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Genetic and phenotypic parameter estimates for growth, yield and meat quality traits in lamb

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ABSTRACT

The Meat and Wool New Zealand Central Progeny Test has evaluated 143 sires from terminal and dual purpose breeds for meat yield and growth. Meat quality traits, including pH, fat and meat colour (CIE L*, CIE a*, CIE b*) have also been measured. This paper determines genetic variation in these quality traits and their correlations with growth and meat yield. Progeny were drafted for slaughter at a threshold live weight of 34 kg at weaning and 36 kg for subsequent slaughters. Fat colour, eye muscle meat colour and meat pH were measured 24 hours post-slaughter, with meat colour measured after a 30 minute bloom. Heritabilities and genetic correlations between traits were calculated from the measurements. Data were analysed with a linear mixed model in ASReml. Results showed significant variation among sires for meat quality. Heritabilities were moderate for most meat quality traits: fat colour (CIE b* 0.42), initial meat colour (CIE L* 0.29, CIE a* 0.19) and pH (0.12). Relationships between meat quality and yield/growth showed that meat CIE L* had a positive genetic correlation with weaning weight (0.42). Simulated index selection for growth rate and meat yield predicted a small increase in meat lightness and decline in fat yellowness (0.231 and -0.227 units per generation and unit selection intensity, respectively).

Keywords: sheep; meat quality; genetic parameters; index selection.

INTRODUCTION

Genetic selection for sheep meat production in New Zealand has traditionally had a heavy emphasis on growth rate (Amer, 2009). The rationale is that high growth rate lambs can be sent for slaughter at an earlier age so as to capture seasonal price premiums, free-up pasture for other livestock and reduce problems associated with feeding livestock in summer-dry conditions. Selection for improved meat yield has also been possible for over twenty years through the use of technologies, including ultrasound scanning and more recently computed tomography (CT) scanning (Young *et al.,* 1996). There has been increased emphasis on meat yield, particularly in the terminal sire breeds, as some meat processors have installed yield-based grading systems and included financial incentives for meat yield in their payment schemes.

Animal performance for growth and meat yield are important to farmers and meat processors, but market signals indicate meat quality traits are becoming increasing important to consumers. There has been little research in sheep into the correlated responses of meat quality traits in programmes based on selection for growth rate and meat yield. Studies in the pork, beef and poultry sectors have shown selection for yield and growth has negatively influenced meat quality (Sellier and Monin, 1994; Dransfield and Sosnicki, 1999; Koohmaraie *et al.*, 2002).

The aim of this research was to estimate the heritabilities and genetic and phenotypic correlations for the meat quality traits of pH and meat colour, along with growth and meat yield traits measured as part of the Meat and Wool New Zealand Central Progeny Test (CPT). From this, the correlated response for the meat quality traits to selection for growth rate and yield are estimated.

MATERIALS AND METHODS

Data were collected from the 6,565 progeny of 143 sires from the Meat and Wool New Zealand CPT. Sires were born over six years and part of three fully pedigree-recorded research flocks. These research flocks are based at AgResearch's Woodlands Research Farm (Southland), Lincoln University's Ashley Dene Pastoral Systems Research Farm (Canterbury) and On-Farm Research's Poukawa Research Station (Hawkes Bay). Mating and farm management has been described by McLean *et al.* (2006). Animals were of 18 different terminal sire and dual purpose breeds.

All progeny from terminal sire rams were slaughtered to collect carcass measurements. Ewe lambs from dual purpose sires were retained to measure maternal traits, while ram lambs and surplus ewe lambs were slaughtered to measure carcass traits. Live weight thresholds to draft for slaughter were derived with the aim of achieving 17 kg carcass weights. Lambs were weaned at an

average of 12 weeks of age and live weight measured (WWT). Animals that reached the live weight threshold of 34 kg at weaning were drafted and slaughtered the following day. Those not reaching the live weight threshold were fed on high quality pasture and weighed every four weeks until they either reached the 36 kg weaned live weight threshold or until the fourth weighing. All animals were slaughtered the day after weighing occurred.

