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Preliminary estimates of genetic parameters for carcass and meat quality traits in Australian sheep

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Abstract. Using performance from progeny born in 2007 and 2008 generated by the Information Nucleus program of the Cooperative Research Centre for Sheep Industry Innovation, preliminary estimates of heritability were obtained for a range of novel carcass and meat attributes of lamb relevant to consumers, including carcass characteristics, meat quality and nutritional value of lamb. Phenotypic and genetic correlations of live animal traits with carcass composition and meat quality traits were also estimated. The data were from progeny located at eight sites, sired by 183 rams from Merino, maternal and terminal meat breeds and were representative of the Merino, Border Leicester × Merino, Terminal × Merino and Terminal × Border Leicester-Merino production types of the Australian sheep industry. Data were available from 7176 lambs for weaning weight, 6771 lambs for ultrasound scanning and 4110 lambs for slaughter traits. For the novel meat quality traits, generally moderate to high heritability estimates were obtained for meat quality measures of shear force (0.27 aged 1 day, 0.38 aged 5 days), intramuscular fat (0.39), retail meat colour (range of 0.09 to 0.44) and myoglobin content (0.22). The nutritional value traits of omega-3 fatty acids and iron and zinc contents tended to have low to moderate heritabilities (0.11–0.37), although these were based on fewer records. Fresh meat colour traits were of low to moderate heritability (0.06–0.21) whereas measures of meat pH were of low heritability (~0.10). For the carcass traits, estimates of heritability were moderate to high for the various measures of carcass fat (0.18–0.50), muscle weight (0.22–0.35), meat yield (0.24–0.35), carcass muscle dimensions (0.25–0.34) and bone weight (0.27). Results indicate that for most lamb carcass and meat quality traits there is sufficient genetic variation for selection to alter successfully these characteristics. Additionally, most genetic correlations of live animal assessments of bodyweight, muscle and subcutaneous fat with the carcass and meat quality traits were favourable. Appropriate definition of breeding objectives and design of selection indexes should be able to account for the small unfavourable relationships that exist and achieve the desired outcomes from breeding programs.

Additional keywords: fat, genetic correlations, heritability, meat colour, meat yield, tenderness.

Introduction

Genetic improvement has been a major factor responsible for the substantial increases in productivity and profitability that have benefited the sheep meat industry in Australia over recent decades. In his comprehensive review of sheep meat breeding in Australia over the past 40 years, Fogarty (2009) concluded that the basis of the genetic gains achieved by the breeding programs implemented in industry flocks was mainly attributable to improvements in growth, leanness and muscling. Overall, the development, implementation and adoption of performance recording and genetic evaluation by the sheep meat industry has been shown to have yielded, over the period post 2000–2005, annual improvements in the terminal sire breed group of $2 per ewe, the Coopworth breed of $1.80 per ewe and the Border Leicester breed of $1.70 per ewe (Swan *et al*. 2009). Over the same period, annual responses of $0.70 per ewe were achieved in the Merino breed. For continued gains to occur in productivity and profitability and to maintain its market acceptability,

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market research conducted by Meat & Livestock Australia has identified that lamb should be lean, nutritious, of high eating quality and visually appealing (Pethick *et al*. 2006).

Sheep Genetics, the national genetic evaluation program, provides Australian sheep breeding values (ASBVs) to the Australian sheep industry based on the LAMBPLAN and MERINOSELECT databases (Brown *et al*. 2006). These ASBVs are then used in the construction of selection indexes for a range of meat and wool breeding objectives for different production systems and specific market specifications that assist breeders in the conduct of their flock breeding programs. Terminal sire breeders can make use of the Carcase Plus index, LAMB2020 index, the Trade $ index and the Export $ index, whereas a range of indexes is available for both maternal sire breeders (Maternal $ indexes) and Merino breeders (Dual Purpose indexes) (Brown *et al*. 2006). As stressed by Fogarty (2009), it is now critical to expand our information on the implications of these current industry breeding programs to cover their impact on the newer and more novel consumer-relevant attributes of lamb to ensure that the sheep meat industry will have in place breeding programs that improve eating quality, visual appeal and the nutritional value of lamb as well as its production.

The development of the new attributes of lamb meat and their inclusion in genetic improvement programs requires a detailed understanding of the extent of genetic variation influencing traits relevant to carcass composition and meat quality, noting that these traits are difficult and expensive to measure in sheep breeding flocks in Australia. The newer traits include measures of fresh and retail meat colour, meat pH, tenderness, intramuscular fat and contents of iron, zinc and fatty acids. For sheep meat, heritability estimates are unavailable for retail colour and mineral content traits, whereas an estimate has been reported for intramuscular fat content (Karamichou *et al*. 2006*b*). Few heritability estimates have been reported for tenderness as measured by shear force (Botkin *et al*. 1969; Karamichou *et al*. 2006*b*; Cloete *et al*. 2008) and fatty acid content of lamb (Karamichou *et al*. 2006*a*; Greeff *et al*. 2007), although several estimates are published for fresh meat colour and pH traits (Fogarty *et al*. 2003; Karamichou *et al*. 2006*b*; Ingham *et al*. 2007; Cloete *et al*. 2008; Greeff *et al*. 2008; Payne *et al*. 2009). The reviews of Fogarty (1995) and Safari and Fogarty (2003) have established that there are many independent estimates of heritability for carcass muscle dimensions and measures of carcass fat and lean, with many of the reports on carcass traits reviewed by these authors also providing estimates of heritability of carcass weight and dressing percentage.

In recognising the lack of genetic parameter estimates for the more novel lamb traits as one of the issues that would affect adoption of breeding technologies and continued genetic improvement in the Australian sheep industry, Banks *et al*. (2006) proposed the concept of an Information Nucleus. The Information Nucleus was established in 2007 and progeny tests key young industry sires for a wide range of traits in many different environments (Fogarty *et al*. 2007). Among its specific aims is the estimation of genetic parameters for traits that are relevant to breeding objectives that improve meat quality. The Information Nucleus progeny are representative of the major production types in the sheep industry, namely Merino, Border Leicester × Merino, Terminal × Merino and Terminal × Border Leicester-Merino. It is planned to generate progeny from five matings. By using data from the progeny born in 2007 and 2008, generated by the Information Nucleus, the present paper reports preliminary estimates of heritability for carcass and meat quality traits and the genetic and phenotypic correlations of these traits with lamb growth and live carcass traits.

