GENETIC CORRELATION ESTIMATES FOR LAMB CARCASS COMPOSITION

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SUMMARY

Genetic correlations were estimated among lamb carcass composition traits recorded on progeny of the Information Nucleus program of the CRC for Sheep Industry Innovation. Genetic correlations among carcass muscle dimensions (depth, width and area) and muscle weights (loin, topside and round) were positive and generally moderate to strong, as were genetic correlations among carcass fat traits (at the 5th rib, GR and C sites and weight of trimmed loin fat). The eye muscle dimensions had weak genetic correlations with the fat traits and bone weight, whereas the fat traits had favourable moderate to strong genetic correlations with topside and round weights, plus hind leg bone weight. Use of index selection in a simple terminal sire breeding program based on live animal traits is expected to yield improvements in most carcass composition traits.

INTRODUCTION

Breeding objectives and selection indexes used in the Australian lamb industry have relied on live animal predictors to improve muscle and fat attributes of the carcass. Rates of genetic gain from breeding programs would be increased by using direct measures of carcass composition traits in genetic evaluations provided by Sheep Genetics, but for this to occur estimates of a range of genetic parameters are needed. This study presents genetic and phenotypic correlation estimates among lamb carcass composition traits. Their heritability and phenotypic variances estimates, plus their relationships with live animal traits, have been reported earlier by Mortimer *et al*. (2010).

MATERIALS AND METHODS

Carcass records were available from 2007 and 2008 drop progeny of the Information Nucleus program of the CRC for Sheep Industry Innovation (Sheep CRC), described by van der Werf *et al*. (2010). Data collection methods have been described elsewhere (Mortimer *et al*. 2010). Briefly, after electrical stimulation and trimming of the hot carcass, fat depth at the GR site was measured while fat depth at the 5th rib (FAT5) was measured on the chilled carcass. Following overnight chilling (3-4°C), eye muscle depth (EMD) of the *m. longissimus thoracis et lumborum,* LL, and its width (EMW) at the 12th and 13th ribs were measured and eye muscle area (EMA) calculated (product of 0.8, depth and width). C site fat depth was measured (FATC, over the maximum depth

of the eye muscle). Weight of the trimmed LL muscle (WTLL) and subcutaneous fat trimmed from it (FATLL) were recorded. From the hindleg, the topside (WTTOP), trimmed of external fat, and round (WTRND) were weighed after removal from the hind leg, together with all the bone of the hindleg (BONE). Table 1 summarises the statistics for each trait.

Bivariate analyses were used to estimate genetic and phenotypic correlations among the carcass components, with covariance estimation performed using ASReml (Gilmour *et al.* 2009). The models fitted to each trait have been described by Mortimer *et al.* (2010). Animal and genetic group were fitted as random effects, together with fixed effects of site, birth year, slaughter group, sire breed, dam breed, sex, birth-rearing type and age of dam, as well as significant interactions. Age of the lamb at slaughter and hot carcass weight were fitted as covariates. Using parameter estimates from Mortimer *et al.* (2010) and this study, correlated responses for the carcass traits over 10 years were predicted from index selection (LAMB2020) applied in a terminal sire breeding program, as described by Swan *et al.* (2009).

Table 1. Summary statistics for the carcass composition traits

Trait	Records	Number of sires	Mean	Standard deviation	Range
EMW (mm)	3781	183	61.3	4.53	40.0 - 76.0
EMD (mm)	3782	183	29.8	3.83	17.0 - 45.0
EMA (cm²)	3781	183	14.7	2.44	7.2 - 23.8
WTLL (gm)	3781	183	354.1	69.78	140.0 - 670.0
WTTOP (gm)	3781	183	602.2	102.5	295.0 - 1190.0
WTRND (gm)	3782	183	447.3	68.44	240.0 - 770.0
FATGR (mm)	4053	183	12.7	5.34	0.5 - 31.0
FATC (mm)	3718	182	4.0	2.43	0.2 - 24.0
FAT5 (mm)	3695	183	7.0	3.15	1.0 - 20.0
FATLL (gm)	3774	183	205.4	101.6	11.0 - 865.0
BONE (gm)	3796	183	914.5	147.9	510.0 - 1645.0

RESULTS AND DISCUSSION

Genetic and phenotypic correlation estimates for the carcass composition traits, adjusted for hot carcass weight, are presented in Tables 1, 2 and 3, as well as predicted correlated responses in the carcass traits (in trait units) from index selection over 10 years (Tables 2 and 3). Among the muscle dimensions (Table 2) and fat depth measures (Table 3), there were high positive genetic correlations, except for a low positive genetic correlation between EMD and EMW. These estimates were consistent with published values (Fogarty 1995; Safari and Fogarty 2003; Ingham *et al*. 2007; Greeff *et al*. 2008). Genetic correlation estimates among muscle weights ranged from 0.29 to 0.50 (Table 2) and were lower than published estimates among predicted weights of primal cuts that were generally greater than 0.9 (Jopson *et al*. 2009; Payne *et al*. 2009; Rius-Vilarrasa *et al*. 2009, 2010). In agreement with the few published estimates (Kenney *et al*. 1995; Waldron *et al*. 1992; Jopson *et al*. 2009), muscle dimensions and weights had positive and generally moderate to strong genetic correlations, although correlations involving loin and topside weights tended to be stronger than those involving round weight. All fat depth measures had strong positive genetic correlations with FATLL (Table 3), similar to estimates reported by Kenney *et al*. (1995).