Slaughters were carried out at The Alliance Group Mataura, Smithfield, Pukeuri and Dannevirke processing plants. Carcass weight (CWT) was measured, followed by grading using the VIAscan® carcass classification system (Hopkins *et al.*, 2004). Total weight of lean tissue in each of the hindleg, loin and shoulder primal cuts was derived from the VIAscan® video images (LEANLEG, LEANLOIN and LEANSHLD, respectively). Carcasses underwent an accelerated aging and conditioning protocol including electrical stimulation and overnight chilling. Carcasses were processed into cuts the day after slaughter. The rack cut was recovered and allowed to sit for a minimum of 30 minutes to allow the cut surface of the meat to bloom. Colour was estimated in the CIE L* a* b* system using a Minolta Colorimeter (Konica Minolta Sensing, Inc., Osaka, Japan) with an 8 mm aperture and calibrated to a standard white tile, where CIE L*, CIE a* and CIE b* are relative lightness, redness and yellowness respectively. Colour measurements were made on both the cut surface of the *M. longissimus lumborum* at the 12th/13th rib and on the untrimmed fat cap covering the cut. Three readings were collected from both the meat and fat colour, and the average values for each

were analysed. While CIE L*, CIE a* and CIE b* were measured for both muscle and fat, results are only presented for CIE L* and CIE a* for meat colour and CIE b* for fat colour (MeatL, MeatA and FatB, respectively). Meat pH was measured at the same time using a temperature-compensated pH meter, again as the average of three replicates measured at the cut site on the *M. longissimus lumborum*.

Data were analysed using linear mixed models. Breed, sex and contemporary group were fitted as fixed effects, and animal fitted as a random effect, for all traits. The fixed effects and covariate terms fitted for each trait are listed in Table 1. Parameter estimates for WWT and CWT were estimated on an age constant basis. LEANLEG, LEANLOIN and LEANSHLD were fitted on a carcass weight adjusted basis.

Variance components were estimated using restricted maximum likelihood (REML) procedures fitting an animal model in ASReml (Gilmour *et al.,* 2006). Univariate analyses were used to estimate heritabilities for each carcass trait. Bivariate analyses were used to estimate the phenotypic and genetic correlations between the various traits. The genetic correlation matrix was bent to ensure it was positive definite.

Selection index gains (Falconer, 1983) were simulated for a progeny tested flock with 80 progeny per sire, 20 of which were slaughtered to collect meat yield measurements. Economic values were set to $0.66 per kg for WWT and $1.58 per kg for CWT, which are the values currently used within the Sheep Improvement Limited (SIL) genetic evaluation programme Geenty, 2000) for a terminal

TABLE 1: Statistical models for the analysis of growth rate, meat yield and meat quality traits measured as part of the Meat and Wool Central Progeny Test. WWT = Wean weight, CWT = Carcass weight, LEANLEG = Weight of lean tissue in hindleg primal cut, LEANLOIN = Weight of lean tissue in loin primal cut, LEANSHLD = Weight of lean tissue in shoulder primal cut, MeatL = CIE L* of cut muscle, MeatA = CIE a* of cut muscle, FatB = CIE b* of fat.

Trait	Terms fitted		
	Fixed effects*	Covariates*	Random effects
WWT	sex, breed, brr, aod, cgwean	bdev	Animal, Dam
CWT	sex, breed, brr, aod, kmob, cgmeat	kdays	Animal
LEANLEG	sex, breed, cgmeat	CWT	Animal
LEANLOIN	sex, breed, cgmeat	CWT	Animal
LEANSHLD	sex, breed, cgmeat	CWT	Animal
pH	sex, breed, cgmeat		Animal
MeatL	sex, breed, cgmeat	pH, pH^2	Animal
MeatA	sex, breed, cgmeat	pH, pH^2	Animal
FatB	sex, breed, cgmeat		Animal

* brr = Birth rearing rank; aod = Age of dam; bdev = Birth day deviation; kdays = Days from birth to slaughter; kmob = Kill mob; byear = Birth year; cgwean = Contemporary group based on flock, birth year, sex and docking mob; cgmeat = Contemporary group based on flock, birth year, sex, docking mob and kill mob.

