Genetic correlations between wool traits and carcass traits in Merino sheep[1]

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ABSTRACT: Genetic correlations between 29 wool production and quality traits and 14 whole carcass measures and carcass component traits were estimated from the Information Nucleus of 8 flocks managed across a range of Australian sheep production environments and genetically linked. Wool data were from over 5,000 Merino progeny born over 5 yr, whereas carcass data were from over 1,200 wether progeny of over 176 sires, slaughtered at about 21 kg carcass weight, on average. Wool traits included yearling and adult records for wool weight, fiber diameter, fiber diameter variation, staple strength, scoured color, and visual scores for breech and body wrinkle. Whole carcass measures included HCW, dressing percentage (DP), and various measures of fat depth and eye muscle dimensions. Carcass components were obtained by dissection, and lean meat yield (LMY) was predicted. Heritability estimates for whole carcass measures ranged from 0.12 ± 0.08 to 0.35 ± 0.10 and ranged from 0.17 ± 0.10 to 0.46 ± 0.10 for carcass dissection traits, with no evidence of important genotype × environment interactions. Genetic correlations indicated that selection for increased clean wool weight will result in reduced carcass fat (-0.17 to -0.34) and DP ($-0.48 \pm$ 0.15), with little effect on carcass muscle. Selection for lower fiber diameter will reduce HCW (-0.48 ± 0.15) as well as carcass fat (0.14 to 0.27) and muscle (0.21 to 0.50). There were high genetic correlations between live animal measures of fat and muscle depth and the carcass traits (generally greater than 0.5 in size). Selection to increase HCW (and DP) will result in sheep with fewer wrinkles on the body (-0.57 ± 0.10) and barer breeches (-0.74 ± 0.12, favorable), with minor deterioration in scoured wool color (reduced brightness and increased yellowness). Selection for reduced fat will also result in sheep with fewer body wrinkles (-0.42 to -0.79). Increasing LMY in Merinos through selection would result in a large reduction in carcass fat and DP (-0.66 to -0.84), with a smaller increase in carcass muscle and some increase in wool weight and wrinkles. Although no major antagonisms are apparent between the wool and carcass traits, developing selection indexes for dual-purpose wool and meat breeding objectives will require accurate estimates of genetic parameters to ensure that unfavorable relationships are suitably considered. The findings will aid development of dual-purpose wool and meat breeding objectives.

Key words: fat, genetic correlations, meat, Merino sheep, muscle, wool

INTRODUCTION

In recent years, incorporation of meat production traits together with traditional fine wool traits into sheep breeding programs is being driven by continued demand for sheep meat (MLA, 2016) and changes in relative prices paid for wool and meat. Consequently, in Australia, dual-purpose breeding objectives have been developed for the Merino (Brown and Swan, 2016) and Dohne Merino (Casey, 2016) breeds. Improved profitability of lamb performance traits and wool production in breeds such as the Targhee is also the aim of the Western Range index in the National Sheep Improvement Program (Ames, IA) in the United States (Notter et al., 2011). Selection criteria for meat production usually include live weight and fat and muscle depth measured over the loin by ultrasound. However, effective breeding programs require information on the genetic relationships between these selection traits and the meat traits measured in the carcass as well as with wool traits. Although several consistent estimates of the genetic variation exist for the major wool and meat production traits (Safari et al., 2005, 2007; Greeff et al., 2008; Huisman et al., 2008; Brown et al., 2016), there are few estimates of genetic correlations between wool and meat traits, particularly for Merino sheep. This second paper of a series reports estimates of genetic and phenotypic correlations between several wool production and quality traits and carcass meat traits, including lean meat yield and the weight of various cuts, from Merino sheep in the Information Nucleus (**IN**; Fogarty et al., 2007; van der Werf et al., 2010). The first paper reported genetic parameters for production and quality traits for wool and meat measured in live animals (Mortimer et al., 2017). These genetic parameters will contribute to calculation of more accurate EBV and selection indexes for gains in dual-purpose breeding objectives.

MATERIALS AND METHODS

Animals

Data were collected from Merino progeny born over 5 yr (2007 to 2011) in the IN breeding program (Fogarty et al., 2007; van der Werf et al., 2010) of the Cooperative Research Centre for Sheep Industry Innovation (**Sheep CRC**; Armidale, Australia). The 8 flocks of the IN were linked through the use of common sires. Each flock was located in a major sheep producing region of Australia (Armidale, NSW; Trangie, NSW, Cowra, NSW; Rutherglen, VIC; Hamilton, VIC; Struan, SA; Turretfield, SA; and Katanning, WA) and managed by local Sheep CRC partner organizations. The design of the IN, including flock management and sire selection procedures (for AI mating with the base dams), are described by van der

Werf et al. (2010) and Geenty et al. (2014). The data were generated from records of 9,135 progeny born to 184 Merino sires and 4,614 Merino dams. The lambs were tail docked and the males were castrated at marking (7 to 43 d). After weaning (90 d), the lambs at each site were managed to achieve target growth rates of 150 g/d. Half of the wether lambs (balanced for sire) were randomly allocated to slaughter groups for slaughter in their first year to achieve a target of an average carcass weight of 21.5 kg for each group. The ewe lambs and the remainder of the wethers were retained for yearling and adult wool trait measurements. The lambs grazed the extensive pastures available at the sites and were supplemented with grain, hay, or feedlot pellets when the pasture supply was restricted (Ponnampalam et al., 2014). The research and data collection activities used a common protocol at each IN site, and all activities were approved by the Animal Ethics Committee for each site.

Wool Traits

The ewes and remaining wethers were shorn as yearlings (300 to 400 d) and adults (>540 d), when greasy fleece weight (**GFW**) was recorded (i.e., yearling GFW and adult GFW [**aGFW**]). Mid-side wool samples were measured for the following traits: clean yield (**YLD**), clean fleece weight (**CFW**), mean fiber diameter (**FD**), FD SD, FD CV (**FDCV**), staple strength (**SS**), staple length (**SL**), and mean fiber curvature. Wool color measurements were performed on the clean scoured and carded samples for brightness and for yellowness (**Y-Z**). A commercial testing laboratory measured the wool traits; details for the procedures are described by the Australian Wool Testing Authority (2000). Within 1 mo after shearing (yearlings and adults), visual traits were scored for breech cover (**BCOV**), breech wrinkle (**BRWR**), and body wrinkle using a 1 to 5 diagrammatic scale (1 the least expression and 5 the most expression of the trait). Breech wrinkle was also scored at marking. Over 5,000 animals were measured for each of the yearling wool production, wool quality, and wool color traits, and over 3,600 animals were measured as adults. The animals measured for the wool traits were the progeny of 184 sires and 3,995 dams. The number of animals scored for the visual traits ranged from 6,035 for marking BRWR to over 3,300 for yearling scores and over 1,800 for adult scores. Numbers of adult wool measurements were reduced due to adult traits not being recorded on the 2011-born wethers as well as 546 wethers being both recorded for yearling wool and visual traits and slaughtered for recording of carcass measurements. Additionally, adult BCOV was not scored on animals born in 2007, 2010, and 2011. Further details of the measurements, including the means and SD and the genetic variances for each of

the yearling wool traits, are reported in the first paper in this series (Mortimer et al., 2017).

Carcass Traits

All lambs were slaughtered at commercial abattoirs. All carcasses were subjected to medium voltage electrical stimulation and trimmed according to AUS-MEAT specifications (AUS-MEAT, 2006), with measurement procedures for the carcass traits described by Gardner et al. (2010). At slaughter, HCW was measured and carcass fat depth at the GR site (**FATGR**; total tissue depth at the 12th rib, 110 mm from the midline) was measured as an estimate of carcass fatness with a GR knife on the hot carcass. Dressing percentage (**DP**) was calculated as the ratio of HCW to preslaughter weight measured the day before slaughter. Carcasses were chilled overnight (3–4°C) and were sampled for measurement of a wide range of carcass and meat quality traits. Carcass fat depth at the fifth rib (**FAT5**), 110 mm from the midline on the chilled carcass, was measured using a ruler. The carcasses were cut between the 12th and 13th ribs, and eye muscle depth (**EMD**), *M. longissimus thoracis et lumborum* (**LL**), and eye muscle width (**EMW**) were measured and used to calculate eye muscle area (**EMA**) as 80% of the product of depth and width. Fat depth over the LL (**FDC**; Wood and MacFie, 1980) measured on the cut surface between the twelfth and thirteenth ribs over the deepest part of the muscle. The LL was excised from the carcass and trimmed of fat (weight of fat trim of the loin [**FATLL**]), and the total weight of the denuded LL (loin muscle weight [**WTLL**]) was recorded. From the hind leg, the topside (Handbook of Australian Meat number 5073; AUS-MEAT, 2006) was removed, trimmed of external fat, and weighed (topside weight [**WTTOP**]). The knuckle (Handbook of Australian Meat number 5072; AUS-MEAT, 2006) was also removed and weighed (round weight [**WTRND**]), along with all the bone of the hind leg (hind leg bone weight [**BONE**]). Lean meat yield (**LMY**) was predicted for each animal using an algorithm based on HCW, FATGR, FATLL, FAT5, EMA, WTLL, WTTOP, WTRND, and BONE (Gardner et al., 2010). The number of records, mean, SD, and the number of sires and dams for each of the carcass measures and carcass dissection traits are shown in Table 1. Genetic and phenotypic correlations were also estimated between the carcass traits and ultrasound measures on live sheep at postweaning and yearling ages for fat depth (postweaning live ultrasound fat [C site; **pwFATUS**] and yearling live ultrasound fat [C site], respectively) and eye muscle depth (postweaning live ultrasound eye muscle depth [**pwEMDUS**] and yearling live ultrasound eye muscle depth, respectively; see Mortimer et al. [2017] for details of the ultrasound traits).

