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Genetic parameters for primal cut meat yield traits in sheep

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ABSTRACT

Lamb carcass grading is changing from classification on carcass weight and tissue depth (GR) to yield grading systems such as VIAscan®. Under the VIAscan® system, farmers receive information on the percentage lean meat yield from the hindleg, loin and shoulder primal cuts, and payments are based on these measurements. Genetic improvement programmes for meat have concentrated on producing age-adjusted breeding values for carcass lean and fat weight from live weight and ultrasonic eye muscle measurements. This has worked well for grading using carcass weight and GR, but does not quantify differences in yield between meat cuts. Carcass and VIAscan® yield data collected for the Meat and Wool New Zealand Central Progeny Test were analysed to determine heritabilities and genetic and phenotypic correlations for meat yield traits. The dataset contained around 6,600 progeny from 143 terminal sire or dual purpose rams. Data were analysed using linear mixed models in ASReml. The results showed significant variation between sires for lean yield traits. Heritabilities for age-adjusted lean weight in the hindleg, loin and shoulder were 0.40, 0.37 and 0.42, respectively. Genetic correlations for age-adjusted weight of lean by carcass region were all high (range 0.94 to 0.96), but were lower (0.62 to 0.85) when adjusted to constant carcass weight.

Keywords: sheep; genetic selection; genetic parameters; meat yield.

INTRODUCTION

Lamb carcass grading in New Zealand has been based on carcass weight and the GR tissue depth over the 12th rib, 11 cm from midline (Kirton, 1989). Payments to producers have been on the basis of the carcass weight and GR 'bin' that each carcass achieves. These two traits have provided estimates of the weight of lean and fat tissue in the carcass (Kirton *et al.*, 1999). The accuracy of the estimates are however, only moderate and consequently there is a significant degree of averaging in the payment system. Meat industry reform has meant that meat processors are now able to develop their own grading systems with some meat processors having introduced equipment to estimate meat yield on-line. As a result, they have changed their payment schemes to reward producers who supply high yielding carcasses, with the yield being measured in each of the hindleg, loin and shoulder primal cuts.

Given that payment systems can now reward for meat yield within a carcass region, there is the need for New Zealand breeding programmes to be able to include selection for meat yield in the breeding objective, particularly in the terminal sire breed industry. This is already possible on an individual cut basis in live animals through the use of computed tomography (CT) scanning (Kvame *et al.*, 2004) and there is the potential to progeny test

rams using the on-line meat plant equipment (McLean *et al.*, 2006). Achieving maximal response to selection is dependent upon accurate estimates of the heritabilities and genetic and phenotypic correlations for the yield traits. There are few published estimates of any of these parameters for sheep in New Zealand.

The Meat and Wool New Zealand Central Progeny Test has been measuring meat yield in The Alliance Group processing plants for six years using the VIAscan® carcass grading system. As such it provides a suitable dataset to provide genetic parameters for the meat yield traits. The aim of this paper was to estimate the heritability, as well as phenotypic and genetic correlations, for the weight of lean tissue in the hindleg, loin and shoulder cuts across rams from both dual purpose and terminal sire breeds, along with carcass traits already recorded in terminal sire breeding programmes.

MATERIALS AND METHODSS

Carcass data were collected from 6,565 lambs slaughtered at four weekly intervals from three to six months of age, with animals drafted to achieve a 17 kg carcass weight. The animals were the progeny of 143 sires and born over six years in three fully pedigree-recorded research resource flocks (Table 1) and evaluated in the Meat and Wool New Zealand Central Progeny Test. Resource flocks included

TABLE 1: Numbers of sires and progeny used by location and year.

Year	Woodlands		Ashley Dene		Poukawa	
	Sires ¹	Progeny	Sires ¹	Progeny	Sires ¹	Progeny
2002	22	605	-	-	-	-
2003	25	682	13	278	-	-
2004	12	505	14	472	-	-
2005	13	401	7	323	11	626
2006	11	372	7	395	8	553
2007	13	331	7	553	10	469
Total		2896		2021		1648

¹ Includes year and site link sires. A total of 143 sires have been evaluated.

TABLE 2: Sire breed representation in the dataset.

Breed	Number of sires
Borderdale	1
Cheviot	1
Composite	15
Coopworth	10
Corriedale	6
Dorper	1
Dorset Down	9
Dorset Horn	2
GrowBulk	3
Hampshire	5
Oxford	1
Oxford Down	1
Perendale	12
Poll Dorset	13
Romney	22
South Suffolk	6
Southdown	5
Suffolk	14
Texel	16
Total	143

AgResearch's Woodlands Research Farm (WDL) in Southland, Lincoln University's Ashley Dene Pastoral Systems Research Farm (AD) in Canterbury and On-Farm Research's Poukawa Research Station (POU) in the Hawkes Bay. A minimum of two rams were used each year to provide genetic linkage across years and sites. The sires comprised 18 individual breeds as well as terminal sire and dual purpose composites (Table 2). Matings and farm management of the animals are described by McLean *et al.* (2006). Coopworth or Romney-cross ewes were predominantly used in the research flocks. All progeny from terminal sire rams and all male and surplus female progeny from the dual purpose sires were slaughtered to collect carcass measurements.