TABLE 2: Summary statistics for the carcass meat traits including the raw mean, phenotypic standard deviation (pSD), coefficient of variation (CV%) and residual standard deviation RSD) measured as part of the Meat and Wool Central Progeny Test. WWT = Wean weight, CWT = Carcass weight, LEANLEG = Weight of lean tissue in hindleg primal cut, LEANLOIN = Weight of lean tissue in loin primal cut, LEANSHLD = Weight of lean tissue in shoulder primal cut, MeatL = CIE L* of cut muscle, MeatA = CIE a* of cut muscle, FatB = CIE b* of fat.

Trait	Mean	pSD	CV%	RSD
WWT (kg)	31.1	4.48	14.4	3.52
CWT (kg)	17.56	1.59	9.1	1.42
LEANLEG (kg)	3.18	0.18	5.6	0.15
LEANLOIN (kg)	2.42	0.11	4.3	0.10
LEANSHLD (kg)	3.79	0.14	3.7	0.13
pH	5.71	0.12	2.1	0.11
MeatL (CIE L*)	37.0	1.71	4.6	1.44
MeatA (CIE a*)	18.5	1.38	7.4	1.24
FatB (CIE b*)	10.3	2.77	26.8	2.12

TABLE 3: Heritabilities, phenotypic and genotypic correlations among meat quality traits and yield traits measured as part of the Meat and Wool Central Progeny Test. Heritabilities are in bold font on the diagonal, genetic and phenotypic correlations are below and above diagonal, respectively. WWT = Wean weight, CWT = Carcass weight, LEANLEG = Weight of lean tissue in hindleg primal cut, LEANLOIN = Weight of lean tissue in loin primal cut, LEANSHLD = Weight of lean tissue in shoulder primal cut, MeatL = CIE L* of cut muscle, MeatA = CIE a* of cut muscle, FatB = CIE b* of fat.

Trait	WWT	CWT	LEANLEG	LEANLOIN	LEANSHLD	pH	MeatL	MeatA	FatB
WWT	**0.09**	0.84	0.14	0.06	-0.01	0.00	0.24	0.07	-0.02
CWT	0.84	**0.20**	0.33	0.26	0.14	-0.06	-0.07	-0.08	0.03
LEANLEG	0.39	0.22	**0.25**	0.64	0.61	0.05	0.04	0.00	-0.10
LEANLOIN	0.13	0.11	0.52	**0.18**	0.47	0.01	0.02	0.00	-0.03
LEANSHLD	0.16	0.02	0.52	0.48	**0.20**	0.03	0.04	0.01	-0.13
pH	0.08	0.03	0.30	-0.12	-0.03	**0.12**	0.00	0.00	0.00
MeatL	0.42	-0.10	0.27	0.02	0.13	0.08	**0.29**	0.29	-0.01
MeatA	-0.08	-0.29	-0.07	-0.06	0.11	-0.02	0.17	**0.19**	-0.01
FatB	-0.13	0.03	-0.34	-0.19	-0.53	-0.03	-0.03	-0.03	**0.42**

sire growth index when meat is not selected. In addition, economic values were estimated for LEANLEG, LEANLOIN and LEANSHLD, such that the value was equal to the equivalent increase in carcass weight given a 54% recovery of lean cuts from the carcass. Two scenarios were tested. The first scenario assumed lean tissue to be of equivalent value regardless of where it was found in the carcass and was set at $2.92 per kg for each of the LEANLEG, LEANLOIN and LEANSHLD cuts. The second scenario used weightings depending on where the lean tissue was located in the carcass at a ratio of 1:2:3 for the shoulder, hindleg and loin, such that the overall value of the three cuts was equal to the first scenario. In Scenario 2, the economic values for LEANLEG, LEANLOIN and LEANSHLD were $3.15, $4.72 and $1.57, respectively.

