GENETIC PARAMETERS FOR EATING QUALITY TRAITS OF AUSTRALIAN LAMB

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SUMMARY

Genetic parameters were estimated for 5 sensory (overall liking, tenderness, juiciness, flavour and liking of odour) and 2 objective eating quality (EQ) traits (intramuscular fat, IMF, and shear force, SF), measured on loin and topside meat cuts (except IMF) produced by progeny from the Information Nucleus of the CRC for Sheep Industry Innovation. Heritabilities for sensory traits were low to moderate for loin and moderate to high for topside cuts. Loin IMF was highly heritable while SF was moderately heritable in both cuts. Genetic correlations among the sensory EQ traits were all positive and high (0.72-1.00). Genetic correlations between loin IMF and sensory traits were moderately positive and lowly positive for loin and topside respectively. SF had stronger, negative correlations with sensory EQ traits in the topside than in the loin. Overall liking may be improved more so through selection on IMF in the loin and SF in the topside.

INTRODUCTION

Whilst breeding programs implemented in the Australian sheep industry have yielded substantial gains in lean meat yield, several studies have indicated that such programs may have also reduced the sensory eating quality (EQ) of lamb meat produced by terminal sire production systems. Breeding programs applied by breeders of terminal sires routinely use Australian Sheep Breeding Values for post weaning expressions of ultrasound eye muscle and fat depths at the C-site as components of breeding objectives and selection indices. Selection using these breeding values has been shown to reduce intramuscular fat (IMF) (e.g. Hopkins *et al.* 2007; Pannier *et al.* 2014b) and sensory EQ scores (e.g. Hopkins *et al.* 2005; Pannier *et al.* 2014a). Research is underway through the CRC for Sheep Industry Innovation to enable EQ traits to be incorporated directly into breeding programs. Contributing to this research, this study aimed to estimate genetic parameters for a range of EQ traits of samples, assessed by untrained consumer panels, from the *m. longissimus lumborum* (short loin) and *m. semimembranosus* (topside) muscles of lambs. Genetic and phenotypic correlations of the sensory EQ traits with IMF and shear force were also estimated.

MATERIALS AND METHODS

The Information Nucleus (IN) program of the CRC for Sheep Industry Innovation (van der Werf *et al.* 2010) produced the lambs that were slaughtered to obtain the meat samples for this study. The sample preparation, cooking procedures and sensory testing protocols applied to grilled loin and topside samples tasted by panels of untrained consumers have been described by Pannier *et al.* (2014a). Briefly, 10 sub-samples prepared from each meat sample of a carcass were grilled under standardised conditions during each consumer tasting session (94 sessions in total) and

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*AGBU is a joint venture of NSW Department of Primary Industries and University of New England tasted to provide 10 consumer responses per meat cut. The EQ traits were assessed by the consumers using a 0-100 scale (100 being most preferred) and for this study included tenderness (Ltend, Ttend), juiciness (Ljuic, Tjuic), liking of flavour (Lflav, Tflav), overall liking (Llike, Tlike) and liking of odour (odour) of loin and topside samples respectively. EQ records, based on the mean of 10 consumer responses for each muscle, were derived from 1414 animals, which were the progeny of 174 sires of various breeds born during 2009-2010, at 2 IN sites (Kirby and Katanning). From their carcasses and those from other animals born during 2007-2011 at all sites and slaughtered by the IN program, samples from the other loin were taken for analysis of IMF (%, 8917 records) and testing of shear force (SF) after 5 days of ageing (LSF, N, 9000 records), as described by Mortimer *et al.* (2014). A topside sample was similarly tested for SF after 5 days of ageing (TSF, N, 4793 records).

For the sensory EQ traits, univariate anlyses were used to estimate phenotypic variances and heritabilities, where models included fixed effects of site, slaughter group, sex, birth type, rearing type, age of dam and age at measurement. Random effects included a direct genetic effect of animal and an effect of consumer tasting session, as well as a fixed effect of genetic group. Univariate analyses of IMF, LSF and TSF fitted fixed and random effects in models as described by Mortimer *et al.* (2014). Genetic and phenotypic correlations among the EQ traits, IMF and shear force values were estimated from bivariate analyses. Variance and covariance estimations were performed using ASReml (Gilmour *et al.* 2014). Table 1 summarises the data for each trait.