Materials and methods

Animals

Data on the crossbred and Merino progeny of the Information Nucleus were recorded at eight sites. The sites were: Kirby Research Station, University of New England, Armidale, NSW; Trangie Agricultural Research Centre, NSW (first mating in 2008); Cowra Agricultural Research and Advisory Station, NSW; DPI Hamilton Centre, Vic.; DPI Rutherglen Centre, Vic.; Struan Research Station, SA; Turretfield Research Station, SA; and Great Southern Agricultural Research Institute, Katanning, WA. In 2007 and 2008, the majority of sires mated to the base ewes at each site were chosen initially on the basis of having performance records available in one of the Sheep Genetics databases, either LAMBPLAN or MERINOSELECT. To further broaden the genetic sampling of the industry, several sires were chosen that did not have performance records in these databases. These sires also were representative of additional bloodlines. The individual sires then were chosen to ensure genetic diversity across the range of economically important sheep production traits (growth, meat, wool, reproduction and disease resistance), with preference given to young sires (1–3 years of age) and those sires expected to be widely used in the industry. Sires were selected from within the Merino, Border Leicester (maternal) and terminal meat breeds and sampled from a broad range of bloodlines and strains. ASBVs from LAMBPLAN and MERINOSELECT for the sires indicated that the sires were generally representative of the range of genetic merit available to the sheep industry. In total, 183 sires were mated by AI in 2007 and 2008, with sires used equally across sites to provide genetic links within each year and 14 sires used in both years to provide genetic links across years. The sires were sampled from the Merino (n = 72), maternal (Border Leicester, n = 36; Texel, n = 5; White Dorper, n = 2; East Friesian, n = 1; Booroola Leicester, n = 1) and terminal meat breeds (Poll Dorset, n = 36; Suffolk, n = 4; White Suffolk, n = 23; Hampshire Down, n = 1; Southdown, n = 1; Ile de France, n = 1). The base ewes used at most sites in each year consisted of ~80% Merino ewes and 20% Border Leicester × Merino ewes, except at Kirby and Turretfield in 2007 and Hamilton and Katanning in both years, where Merino ewes only were mated. As base ewes were drawn from both pedigreed and commercial flock sources, the amount of pedigree available on the base ewes varied from no pedigree to full pedigree. For example, the Merino base ewes at Cowra, Katanning, Struan, Trangie and Turretfield were from Merino research resource flocks described by Safari *et al*. (2007*a*). Information on the genetic relationships among the sires and base ewes was made available by Sheep Genetics and was used in the statistical analyses. For the data considered in the present study, Table 1 shows the numbers of sires, dams and progeny at each site in each year. The data comprised records on 7176 lambs weaned from the 183 sires and 4194 dams, of which 6771 animals

Table 1. Numbers of sires, dams and progeny for lambs weaned, lambs scanned and lambs slaughtered at each site and year

Year	Sires	Lambs weaned		Lambs scanned		Lambs slaughtered	
		Dams	Progeny	Dams	Progeny	Dams	Progeny
				Armidale			
2007	50	439	532	434	524	211	233
2008	75	600	718	532	615	347	391
				Trangie[A]			
2007	–	–	–	–	–	–	–
2008	37	321	519	313	491	202	301
				Cowra			
2007	46	293	444	221	307	199	285
2008	37	188	274	182	265	114	148
				Rutherglen			
2007	49	314	423	304	407	207	292
2008	45	313	505	311	502	205	309
				Hamilton			
2007	50	280	344	272	329	180	208
2008	47	304	344	194	220	173	192
				Struan			
2007	50	308	459	299	440	189	263
2008	43	181	215	179	212	117	131
				Turretfield			
2007	49	312	440	313	440	200	262
2008	36	343	501	336	486	189	238
				Katanning			
2007	59	508	678	507	671	302	367
2008	83	569	780	601	862	379	490
Total	183[B]	4194[C]	7176	4025	6771	2809	4110

[A]No matings at Trangie in 2007.
[B]Link sires were used across sites in each year, with 14 of the sires used in both years.
[C]Ewes were used in both years within each site.

had records from ultrasound scanning and 4110 animals were grown out and slaughtered. The objectives and design of the Information Nucleus have been described in more detail by Fogarty *et al*. (2007).

Live animal measurements

Weaning weight (WWT) of the lambs at each site was recorded at ~12–13 weeks of age. Live animal ultrasound measurements of subcutaneous fat depth (FATUS) and eye muscle depth (EMDUS), 45 mm from the midline over the 12th rib, were obtained by Sheep Genetics-accredited operators. All terminal and maternal lambs were scanned before the first draft of these lambs for slaughter, whereas all Merino lambs were scanned before the slaughter of the first draft of Merino wethers. Liveweight at scanning (WTUS) was recorded. Prior to slaughter, lambs were managed at each site to have target growth rates of 200 g/day for crossbred lambs and 150 g/day for Merino lambs.