RESULTS

Trait summary statistics are presented in Table 2, including the raw means, phenotypic standard deviations, residual; standard deviations and coefficients of variation. Standard errors for the heritabilities ranged between 0.034 and 0.049, and the corresponding range for genetic correlation estimates was 0.078 to 0.203.

Heritabilities

The derived heritability estimates are presented in Table 3. Heritabilities were low to moderate for growth traits being 0.09 and 0.20 for WWT and CWT, respectively and moderate for most meat yield traits, ranging from 0.18 to 0.25. Estimates were moderate for the meat quality traits of meat lightness (MeatL; 0.29); fat yellowness (FatB; 0.42); and meat redness (MeatA; 0.19). Meat pH had a low heritability at 0.12.

TABLE 4: Predicted response to index selection for growth rate and meat yield per generation and per unit of selection intensity. Scenario 1 assigns meat yield an equal value across all cuts while Scenario 2 weights cuts according to region at a ratio of 1:2:3 for the shoulder, hindleg and loin, respectively. WWT = Wean weight, CWT = Carcass weight, LEANLEG = Weight of lean tissue in hindleg primal cut, LEANLOIN = Weight of lean tissue in loin primal cut, LEANSHLD = Weight of lean tissue in shoulder primal cut, MeatL = CIE L* of cut muscle, MeatA = CIE a* of cut muscle, FatB = CIE b* of fat.

Trait	Scenario 1	Scenario 2
WWT (kg)	1.088	1.086
CCW (kg)	0.520	0.520
LEANLEG (kg)	0.037	0.037
LEANLOIN (kg)	0.009	0.009
LEANSHLD (kg)	0.012	0.012
pH	0.003	0.003
MeatL (CIE L*)	0.231	0.231
MeatA (CIE a*)	-0.069	-0.072
FatB (CIE b*)	-0.227	-0.214

Genetic correlations

Derived genetic and phenotypic correlations are presented in Table 3. The genetic correlation between meat lightness and weaning weight was moderate and positive at 0.42 ± 0.15, but the correlation between meat lightness and carcass weight was not statistically different from zero (-0.10 ± 0.16). The genetic correlations for the growth traits with meat pH, MeatA or FatB were all not significantly different from zero (P >0.05).

Genetic correlations between each of the three meat yield traits of LEANLEG, LEANLOIN and LEANSHLD and the meat quality traits of pH, MeatL and MeatA were all not significantly different from zero (P >0.05). LEANLEG and LEANSHLD were found to have a negative genetic correlation with FatB (LEANLEG = -0.34 ± 0.11 and LEANSHLD = -0.53 ± 0.11). The genetic correlation between LEANLOIN and FatB was not significantly different from zero (P >0.05).

None of the genetic correlations between the meat quality traits were found to be significantly different from zero (P >0.05).

Phontypic correlations are listed for completeness.

Index selection

Index selection based on growth rate and meat yield resulted in increases in all of the growth and yield traits in both Scenario 1 where lean meat was equally valued throughout the carcass and Scenario 2 where the higher value cuts were weighted accordingly (Table 4). Increases per round of selection, that is per generation and unit of selection intensity, in the carcass weight adjusted traits ranged from 0.009 to 0.037 kg and were lower than for the age adjusted growth traits with a range 0.52 to 1.09 kg. The trends in the meat quality traits were similar across both scenarios. Selection for growth and meat yield traits without selection for the meat quality traits resulted in a small increase in pH of 0.003 in both scenarios and values for MeatA of -0.069 and -0.072 for Scenarios 1 and 2, respectively. There was a moderate increase in MeatL and a fall in FatB in response to selection for growth rate and meat quality of 0.231 and -0.227, respectively in Scenario 1.

