genetic correlations between wool traits and carcass traits in Merino sheep. *Journal of Animal Science* **95**, 2385-98.

Mortimer S.I., van der Werf J.H., Jacob R.H., Hopkins D.L., Pannier L., Pearce K.L., Gardner G.E., Warner R.D., Geesink G.H., Edwards J.E., Ponnampalam E.N., Ball A.J., Gilmour A.R. & Pethick D.W. (2014) Genetic parameters for meat quality traits of Australian lamb meat. *Meat Sci* **96**, 1016-24.

Mortimer S.I., van der Werf J.H.J., Jacob R.H., Pethick D.W., Pearce K.L., Warner R.D., Geesink G.H., Hocking Edwards J.E., Gardner G.E., Ponnampalam E.N., Kitessa S.M., Ball A.J. & Hopkins D.L. (2010) Preliminary estimates of genetic parameters for carcass and meat quality traits in Australian sheep. *Animal Production Science* **50**, 1135-44.

Safari E., Fogarty N.M. & Gilmour A.R. (2005) A review of genetic parameter estimates for wool, growth, meat and reproduction traits in sheep. *Livestock Production Science*, 271 - 89

van der Werf J.H.J., Kinghorn B.P. & Banks R.G. (2010) Design and role of an information nucleus in sheep breeding programs. *Animal Production Science*, 998 - 1003.



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