RESULTS AND DISCUSSION

Apart from odour, phenotypic variances and heritabilities of sensory EQ traits were lower for loin compared to topside samples, although the standard errors were relatively large for the heritability estimates of both meat cuts (Table 1). Heritabilities for EQ traits of loin samples were low to moderate while those assessed on topside samples were moderate to high. Irrespective of meat cut, odour was of very low heritability. These results, though based on relatively small numbers of records, confirm that the genetic variation in EQ traits is sufficient to be exploited through selection. Previously, the much smaller study of Karamichou *et al.* (2007), using trained taste panel assessments of loin samples (350 records), had shown that equivalent lamb sensory traits to those assessed in the present study were of low (0.05±0.09 for overall liking) to high heritability (0.31±0.17 for juiciness). While IMF had a high heritability (0.53), SF when measured in either the loin (0.24) or topside samples (0.29) was of moderate heritability. These estimates were consistent with estimates from a subset of the IN data used in this study and earlier estimates reviewed by Mortimer *et al.* (2014).

Within each meat cut, genetic correlations among the sensory EQ traits were positive, with all estimates greater than 0.90 in size (Table 2, with results not shown for the odour traits due to low estimates of genetic variance and heritability). Phenotypic correlations were also high, though slightly lower than the genetic correlations. Johnston *et al.* (2003) reported that untrained panel assessments of sensory scores for tenderness, juiciness, flavour and overall acceptability of beef produced by temperate and tropically adapted cattle breeds were highly correlated, both genetically and phenotypically. The genetic correlations between the same EQ traits assessed in each of the loin and topside samples were between 0.87, for Ltend with Ttend, and 1.00, for Ljuic with Tjuic, and tended to be associated with larger standard errors. For the remaining combinations of sensory scores, assessments in loin and topside samples were positively and highly correlated genetically, ranging from 0.72 to 1.00. However, phenotypic correlations between assessments in loin and topside samples were much weaker, ranging from 0.28 to 0.36.

Very similar to the results of Karamichou *et al.* (2006) and Mortimer *et al.* (2014), IMF and LSF had a high, negative genetic correlation (-0.64, Table 2). However, a low negative genetic correlation (-0.21) was estimated between IMF measured in the loin and SF measured in the

Table 1. Descriptive statistics for lamb eating quality traits of loin and topside cuts (0-100 scale, 100 most preferred), intramuscular fat (IMF, %) and shear force after ageing for 5 days (SF, N) and estimates of phenotypic variance (σ^2_P) and direct heritability (h^2)

	Mean	SD	Minimum	Maximum	σ^2_P	h^2
Loin						
Tenderness	73.2	9.4	32.4	92.7	64.9 (2.74)	0.20 (0.07)
Juiciness	67.3	9.4	30.3	94.8	64.0 (2.67)	0.18 (0.07)
Flavour	71.1	8.0	40.5	91.2	49.5 (2.04)	0.10 (0.06)
Overall liking	72.3	8.4	40.6	93.9	53.8 (2.23)	0.15 (0.07)
Odour	69.9	6.4	46.1	87.0	32.0 (1.31)	0.04 (0.06)
IMF	4.3	1.018	1.5	10.5	0.67 (0.01)	0.53 (0.04)
SF5	27.5	9.8	10.8	95.1	58.53 (1.08)	0.24 (0.03)
Topside						
Tenderness	47.7	12.0	12.9	83.9	110.9 (4.85)	0.36 (0.09)
Juiciness	48.1	10.3	20.9	78.9	81.4 (3.45)	0.24 (0.08)
Flavour	55.2	9.4	27.8	84.4	69.9 (2.92)	0.17 (0.07)
Overall liking	52.1	10.4	20.8	84.2	85.5 (3.68)	0.30 (0.09)
Odour	66.2	6.8	44.6	84.5	36.4 (1.48)	0.03 (0.06)
SF5	41.8	12.3	15.3	98.9	84.4 (1.97)	0.29 (0.04)

Table 2. Genetic (below diagonal) and phenotypic (above diagonal) correlations among lamb eating quality traits of loin and topside cuts, intramuscular fat and shear force