Slaughter animals were weaned at an average of 12 weeks of age and live weight was measured. All animals over the live weight threshold of 34 kg at weaning were drafted and slaughtered the following day. Lambs below the target live weight were fed *ad libitum* on high quality pasture and weighed at further four-weekly intervals. All animals over 36 kg live weight at each of the post-weaning measurement times were drafted to slaughter the following day, with all remaining animals going for slaughter at the fourth weighing.

TABLE 3: Summary statistics for the carcass meat traits including the raw mean, phenotypic standard deviation (pSD) coefficient of variation (CV%) and residual standard deviation (RSD). CWT = On-line carcass weight, EMA = Eye muscle area, LEAN = Total weight of lean tissue, FAT = Total weight of fat, LEANLEG = Weight of lean tissue in hind leg, LEANLOIN = Weight of lean tissue in loin, LEANSHLD = Weight of lean tissue in shoulder.

Trait	Mean	pSD	CV%	RSD
CWT (kg)	17.56	1.71	9.7	1.41
EMA (cm ²)	11.48	1.87	16.2	1.07
LEAN (kg)	9.26	1.09	11.8	0.83
FAT (kg)	4.76	0.32	6.7	0.25
LEANLEG (kg)	3.18	0.38	10.0	0.29
LEANLOIN (kg)	2.42	0.29	12.0	0.23
LEANSHLD (kg)	3.79	0.34	10.8	0.26

TABLE 4: Genetic parameters for age-adjusted carcass and meat traits. Heritabilities are in bold on the diagonal. Genetic correlations are below the diagonal and phenotypic correlations are above. CWT = On-line carcass weight, EMA = Eye muscle area, LEAN = Total weight of lean tissue, FAT = Total weight of fat, LEANLEG = Weight of lean tissue in hind leg, LEANLOIN = Weight of lean tissue in loin, LEANSHLD = Weight of lean tissue in shoulder.

Trait	CCW	EMA	FAT	LEAN	LEANLEG	LEANLOIN	LEANSHLD
CCW	0.32	0.32	0.72	0.92	0.87	0.91	0.91
EMA	0.41	0.41	0.29	0.48	0.46	0.47	0.48
FAT	0.65	0.23	0.40	0.44	0.35	0.49	0.47
LEAN	0.92	0.72	0.30	0.41	0.98	0.96	0.97
LEANLEG	0.87	0.69	0.21	0.99	0.40	0.92	0.92
LEANLOIN	0.94	0.72	0.39	0.97	0.94	0.37	0.90
LEANSHLD	0.91	0.71	0.33	0.98	0.96	0.94	0.42

Slaughters were carried out at the Alliance Groups Matura, Smithfield, Pukeuri and Dannevirke processing plants. Carcasses were weighed on-line (CWT) prior to grading and then graded using the VIAscan® carcass classification system which is based on video image analysis. The weights of lean tissue in the hindleg, loin and shoulder primal cuts (LEANLEG, LEANLOIN and LEANSHLD, respectively) were estimated from the video images. Total weight of lean tissue (LEAN) was defined as the sum of lean measured in the hindleg, loin and shoulder cuts. Total weight of fat in the carcass (FAT) was calculated as carcass weight less the weight of LEAN and estimated weight of bone. Literature estimates of bone weight are around 18% of carcass weight (e.g. Kirton *et al.*, 1985). However, bone weight was set at 20% of carcass weight in order to keep the mean estimated fat weight below the level of 30% of carcass weight observed in heavy weight carcasses (e.g. Young *et al.*, 1996). After grading, carcasses went through an accelerated aging and conditioning protocol and

were further processed the following day. The rack cut was collected and the distal end of the *M. longissimus lumborum* was either photographed or traced for subsequent eye muscle area (EMA) measurement.

Data were analysed using linear mixed models (ASReml; Gilmour *et al.*, 2006). All parameter estimates were calculated on an age constant basis. Fixed effects were fitted for birth and rearing rank, age of dam, sex and contemporary group (flock, year of birth, weaning mob and slaughter mob). Birth day deviation was fitted as a covariate for all traits. Variance components were estimated using REML procedures fitting an animal model. Univariate analyses were used to estimate heritabilities for each carcass trait. Phenotypic and residual standard deviations were calculated for each trait from the output of the univariate REML analyses. Bivariate analyses were used to estimate the phenotypic and genetic correlations between the various traits. The variance/covariance matrices were bent where appropriate using a weighted bending method (Jorjani *et al.*, 2002; 2003) to ensure the matrices were positive definite. The accuracy of weightings were set a hundred-fold higher for the variance parameters than for the covariance parameters.