Table 1. The number of records, mean, SD, and number of sires and dams for the carcass traits[1]

Carcass traits	No.	Mean	SD	Sires	Dams
Carcass measures					
HCW, kg	1,331	21.1	3.2	178	1,193
DP, %	1,262	43.6	3.5	178	1,129
FATGR, mm	1,336	10.7	4.6	179	1,196
FATC, mm	1,281	3.3	2.0	177	1,152
FAT5, mm	1,288	5.6	2.7	177	1,157
EMW, mm	1,289	59.5	4.7	177	1,160
EMD, mm	1,289	27.4	3.6	177	1,160
EMA, cm^2	1,289	13.1	2.2	177	1,160
Carcass dissection					
LMY, %	1,249	58.4	2.5	176	1,128
WTLL, g	1,292	319.4	60.7	177	1,162
WTTOP, g	1,291	541.3	95.5	177	1,162
WTRND, g	1,293	426.9	63.7	177	1,162
FATLL, g	1,290	159.0	92.2	177	1,160
BONE, g	1,289	912.4	131.9	177	1,160

[1]DP = dressing percentage; FATGR = carcass fat depth at the GR site located at the 12th rib, 110 mm from the midline; FATC = carcass 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; FAT5 = carcass fat depth at the fifth rib; EMW = eye muscle width; EMD = eye muscle depth; EMA = eye muscle area; LMY = lean meat yield; WTLL = loin muscle weight; WTTOP = topside weight; WTRND = round weight; FATLL = weight of fat trim of the loin; BONE = hind leg bone weight.

Statistical Analyses

General linear mixed models and REML methods, applied with ASReml software (Gilmour et al., 2015), were used to estimate fixed effects, variance components, and genetic parameters. Before estimating the variance components, mixed linear sire models initially were fitted to the wool traits and the carcass traits separately to identify significant environmental effects. The fixed effects included site (8 levels), year of birth (5 levels), sex (2 levels; wool traits only), sheep type (3 levels: ultra/super fine, fine fine/medium, and medium/strong), type of birth and rearing (6 levels: 11, 21, 22, 31, 32, and 33 for number of lambs born and reared, respectively, and dam age (7 levels: 2 to greater than or equal to 7 yr of age; see Mortimer et al. [2017] for more details). For the carcass traits, slaughter group was also fitted as well as age of the lamb as a linear covariate. Significant ($P < 0.05$) 2-way interactions were included in the final model.

Univariate mixed animal model analyses were then used to obtain estimates of variance components for each trait, using the linear mixed model as described by Swan et al. (2016). Random effects fitted in the final model included animal and genetic group, with the genetic group effect defined by Merino flock of origin (bloodline) or sheep type (Swan et al., 2016). The number of genetic groups appropriate to each trait ranged from 124 to 134. The genetic groups for each trait were derived from the

Table 2. Estimates of phenotypic variance and the proportions due to additive genetic variance (h^2), genetic group (b^2)[1], and sire × site (s^2; SE) for the carcass traits

Trait[2]	Phenotypic variance	CV, %	Heritability (h^2)	Genetic group (b^2)	Sire × site (s^2)
Carcass measures					
HCW, kg	5.03	10.6	0.35 (0.10)	0.68 (0.48)	–
DP, %	6.53	5.9	0.21 (0.11)	0.24 (0.41)	0.16 (0.05)
FATGR, mm	10.95	30.9	0.23 (0.11)	0.55 (0.65)	0.10 (0.04)
FATC, mm	2.58	49.1	0.29 (0.10)	0.10 (0.27)	–
FAT5, mm	4.60	38.0	0.21 (0.08)	0.00 (0.00)	–
EMW, mm	14.51	6.4	0.29 (0.09)	0.12 (0.25)	–
EMD, mm	8.38	10.6	0.12 (0.08)	0.07 (0.45)	–
EMA, cm²	3.18	13.6	0.19 (0.08)	0.08 (0.26)	–
Carcass dissection					
LMY, %	3.891	3.4	0.29 (0.11)	0.09 (0.26)	0.08 (0.04)
WTLL, g	2,205.9	14.7	0.46 (0.10)	0.20 (0.20)	–
WTTOP, g	3,700.5	11.2	0.34 (0.11)	0.47 (0.41)	–
WTRND, g	2,054.0	10.6	0.38 (0.11)	0.53 (0.43)	–
FATLL, g	3,015.9	34.5	0.17 (0.10)	0.60 (0.77)	0.08 (0.04
BONE, g	7,757.5	9.7	0.29 (0.11)	0.94 (0.65)	0.06 (0.04)

[1]b^2 = ratio of genetic group to additive genetic variance.

[2]DP = dressing percentage; FATGR = carcass fat depth at the GR site total tissue depth at the 12th rib, 110 mm from the midline; FATC = carcass 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; FAT5 = carcass fat depth at the fifth rib; EMW = eye muscle width; EMD = eye muscle depth; EMA = eye muscle area; LMY = lean meat yield; WTLL = loin muscle weight; WTTOP = topside weight; WTRND = round weight; FATLL = weight of fat trim of the loin; BONE = hind leg bone weight.

pedigrees of animals having observations for that trait. As well, the importance of the random effects of sire × site interaction and dam (representing a maternal effect comprising both maternal genetic and maternal environmental effects) was assessed by sequentially adding these effects to the model. Following inclusion in the model, a significant increase in the log-likelihood value from that of a reduced model indicated that a random effect should be retained. The maternal environmental effect was not significant for all carcass traits and was removed from the final model for these traits. As described by Mortimer et al. (2017), variance ratios for each trait, including heritabilities, were estimated from these univariate analyses. The phenotypic variance was the sum of the additive genetic, maternal (when fitted for wool traits only), sire × site (when fitted), and the residual variances. As appropriate for each trait, the ratios of maternal (wool traits only) and sire × site variances to phenotypic variance were estimated. The ratio of genetic group variance to additive genetic variance was also calculated as a comparison of the relative size of the between genetic group variance with the within genetic group variance. Bivariate analyses involving all combinations of traits at each stage of measurement were used to estimate phenotypic and genetic covariances, where fixed effects and

significant 2-way interactions were fitted based on the univariate analyses. All significant random effects from the univariate models were included in the random bivariate models, although simpler random models were used in the few instances where convergence did not occur. Phenotypic and genetic correlations, and their SE, were estimated from the appropriate covariances using ASReml. Because no males were measured for both carcass and adult traits, the environmental covariances of adult wool traits with carcass traits are 0 and phenotypic correlations could not be estimated.

RESULTS AND DISCUSSION

Heritability

The estimates of variance components and heritability for the wool production and quality traits and visual scores were reported by Mortimer et al. (2017) and are not repeated here. There were high heritability estimates for the major wool production and wool quality traits whereas other wool quality, wool color, and visual traits were more moderately heritable, which is consistent with the review of Safari et al. (2005) and more recent reports from several large Merino data sets (Asadi Fozi et al., 2005; Safari et al., 2007; Huisman et al., 2008; Swan et al., 2008, 2016; Brown et al., 2010, 2013).

Carcass Measures Traits. The estimates of heritability for the carcass traits were generally moderate (range 0.12 ± 0.08 to 0.46 ± 0.10; Table 2). There were moderate to large genetic group effects for HCW, FATGR, and DP and all of the carcass dissection traits except LMY. This reflects the large range in Merino bloodlines in the industry and their varying emphasis on wool and meat in their past breeding programs. Studies comparing a range of Merino strains have reported differences for DP (Fogarty et al., 2003) and FATGR and FATC adjusted for HCW as well as small differences in the carcass eye muscle measures (Fogarty et al., 2003; Hopkins et al., 2005, 2007a). Across these studies, the finer wool types had the greater carcass fat levels when adjusted for carcass weight, as a consequence of their lighter carcasses and, to a lesser extent, differing mature weights (Hopkins et al., 2007a). Despite medium wool Merinos having lighter carcasses than broad wool Merinos, Hopkins et al. (2007a) concluded that these strains would produce similar yields of saleable meat, which is consistent with the absence of strain (or bloodline) differences in LMY observed in the present study. The sire × site effect was small or not significant for most traits, indicating that genotype × environment interactions were generally not important for these carcass traits. The estimates of heritability for the various carcass measures are generally consistent with previous reports summarized in reviews by

Table 3. Estimates of genetic and phenotypic correlations (SE) between yearling wool traits and carcass measures traits