Carcass and meat quality measurements

Lambs were slaughtered at commercial abattoirs at an average target carcass weight of 22 kg for wethers and 21 kg for ewes. All lambs had a fasted weight recorded 1 week before slaughter. Using this weight, the lambs were then allocated to a slaughter group by stratified random sampling, balancing for weight within sex, sire and production type (except the Merino wethers, as they tended to reach target weights later). The 2007-born lambs were slaughtered in 30 groups (age range of 5–15 months across groups) and the 2008-born lambs were slaughtered in 29 groups (age range of 5–17 months across groups). The post-slaughter sampling protocol for the carcass and meat quality traits was as described by Pearce (2009), whereas measurement procedures were as described for the carcass traits by Gardner *et al*. (2010), for the nutritional value traits by Pannier *et al*. (2010) and for the meat quality traits by Warner *et al*. (2010). Briefly, all carcasses were electrically stimulated and trimmed according to AUS-MEAT specifications (Anon. 1992). At slaughter, hot carcass weight (HCWT) was recorded and carcass fat at the GR site (FATGR, total tissue depth at the 12th rib, 110 mm from the midline) was measured with a GR knife on the hot carcass. Fat depth at the 5th rib (FAT5), 110 mm from the midline on the chilled carcass, was measured with a ruler. Dressing percentage (DP) was calculated as the ratio of HCWT to fasted pre-slaughter weight recorded the day before slaughter. Carcasses were chilled overnight (3−4°C) and measured and sampled for a wide range of carcass and meat quality traits. Following overnight chilling, the carcasses were cut between the 12th and 13th ribs. Depth of the muscle (EMD), *M. longissimus thoracis et lumborum*; LL, and its width (EMW) were measured and used to calculate eye muscle area (EMA) as 80% of the product of depth and width. Fat depth was measured at the C site (FATC, depth of fat over the maximum depth of the eye muscle). pH of the LL (pHLL) and the *M. semitendinsous* (pHST) was measured using several different pH meters linked to pH electrodes calibrated at chiller temperatures (3−4°C). The cut surface of the LL at the 12th rib was exposed to the air at ambient temperature for 30–40 min and the meat colour measured with Minolta Chroma meters (Models CR-300 and CR-400) set on the L^*, a^*, b^* system (where L^* (CFL^*) measures relative lightness, a^* (CFa^*) relative redness and b^* (CFb^*) relative yellowness). Three measurements were taken at different positions and an average value was used for analysis. At 24 h post-mortem, the LL muscle was excised from the carcass. After removal of subcutaneous fat and silver skin, two 40-g samples of diced muscle were collected. Iron and zinc contents were measured on one sample, whereas a range of fatty acids was measured on the other sample, including α-linolenic acid (ALA), eicosapentaenoic acid (EPA), docosapentaenoic acid (DPA) and docosahexaenoic acid (DHA). Myoglobin content (MYO) was measured on a sample (1 g) taken from the loin using methods described by Trout (1991). A sample (50 g) was also taken for analysis of intramuscular fat. The percentage of intramuscular fat (IMF) was determined using a near infrared procedure (NIR) with a Technicon Infralyser 450. The method was further described by Perry *et al*. (2001). For measurement of retail colour stability, a 3-cm slice from the cranial end of the LL was taken, vacuum packed and aged for 5 days. After 5 days, a fresh surface was cut on each sample and these were then placed individually on black foam trays and over wrapped with PVC food film wrap. After a blooming period of 30–40 min, each sample was measured (initial colour values) with Hunter Laboratory meters (Models 45/0-L),

with an aperture size of 25 mm. Samples were displayed in a chiller at 3–4°C under lighting (1000 l×) and measured once a day for 4 days (final colour value). Each sample was measured twice at each measurement time and the two values were averaged for analysis. Measurements recorded on Day 3 of *L** (RC*L**), *a** (RC*a**), *b** (RC*b**) and oxymyoglobin : metmyoglobin ratio (RCR) were considered in the present study. RCR, an indicator of colour stability during retail display, was measured using methods described by Jacob *et al*. (2007). The ratio was calculated as the percentage of light reflectance at wavelength 630 nm to the percentage of light reflectance at wavelength 580 nm. A section of the LL also was divided into two portions (65 g) for shear force testing, which were frozen after 1 or 5 days (aged 1 or 5 days). The 5-day samples were vacuum packed and held chilled (3–4°C) until preparation and freezing on Day 5. Samples for shear force testing were cooked from frozen for 35 min in plastic bags at 71°C in a water bath, before being tested using a Lloyd texture analyser (Model LRX, Lloyd Instruments, Hampshire, UK) with a Warner–Bratzler shear blade fitted as described by Hopkins *et al*. (2010). During preparation of the LL, the weight of subcutaneous fat trimmed to 25 mm from the lateral edge of the muscle (FATLL) was recorded, as was the total weight of the denuded LL (WTALL). From the hindleg (HAM 4816), the topside (HAM 2000) was removed, trimmed of external fat and weighed (WTTOP). The knuckle (HAM 5072) was also removed and weighed (WTRND), along with all the bone of the hindleg (BONE). Lean meat yield (LMY) was predicted for each animal by using an algorithm based on HCWT, FATGR, FATLL, FAT5, EMA, WTLL, WTTOP, WTRND and BONE (G. E. Gardner, unpubl. data).

Data were available from animals born in both years for the live animal and carcass traits, as well as some meat quality traits (pH, the fresh meat colour traits and IMF). For the remaining meat quality traits and nutritional value traits, records were available only from animals born in 2007, with the retail colour traits only recorded on progeny at Cowra, Hamilton, Rutherglen and Katanning.

Statistical analyses

Variance and covariance components were estimated from the data by using the software ASReml (Gilmour *et al*. 2009), applying restricted maximum likelihood procedures to fit a mixed linear model. Initially, the model for the univariate analyses included the fixed effects of site (eight, seven or four levels as appropriate for each trait), year (two levels as appropriate), management group (group at weaning, ultrasound scanning and slaughter as appropriate), sire breed, dam breed (Merino, Merino × Border Leicester), sex (male, female), type of birth and rearing (11, 21, 22, 31, 32, 33 for lambs born and reared, respectively) and dam age (from 1 to >7 years of age). Age of the lamb was fitted as a linear covariate. Weight at ultrasound scanning was included as a covariate for the ultrasound-scanning traits. For the carcass traits, hot carcass weight was included as a linear covariate for all traits except dressing percentage and lean meat yield. Meat ultimate pH of the LL was also included as a covariate for the analyses of fresh and retail colour traits and shear force traits. The data for the fatty acids were log-transformed before analysis, where the model also included intramuscular fat as a covariate. Significant ($P < 0.05$) two-way interactions were included in the final model. Variance components were estimated from univariate analyses that fitted random effects of animal and dam. The animal effect represented the additive genetic variance, whereas the dam effect represented a maternal variance, combining the maternal genetic and maternal environmental variances. Where data were available for dams with progeny born in 2 years, the dam × year interaction, representing environmental variation between litters, was included. To account for the base animals being from different breeds and strains, genetic group, defined using mixed model equations derived by Quaas (1988), was fitted as a random effect in the model. A random sire × site interaction was included in the model. A series of random models were fitted to the data for each trait to assess the importance of the maternal effects and the sire × site interaction. Each of these random effects was retained if its inclusion resulted in a significant increase in the log-likelihood value for the model. Heritabilities for each trait were estimated from the univariate analyses, whereas estimates of phenotypic and genetic correlations of the live animal traits with the carcass and meat quality traits were estimated from bivariate analyses.

