THE GENETIC RELATIONSHIPS BETWEEN INTRAMUSCULAR FAT MEASURED IN FOUR DIFFERENT LAMB MUSCLES

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SUMMARY

Intramuscular fat percentage (IMF) is a key determinant of eating quality in red meat. Measures of IMF from the short loin muscle (*M. longissimus lumborum*, LL) are currently used as selection criteria in Sheep Genetics eating quality indexes. To understand how routine selection on the short loin impacts IMF across the whole carcase, this pilot study examines IMF data collected from three additional muscles from the fore quarter (*Muscularis supraspinatus*, SS) and hind quarter (*Musculus semimembranosus*, SM; *Muscularis semitendinosus*, ST) of the carcase. The heritability of IMF was relatively high and consistent across the SS, LL and ST muscles, and lower in the SM. The genetic correlation estimate between IMF measured in the different muscles were all positive, ranging from 0.49 ± 0.13 to 0.97 ± 0.10. Therefore, IMF measurements from the short loin, which is currently being used as selection criteria for eating quality, will be a useful indicator for IMF across muscles from other parts of the carcase. Further, the genetic selection to increase IMF in one muscle should result in an increase in IMF in the other muscles, although at differing rates.

INTRODUCTION

Intramuscular fat (IMF) is a key determinant of eating quality in red meat as it has been found to have a positive influence on flavour, juiciness and tenderness (Hopkins *et al.* 2006; Pannier *et al.* 2014). Currently used as a selection criteria in Sheep Genetics eating quality indexes (Swan *et al.* 2015), IMF is extracted from the short loin using near-infra red technology. Most research has focused around IMF measured in the loin muscle, with very little research on other muscles.

Pre-adjusted IMF phenotypes measured on different muscles have been found to have moderately positive phenotypic correlations, ranging from 0.24 to 0.68 (Anderson *et al.* 2015). However, there are no reports on genetic relationship between IMF across different muscles. The objective of this pilot study was to estimate genetic correlations between IMF in different muscles from the fore-quarter, saddle (or loin) and hind-quarter sections of the lamb carcase.

MATERIALS AND METHODS

Data. Data was collected on 400 lambs slaughtered from the 2011-drop of the Information Nucleus Flock from the Katanning site (Fogarty *et al.* 2007) and 1,111 lambs slaughtered from the 2017-drop from the MLA Resource Flock (900 from the Kirby site and 211 from the Katanning site). Lambs were slaughtered at an average age of 280 ± 44 (± SD) days and an average hot carcase weight of 23.7 ± 3.3 kg. There were no common sires between the 2017 and 2011 drop lambs, with 64 sires in common across the two sites in the 2017 drop. In addition to the standard carcase traits measured

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(including IMF measured on the loin), three additional muscles were measured for IMF. In total, there were four muscles that were measured for IMF from the fore, saddle and hind section of the carcass:

- Fore-quarter: *Muscularis supraspinatus* (SS)
- Saddle: *M. longissimus lumborum* (LL)
- Hind-quarter: *Musculus semimembranosus* (SM) and *Muscularis semitendinosus* (ST).

All carcase traits, including IMF, were measured according to the Information Nucleus Flock operations manual (Sheep CRC 2009). The collection of IMF from additional muscles was as described in Anderson *et al.* 2015. Due to carcass imperfections and muscle trimming, IMF measures could not always be obtained for all muscles and or carcasses. Table 1 provides a summary of the number of samples, means and standard deviation for each muscle within each flock. Across the four muscles, IMF ranged from 2.16% to 11.79%, with an average of 4.71%.

Table 1. Summary of intramuscular fat (%) records available in muscles* from the fore-quarter, saddle and hind-quarter, sampled from lambs slaughtered from the Katanning 2011-drop, Katanning 2017-drop and the Kirby 2017-drop (*n* = 1,383)

			Fore-quarter	Saddle (loin)	Hind-quarter	
Site	Drop		SS	LL	SM	ST
Katanning	2011	Count	337	344	341	338
		Mean (*SD*)	5.04 (1.10)	4.36 (0.84)	3.69 (0.78)	4.87 (1.18)
Katanning	2017	Count	134	199	194	199
		Mean (*SD*)	6.29 (1.40)	5.00 (0.98)	4.07 (1.07)	5.63 (1.20)
Kirby	2017	Count	187	837	761	830
		Mean (*SD*)	5.44 (0.86)	4.95 (1.10)	3.92 (0.58)	5.25 (1.07)
Overall		Count	658	1380	1296	1367
		Mean (*SD*)	5.40 (1.21)	4.56 (1.05)	3.89 (0.74)	5.20 (1.14)

*SS: *Muscularis supraspinatus*; LL: *M. longissimus lumborum*; SM: *Musculus semimembranosus*; ST: *Muscularis semitendinosus*

Analysis. The IMF traits were analysed using a multivariate sire model in ASReml (Gilmour *et al*. 2009). An animal model was explored but due to the small number of records, a sire model was preferred. Fixed effects included birth type, rearing type, age, age of dam, age of dam squared, sire breed, dam breed and hot carcase weight. Contemporary group was defined by breed, flock, management group, sex, date of measurement and kill group. Maternal effects and genetic groups were not tested as there was insufficient data. Therefore, the genetic components estimated from this genetically diverse resource population are expected to be larger than estimates reported in literature (Walkom and Brown 2016). This was further exacerbated by the subsampling of the Australian sheep population in this study.