Carcass measures traits[1]	Yearling wool traits[2]								
	yGFW	yYLD	yCFW	yFD	yFDSD	yFDCV	ySS	ySL	yCUR
Genetic correlations									
HCW	0.09 (0.11)	−0.06 (0.11)	0.02 (0.11)	0.28 (0.10)	0.02 (0.11)	−0.23 (0.11)	−0.04 (0.12)	0.41 (0.10)	−0.01 (0.11)
DP	−0.50 (0.14)	0.11 (0.14)	−0.48 (0.15)	0.06 (0.13)	−0.34 (0.14)	−0.52 (0.15)	−0.11 (0.15)	0.37 (0.14)	0.05 (0.14)
FATGR	−0.17 (0.14)	−0.05 (0.13)	−0.26 (0.14)	0.23 (0.11)	−0.10 (0.13)	−0.33 (0.13)	−0.15 (0.14)	0.46 (0.12)	0.07 (0.13)
FATC	−0.11 (0.13)	−0.18 (0.13)	−0.17 (0.13)	0.14 (0.11)	−0.04 (0.13)	−0.20 (0.13)	0.01 (0.14)	0.16 (0.12)	0.13 (0.13)
FAT5	−0.26 (0.16)	−0.22 (0.16)	−0.34 (0.16)	0.27 (0.14)	−0.08 (0.16)	−0.35 (0.15)	0.17 (0.17)	0.23 (0.15)	0.36 (0.15)
EMW	0.07 (0.14)	−0.07 (0.14)	0.05 (0.14)	0.06 (0.12)	0.16 (0.14)	0.14 (0.14)	−0.14 (0.15)	0.09 (0.13)	−0.10 (0.14)
EMD	0.03 (0.19)	0.02 (0.19)	0.05 (0.19)	0.50 (0.21)	0.04 (0.19)	−0.37 (0.20)	0.37 (0.21)	0.22 (0.18)	0.12 (0.19)
EMA	0.10 (0.17)	0.00 (0.16)	0.11 (0.17)	0.38 (0.17)	0.11 (0.16)	−0.19 (0.17)	0.18 (0.18)	0.26 (0.16)	−0.02 (0.16)
Phenotypic correlations									
HCW	0.23 (0.03)	0.02 (0.04)	0.21 (0.03)	0.15 (0.04)	−0.04 (0.04)	−0.15 (0.04)	−0.04 (0.05)	0.10 (0.05)	0.02 (0.04)
DP	−0.07 (0.04)	0.16 (0.04)	−0.01 (0.04)	0.05 (0.04)	−0.25 (0.04)	−0.38 (0.04)	0.01 (0.05)	0.18 (0.05)	0.03 (0.05)
FATGR	0.09 (0.03)	0.04 (0.04)	0.08 (0.04)	0.08 (0.04)	−0.07 (0.04)	−0.16 (0.04)	−0.02 (0.05)	0.12 (0.05)	0.02 (0.04)
FATC	0.09 (0.04)	0.01 (0.05)	0.09 (0.04)	0.12 (0.04)	−0.04 (0.05)	−0.15 (0.05)	0.02 (0.05)	−0.02 (0.05)	0.034 (0.05)
FAT5	0.03 (0.04)	0.04 (0.04)	0.06 (0.04)	0.13 (0.04)	0.00 (0.04)	−0.09 (0.04)	0.06 (0.05)	0.06 (0.05)	0.13 (0.04)
EMW	0.18 (0.04)	−0.04 (0.04)	0.16 (0.04)	0.04 (0.04)	0.03 (0.05)	0.01 (0.05)	−0.02 (0.05)	0.06 (0.05)	0.00 (0.05)
EMD	0.15 (0.04)	0.02 (0.04)	0.15 (0.04)	0.07 (0.04)	0.00 (0.05)	−0.06 (0.05)	0.02 (0.05)	−0.04 (0.05)	−0.01 (0.05)
EMA	0.21 (0.04)	0.00 (0.04)	0.20 (0.04)	0.07 (0.04)	0.01 (0.05)	−0.05 (0.05)	0.01 (0.05)	0.01 (0.05)	−0.01 (0.05)

[1]DP = dressing percentage; FATGR = carcass fat depth at the GR site located at the 12th rib, 110 mm from the midline; FATC = carcass 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; FAT5 = carcass fat depth at the fifth rib; EMW = eye muscle width; EMD = eye muscle depth; EMA = eye muscle area.

[2]yGFW = yearling greasy fleece weight; yYLD = yearling clean yield; yCFW = yearling clean fleece weight; yFD = yearling fiber diameter; yFDSD = yearling fiber diameter SD; yFDCV = yearling fiber diameter CV; ySS = yearling staple strength; ySL = yearling staple length; yCUR = yearling fiber curvature.

Fogarty (1995) and Safari et al. (2005) as well as more recent reports for Merino rams (Greeff et al., 2008) and multibreed sheep populations (Bolormaa et al., 2016).

Carcass Dissection Traits. Heritability estimates have been moderate to high from the relatively few studies that have estimated genetic variances for carcass dissection traits in sheep, with our results consistent with those earlier estimates. These earlier reports for heritability include 0.36 for WTLL and 0.37 for total lean (Waldron et al., 1992), 0.27 ± 0.06 for meat in 3 primal cuts (Kenney et al., 1995), 0.27 ± 0.11 for lean in the shoulder (Conington et al., 1998), 0.41 for WTLL and 0.24 to 0.31 for lean in various other cuts (Johnson et al., 2006), 0.46 for lean in the carcass (van Heelsum et al., 2006), 0.37 for lean in the loin (Jopson et al., 2009), and 0.32 ± 0.14 for WTLL and 0.24 ± 0.14 for WTTOP (Lorentzen and Vangen, 2012). There have also been other studies reporting heritabilities of 0.2 to 0.5 for lean using video image analysis (Rius-Vilarrasa et al., 2009; Einarsson et al., 2015; Johnson et al., 2015a,b) and computer tomography (**CT**; Jones et al., 2004; Karamichou et al., 2006; Kvame and Vangen, 2007; Lambe et al., 2008) procedures. Our results of 0.34 to 0.46 for heritability of WTLL, WTTOP, and WTRND are consistent with these literature estimates, indicating moderate genetic variance for lean, which should be responsive to selection given the level of phenotypic variance avail-

able. The estimates of heritability for carcass fat tend to be lower than those for carcass lean in our results as well as in the literature above. However, the considerably greater phenotypic variability in carcass fat indicates that selection to change fat levels could lead to relatively larger changes than selection for carcass lean.

Genetic Correlations

Wool Production Traits with Carcass Measures Traits. The estimates of genetic and phenotypic correlations between yearling wool traits and lamb carcass measures are shown in Table 3, with the genetic correlations for adult wool traits available in Supplementary Table S1 (see the online version of the article at http://journalofanimalscience.org). The genetic correlations between yearling wool production (yearling GFW and yearling CFW) and carcass fat traits were negative and low (range −0.11 ± 0.13 to −0.34 ± 0.16), whereas those with adult wool production (aGFW and adult CFW [**aCFW**]) were more strongly negative (range −0.33 ± 0.13 to −0.54 ± 0.14; Supplementary Table S1 [see the online version of the article at http://journalofanimalscience.org]). The genetic correlations between carcass muscle traits and wool production at both yearling and adult ages were negligible. This is consistent with reports for ultrasound measures of fat and muscle at young ages (Safari et al.,

Table 4. Estimates of genetic and phenotypic correlations (SE) between yearling wool traits and carcass dissection traits

Carcass dissection traits[1]	Yearling wool traits[2]								
	yGFW	yYLD	yCFW	yFD	yFDSD	yFDCV	ySS	ySL	yCUR
Genetic correlations									
LMY	0.16 (0.15)	0.02 (0.14)	0.20 (0.15)	−0.09 (0.12)	0.12 (0.14)	0.22 (0.15)	0.11 (0.15)	−0.22 (0.14)	−0.15 (0.14)
WTLL	0.07 (0.12)	−0.16 (0.11)	−0.04 (0.12)	0.21 (0.10)	−0.06 (0.11)	−0.27 (0.11)	0.04 (0.13)	0.33 (0.11)	−0.07 (0.11)
WTTOP	0.09 (0.12)	−0.08 (0.12)	0.03 (0.12)	0.25 (0.10)	−0.05 (0.12)	−0.27 (0.11)	−0.02 (0.13)	0.35 (0.11)	0.05 (0.12)
WTRND	0.12 (0.12)	0.04 (0.11)	0.10 (0.12)	0.24 (0.10)	0.03 (0.11)	−0.20 (0.11)	−0.05 (0.12)	0.37 (0.10)	−0.12 (0.11)
FATLL	−0.11 (0.16)	−0.17 (0.16)	−0.20 (0.16)	0.24 (0.13)	−0.23 (0.15)	−0.45 (0.14)	−0.02 (0.17)	0.44 (0.14)	0.02 (0.15)
BONE	0.19 (0.12)	0.02 (0.12)	0.16 (0.12)	0.25 (0.10)	0.18 (0.12)	−0.04 (0.12)	−0.11 (0.13)	0.30 (0.11)	0.03 (0.12)
Phenotypic correlations									
LMY	0.04 (0.04)	−0.06 (0.04)	0.02 (0.04)	−0.08 (0.04)	0.06 (0.04)	0.13 (0.04)	0.00 (0.05)	−0.12 (0.05)	−0.10 (0.04)
WTLL	0.20 (0.03)	0.03 (0.04)	0.18 (0.03)	0.11 (0.04)	−0.06 (0.04)	−0.15 (0.04)	−0.02 (0.05)	0.07 (0.05)	−0.01 (0.04)
WTTOP	0.20 (0.03)	−0.02 (0.04)	0.18 (0.03)	0.11 (0.04)	−0.07 (0.04)	−0.16 (0.04)	−0.07 (0.05)	0.08 (0.05)	0.01 (0.04)
WTRND	0.21 (0.03)	−0.01 (0.04)	0.19 (0.03)	0.09 (0.04)	0.00 (0.04)	−0.07 (0.04)	−0.03 (0.05)	0.01 (0.05)	0.00 (0.04)
FATLL	0.09 (0.03)	0.04 (0.04)	0.10 (0.04)	0.13 (0.04)	−0.05 (0.04)	−0.16 (0.04)	0.01 (0.04)	0.11 (0.05)	0.00 (0.04)
BONE	0.20 (0.03)	0.02 (0.04)	0.19 (0.03)	0.07 (0.04)	0.00 (0.04)	−0.06 (0.04)	−0.10 (0.05)	0.03 (0.05)	0.02 (0.04)