Results

Heritability

Heritability estimates for the live animal traits, carcass and meat quality traits measured on 2007- and 2008-born progeny are shown in Table 2 and heritability estimates for the meat quality and nutritional value traits, measured on 2007-born progeny only, are shown in Table 3. Estimates of the maternal variance components for the various traits, where significant, are also presented. For the meat tenderness traits, heritability estimates were moderate to high for SHF1 (0.27 ± 0.07), SHF5 (0.38 ± 0.08) and IMF (0.39 ± 0.05). Iron content had a low heritability estimate of 0.12 ± 0.05, whereas zinc content was moderately heritable (0.21 ± 0.06). Myoglobin content was moderately heritable (0.22 ± 0.06). Heritability estimates for the fatty acids ranged from 0.11 ± 0.05 for DPA to 0.37 ± 0.09 for ALA. The fresh meat colour traits had low heritability estimates of 0.06 ± 0.03 for CF*a** and 0.13 ± 0.04 for CF*b** and a moderate estimate of 0.21 ± 0.04 for CF*L**. For the corresponding meat retail colour traits where estimates were based on much fewer records, heritability estimates were at least moderate in size for RC*a** (0.29 ± 0.09), RC*L** (0.44 ± 0.10) and RCR (0.40 ± 0.10) but low for RC*b** (0.09 ± 0.06). Both measures of meat pH had low heritability estimates (~0.10). HCWT and LMY had high heritability estimates (both ~0.35), whereas the estimate for DP was moderate (0.24 ± 0.05). The heritability estimates for the muscle dimensions, muscle weights and fat measurements were generally moderate (range of 0.18 for FATLL and FAT5 to 0.25 for EMD). Exceptions were the high heritability estimates for EMW (0.34 ± 0.05), EMA (0.30 ± 0.05), WTLL (0.35 ± 0.05) and FATGR (0.50 ± 0.05). Bone weight was moderately heritable (0.27 ± 0.05). The heritability estimates for the liveweights were generally moderate in size (0.14 ± 0.03 for WWT and 0.27 ± 0.04 for WTUS). Ultrasound fat depth (0.15 ± 0.03) and muscle depth (0.23 ± 0.03) were moderately heritable.

The maternal genetic and environmental effects and/or litter effects were important for several traits, including WWT, WTUS,

Table 2. Number of records, predicted means and estimates of phenotypic variance (σ^2_P), heritability (h^2), maternal environmental variance (c^2) and litter variance (l^2), and their standard errors, for live animal, carcass and meat quality traits recorded on 2007 and 2008 drop Information Nucleus progeny

Trait	Records	Mean	σ^2_P	h^2	c^2	l^2
Live animal traits						
Weaning weight (WWT, kg)	7176	27.8	13.90	0.14 ± 0.03	0.23 ± 0.02	–
Scanning weight (WTUS, kg)	6682	45.7	22.75	0.27 ± 0.04	0.13 ± 0.03	0.06 ± 0.03
Ultrasound muscle depth (EMDUS, mm)	6771	26.6	4.55	0.23 ± 0.03	–	–
Ultrasound fat depth (FATUS, mm)	6768	3.5	0.41	0.15 ± 0.03	0.07 ± 0.02	–
Carcass traits						
Carcass weight (HCWT, kg)	4110	21.6	5.47	0.35 ± 0.06	0.00	0.13 ± 0.03
Dressing percent (DP, %)	3684	53.8	4.84	0.24 ± 0.05	0.09 ± 0.03	–
Lean meat yield (LMY, %)	3568	46.3	6.26	0.34 ± 0.05	–	–
Eye muscle width (EMW, mm)	3781	55.6	12.10	0.34 ± 0.05	–	–
Eye muscle depth (EMD, mm)	3782	27.1	6.86	0.25 ± 0.05	–	–
Eye muscle area (EMA, cm^2)	3781	11.6	2.65	0.30 ± 0.05	–	–
Loin muscle weight (WTLL, gm)	3781	263.3	1304.3	0.35 ± 0.05	–	–
Topside weight (WTTOP, gm)	3782	388.9	1850.8	0.22 ± 0.05	0.01 ± 0.05	0.19 ± 0.06
Round weight (WTRND, gm)	3795	364.4	1162.4	0.24 ± 0.05	0.09 ± 0.03	–
Carcass fat depth GR site (FATGR, mm)	4053	21.6	7.42	0.50 ± 0.05	–	–
Carcass fat depth C site (FATC, mm)	3718	7.6	2.82	0.23 ± 0.04	–	–
Carcass fat depth 5th rib (FAT5, mm)	3695	16.3	4.87	0.18 ± 0.04	–	–
Weight of fat trimmed from the loin (FATLL, gm)	3774	288.5	2543.1	0.18 ± 0.04	0.06 ± 0.03	–
Hind leg bone weight (BONE, gm)	3796	671.4	3572.7	0.27 ± 0.05	0.09 ± 0.03	–
Meat quality traits						
Fresh meat colour *L** (CF*L**)	3432	35.5	3.21	0.21 ± 0.04	–	–
Fresh meat colour *a** (CF*a**)	3431	21.8	1.43	0.06 ± 0.03	0.08 ± 0.03	–
Fresh meat colour *b** (CF*b**)	3431	3.9	0.97	0.13 ± 0.04	0.09 ± 0.03	–
Meat pH loin muscle (pHLL)	3709	5.5	0.006	0.10 ± 0.03	–	–
Meat pH round (pHST)	3766	5.6	0.025	0.09 ± 0.04	–	–
Intramuscular fat (IMF, %)	3811	5.7	0.63	0.39 ± 0.05	–	–

Table 3. Number of records, predicted means and estimates of phenotypic variance (σ^2_P), heritability (h^2) and maternal environmental variance (c^2), and their standard errors, for meat quality and nutritional value traits recorded on 2007 drop Information Nucleus progeny