TABLE 5: Genetic parameters for age-adjusted and estimated carcass weight adjusted lean yield using the method of Dodds (1991). Heritabilities are in bold on the diagonal. Genetic correlations are below the diagonal and phenotypic correlations are above. CWT = On-line carcass weight, LEANLEG = Weight of lean tissue in hind leg, LEANLOIN = Weight of lean tissue in loin, LEANSHLD = Weight of lean tissue in shoulder.

Trait	CCW	LEANLEG	LEANLOIN	LEANSHLD
CCW	0.32	0	0	0
LEANLEG	0.20	0.42	0.62	0.64
LEANLOIN	0.26	0.76	0.30	0.44
LEANSHLD	0.30	0.85	0.62	0.45

RESULTS

Summary statistics for the carcass traits are presented in Table 3, including the raw means, phenotypic standard deviations, coefficients of variation and residual standard deviation.

Table 4 presents the estimates of the heritabilities and the genetic and phenotypic correlations among the carcass

and meat yield measurements. All traits were analysed on an age-constant basis. Heritabilities for traits were all moderate to high, ranging from 0.32 for CCW to 0.42 for LEANSHLD. LEANLOIN had the lowest heritability of the three lean weights traits of 0.37, compared to 0.40 and 0.42 for LEANLEG and LEANSHLD, respectively. Standard errors for the heritabilities ranged between 0.041 and 0.047 and corresponding range for genetic correlation estimates was 0.002 and 0.086.

All of the genetic correlations between traits were positive to varying degrees. The hindleg, loin and shoulder lean weights were all highly genetically correlated with each other with a range of range 0.94 to 0.96, and with carcass weight with a range 0.87 to 0.94. Genetic correlations for the three cuts compared to EMA were moderate to high, ranging from 0.69 to 0.72. LEANLOIN had the greatest genetic correlation with EMA at 0.72. The three lean cuts had somewhat lower genetic correlations with FAT ranging from 0.21 to 0.33.

DISCUSSION

Genetic improvement programmes for sheep meat production have concentrated on producing breeding values for age-adjusted weight of lean and fat in the carcass. This has been based on measurements of live weight and ultrasonic eye muscle dimensions, although there has been some use of carcass measurements from CT scanning and from progeny tests (Jopson *et al.*, 1995; Johnson *et al.*, 2002). This has served the sheep industry well under a carcass weight and GR carcass grading system. However, meat companies are now implementing carcass payment systems based on yield of lean tissue within carcass regions. Breeding values for the total weight of lean and fat do not give information on the differences in the yield of meat within and between regions in a carcass.

The estimates for CCW, LEAN, and EMA are in reasonable agreement with previous estimates for sheep in New Zealand (Waldron *et al.*, 1992). FAT as calculated here has a substantially lower coefficient of variation than for other published estimates. This is not unexpected given that it is estimated here by difference.

The results also show that weights of lean meat within a carcass region are highly correlated genetically with both carcass weight and total lean weight. As such, current selection programmes have been making progress in improving the weight of lean meat within specific regions of a carcass. However, while the genetic correlations between carcass weight and the weight of lean in the three cuts are high, there are differences between the cuts meaning that the selection response could be

improved through incorporating the three lean meat weights as traits in the overall breeding objective.

The magnitude of the difference in selection response is somewhat masked when the genetic parameters are presented on an age-adjusted basis. Differences in meat yield, that is the weight of meat per unit of carcass weight or per unit of cut weight, are of great importance to the meat processor. The meat processor purchases a carcass and maximises returns by being able to recover a high proportion of that weight of carcass as saleable meat. If we transform the genetic parameters for carcass weight and the weights of lean in the three primal cuts using the method of Dodds (1991), we see that the genetic correlations between the weight of lean in the three cuts and carcass weight are somewhat lower with a range of 0.20 to 0.30 (Table 5). Also of note is that the genetic correlations between the three lean cuts are reduced to range between 0.62 and 0.85. These values are similar to the carcass weight adjusted values presented in Payne *et al.* (2009), although the genetic correlations between the three traits were lower in the later study with a range of 0.48 to 0.52. This may be explained in part in that breed was included as a fixed effect in that study. This demonstrates that selection for meat yield is different to selection for growth rate and that estimates of weight of lean by region in the carcass will improve selection response in breeding programmes for meat production.

The value of meat per unit weight varies widely between cuts of meat at point of sale, with the loin and rack cuts generally having the highest value per kilogram, products from the hind leg generally being intermediate in value and products from the shoulder generally having the lowest value. Currently the payment systems based on yield grading provides information by region, namely the hindleg, shoulder and the combined loin and rack cuts, but do not pay a premium for having additional yield in the higher value cuts. Given that there is currently no premium paid for the distribution of the meat, the argument could be made that the selection should be made on measures of overall meat yield, which is LEAN as defined above. However, it seems likely that some sort of differential by carcass region will be paid in the future as yield based payment systems evolve, to give a better reflection of the true value of the additional yield recovered from the carcass. As such, breeding programmes should include breeding values for each of the three regions in anticipation of future differential payments.

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