[1]LMY = lean meat yield; WTLL = loin muscle weight; WTTOP = topside weight; WTRND = round weight; FATLL = weight of fat trim of the loin; BONE = hind leg bone weight.

[2]yGFW = yearling greasy fleece weight; yYLD = yearling clean yield; yCFW = yearling clean fleece weight; yFD = yearling fiber diameter; yFDSD = yearling fiber diameter SD; yFDCV = yearling fiber diameter CV; ySS = yearling staple strength; ySL = yearling staple length; yCUR = yearling fiber curvature.

2005; Mortimer et al., 2017). There were negative genetic correlations between DP and wool production at yearling (−0.5) and adult (−0.7) ages, which is expected because heavier pelts will result in a lower carcass DP. From examining the effect of EBV, known as Australian Sheep Breeding Values (**ASBV**), of the sire on carcass characteristics of IN progeny of terminal, maternal, and Merino breed sires, Gardner et al. (2015) also reported an unfavorable effect of increasing sire ASBV for yearling GFW reducing DP. There appears to be a low negative genetic relationship between wool scouring yield (YLD) and carcass fat measures (−0.20 to −0.41 for adult YLD). The genetic correlations between carcass fat traits and yearling FD (**yFD**) and yearling SL were generally low positive and low negative with yearling FDCV, with the adult wool traits being similar to the yearling traits. Eye muscle depth was moderately positively related to FD (0.50 ± 0.21 for yFD and 0.57 ± 0.20 for adult FD) as well as SS (0.51 ± 0.23 for adult SS). Hot carcass weight had low positive genetic correlations with FD and SL and negative correlations with FDCV for both yearling and adult wool measures. The other genetic correlations were generally negligible and smaller than their SE, and the phenotypic correlations were generally small and negligible. Although previous studies have adjusted the carcass traits for carcass weight, the genetic correlation estimates were generally consistent with reported estimates of carcass measures with GFW, CFW, FD, yield, FD variability, SS, and fiber curvature (Fogarty et al., 2003; Greeff et al., 2003, 2005, 2008; Ingham et al., 2007).

Wool Production Traits with Carcass Dissection Traits. The estimates of genetic and phenotypic corre-lations between yearling wool production and quality traits and carcass dissection traits are shown in Table 4, with the genetic correlations for adult wool traits available in Supplementary Table S2 (see the online version of the article at http://journalofanimalscience.org). The genetic correlations between wool production (GFW and CFW) and LMY were positive and low for yearling wool and moderate for adult wool (0.38 ± 0.15 for aGFW and 0.42 ± 0.16 for aCFW), although the correlations were negligible for the weights of the various lean cuts. However, there were low positive genetic correlations between the lean cuts and FD and SL, with negative correlations for FDCV at both yearling and adult ages. There were low negative correlations between yearling fleece weight and FATLL, but these correlations were more negative for adult wool (−0.55 ± 0.16 aGFW and −0.46 ± 0.15 aCFW). There were also positive genetic correlations between FATLL and yFD and yearling SL and negative correlations with yearling FD SD and year-ling FDCV, which did not change at adult ages. The low positive genetic correlations between BONE and FD and SL were similar for yearling and adult wool. These re-sults are somewhat contrary to a report by Lambe et al. (2008) for GFW and carcass traits predicted by CT pro-cedures in Scottish Blackface sheep, where adult fleece weight was genetically uncorrelated with the carcass traits. For wool-producing breeds, selection to increase fleece weight, particularly when based on adult expres-sions, is expected to slightly lower DP and reduce car-cass fat levels, which may not be favorable in relatively lean breeds such as the Merino. The impact on carcass fat traits would be further increased where selection for

Table 5. Estimates of genetic and phenotypic correlations (SE) between yearling wool color and visual traits and carcass measures traits

Carcass measures traits[1]	Yearling wool color and visual traits[2]					
	yY	y(Y-Z)	yBCOV	mBRWR	yBRWR	yBDWR
Genetic correlations						
HCW	−0.36 (0.12)	0.20 (0.11)	−0.74 (0.12)	−0.44 (0.11)	−0.52 (0.11)	−0.57 (0.10)
DP	−0.30 (0.17)	0.02 (0.14)	−0.82 (0.19)	−0.55 (0.15)	−0.92 (0.14)	−0.98 (0.15)
FATGR	−0.20 (0.16)	0.06 (0.13)	−0.52 (0.18)	−0.55 (0.14)	−0.72 (0.15)	−0.79 (0.14)
FATC	−0.16 (0.15)	0.14 (0.13)	−0.56 (0.17)	−0.12 (0.14)	−0.40 (0.15)	−0.42 (0.14)
FAT5	0.25 (0.18)	−0.01 (0.15)	−0.43 (0.22)	−0.48 (0.16)	−0.65 (0.17)	−0.75 (0.16)
EMW	−0.19 (0.16)	−0.11 (0.05)	−0.50 (0.17)	−0.26 (0.15)	−0.12 (0.15)	−0.13 (0.15)
EMD	−0.25 (0.22)	0.15 (0.19)	−0.09 (0.25)	−0.06 (0.21)	−0.30 (0.21)	−0.23 (0.19)
EMA	−0.29 (0.19)	0.31 (0.17)	−0.33 (0.21)	−0.16 (0.18)	−0.21 (0.18)	−0.21 (0.17)
Phenotypic correlations						
HCW	−0.07 (0.04)	0.12 (0.04)	−0.20 (0.04)	−0.14 (0.03)	−0.22 (0.04)	−0.18 (0.04)
DP	0.00 (0.05)	−0.02 (0.05)	−0.14 (0.04)	−0.17 (0.03)	−0.46 (0.04)	−0.49 (0.03)
FATGR	−0.01 (0.04)	0.01 (0.04)	−0.15 (0.04)	−0.13 (0.03)	−0.17 (0.04)	−0.16 (0.04)
FATC	0.00 (0.05)	0.06 (0.04)	−0.10 (0.04)	−0.09 (0.04)	−0.17 (0.05)	−0.16 (0.05)
FAT5	0.00 (0.05)	0.05 (0.04)	−0.13 (0.04)	−0.08 (0.04)	−0.12 (0.05)	−0.12 (0.05)
EMW	−0.04 (0.05)	0.08 (0.04)	−0.10 (0.04)	−0.05 (0.04)	−0.11 (0.05)	−0.01 (0.05)
EMD	0.00 (0.05)	0.06 (0.05)	0.08 (0.05)	−0.01 (0.04)	−0.09 (0.05)	−0.09 (0.05)
EMA	−0.03 (0.05)	0.09 (0.04)	−0.11 (0.04)	−0.02 (0.04)	−0.12 (0.05)	−0.07 (0.05)

[1]DP = dressing percentage; FATGR = carcass fat depth at the GR site located at the 12th rib, 110 mm from the midline; FATC = carcass 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; FAT5 = carcass fat depth at the fifth rib; EMW = eye muscle width; EMD = eye muscle depth; EMA = eye muscle area.

[2]yY = yearling scoured wool brightness; y(Y-Z) = yearling scoured wool yellowness; yBCOV = yearling breech cover; mBRWR = marking breech wrinkle; yBRWR = yearling breech wrinkle; yBDWR = yearling body wrinkle.

finer wool diameter also occurs, which is likely to lead to reductions in HCW, eye muscle dimensions, carcass lean cuts, and bone weight. Although selection for increased SL will result generally in higher mean performances in the carcass traits, the larger responses are expected for HCW, DP, FATGR, FATLL, and the muscle weights.