Trait	Records	Mean	σ^2_P	h^2	c^2
Meat quality traits					
Shear force aged 5 days (SHF5, N)	1759	20.3	39.20	0.38 ± 0.08	–
Shear force aged 1 day (SHF1, N)	1637	29.4	59.30	0.27 ± 0.07	–
Retail colour *L** (RC*L**)	1156	44.4	3.98	0.44 ± 0.10	–
Retail colour *a** (RC*a**)	1156	18.8	2.51	0.29 ± 0.09	–
Retail colour *b** (RC*b**)	1156	20.2	2.04	0.09 ± 0.06	–
Retail colour ratio (RCR)	1156	3.3	0.28	0.40 ± 0.10	–
Myoglobin (MYO, mg/g)	1897	6.4	1.56	0.22 ± 0.06	–
Nutritional value traits – minerals					
Zinc content (Zn, mg/kg wet muscle tissue)	1915	29.6	12.83	0.21 ± 0.06	–
Iron content (Fe, mg/kg wet muscle tissue)	1915	27.7	12.77	0.12 ± 0.05	–
Nutritional value traits – omega-3 fatty acids					
α-Linolenic acid (ALA, mg/100 g wet muscle tissue)	1916	3.759[A]	0.027	0.37 ± 0.09	0.28 ± 0.05
Eicosapentaenoic acid (EPA, mg/100 g wet muscle tissue)	1919	3.169	0.039	0.29 ± 0.07	–
Docosapentaenoic acid (DPA, mg/100 g wet muscle tissue)	1921	3.589	0.030	0.11 ± 0.05	–
Docosahexaenoic acid (DHA, mg/100 g wet muscle tissue)	1915	2.392	0.051	0.25 ± 0.06	

[A]Means, variances and variance ratios for omega-3 fatty acids were estimated by using transformed data.

FATUS, HCWT, DP, WTTOP, WTRND, FATLL, BONE, CF*a**, CF*b** and ALA. However, the amount and structure of these data, where the pedigree was unavailable for some dams, the majority of the dams had only one progeny recorded for the traits and the dams themselves did not have records in the data, limited the ability to partition the effects into their genetic and environmental components. Nevertheless, the evidence suggests that maternal effects need to be included in models

for the estimation of genetic parameters for carcass and meat quality traits and evaluated for their importance (Safari *et al.* 2005). Ingham *et al.* (2007) also have reported that small maternal effects and litter effects were present for some carcass traits in their data from crossbred sheep.

Correlations

Estimates of genetic correlations between the live animal traits and the carcass, meat quality and nutritional value traits, which were adjusted for carcass weight, are shown in Table 4, whereas Table 5 presents the corresponding phenotypic correlation estimates. These tables also include correlation estimates among the live animal traits.

Both liveweights had generally weak negative genetic correlations with the fresh meat colour traits, but had moderate positive genetic correlations with shear force aged 5 days (0.45 ± 0.15 for WWT, 0.30 ± 0.15 for WTUS). The liveweights had small negative genetic correlations with IMF. Both EMDUS and CFATUS had moderate positive genetic correlations with CF*a** (0.34 ± 0.16 for EMDUS and 0.54 ± 0.16 for FATUS) and CF*b** (0.50 ± 0.13 for EMDUS and 0.41 ± 0.15 for FATUS).

The liveweights had very strong positive genetic correlations with HCWT (0.80 ± 0.06 for WWT and 0.92 ± 0.02 for WTUS), but had weak positive genetic correlations with DP and LMY. The liveweights were moderately correlated with EMW (0.30 ± 0.11 for WWT, 0.43 ± 0.09 for WTUS), but had weaker correlations with EMD and EMA. The liveweights had positive genetic correlations with all muscle weights, but they were strongest with WTTOP (0.42 ± 0.13 for WWT, 0.66 ± 0.09 for WTUS) and WTRND (0.65 ± 0.10 for WWT, 0.64 ± 0.08 for WTUS). Both liveweights had generally moderate negative correlations with all fat measures (–0.35 to –0.64). Weight of fat trimmed from the loin had low negative genetic correlations with WWT (–0.39 ± 0.14) and WTUS (–0.23 ± 0.13). Bone weight had strong positive genetic correlations with both liveweights (0.76 ± 0.08 for WWT, 0.79 ± 0.06 for WTUS).

Of the correlations with the yield traits, EMDUS had a strong positive genetic correlation with DP (0.58 ± 0.10), whereas FATUS had a strong negative correlation with LMY (–0.64 ± 0.09). EMDUS was strongly genetically correlated with its corresponding carcass measurement, EMD (0.82 ± 0.06), and EMA (0.64 ± 0.08), but uncorrelated with EMW. FATUS had a low negative correlation with EMW and a positive correlation with EMD (both correlations ~0.30 in size). EMDUS had a moderate positive genetic correlation with WTLL (0.43 ± 0.09), and FATUS had low negative genetic correlations with the muscle weights (–0.21 to –0.34). EMDUS had moderate positive genetic correlations with FATGR and FAT5. FATUS was strongly positively correlated with its corresponding carcass measure, FATC (0.81 ± 0.08), and FAT5 (0.79 ± 0.09). Trimmed loin fat weight had strong positive genetic correlations with EMDUS (0.50 ± 0.12) and FATUS (0.84 ± 0.09). Bone weight was negatively correlated with EMDUS (–0.33 ± 0.11) and FATUS (–0.42 ± 0.12). The phenotypic

Table 4. Estimates of genetic correlations, with their standard errors, between live animal traits and carcass and meat quality traits measured on Information Nucleus progeny