DISCUSSION

Meat quality traits such as meat colour and pH are important in that they have repeatedly been found to be important in consumer preference studies. For example, meat colour has been show to be an important factor in a consumers meat purchasing decisions (Clydesdale, 1991; Kubberød *et al.*, 2002). Similarly meat pH has been shown to affect the consumer traits meat colour, shelf-life (Seideman *et al.*, 1984) and tenderness (Watanabe *et al.*, 1996). There has been significant research effort into understanding factors influencing meat quality in the meat processing plant and on farm (Geesink *et al.*, 2000). However, there is currently no way of routinely collecting large numbers of objective meat quality measurements in a timely manner and incorporating them into sheep breeding programmes. Breeding for meat quality traits is unlikely to attain widespread application until it is possible to routinely measure meat quality in the processing plant, and for farmers to receive sufficient payment for improvements in meat quality to compete with the economic benefits of improving growth rate and meat yield in their animals.

Genetic selection for extremes in growth rates and yield in other species have resulted in negative responses in meat quality as reviewed in Sellier and Monin (1994), Dransfield and Sosnicki (1999) and Koohmaraie *et al.* (2002). Reproduction rates and the predominant dual purpose function of sheep in New Zealand means that selection for growth and yield are unlikely to be as intensive as in the pork and poultry industries. However, terminal sire sheep breeding programmes do have a strong emphasis on selection for fast growth and high yield, with the aim of increasing meat production and efficiency. It is therefore important to study the impact of selection decisions on meat quality traits if quality is not to be inadvertently affected.

Genetic parameters for growth, yield and some basic meat quality measures are presented to be able to quantify the effects of current and potential future

selection practices for growth and meat yield. The decision to adjust for breed effects in the analysis is somewhat moot, in that there is considerable variation in the representation of the breeds in this study with some breeds only being represented by one ram. However, failure to adjust for these effects means that a single breed may have a high leverage on the results. Heritabilities for the growth traits are at the lower end of the published range (Waldron *et al.*, 1992; Greeff *et al.*, 2008), possibly due to the adjustment for breed effects in the analysis. The analysis was run both with and without breed effects. The models adjusted for breed effects were deemed to give more conservative estimates (N.B. Jopson, Unpublished data).

The above results show that selection for growth rate and meat yield does not produce a significant correlated response in the majority of meat quality traits measured here. For the three meat quality traits pH, MeatL and MeatA, the only significant genetic correlation was between weaning weight and MeatL, where selection for increased weaning weight would tend to make the meat lighter or paler. Selection for increased meat yield would produce no correlated change on meat colour, but would tend to produce fat that was less yellow due to the significant negative genetic correlations with LEANLEG and LEANSHLD.

While the majority of the genetic correlations between the meat quality traits and the growth and yield traits were not significantly different from zero, it is of interest to examine the selection index results. Combining the growth rate and meat yield traits in a selection index did result in a moderate increase change in MeatL of 0.23 colour units per generation and per unit of selection intensity. This response in CIE L* equates to 0.085 units per year assuming an average selection intensity across sexes of 1.2 and an average generation interval of 3.25 years, or around 12 years of selection to change CIE L* by one unit.

Estimated response in meat pH to selection was very low at 0.003 units per generation and unit selection intensity. Meat pH is a very important meat quality trait in that it is known to influence tenderness, colour and shelf life (Seideman *et al.*, 1984; Watanabe *et al.*, 1996). While pH was moderately heritable in this and other studies (Greeff *et al.*, 2008), the phenotypic standard deviation was low (0.12) meaning that selection is unlikely to produce a large change in pH.

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