RESULTS AND DISCUSSION

The variance component and heritability for the IMF traits are presented in Table 2. These heritabilities are higher than presented in literature due to the inability to completely take into account breed and maternal effects in this subset of a genetically diverse reference population (Walkom and Brown 2016). Nevertheless, the heritability estimate for IMF measured in the LL (0.60 ± 0.10) reflects the estimate of 0.48 ± 0.05 reported by Mortimer *et al.* (2014), which included genetic groups in their

analysis of LL samples from the same sheep resource population. The genetic and phenotypic variation was lowest in the SM muscle. Meanwhile, the SS and ST muscles exhibited the greatest genetic and phenotypic variation, which exhibited more than double the variation observed in the SM muscle.

Table 2. Genetic parameter estimates ± SE for intramuscular fat traits measured in four muscles* from the fore-quarter, saddle and hind-quarter (*n* = 1,383)

	Fore-quarter	Saddle		Hind-quarter
Genetic parameter estimate	SS	LL	SM	ST
Phenotypic variance	1.00 ± 0.07	0.85 ± 0.04	0.43 ± 0.02	1.10 ± 0.05
Residual variance	0.76 ± 0.05	0.73 ± 0.03	0.41 ± 0.02	0.89 ± 0.04
Sire variance	0.24 ± 0.06	0.13± 0.03	0.03 ± 0.01	0.18 ± 0.03
Heritability	0.96 ± 0.19	0.60 ± 0.10	0.25 ± 0.08	0.68 ± 0.11

*SS: *Muscularis supraspinatus*; LL: *M. longissimus lumborum*; SM: *Musculus semimembranosus*; ST: *Muscularis semitendinosus*

The phenotypic correlations between IMF traits from the multivariable analysis were all positive (Table 3). The genetic correlations were also positive and stronger, ranging from 0.49 ± 0.13 to 0.97 ± 0.10. Therefore, IMF measurements from the LL muscle (short loin) will be a useful indicator for IMF across muscles from other parts of the carcase. Further, the genetic selection to increase IMF in one muscle should result in an increase in IMF in the other muscles, although at differing rates.

Table 3. Genetic correlations (below diagonal) and phenotypic correlations (above diagonal) for IMF measured in four muscles* from the fore-quarter, saddle and hind-quarter (*n* = 1,383)

	Fore-quarter	Saddle	Hind-quarter	
	SS	LL	SM	ST
SS		0.30 ± 0.03	0.30 ± 0.03	0.37 ± 0.04
LL	0.68 ± 0.11		0.44 ± 0.02	0.53 ± 0.02
SM	0.76 ± 0.17	0.97 ± 0.10		0.34 ± 0.03
ST	0.49 ± 0.13	0.70 ± 0.08	0.71 ± 0.13	

*SS: *Muscularis supraspinatus*; LL: *M. longissimus lumborum*; SM: *Musculus semimembranosus*; ST: *Muscularis semitendinosus*

Although more data will improve the accuracy of these estimates by reducing standard errors, this pilot study demonstrates that there are no detrimental consequences on the eating quality of the entire carcase when selecting on only measurements taken from the loin. These results also suggest that IMF should be recorded in the SS muscle, as this was the muscle that exhibits the most genetic variability. However, the muscle from which IMF samples are taken routinely should also consider the ease of sampling and the financial value of muscle.

Variation in the functional requirements of muscles leads to differences in muscle fibre type, the proportion of oxidative fibres and in turn the levels of triglycerides and IMF in the muscle (Hocquette *et al.* 2010). Muscles associated with posture tend to have more oxidative fibers and higher IMF (Picard *et al*. 2002; Anderson *et al*. 2015), which is reflected in the lower mean and heritability observed for the SM.

CONCLUSIONS

Intramuscular fat percentage (IMF) is a key determinant of eating quality in red meat. The analysis of IMF measures from four different muscles from 1,383 lambs suggests that the heritability of IMF was relatively high and consistent across the SS, LL and ST muscles, and lower in the SM. There were moderate to high genetic correlations between IMF across the four muscles. Therefore, IMF measurements from the short loin (LL), which is currently being used as selection criteria for eating quality, will be a useful indicator for IMF across muscles from other parts of the carcase.

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