Trait	WWT	WTUS	EMDUS	FATUS
		Live animal traits		
WTUS	0.85 ± 0.04			
EMDUS	–0.36 ± 0.10	–0.24 ± 0.10		
FATUS	–0.32 ± 0.12	–0.08 ± 0.12	0.57 ± 0.08	
		Carcass traits		
HCWT	0.80 ± 0.06	0.92 ± 0.02	0.23 ± 0.10	–0.06 ± 0.12
DP	0.03 ± 0.15	0.27 ± 0.13	0.58 ± 0.10	0.16 ± 0.14
LMY	0.19 ± 0.13	0.15 ± 0.11	0.08 ± 0.11	–0.64 ± 0.09
EMW	0.30 ± 0.11	0.43 ± 0.09	0.07 ± 0.11	–0.32 ± 0.11
EMD	0.01 ± 0.13	–0.02 ± 0.12	0.82 ± 0.06	0.29 ± 0.12
EMA	0.17 ± 0.13	0.21 ± 0.11	0.64 ± 0.08	0.03 ± 0.12
WTLL	0.10 ± 0.13	0.27 ± 0.09	0.43 ± 0.09	–0.21 ± 0.12
WTTOP	0.42 ± 0.13	0.66 ± 0.09	0.20 ± 0.12	–0.25 ± 0.14
WTRND	0.65 ± 0.10	0.64 ± 0.08	–0.03 ± 0.12	–0.34 ± 0.12
FATGR	–0.64 ± 0.07	–0.49 ± 0.08	0.42 ± 0.09	0.37 ± 0.11
FATC	–0.40 ± 0.12	–0.39 ± 0.11	0.11 ± 0.12	0.81 ± 0.08
FAT5	–0.45 ± 0.12	–0.35 ± 0.12	0.42 ± 0.12	0.79 ± 0.09
FATLL	–0.39 ± 0.14	–0.23 ± 0.13	0.50 ± 0.12	0.84 ± 0.09
BONE	0.76 ± 0.08	0.79 ± 0.06	–0.33 ± 0.11	–0.42 ± 0.12
		Meat quality traits		
CF*L**	–0.12 ± 0.14	–0.17 ± 0.12	–0.03 ± 0.13	–0.14 ± 0.14
CF*a**	–0.08 ± 0.20	–0.09 ± 0.18	0.34 ± 0.16	0.54 ± 0.16
CF*b**	0.02 ± 0.18	–0.19 ± 0.16	0.50 ± 0.13	0.41 ± 0.15
pHLL	–0.04 ± 0.18	–0.11 ± 0.16	–0.18 ± 0.16	–0.05 ± 0.17
IMF	–0.19 ± 0.11	–0.10 ± 0.10	0.03 ± 0.11	0.12 ± 0.11
SHF5	0.45 ± 0.15	0.30 ± 0.15	0.15 ± 0.17	–0.10 ± 0.16

Table 5. Estimates of phenotypic correlations, with their standard errors, between live animal traits and carcass and meat quality traits recorded on Information Nucleus progeny

Trait	WWT	WTUS	EMDUS	FATUS
		Live animal traits		
WTUS	0.72 ± 0.01			
EMDUS	–0.09 ± 0.02	–0.07 ± 0.02		
FATUS	–0.17 ± 0.01	0.08 ± 0.02	0.38 ± 0.01	
		Carcass traits		
HCWT	0.59 ± 0.01	0.82 ± 0.01	0.18 ± 0.02	0.10 ± 0.02
DP	0.11 ± 0.02	0.17 ± 0.02	0.25 ± 0.02	0.16 ± 0.02
LMY	0.01 ± 0.02	–0.09 ± 0.02	–0.03 ± 0.02	–0.23 ± 0.02
EMW	0.05 ± 0.02	0.09 ± 0.02	0.06 ± 0.02	–0.13 ± 0.02
EMD	–0.03 ± 0.02	–0.05 ± 0.02	0.30 ± 0.02	0.07 ± 0.02
EMA	0.00 ± 0.02	0.00 ± 0.02	0.26 ± 0.02	–0.01 ± 0.02
WTLL	0.05 ± 0.02	0.09 ± 0.02	0.18 ± 0.02	–0.07 ± 0.02
WTTOP	0.09 ± 0.02	0.19 ± 0.02	0.06 ± 0.02	–0.13 ± 0.02
WTRND	0.17 ± 0.02	0.24 ± 0.02	–0.05 ± 0.02	–0.15 ± 0.02
FATGR	–0.27 ± 0.02	–0.15 ± 0.02	0.24 ± 0.02	0.34 ± 0.02
FATC	–0.12 ± 0.02	–0.07 ± 0.02	0.08 ± 0.02	0.31 ± 0.02
FAT5	–0.10 ± 0.02	–0.07 ± 0.02	0.08 ± 0.02	0.18 ± 0.02
FATLL	–0.19 ± 0.02	–0.06 ± 0.02	0.15 ± 0.02	0.29 ± 0.02
BONE	0.34 ± 0.02	0.40 ± 0.02	–0.15 ± 0.02	–0.19 ± 0.02
		Meat quality traits		
CF*L**	–0.03 ± 0.02	–0.10 ± 0.02	–0.05 ± 0.02	–0.01 ± 0.02
CF*a**	0.01 ± 0.02	0.02 ± 0.02	0.05 ± 0.02	0.05 ± 0.02
CF*b**	0.00 ± 0.02	–0.04 ± 0.02	0.06 ± 0.02	0.06 ± 0.02
pHLL	0.05 ± 0.02	0.01 ± 0.02	–0.04 ± 0.02	–0.04 ± 0.02
IMF	–0.09 ± 0.02	0.00 ± 0.02	0.03 ± 0.02	0.10 ± 0.02
SHF5	0.09 ± 0.03	0.06 ± 0.03	–0.04 ± 0.03	–0.09 ± 0.03

correlations of the liveweights and ultrasound measurements with the carcass and meat quality traits were generally small and less than 0.2 in size, with the exception of the stronger correlations involving carcass weight and bone weight.

Among live animal traits, WWT had a very strong positive genetic correlation with WTUS (0.85 ± 0.04). Both liveweights had low to moderate negative genetic correlations with EMDUS and FATUS. EMDUS and FATUS had a strong positive genetic correlation (0.57 ± 0.08). The genetic correlations were generally higher than the corresponding phenotypic correlations. These genetic correlation estimates were consistent with estimates presented and reviewed by Huisman and Brown (2008, 2009).

Discussion

The present study reports preliminary estimates of genetic parameters for carcass and meat quality traits recorded on progeny of the Information Nucleus. With the completion of data recording on the five planned drops of progeny of the Information Nucleus, a large and unique dataset will be available to provide the Australian sheep industry with information on the quantitative genetics of new and novel meat traits and their relationships with a comprehensive range of carcass, meat quality and growth traits, as well as reproduction, wool production and quality and disease resistance traits. The genetic parameter estimates will contribute to the expansion of the range of ASBVs provided by Sheep Genetics to the sheep industry to include novel carcass and meat quality traits and, as appropriate, enable these traits to be part of industry breeding objectives and among the selection criteria traits used in breeding programs.