Wool Color and Visual Traits with Carcass Measures Traits. The estimates of genetic and phenotypic correlations between yearling wool color and visual traits and carcass traits are shown in Table 5, with the genetic correlations for adult wool and visual traits available in Supplementary Table S3 (see the online version of the article at http://journalofanimalscience.org). For HCW, there were low unfavorable genetic correlations with yearling scoured wool brightness (**yY**; −0.36 ± 0.12) and yearling Y-Z (0.20 ± 0.11) but moderate to high favorable correlations with BCOV and BRWR scores (−0.44 to −0.74). There were also highly favorable (negative) genetic correlations between DP and BCOV and BRWR scores (−0.55 to −0.98), with an unfavorable correlation with yY. There were also moderate to high negative genetic correlations between the various measures of carcass fat and BCOV and BRWR scores, whereas the correlations with eye muscle traits were generally negligible. The corresponding genetic correlations with the adult wool traits showed a pattern and magnitude similar to those of the yearling traits.

Wool Color and Visual Traits with Carcass Dissection Traits. The estimates of genetic and phenotypic correlations between yearling wool color and visual traits and carcass dissection traits are shown in Table 6, with the genetic correlations for adult wool and visual traits available in Supplementary Table S4 (see the online version of the article at http://journalofanimalscience.org). There were generally moderate to high and favorable (negative) genetic correlations between the visual traits and muscle and bone weights, although those for LMY were unfavorable with wrinkle scores. Most of the carcass dissection traits were unfavorably correlated with yY and yearling Y-Z. The corresponding genetic correlations with the adult wool traits showed a pattern and magnitude similar to those of the yearling traits. Genetically increasing LMY, or reducing carcass fat, is expected to be accompanied by increased skin wrinkliness and reduced bareness of the breech, although negligible changes will occur in BCOV and marking BRWR in response to selection for LMY. In contrast, the similar patterns of genetic correlation of HCW and DP with the yearling wool color and visual traits, patterns that were also observed for the muscle and bone weights, indicate that genetic improvement of HCW and DP will lead to sheep with fewer wrinkles on the body (plainer-bodied sheep) having barer breeches but with minor deterioration in wool color.

Table 6. Estimates of genetic and phenotypic correlations (SE) between yearling wool color and visual traits and carcass dissection traits

Carcass dissection traits[1]	Yearling wool color and visual traits[2]					
	yY	y(Y-Z)	yBCOV	mBRWR	yBRWR	yBDWR
Genetic correlations						
LMY	−0.06 (0.16)	0.13 (0.14)	0.03 (0.20)	0.02 (0.16)	0.46 (0.17)	0.51 (0.18)
WTLL	−0.27 (0.13)	0.20 (0.11)	−0.61 (0.13)	−0.46 (0.11)	−0.34 (0.12)	−0.48 (0.11)
WTTOP	−0.28 (0.13)	0.13 (0.11)	−0.68 (0.12)	−0.54 (0.11)	−0.44 (0.11)	−0.51 (0.10)
WTRND	−0.46 (0.12)	0.25 (0.11)	−0.80 (0.11)	−0.57 (0.10)	−0.44 (0.11)	−0.46 (0.11)
FATLL	−0.34 (0.18)	0.07 (0.15)	−0.01 (0.04)	−0.60 (0.16)	−0.68 (0.17)	−0.73 (0.17)
BONE	−0.36 (0.13)	0.26 (0.11)	−0.69 (0.13)	−0.37 (0.13)	−0.26 (0.13)	−0.37 (0.12)
Phenotypic correlations						
LMY	−0.04 (0.04)	0.04 (0.04)	0.06 (0.04)	0.07 (0.04)	0.06 (0.05)	0.11 (0.05)
WTLL	−0.02 (0.04)	0.10 (0.04)	−0.18 (0.04)	−0.13 (0.03)	−0.14 (0.04)	−0.12 (0.04)
WTTOP	−0.03 (0.04)	0.10 (0.04)	−0.19 (0.04)	−0.15 (0.03)	−0.19 (0.04)	−0.12 (0.04)
WTRND	−0.10 (0.04)	0.11 (0.04)	−0.18 (0.04)	−0.11 (0.04)	−0.16 (0.04)	−0.10 (0.04)
FATLL	−0.02 (0.04)	0.07 (0.04)	−0.17 (0.04)	−0.15 (0.03)	−0.17 (0.04)	−0.18 (0.04)
BONE	−0.09 (0.04)	0.12 (0.04)	−0.15 (0.04)	−0.08 (0.03)	−0.14 (0.04)	−0.09 (0.04)

[1]LMY = lean meat yield; WTLL = loin muscle weight; WTTOP = topside weight; WTRND = round weight; FATLL = weight of fat trim of the loin; BONE = hind leg bone weight.

[2]yY = yearling scoured wool brightness; y(Y-Z) = yearling scoured wool yellowness; yBCOV = yearling breech cover; mBRWR = marking breech wrinkle; yBRWR = yearling breech wrinkle; yBDWR = yearling body wrinkle.

Ultrasound Traits with Carcass Measures Traits. The estimates of genetic and phenotypic correlations between ultrasound traits and carcass traits are shown in Table 7. Genetic correlations between ultrasound measures of fat depth measured at the C site on live animals and the various carcass measures of fat depth were generally high (0.63 to 0.94), consistent with other reports where ultrasound fat depth was adjusted for live weight and measures of carcass fat depth were adjusted for carcass weight (Waldron et al., 1992; Greeff et al., 2008; Mortimer et al., 2010; Maximini et al., 2012; Brito et al., 2015; Einarsson et al., 2015). Genetic correlations between ultrasound EMD and carcass EMD and EMA were also high (0.82 to 0.99), although they were lower with carcass EMW (0.32 to 0.36), which confirms previous estimates (Greeff et al., 2008; Mortimer et al., 2010; Maximini et al., 2012). Increases in sire ASBV for pwFATUS and pwEMDUS have been associated with the carcasses of the crossbred progeny having greater fat at the GR and C sites (Hegarty et al., 2006a,b; Hopkins et al., 2007b) and larger EMD and EMA, respectively (Hegarty et al., 2006a; Hopkins et al., 2007b), where carcass measures were adjusted for HCW. For Merinos, these effects of the sire ASBV were also observed on the various carcass fat measures but not the carcass muscle measures (Gardner et al., 2010). The genetic correlations between ultrasound muscle depth and carcass fat measures were positive and moderate to high (0.43 to 0.93), as previously observed (Waldron et al., 1992; Greeff et al., 2008; Mortimer et al., 2010; Maximini et al., 2012; Brito et al., 2015), although a low negative correlation involving FATGR has been reported

(Einarsson et al., 2015). Significant regression coefficients of sire breeding value for pwEMDUS on carcass fat measures have been reported for second-cross progeny of Poll Dorset sires (Hegarty et al., 2006b), although the coefficients were positive for FATGR and negative for FATC. In contrast, the genetic correlations were generally negligible between ultrasound fat depth and carcass muscle measures, as earlier reported (Greeff et al., 2008; Mortimer et al., 2010; Maximini et al., 2012; EMA only). This result agrees with no effect being observed for sire pwFATUS ASBV on loin muscle depth in crossbred progeny of Poll Dorset sires (Hegarty et al., 2006a; Hopkins et al., 2007b) and the loin muscle measures in Merinos (Gardner et al., 2010). However, a negative effect of the sire pwFATUS ASBV on loin muscle area was reported by Hopkins et al. (2007b). The ultrasound measures were all highly genetically correlated with DP and moderately to highly correlated with HCW, similar to the genetic correlations with postweaning and yearling live weights (Mortimer et al., 2017). The estimates were consistent with those reported by Greeff et al. (2008) and Brito et al. (2015; HCW only), although in meat sheep breeds, the genetic relationships with HCW tended to be not significantly different from 0 from analyses where the ultrasound traits were adjusted for live weight (Conington et al., 1998; van Heelsum et al., 2006; Karamichou et al., 2007; Rius-Vilarrasa et al., 2009; Mortimer et al., 2010). This is consistent with sire ASBV for the ultrasound traits having no effect on HCW of carcasses of progeny of Poll Dorset sires (Hopkins et al., 2007b) and Merinos (Gardner et al., 2010), whereas in more recent work using IN data across breeds,

Table 7. Estimates of genetic and phenotypic correlations (SE) between ultrasound traits and carcass measures traits

Carcass measures traits[1]	Ultrasound traits[2]			
	pwFATUS	pwEMDUS	yFATUS	yEMDUS
Genetic correlations				
HCW	0.40 (0.16)	0.75 (0.16)	0.59 (0.12)	0.51 (0.11)
DP	0.86 (0.27)	0.66 (0.20)	0.74 (0.18)	0.63 (0.17)
FATGR	0.89 (0.14)	0.92 (0.23)	0.92 (0.09)	0.71 (0.15)
FATC	0.94 (0.16)	0.93 (0.24)	0.75 (0.14)	0.43 (0.15)
FAT5	0.63 (0.22)	0.74 (0.30)	0.82 (0.17)	0.54 (0.18)
EMW	−0.18 (0.22)	0.36 (0.26)	−0.02 (0.17)	0.32 (0.16)
EMD	0.25 (0.29)	0.89 (0.19)	0.37 (0.21)	0.86 (0.16)
EMA	0.04 (0.25)	0.99 (0.25)	0.25 (0.19)	0.82 (0.14)
Phenotypic correlations				
HCW	0.30 (0.03)	0.39 (0.03)	0.37 (0.04)	0.47 (0.04)
DP	0.18 (0.03)	0.18 (0.03)	0.33 (0.04)	0.49 (0.04)
FATGR	0.39 (0.03)	0.32 (0.03)	0.48 (0.03)	0.47 (0.04)
FATC	0.28 (0.03)	0.22 (0.03)	0.44 (0.04)	0.31 (0.05)
FAT5	0.28 (0.03)	0.25 (0.03)	0.26 (0.04)	0.30 (0.05)
EMW	0.02 (0.04)	0.17 (0.03)	0.01 (0.05)	0.25 (0.05)
EMD	0.13 (0.03)	0.26 (0.03)	0.22 (0.05)	0.47 (0.04)
EMA	0.11 (0.03)	0.27 (0.03)	0.17 (0.05)	0.48 (0.04)

[1]DP = dressing percentage; FATGR = carcass fat depth at the GR site located at the 12th rib, 110 mm from the midline; FATC = carcass 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; FAT5 = carcass fat depth at the fifth rib; EMW = eye muscle width; EMD = eye muscle depth; EMA = eye muscle area.