While hind leg bone weight had moderate to strong, negative genetic correlations with the carcass fat measures (range of -0.42 to -0.66), its genetic correlations were positive with EMW, WTTOP and WTRND and not different from zero for EMD, EMA and WTLL (Table 4). The few published genetic correlation estimates that have been reported between these traits are in the same

direction (Kenney *et al*. 1995; Conington *et al*. 1998; Jones *et al*. 1999). The weak genetic

Table 2. Genetic (below diagonal) and phenotypic (above diagonal) correlation estimates (s.e.) among carcass muscle traits and predicted responses over 10 years from index selection

	EMW	EMD	EMA	WTLL	WTTOP	WTRND
EMW		0.14(0.02)	0.62(0.01)	0.33(0.02)	0.25(0.02)	0.17(0.02)
EMD	0.24(0.11)		0.86(0.00)	0.26(0.02)	0.18(0.02)	0.09(0.02)
EMA	0.71(0.06)	0.85(0.03)		0.38(0.02)	0.27(0.02)	0.16(0.02)
WTLL	0.59(0.08)	0.46(0.10)	0.65(0.07)		0.31(0.02)	0.19(0.02)
WTTOP	0.60(0.09)	0.26(0.13)	0.50(0.11)	0.50(0.09)		0.32(0.02)
WTRND	0.45(0.10)	0.14(0.13)	0.35(0.11)	0.29(0.10)	0.42(0.12)	
Response	2.0 mm	2.1 mm	1.5 cm^2	27.9 gm	32.4 gm	21.6 gm

Table 3. Genetic (below diagonal) and phenotypic (above diagonal) correlation estimates (s.e.) among carcass fat traits and bone weight and predicted responses over 10 years from index selection

	FATGR	FATC	FAT5	FATLL	BONE
FATGR		0.41(0.01)	0.35(0.02)	0.45(0.01)	-0.33(0.02)
FATC	0.78(0.06)		0.24(0.02)	0.37(0.02)	-0.19(0.02)
FAT5	0.73(0.08)	0.84(0.08)		0.26(0.02)	-0.16(0.02)
FATLL	0.55(0.13)	0.85(0.07)	0.80(0.10)		-0.27(0.02)
BONE	-0.66(0.07)	-0.62(0.10)	-0.42(0.12)	-0.53(0.12)	
Response	-0.5 mm	-0.5 mm	0 mm	7.6 gm	30.0 gm

Table 4. Genetic and phenotypic correlation estimates (s.e.) among carcass component traits

	EMW	EMD	EMA	WTLL	WTTOP	WTRND
Genetic correlations						
FATGR	-0.18(0.09)	0.09(0.11)	-0.02(0.10)	-0.02(0.09)	-0.51(0.09)	-0.41(0.09)
FATC	-0.33(0.11)	-0.03(0.14)	-0.19(0.13)	-0.26(0.11)	-0.58(0.11)	-0.36(0.12)
FAT5	-0.21(0.12)	0.22(0.14)	0.03(0.14)	-0.25(0.12)	-0.37(0.13)	-0.33(0.13)
FATLL	-0.20(0.13)	0.11(0.15)	-0.05(0.14)	0.10(0.12)	-0.31(0.15)	-0.30(0.14)
BONE	0.29(0.11)	-0.16(0.13)	0.04(0.13)	0.13(0.11)	0.49(0.12)	0.61(0.10)
Phenotypic correlations						
FATGR	-0.15(0.02)	0.11(0.02)	0.01(0.02)	-0.01(0.02)	-0.14(0.02)	-0.20(0.02)
FATC	-0.14(0.02)	-0.01(0.02)	-0.08(0.02)	-0.11(0.02)	-0.15(0.02)	-0.15(0.02)
FAT5	-0.14(0.02)	0.03(0.02)	-0.05(0.02)	-0.09(0.02)	-0.13(0.02)	-0.15(0.02)
FATLL	-0.13(0.02)	0.00(0.02)	-0.07(0.02)	0.04(0.02)	-0.13(0.02)	-0.18(0.02)
BONE	0.13(0.02)	-0.04(0.02)	0.03(0.02)	0.00(0.02)	0.23(0.02)	0.29(0.02)

correlation estimates, generally not different from zero (Table 4), suggest selection that increases muscle dimensions is expected to only lead to small changes in the carcass fat measures. These genetic associations are generally consistent with those reported by Fogarty (1995), Kenney *et al*. (1995), Safari and Fogarty (2003), Ingham *et al*. (2007), Greeff *et al*. (2008) and Jopson *et al*. (2009). In contrast, the stronger negative genetic correlations of topside and round weights with the carcass fat measures (range of -0.30 to –0.58) indicate that selection to reduce carcass fat levels would be expected to result in substantial increases in the weights of these cuts. Such selection would result in much smaller changes in loin weight, based on its weaker genetic correlations with the fat traits (Table 4). Published values of genetic correlations between carcass fat traits and

carcass lean traits are variable (Conington *et al*. 1998; Jones *et al*. 1999; Jopson *et al*. 2009). Overall, the phenotypic correlations among the carcass composition traits followed a similar pattern to those of the genetic correlation estimates, but were often weaker.

Over 10 years, predicted increases from index selection were about 2 mm for carcass muscle width and depth, while predicted increases were 1.5 cm^2 for carcass eye muscle area (Table 2). Hind leg muscle weights were predicted to increase between 21.6 and 32.4 gm. Carcass fat depth at the GR and C sites were predicted to reduce by 0.5 mm over the 10 years, but with no change in fat depth at the 5th rib and an increase in loin fat weight of 7.6 gm (Table 3). Bone weight was predicted to increase by 30 gm. These results show that an index currently used in the Australian sheep meat industry that emphasises growth and carcass traits is predicted to yield generally improved levels of performance in lamb carcass composition traits. However, some selection indexes may need to be modified for use in certain flocks to allow some carcass composition traits, such as fat depths, to be maintained at acceptable levels.

ACKNOWLEDGEMENTS

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