Preliminary estimates of heritability for the more novel carcass and meat quality traits were generally moderate to high for meat quality measures of shear force (0.27 aged 1 day, 0.38 aged 5 days) and retail meat colour (range of 0.09 to 0.44), although these estimates were based on fewer records and had higher standard errors than the other traits, and intramuscular fat (0.39). These estimates suggested that there is genetic variation for these traits in the Australian sheep population that could be utilised by sheep breeding programs. These traits are expected to respond to selection, with gains being greater for intramuscular fat and the shear force traits which are of higher heritability and have coefficients of variation >10%. Heritability estimates were low to moderate for the fresh meat colour measures (range of 0.06–0.21) and meat pH (~0.10), with these traits tending to have coefficients of variation of <5%. Consequently, selection gains will be slower for these traits.

Our estimate of intramuscular fat (0.39) was higher than an estimate of 0.32 in Scottish Blackface sheep (Karamichou *et al*. 2006*b*). For shear force, an estimate of 0.39 in Scottish Blackface sheep has been reported by Karamichou *et al*. (2006*b*), whereas an estimate of 0.44 in South African terminal crossbred lambs has been reported by Cloete *et al*. (2008). Previously, heritability of shear force had been estimated at 0.28 by Botkin *et al*. (1969), using records from the progeny of Rambouillet, Columbia and Corriedale sires. The nutritional value traits tended to have low to moderate heritabilites (range of 0.11–0.29), with the exception of ALA, which had a higher heritability. The preliminary estimates for the fatty acids support the conclusions of Karamichou *et al*. (2006*a*) and Greeff *et al*. (2007) that it may be possible to improve omega-3 fatty acids in sheep through selection. We are unaware of heritability estimates for iron and zinc content of sheep meat, although zinc concentration of milk of dairy cattle has been estimated to be high (van Hulzen *et al*. 2009) and zinc concentration of serum in Angus cattle has been estimated to be of moderate heritability (Morris *et al*. 2006). Myoglobin content was of moderate heritability, which was similar to an estimate of 0.27 for soluble myoglobin in pork LM (Newcom *et al*. 2004), but much lower than an estimate of 0.85 for myoglobin content of Angus steaks (King *et al*. 2010). This perhaps is surprising, given that the estimates for fresh colour were low and myoglobin is the major pigment responsible for meat colour (Mancini and Hunt 2005). The heritability estimates for the meat colour traits were similar to estimates for colour *L** (0.21 *v.* 0.23 and 0.18), colour *a** (0.06 *v.* 0.10 and 0.10) and colour *b** (0.13 *v.* 0.10 and 0.12) of Ingham *et al*. (2007) and Greeff *et al*. (2008). Meat pH was less heritable in the present study (0.10 for the loin measure) than in the studies of Ingham *et al*. (2007) (0.18) and Greeff *et al*. (2008) (0.22). Our estimate for meat pH was similar to an estimate (0.12) from a New Zealand study using a range of terminal and dual purpose breeds (Payne *et al*. 2009), but that study's estimates for colour *L** (0.29) and *a** (0.19) were higher than our estimates.

Preliminary estimates of heritability were moderate to high for measures of meat yield (range of 0.24–0.35), carcass muscle dimensions (0.25–0.34), muscle weight (0.22–0.35), carcass fat (0.18–0.50) and bone weight (0.27). Estimates from our study compare well with those from other studies. The review of Safari *et al*. (2005) provided mean heritability estimates that were generally high for meat yield (range of 0.20–0.35), carcass muscle dimensions (0.30–0.41), carcass fat (0.32 for GR site, 0.30 for C site) and low for fresh meat colour (0.04–0.16) and meat pH (0.18). The earlier review of Fogarty (1995) reported mean heritability estimates of 0.31 for carcass fat at the C site and 0.29 for carcass eye muscle width. Since these reviews, Ingham *et al*. (2007), using crossbred lamb data, and Greeff *et al*. (2008), using Merino data, have provided estimates for the various traits recorded under Australian conditions. Our estimate for HCWT (0.35) was very similar to their estimates of 0.37 and 0.36, respectively, whereas our estimate for DP (0.24) was similar to the estimate of Greeff *et al*. (2008) (0.25), but lower than the estimate of Ingham *et al*. (2007) (0.35). For carcass muscle dimensions, our estimates were similar to that for EMW reported by Greeff *et al*. (2008) (0.34 *v.* 0.29), similar to that reported for EMD by Greeff *et al*. (2008) (0.25 *v.* 0.22), but lower than the estimate of 0.39 of Ingham *et al*. (2007), and similar to that reported for EMA by Ingham *et al*. (2007) (0.35 *v.* 0.32), but higher than the estimate of 0.26 of Greeff *et al*. (2008). Our heritability estimate for FATGR (0.50) was more similar to that of Ingham *et al*. (2007) (0.47) than that of Greeff *et al*. (2008) (0.28) and this probably reflects the wider range of types included in the study of Ingham *et al*. (2007), with Greeff *et al*. (2008) studying only Merino animals. In contrast, our heritability estimate (0.23) for FATC was more similar to that of Greeff *et al*. (2008) (0.20) than the estimate of Ingham *et al*. (2007) (0.44). From detailed measurements of carcasses of crossbred lambs raised under Australian conditions, genetic parameters for a wide range of carcass components have been estimated previously by

Kenney *et al*. (1995). Where traits were similar, our estimates for BONE (0.27 *v.* 0.35), FAT5 (0.18 *v.* 0.31) and FATLL (0.18 *v.* 0.30) tended to be lower than the estimates of Kenney *et al*. (1995).

The heritability estimates for the live animal traits were at the lower end of the range of literature estimates reported for WWT (e.g. Fogarty 1995; Safari *et al*. 2005, 2007*b*; Ingham *et al*. 2007; Greeff *et al*. 2008; Huisman *et al*. 2008) and ultrasound fat depth, adjusted for liveweight (e.g. Fogarty 1995; Safari *et al*. 2005; Greeff *et al*. 2008; Huisman *et al*. 2008). For liveweight at scanning, our estimate agreed with those reported for post-weaning weight by Fogarty (1995), Safari *et al*. (2005), Ingham *et al*. (2007) and Huisman *et al*. (2008), for liveweight at scanning by Greeff *et al*. (2008) and yearling weight by Safari *et al*. (2007*b*). The heritability estimate for ultrasound eye muscle depth, adjusted for liveweight, was similar to those reported by Fogarty (1995), Safari *et al*. (2005), Greeff *et al*. (2008) and, at post-weaning, Huisman *et al*. (2008).