[2]pwFATUS = postweaning live ultrasound fat (C site); pwEMDUS = postweaning live ultrasound eye muscle depth; yFATUS = yearling live ultrasound fat (C site); yEMDUS = yearling live ultrasound eye muscle depth.

Table 8. Estimates of genetic and phenotypic correlations (SE) between ultrasound traits and carcass dissection traits

Carcass dissection traits[1]	Ultrasound traits[2]			
	pwFATUS	pwEMDUS	yFATUS	yEMDUS
Genetic correlations				
LMY	−0.67 (0.21)	−0.12 (0.28)	−0.82 (0.15)	−0.16 (0.18)
WTLL	0.55 (0.18)	0.84 (0.10)	0.41 (0.13)	0.76 (0.10)
WTTOP	0.22 (0.19)	0.76 (0.20)	0.56 (0.12)	0.64 (0.11)
WTRND	0.13 (0.18)	0.47 (0.20)	0.39 (0.14)	0.39 (0.13)
FATLL	0.86 (0.18)	0.83 (0.16)	0.98 (0.11)	0.90 (0.16)
BONE	−0.11 (0.19)	0.27 (0.22)	0.28 (0.14)	0.34 (0.13)
Phenotypic correlations				
LMY	−0.27 (0.03)	−0.11 (0.03)	−0.34 (0.04)	−0.15 (0.05)
WTLL	0.18 (0.03)	0.38 (0.03)	0.22 (0.04)	0.52 (0.04)
WTTOP	0.14 (0.04)	0.32 (0.03)	0.22 (0.04)	0.45 (0.04)
WTRND	0.13 (0.04)	0.26 (0.03)	0.16 (0.04)	0.32 (0.05)
FATLL	0.32 (0.03)	0.31 (0.03)	0.41 (0.04)	0.39 (0.04)
BONE	0.11 (0.04)	0.25 (0.03)	0.16 (0.04)	0.30 (0.05)

[1]LMY = lean meat yield; WTLL = loin muscle weight; WTTOP = topside weight; WTRND = round weight; FATLL = weight of fat trim of the loin; BONE = hind leg bone weight.

[2]pwFATUS = postweaning live ultrasound fat (C site measured on the cut surface between the 12th and 13th ribs over the maximum depth of the eye muscle); pwEMDUS = postweaning live ultrasound eye muscle depth; yFATUS = yearling live ultrasound fat (C site); yEMDUS = yearling live ultrasound eye muscle depth.

Gardner et al. (2015) showed that increasing the sire ASBV for the ultrasound traits increased HCW and DP.

Ultrasound Traits with Carcass Dissection Traits. The estimates of genetic and phenotypic correlations between ultrasound traits and carcass dissection traits are shown in Table 8. There were high genetic correlations between ultrasound EMD and WTLL and WTTOP (0.64 to 0.84), although those with WTRND were smaller (0.39 and 0.47) and those with LMY were negligible. There were also high genetic correlations between ultrasound EMD and FATLL (0.83 and 0.90) but smaller with BONE (0.27 and 0.34). Similarly, there were high genetic correlations between ultrasound fat and FATLL (0.86 and 0.98), although those between ultrasound fat depth and the various muscles were smaller. The genetic correlations between ultrasound fat and LMY were highly negative (−0.67 and −0.82), whereas those between ultrasound muscle depth and LMY were weakly negative (−0.12 and −0.16). Overall, these patterns of genetic correlations were similar to but generally weaker than those estimated from an earlier sampling of the IN progeny that also included progeny of terminal and maternal breed sires (Mortimer et al., 2010). The genetic correlations were consistent with reported significant positive regressions of sire pwEMDUS on eye muscle and topside weights (Hegarty et al., 2006a) and carcass fat (Hegarty et al., 2006a). However, they contrasted with the significant positive regressions reported for this ASBV on measures of carcass lean (Hopkins et al., 2007b; Anderson et al., 2015) and the nonsignificant effect of the ASBV on carcass fat measured by CT methods in Merinos (Anderson et al., 2016). On the other hand, the genetic correlations agreed with significant positive regressions reported for sire pwFATUS ASBV on carcass fat measures (Hegarty et al., 2006a; Hopkins et al., 2007b; Anderson et al., 2015, 2016) and carcass lean (Hopkins et al., 2007b; Anderson et al., 2015). However, previous reports found no significant effect of the sire pwFATUS ASBV on weights of loin (Hegarty et al., 2006a) and topside muscles (Hegarty et al., 2006a; Gardner et al., 2010). The expectation of high genetic correlations between ultrasound fat depth and carcass fat and between ultrasound EMD and carcass lean are supported by studies involving CT predictions. Jones et al. (2004) reported genetic correlations between ultrasound measures and CT predictions ranging from 0.41 to 0.64 for fat and 0.42 to 0.53 for muscle for Texel, Suffolk, and Charollais breeds. Similar genetic correlations in Scottish Blackface sheep were reported by Lambe et al. (2008) for fat (0.62 ± 0.17) and muscle (0.13 ± 0.15) as well as by Kvame and Vangen (2007) in Norwegian White sheep (0.82 ± 0.10 and 0.70 ± 0.13 for

fat and muscle, respectively). Although our phenotypic correlations were lower than the corresponding genetic correlations, in the CT studies, the phenotypic correlations were generally similar to or greater than the corresponding genetic correlations.

Carcass Measures Traits. The estimates of genetic and phenotypic correlations among the carcass measures are shown in Table 9. The genetic correlation between HCW and DP was high (0.78 ± 0.09) and those between HCW and carcass fat (0.47 to 0.57) tended to be slightly higher than those with muscle (0.31 to 0.42). Few estimates of genetic correlations among carcass measures in sheep are available. Literature estimates of the genetic correlations of HCW with both carcass fat and muscle are moderately to strongly positive (Safari et al., 2005; Ingham et al., 2007). Dressing percent was highly genetically correlated with carcass fat (0.76 to 0.96) but negligible to lowly correlated with carcass muscle (0.13 to 0.42), whereas Safari et al. (2005) and Ingham et al. (2007) reported genetic correlations with carcass fat that were weak. The various carcass fat measures were highly genetically correlated, as was EMA with EMD and EMW, although there was only a moderate correlation between EMW and EMD (0.38 ± 0.26). The genetic correlations between the carcass fat and muscle measures were generally negative, although negligible in magnitude. These genetic relationships are generally consistent with literature estimates (Safari et al., 2005; Ingham et al., 2007). The phenotypic correlations between HCW and the carcass traits were similar to the genetic correlations, whereas those with DP tended to be lower. The phenotypic correlations among the fat measures were lower than the corresponding genetic correlations, although those among the muscle measures were similar. The phenotypic correlations between the carcass fat and muscle measures were generally negligible, although positive.

Carcass Dissection Traits. The estimates of genetic and phenotypic correlations among the carcass dissection traits are shown in Table 10. Lean meat yield was highly negatively genetically correlated with FATLL, but the correlations with BONE and the meat cuts were generally negligible. Across a range of meat sheep breeds, genetic correlations have tended to be positive and moderate to very strong for similar traits derived using a carcass dissection method (Conington et al., 1998), CT prediction (Jones et al., 2004), or VIAscan carcass grading system (Jopson et al., 2009; Johnson et al., 2015a,b). Bone weight was highly genetically correlated with the various meat cuts but was only lowly correlated with FATLL. There were high genetic correlations among the various meat cuts, although the estimates were at the lower end of the range reported among individual primal cuts assessed using VIAscan carcass grading (Jopson et al., 2009; Rius-Vilarrasa et al., 2009;

Einarsson et al., 2015; Johnson et al., 2015a,b). The phenotypic correlations tended to be similar to or slightly lower than the corresponding genetic correlations.