	Ltend	Ljuic	Lflav	Llike	Ttend	Tjuic	Tflav	Tlike	IMF	LSF	TSF
Ltend		0.78	0.76	0.84	0.35	0.33	0.31	0.35	0.20	-0.34	-0.21
Ljuic	0.93 (0.07)		0.78	0.83	0.29	0.36	ne	0.33	0.23	-0.23	-0.17
Lflav	0.94 (0.11)	0.99 (0.10)		ne	0.28	0.31	0.34	0.34	0.22	-0.24	-0.16
Llike	0.95 (0.06)	0.90 (0.08)	ne[1]		0.32	0.34	ne	0.36	0.24	-0.28	-0.18
Ttend	0.87 (0.14)	0.72 (0.19)	0.90 (0.25)	0.93 (0.17)		0.82	ne	0.89	0.11	-0.19	-0.45
Tjuic	0.93 (0.17)	1.00 (0.18)	0.98 (0.26)	0.99 (0.19)	0.94 (0.05)		ne	0.86	0.15	-0.13	-0.34
Tflav	1.00 (0.20)	ne	0.94 (0.29)	ne	ne	ne		0.91	0.12	-0.12	-0.31
Tlike	0.88 (0.15)	0.80 (0.19)	0.90 (0.25)	0.93 (0.18)	0.98 (0.02)	0.94 (0.04)	0.99 (0.03)		0.13	-0.17	-0.41
IMF	0.48 (0.15)	0.49 (0.15)	0.60 (0.20)	0.59 (0.16)	0.15 (0.14)	0.34 (0.16)	0.36 (0.19)	0.27 (0.15)		-0.29	-0.12
LSF	-0.45 (0.17)	-0.43 (0.19)	-0.49 (0.23)	-0.44 (0.20)	-0.58 (0.15)	-0.74 (0.18)	-0.74 (0.22)	-0.60 (0.16)	-0.64 (0.06)		0.36
TSF	-0.55 (0.17)	-0.38 (0.19	-0.48 (0.23)	-0.47 (0.20)	-0.85 (0.09)	-0.80 (0.13)	-0.91 (0.15)	-0.84 (0.11)	-0.21 (0.09)	0.59 (0.08)	

[1] ne, not estimable.

topside. At the same time, the genetic correlation between SF in the loin and topside was 0.59. These results suggest that tenderness of the two muscles may be influenced by different genes. Johnston *et al.* (2001) had earlier concluded that very different genes could be influencing the expression of tenderness in the two muscles, after estimating a genetic correlation of 0.34 between shear force in the loin and topside muscles from tropically adapted beef breeds. This was thought to be due to different levels of connective tissue in the 2 muscles as shear force measurement is an indicator of tenderness due to the myofibrillar component rather than connective tissue. For lamb cuts, total fat content of topside cuts has been reported to be lower than loin cuts (Ponnampalam *et al.* 2010) and may also be an influence.

Genetic correlations of loin IMF with EQ traits were moderately positive for the loin samples (range of 0.48 to 0.60), but lowly positive for topside samples (range of 0.15 to 0.36; Table 2), which agrees with the strong, positive genetic relationships of IMF with juiciness and flavour assessed in lamb loins reported by Karamichou *et al.* (2006). In contrast, SF was negatively correlated with EQ traits, irrespective of meat cut. Genetic correlations of LSF and TSF with sensory scores assessed on loin samples were moderate (ranges of -0.43 to -0.49 and -0.38 to -0.55), while the corresponding genetic correlations with EQ traits assessed on topside samples were much stronger (ranges of -0.58 to -0.74 and -0.80 to -0.91). Using the standard equation to estimate correlated response and assuming constant selection intensity, selection for increased IMF is predicted to yield about 100% and 70% more response in Llike than selection for reduced LSF and TSF respectively. In contrast, about 50% and 130% greater correlated responses in Tlike are likely from selection for reduced LSF and TSF respectively versus selection for increased IMF.

Conclusions. There is scope to improve sensory EQ properties of lamb loin and topside cuts through selection. Selection on EQ traits assessed on either meat cut can be expected to improve sensory traits of the other meat cut. Though using both traits in breeding programs would be beneficial, it seems that IMF may be the better indicator trait to improve overall liking of the loin, while SF, particularly assessed on the topside, could be a better indicator trait to improve consumer overall liking of the topside. The estimates of this study are preliminary and many more records are needed to obtain accurate genetic parameter estimates for EQ traits, through both pedigree- and genomics-based approaches.

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