Until recently, there were very few published estimates of genetic correlations of the carcass and meat quality traits with liveweights and muscle depth in live animals, although there were a moderate number of correlation estimates between liveweight and live assessments of fat depth (Safari *et al*. 2005). There have been no published correlation estimates of the live animal traits with intramuscular fat and shear force. The genetic correlations between the liveweights and the fresh meat colour traits were small and sometimes close to zero, which was similar to the estimates of Ingham *et al*. (2007) and Greeff *et al*. (2008). These estimates differed from an estimate between weaning weight and meat L^* of 0.42 reported by Payne *et al*. (2009). Whereas the present study found strong positive genetic correlations of both EMDUS and FATUS with meat colour a^* and b^*, Greeff *et al*. (2008), in contrast, reported that the ultrasound traits were uncorrelated genetically with the meat colour traits. Khliji *et al*. (2010) found that for fresh lamb, on average, consumers considered meat colour acceptable when a^* and L^* values were equal to or exceeded 9.5 and 34, respectively, whereas the b^* value was an unimportant influence on consumer acceptability scores. The very small genetic correlations between meat ultimate pH and all live animal traits are generally consistent with estimates from Australian (Ingham *et al*. 2007; Greeff *et al*. 2008) and New Zealand (Payne *et al*. 2009) studies.

The liveweights had strong positive genetic correlations with HCWT, which was in agreement with the estimates of Kenney *et al*. (1995), Ingham *et al*. (2007) and Greeff *et al*. (2008) for correlations involving weaning weight (0.86, 0.74 and 0.64, respectively) and of Ingham *et al*. (2007) for post-weaning weight (0.80) and Greeff *et al*. (2008) for weight at ultrasound scanning (0.89). The ultrasound measurement of muscle in our data was strongly correlated with DP in the present study, whereas Greeff *et al*. (2008) reported positive genetic correlations with DP (0.47) and HCWT (0.70). Ultrasound subcutaneous fat depth was weakly correlated genetically with HCWT and DP in the present study, whereas Greeff *et al*. (2008) reported moderate, positive genetic correlations (0.37 with HCWT and 0.45 with DP). For the genetic correlations involving the carcass muscle dimensions, the stronger genetic correlations (greater than ~0.3 in size) were for EMW with WWT, WTUS and FATUS, for EMD with EMDUS and FATUS and for EMA with FATUS. The preliminary estimates of these genetic relationships were similar to the estimates reported by Kenney *et al*. (1995), Ingham *et al*. (2007) and Greeff *et al*. (2008). The high positive genetic correlations of EMDUS with EMD and EMA were very similar to estimates reported by Greeff *et al*. (2008) (0.82 and 0.63, respectively). For the muscle weights, EMDUS had the strongest genetic correlation with WTLL, whereas the liveweights had the strongest genetic correlations with WTTOP and WTRND. The genetic correlations between the liveweights and all carcass fat measures, adjusted for carcass weight, were all negative and strong. Ingham *et al*. (2007) and Greeff *et al*. (2008) reported genetic correlation estimates for WWT with FATGR and FATC that were very weak and close to zero. These studies also reported estimates close to zero for post-weaning weight with FATGR and FATC (Ingham *et al*. 2007) and scanning weight with FATC, but not FATGR (0.33) (Greeff *et al*. 2008). Kenney *et al*. (1995) reported a genetic correlation of 0.65 between hind-leg bone weight and weaning weight, which is consistent with the estimate (0.76) in the present study.

Overall, the preliminary genetic correlations indicated that genetically heavier animals will be associated with heavier carcass weights, greater carcass eye muscle widths, increased muscle weights (but less so for loin weight), reduced carcass fat measures at a constant carcass weight, heavier hind-leg bone weight and an unfavourable increase in shear force values (less tender). These animals would also have slightly greater lean meat yields. Selecting animals for greater muscling based on ultrasound eye muscle depth is expected to be associated with increased dressing percentage, increased carcass eye muscle depth and area, increased loin muscle weight, increased carcass fat measures at a constant carcass weight, reduced hind-leg bone weight and increases in the redness (a^*) and yellowness (b^*) of the meat. These animals would also produce meat having slightly greater shear force values. Genetically leaner animals based on ultrasound fat depth assessment, are expected to be associated with increased lean meat yield, increased carcass eye muscle width but lower eye muscle depth, increased muscle weights, reduced carcass fat levels, heavier hind-leg bone weights and an unfavourable reduction in the redness (a^*) and a decrease in yellowness (b^*) of the meat. Intramuscular fat in meat from these animals would be very slightly reduced.

Implications

The preliminary genetic parameter estimates reported in the present study have provided the first information on a wide range of novel carcass and meat quality traits considered to be important for consumer acceptability, eating quality and nutritional value of Australian lamb. Moderate to high heritabilities for most carcass and meat quality traits indicated that there is sufficient genetic variation present in these traits for selection to be successful in altering these characteristics in lamb. Most genetic relationships of live animal assessments of bodyweight, muscle and subcutaneous fat with the carcass and meat quality traits were favourable, so there may be value in using some of the carcass traits as selection criteria. Unfavourable genetic relationships did exist for some combinations of traits, e.g. between the liveweights and shear force; ultrasound muscle

depth and shear force; ultrasound fat depth and meat redness; and ultrasound fat depth and intramuscular fat. However, the genetic relationships are small and appropriate definition of breeding objectives and design of selection indexes should be able to account for these relationships and achieve the desired outcomes from breeding programs.

Based on the extent of genetic variation, intramuscular fat and shear force are among the most promising candidates for inclusion in sheep breeding objectives. The ease and cost of measurement of many of the meat quality traits is likely to limit the ability to incorporate these traits directly into current industry breeding programs, at least on-farm, and make genetic improvement. However, the development of genomic breeding values for carcass and meat quality traits being undertaken by the Cooperative Research Centre for Australian Sheep Innovation (Daetwyler *et al*. 2010) and their use in improving the accuracy of ASBVs provided by Sheep Genetics will potentially provide a means to overcome or at least reduce this constraint. As well, modelling is required to evaluate the potential role of the carcass and meat quality traits in breeding objectives for a range of sheep production systems and market specifications. This will identify the need for these traits to be monitored for unfavourable changes from current industry breeding objectives versus their inclusion in breeding objectives, either as individual objective traits or as a part of subindexes (Swan *et al*. 2007).

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