Carcass Measures with Dissection Traits. The estimates of genetic and phenotypic correlations between the carcass measures and dissection traits are shown in Table 11. Hot carcass weight was highly genetically correlated with all the carcass dissection traits (0.62 to 0.89), except LMY, which was low and negative (-0.22 ± 0.17). Similarly, DP was highly genetically correlated with all the carcass dissection traits (0.48 to 0.98), except LMY, which was highly negative (-0.66 ± 0.17). Carcass weight has been shown to have high positive genetic correlations with VIAscan assessments of various primal cuts (Jopson et al., 2009; Rius-Vilarrasa et al., 2009; Johnson et al., 2015a,b). Lean meat yield was highly negatively genetically correlated with the carcass fat measures (-0.71 to -0.84), whereas those with the muscle measures were moderate to highly positive (0.46 to 0.63). These genetic relationships were generally consistent with those of carcass total lean with carcass fatness and various primal cuts (Jopson et al., 2009; Johnson et al., 2015a,b) and a moderate negative genetic correlation of LMY with FATGR (Einarsson et al., 2015). The carcass fat measures were highly genetically correlated with FATLL (0.86 to 0.96), low to moderately correlated with the various meat cuts (0.20 to 0.45), and negligibly correlated with BONE. For these same traits, estimates based on multibreed data from the IN program, adjusted for HCW, were similar between carcass fat measures and FATLL (strongly positive), but genetic correlations of the carcass fat measures with the meat cuts and BONE were moderately negative and strongly negative, respectively (Mortimer et al., 2011). In maternal and terminal sire breeds, VIAscan-assessed FATGR also had moderate negative genetic correlations with various primal cuts (Johnson et al., 2015a,b). In contrast to the fat measures, the carcass muscle measures were moderately to highly genetically correlated with the various meat cuts (0.38 to 0.76), negligibly genetically correlated with FATLL, and lowly genetically correlated with BONE (0.21 to 0.39). These genetic correlation estimates were consistent with those reported by Mortimer et al. (2011). The phenotypic correlations were generally the same sign as the corresponding genetic correlations and were similar or slightly smaller in magnitude.

Conclusions

This study has established for maternal and wool-producing breeds, such as the Merino, that a range of carcass fat and lean traits are of moderate to high heritability. For both the carcass traits previously reported in the literature and the new traits reported in this study,

Table 9. Estimates of genetic (below diagonal) and phenotypic (above diagonal) correlations (SE) among carcass measures traits[1]

	HCW	DP	FATGR	FATC	FAT5	EMW	EMD	EMA
HCW	–	0.58 (0.02)	0.58 (0.02)	0.40 (0.03)	0.37 (0.03)	0.34 (0.03)	0.35 (0.03)	0.43 (0.03)
DP	0.78 (0.09)	–	0.43 (0.03)	0.27 (0.03)	0.21 (0.03)	0.20 (0.03)	0.20 (0.03)	0.24 (0.03)
FATGR	0.57 (0.11)	0.96 (0.11)	–	0.53 (0.02)	0.50 (0.02)	0.07 (0.03)	0.26 (0.03)	0.24 (0.03)
FATC	0.47 (0.14)	0.88 (0.17)	0.92 (0.10)	–	0.34 (0.03)	−0.02 (0.03)	0.15 (0.03)	0.10 (0.03)
FAT5	0.56 (0.17)	0.76 (0.23)	0.95 (0.14)	0.83 (0.16)	–	−0.05 (0.03)	0.14 (0.03)	0.08 (0.03)
EMW	0.31 (0.16)	0.13 (0.23)	−0.15 (0.21)	−0.40 (0.20)	−0.14 (0.24)	–	0.23 (0.03)	0.65 (0.02)
EMD	0.39 (0.21)	0.42 (0.29)	−0.04 (0.28)	0.04 (0.28)	0.04 (0.33)	0.38 (0.26)	–	0.88 (0.01)
EMA	0.42 (0.18)	0.30 (0.25)	−0.15 (0.24)	−0.25 (0.25)	−0.13 (0.28)	0.83 (0.11)	0.83 (0.10)	–

[1]DP = dressing percentage; FATGR = carcass fat depth at the GR site located at the 12th rib, 110 mm from the midline; FATC = carcass 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; FAT5 = carcass fat depth at the fifth rib; EMW = eye muscle width; EMD = eye muscle depth; EMA = eye muscle area.

Table 10. Estimates of genetic (below diagonal) and phenotypic (above diagonal) correlations (SE) among carcass dissection traits[1]

	LMY	WTLL	WTTOP	WTRND	FATLL	BONE
LMY	–	0.11 (0.03)	0.10 (0.03)	0.22 (0.03)	−0.42 (0.03)	0.07 (0.03)
WTLL	0.13 (0.19)	–	0.67 (0.02)	0.54 (0.02)	0.44 (0.02)	0.53 (0.02)
WTTOP	0.04 (0.20)	0.73 (0.08)	–	0.69 (0.02)	0.41 (0.03)	0.69 (0.02)
WTRND	0.29 (0.18)	0.49 (0.12)	0.82 (0.07)	–	0.37 (0.03)	0.67 (0.02)
FATLL	−0.79 (0.17)	0.57 (0.15)	0.48 (0.17)	0.34 (0.17)	–	0.30 (0.03)
BONE	0.19 (0.20)	0.56 (0.12)	0.86 (0.06)	0.86 (0.07)	0.22 (0.20)	–

[1]LMY = lean meat yield; WTLL = loin muscle weight; WTTOP = topside weight; WTRND = round weight; FATLL = weight of fat trim of the loin; BONE = hind leg bone weight.

Table 11. Estimates of genetic and phenotypic correlations (SE) between carcass measures traits and carcass dissection traits

Carcass measures traits[1]	Carcass dissection traits[2]					
	LMY	WTLL	WTTOP	WTRND	FATLL	BONE
Genetic correlations						
HCW	−0.22 (0.17)	0.70 (0.08)	0.95 (0.04)	0.83 (0.06)	0.62 (0.13)	0.89 (0.05)
DP	−0.66 (0.17)	0.68 (0.15)	0.72 (0.14)	0.56 (0.16)	0.98 (0.16)	0.48 (0.18)
FATGR	−0.84 (0.10)	0.44 (0.14)	0.45 (0.15)	0.28 (0.16)	0.96 (0.06)	0.11 (0.18)
FATC	−0.81 (0.14)	0.39 (0.16)	0.32 (0.17)	0.20 (0.17)	0.93 (0.12)	0.10 (0.18)
FAT5	−0.71 (0.17)	0.37 (0.19)	0.44 (0.20)	0.32 (0.21)	0.86 (0.19)	0.16 (0.21)
EMW	0.58 (0.18)	0.58 (0.14)	0.44 (0.16)	0.38 (0.16)	0.05 (0.24)	0.39 (0.17)
EMD	0.46 (0.30)	0.69 (0.19)	0.49 (0.21)	0.40 (0.23)	0.05 (0.32)	0.21 (0.25)
EMA	0.63 (0.23)	0.76 (0.14)	0.54 (0.17)	0.45 (0.19)	0.01 (0.28)	0.36 (0.21)
Phenotypic correlations						
HCW	−0.29 (0.03)	0.71 (0.02)	0.78 (0.01)	0.74 (0.01)	0.59 (0.02)	0.74 (0.01)
DP	−0.37 (0.03)	0.35 (0.03)	0.36 (0.03)	0.31 (0.03)	0.37 (0.03)	0.27 (0.03)
FATGR	−0.56 (0.02)	0.42 (0.03)	0.38 (0.03)	0.28 (0.16)	0.67 (0.02)	0.26 (0.03)
FATC	−0.39 (0.03)	0.26 (0.03)	0.24 (0.03)	0.20 (0.03)	0.52 (0.02)	0.19 (0.03)
FAT5	−0.44 (0.02)	0.25 (0.03)	0.24 (0.03)	0.17 (0.03)	0.44 (0.02)	0.15 (0.03)
EMW	0.26 (0.03)	0.41 (0.03)	0.40 (0.03)	0.34 (0.03)	0.08 (0.03)	0.33 (0.03)
EMD	0.12 (0.03)	0.39 (0.03)	0.36 (0.03)	0.28 (0.03)	0.19 (0.03)	0.25 (0.03)
EMA	0.22 (0.03)	0.49 (0.02)	0.46 (0.02)	0.38 (0.03)	0.18 (0.03)	0.35 (0.03)

[1]DP = dressing percentage; FATGR = carcass fat depth at the GR site located at the 12th rib, 110 mm from the midline; FATC = carcass 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; FAT5 = carcass fat depth at the fifth rib; EMW = eye muscle width; EMD = eye muscle depth; EMA = eye muscle area.

[2]LMY = lean meat yield; WTLL = loin muscle weight; WTTOP = topside weight; WTRND = round weight; FATLL = weight of fat trim of the loin; BONE = hind leg bone weight.

it is evident that carcass traits will respond to selection. There is also no evidence that genotype × environment interactions are important for these carcass traits. This study provides estimates of genetic correlations for a greatly expanded range of wool production and quality traits with carcass composition traits, which will be useful for designing and evaluating the efficacy of various selection indexes in altering the composition of carcasses produced by dual-purpose breeds. The genetic correlations reported herein underline the need to carefully consider the emphasis on carcass composition traits in designing breeding programs that aim to improve both wool and meat production and meet market specifications and consumer requirements for lamb products.

Traditional wool breeding programs emphasize selection for increased wool weight, with possibly reduced FD. From our results, selection for increased wool weight will result in a correlated reduction in carcass fat and DP with little effect on carcass muscle, whereas selection for lower FD will reduce HCW as well as carcass fat and muscle. There were high genetic correlations between the ultrasound measures of fat and muscle depth in live sheep and the carcass measures and carcass dissection traits for fat and muscle, respectively. This shows that these ultrasound traits can be used in selection programs to successfully change carcass traits. Selection to increase HCW (and DP) will result in plainer-bodied (less wrinkle) and barer breech sheep (favorable) with minor deterioration in scoured wool color (reduced brightness and increased yellowness). Selection for reduced fat will also result in plainer-bodied sheep. Breeding values for LMY are now available for meat sheep (Sheep Genetics, 2016). The genetic correlations reported in our study indicate that selection for increased LMY in Merinos would result in a large reduction in carcass fat and DP, with a smaller increase in carcass muscle and some increase in wool weight and wrinkles. The results of this study indicate that although there are no major antagonisms between the wool and carcass traits, care needs to be exercised in selection for both objectives to ensure that the unfavorable correlations are taken into account. These genetic parameters will contribute to calculation of more accurate EBV and selection indexes for gains in dual-purpose wool and meat breeding objectives.

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1   **Supplementary Table S1.** Estimates of genetic correlations (± SE) between adult wool traits[1] and carcass measures traits[2]

	aGFW	aYLD	aCFW	aFD	aFDSD	aFDCV	aSS	aSL	aCUR
HCWT	-0.10 ± 0.11	-0.08 ± 0.11	-0.13 ± 0.11	0.34 ± 0.10	-0.03 ± 0.11	-0.30 ± 0.11	0.16 ± 0.13	0.37 ± 0.10	0.00 ± 0.11
DP	-0.69 ± 0.15	-0.03 ± 0.15	-0.69 ± 0.16	0.10 ± 0.13	-0.42 ± 0.15	-0.62 ± 0.16	0.10 ± 0.17	0.43 ± 0.15	0.11 ± 0.15
FATGR	-0.48 ± 0.13	-0.20 ± 0.14	-0.54 ± 0.14	0.23 ± 0.12	-0.19 ± 0.13	-0.43 ± 0.13	0.02 ± 0.15	0.37 ± 0.12	0.15 ± 0.14
FATC	-0.33 ± 0.13	-0.22 ± 0.13	-0.38 ± 0.13	0.17 ± 0.12	-0.14 ± 0.13	-0.33 ± 0.13	-0.01 ± 0.15	0.28 ± 0.12	0.21 ± 0.13
FAT5	-0.42 ± 0.16	-0.41 ± 0.16	-0.51 ± 0.16	0.20 ± 0.15	-0.15 ± 0.16	-0.36 ± 0.16	0.16 ± 0.18	0.31 ± 0.15	0.28 ± 0.16
EMW	0.17 ± 0.14	0.09 ± 0.14	0.16 ± 0.14	0.18 ± 0.13	0.05 ± 0.14	-0.08 ± 0.14	0.10 ± 0.16	0.20 ± 0.13	-0.11 ± 0.14
EMD	-0.21 ± 0.18	-0.09 ± 0.18	-0.21 ± 0.18	0.57 ± 0.20	0.12 ± 0.19	-0.30 ± 0.19	0.51 ± 0.23	0.35 ± 0.18	0.43 ± 0.19
EMA	-0.04 ± 0.16	0.00 ± 0.17	-0.05 ± 0.16	0.54 ± 0.17	0.09 ± 0.17	-0.29 ± 0.17	0.40 ± 0.19	0.37 ± 0.16	0.20 ± 0.16

2   [1]aGFW = adult greasy fleece weight; aYLD = adult clean yield; aCFW = adult clean fleece weight; aFD = adult fiber diameter; aFDSD = adult

3   fiber diameter standard deviation; aFDCV = adult fiber diameter coefficient of variation; aSS = adult staple strength; aSL = adult staple length;

4   aCUR = adult fiber curvature.

5   [2]HCWT = hot carcass weight; DP = dressing percent, FATGR = carcass fat depth at the GR site; FATC = carcass fat depth at the C site; FAT5 =

6   carcass fat depth at the 5th rib; EMW = eye muscle width; EMD = eye muscle depth; EMA = eye muscle area.

7 **Supplementary Table S2.** Estimates of genetic correlations (± SE) between adult wool traits[1] and carcass dissection traits[2]

	aGFW	aYLD	aCFW	aFD	aFDSD	aFDCV	aSS	aSL	aCUR
LMY	0.38 ± 0.15	0.22 ± 0.15	0.42 ± 0.16	0.01 ± 0.13	0.21 ± 0.15	0.24 ± 0.15	0.11 ± 0.16	-0.16 ± 0.14	-0.15 ± 0.15
WTLL	-0.07 ± 0.11	-0.08 ± 0.12	-0.11 ± 0.11	0.26 ± 0.10	-0.09 ± 0.12	-0.32 ± 0.11	0.12 ± 0.13	0.40 ± 0.11	0.02 ± 0.12
WTTOP	-0.04 ± 0.11	-0.14 ± 0.12	-0.09 ± 0.11	0.29 ± 0.10	0.02 ± 0.12	-0.23 ± 0.12	0.14 ± 0.13	0.33 ± 0.11	0.03 ± 0.12
WTRND	-0.04 ± 0.11	0.05 ± 0.12	-0.04 ± 0.11	0.33 ± 0.10	0.05 ± 0.12	-0.22 ± 0.11	0.20 ± 0.13	0.29 ± 0.11	-0.11 ± 0.12
FATLL	-0.55 ± 0.16	-0.38 ± 0.17	-0.46 ± 0.15	0.22 ± 0.14	-0.22 ± 0.16	-0.42 ± 0.16	-0.08 ± 0.17	0.48 ± 0.15	0.13 ± 0.16
BONE	0.05 ± 0.12	0.03 ± 0.12	0.06 ± 0.12	0.35 ± 0.11	0.20 ± 0.12	-0.05 ± 0.12	0.10 ± 0.14	0.26 ± 0.11	0.02 ± 0.12

8 [1]See Table S1 for traits.

9 [2]LMY = lean meat yield; WTLL = loin muscle weight; WTTOP = topside weight; WTRND = round weight; FATLL = weight of fat trim of the

10 loin; BONE = hind leg bone weight.

Supplementary Table S3. Estimates of genetic correlations (± SE) between adult wool color and visual traits[1] and carcass measures traits[2]

	aY	a(Y-Z)	aBCOV	aBRWR	aBDWR
HCWT	-0.21 ± 0.14	0.18 ± 0.12	-0.61 ± 0.18	-0.49 ± 0.12	-0.61 ± 0.12
DP	-0.29 ± 0.18	0.06 ± 0.16	-0.80 ± 0.26	-0.77 ± 0.18	-0.92 ± 0.21
FATGR	-0.32 ± 0.16	0.09 ± 0.14	-0.65 ± 0.22	-0.73 ± 0.16	-0.73 ± 0.17
FATC	-0.04 ± 0.19	0.15 ± 0.14	-0.46 ± 0.22	-0.44 ± 0.16	-0.34 ± 0.16
FAT5	-0.04 ± 0.19	0.00 ± 0.17	-0.70 ± 0.27	-0.78 ± 0.18	-0.54 ± 0.20
EMW	-0.14 ± 0.17	0.41 ± 0.14	-0.51 ± 0.24	0.05 ± 0.16	-0.17 ± 0.17
EMD	-0.18 ± 0.23	0.03 ± 0.20	0.17 ± 0.33	-0.15 ± 0.22	-0.15 ± 0.22
EMA	-0.21 ± 0.20	0.26 ± 0.18	-0.22 ± 0.28	-0.08 ± 0.19	-0.20 ± 0.19

[1]aY = adult scoured wool brightness, a(Y-Z) = adult scoured wool yellowness; aBCOV = adult breech cover, aBRWR = adult breech wrinkle; aBDWR = adult body wrinkle.

[2]See Table S1 for traits.

3

15 **Supplementary Table S4.** Estimates of genetic correlations (± SE) between adult wool color and visual traits[1] and carcass dissection traits[2]

	aY	a(Y-Z)	aBCOV	aBRWR	aBDWR
LMY	0.15 ± 0.18	0.13 ± 0.16	0.33 ± 0.26	0.46 ± 0.19	0.34 ± 0.19
WTLL	-0.06 ± 0.14	0.17 ± 0.12	-0.52 ± 0.19	-0.38 ± 0.13	-0.59 ± 0.12
WTTOP	-0.24 ± 0.14	0.11 ± 0.13	-0.70 ± 0.18	-0.45 ± 0.13	-0.53 ± 0.13
WTRND	-0.29 ± 0.13	0.23 ± 0.12	-0.57 ± 0.18	-0.43 ± 0.12	-0.50 ± 0.12
FATLL	-0.29 ± 0.19	0.07 ± 0.16	-0.97 ± 0.27	-0.85 ± 0.17	-0.84 ± 0.20
BONE	-0.12 ± 0.15	0.23 ± 0.13	-0.46 ± 0.20	-0.27 ± 0.14	-0.42 ± 0.13

16 [1]See Table S3 for traits.

17 [2]See Table S2 for traits.