BRIEF COMMUNICATION: Genetic parameters for growth, carcass and meat quality traits in New Zealand sheep

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Introduction

To be competitive with other livestock industries, sheep farmers require rapidly growing animals producing tasty meat, which are grazed under exemplary welfare conditions all at a viable final cost to consumers. Genetic selection has played an important role in improving productivity in sheep farming in New Zealand. Meat sheep breeding programmes around the world have focused on selection for fast growth and high lean yield. However, there is evidence that continued selection for higher lean meat yield may adversely affect aspects of quality (Hopkins et al. 2005; Karamichou et al. 2006). Therefore, it is important to ensure that selection for growth and leanness does not inadvertently affect meat eating quality. For the lamb industry to remain competitive in the long-term, lamb carcass and meat quality traits need to be continually improved along with productivity traits. Meat quality is made up of traits such as meat redness indicating freshness; tenderness; marbling; and pH. These influence the eating experience and the probability of consumer repurchase. In order to make genetic progress in quality traits, knowledge of their genetic architecture is crucial to define the selection criteria and the likely outcomes. The objectives of this study were to: 1) estimate heritabilities for growth, carcass and meat quality traits and 2) estimate phenotypic and genetic correlations among those traits in New Zealand sheep.

Material and methods

Data

Performance records (Table 1) were obtained from animals born between 2010 and 2013 in the FarmIQ Progeny Test flocks. These animals were primarily of progeny from terminal sire composites and Texels mated to a variety of maternal breeds. The average number of progeny recorded per sire was 23. The traits included live weight at 6 months (LW6), pre-slaughter live weight (PRESLT), hot carcass weight (CWT), ultrasonic eye-muscle depth (EMD), ultrasonic eye-muscle width (EMW), ultrasonic fat depth (FDM), carcass measurement of buttocks circumference (CBUTT), depth of tissue at the GR site over the 12th rib at a distance of 110 mm from mid-line (CGRM), number of rib pairs (NRIB), loin meat pH (LPH), marbling score (MARB), tenderness (shear force, LKGF) and loin redness measured after blooming within a semipermeable wrap for 24 hours (A24).

Table 1 Descriptive statistics for growth, carcass and meat quality traits and the final models used for estimation of variance components for New Zealand sheep.

	Descriptive analysis[1]				Final models		
Trait[2]	N	Mean ± SD	Range	RSD	Fixed effects[3]	Covariate[4]	Random
LW6 (kg)	13,369	37.00 ± 5.32	20.80 – 53.20	4.58	sex, cg	bdev, breed	Animal
PRESLT (kg)	14,564	41.67 ± 6.14	23.00 – 60.20	4.60	sex, cg	bdev, breed	Animal
CWT (kg)	13,089	17.93 ± 3.31	08.40 – 27.90	2.49	sex, cg	bdev, breed	Animal
EMD (mm)	8,610	24.83 ± 2.42	18.00 – 32.00	2.16	sex, cg	bdev, breed	Animal
EMW (mm)	8,628	64.19 ± 5.03	49.00 – 79.00	4.79	sex, cg	bdev, breed	Animal
FDM (mm)	8,604	02.61 ± 1.08	00.00 – 05.00	0.98	sex, cg	bdev, breed	Animal
CBUTT (cm)	14,366	65.04 ± 3.25	55.20 – 75.00	2.60	sex, cg	bdev, breed	Animal
CGRM (mm)	14,234	05.16 ± 3.39	00.00 – 16.00	2.58	sex, cg	bdev, breed	Animal
NRIB	12,552	13.01 ± 0.33	12.00 – 14.00	0.32		breed	Animal
LPH	9,338	05.81 ± 0.16	05.48 – 06.43	0.15	sex, cg	CWT	Animal
MARB	9,420	03.05 ± 0.58	01.50 – 04.50	0.54	sex, cg	bdev, CWT	Animal
LKGF (kgf)	9,372	06.47 ± 2.23	01.45 – 13.50	1.87	sex, cg	CWT, LPH, LPH[2]	Animal
A24	9,570	16.73 ± 2.55	09.37 – 24.44	1.42	sex, cg	bdev, CWT, LPH	Animal

[1]N: number of observations; SD: standard deviation; RSD: residual standard deviation; [2]LW6: live weight at 6 months, PRESLT: pre-slaughter live weight, CWT: hot carcass weight, EMD: ultrasonic eye-muscle depth, EMW: ultrasonic eye-muscle width, FDM: ultrasonic fat depth, CBUTT: carcass measurement of buttocks circumference, CGRM: depth of tissue at the GR site over the 12th rib at a distance of 110 mm from mid-line, LPH: loin meat pH, MARB: marbling score 1-5 scale, LKGF: tenderness (shear force) and A24: CIE a* after 24 hours; [3]cg: contemporary group; [4]bdev: birthday deviation, breed: breed proportions.

Slaughter procedure

Lambs were slaughtered in commercial plants with the carcasses electrically stimulated. Animals were randomly selected to be slaughtered on given dates. On the day of slaughter, CGRM, CBUTT, NRIB and CWT measurements were collected. The following day, 24 hours after slaughter, the carcasses were processed into primal cuts. The boneless loins were vacuum packed and stored at -1°C for eight weeks. At eight weeks, pH was measured of the *longissimus dorsi* muscle. Three 2-cm thick slices of the loin were placed on small plastic trays and wrapped using semi-permeable cling film and stored at 4°C. Marbling was visually scored (1-5 scale). Loin redness was measured 24 hours after blooming using a Minolta Chromometer (Konica Minolta Sensing, Inc., Osaka Japan). LKGF was measured on a loin frozen 24 hours after slaughter using the MIRINZ protocol (http://www.mirinz.org.nz/).

Statistical analysis

Traits that showed a relation between the mean and variance were scaled as appropriate to homogenise the variance (Brown et al., 2005). They were expressed as a proportion of their contemporary group (CG) mean multiplied by the global mean for each trait. The traits that were scaled in this way were: LW6, PRESLT, CWT, CGRM, FDM and LPH. CG for each trait was defined by flock, birth year, sex, weaning mob and trait measurement/ slaughter mob.

Data were analysed using linear mixed models. Fixed effects models were selected for each trait separately via backwards elimination using the GLM procedure (SAS Inst. Inc., Cary, NC). Model building was carried out on the pre-processed dataset. The fixed effects and covariate terms fitted for each trait are listed in Table 1.

Variance and covariance components were estimated using restricted maximum likelihood (REML) procedures fitting an animal model in ASReml (Gilmour et al. 2009). Heritabilities were obtained by running univariate analyses for each trait and bivariate analyses were used to estimate the phenotypic and genetic correlations between the various traits. Due to the presence of a large number of animals with unknown ancestry, we also fitted a genetic group effect (phantom parents) to take into account possible genetic differences in founders animals contributing to ewes and rams in different birth years. For this study, the groups were created based on the year of birth and sex of the unknown parent.

Results and discussion

Table 2 presents the heritabilities of traits and genetic and phenotypic correlations among the traits. Heritabilities were moderate to high for all growth and carcass traits, ranging from 0.19 for CWT to 0.37 for EMD. Estimates for the meat-quality traits ranged from 0.09 for LPH to 0.31 for MARB. The heritability estimates suggest that most of the traits studied are under moderate genetic control so that genetic gains could be achieved by selection. In general, the estimates obtained in this study are in agreement with those presented in the literature (e.g., Payne et al. 2009; Mortimer et al. 2014), except NRIB, for which we did not find other estimates reported in the sheep literature.

Birth-rearing rank (number of lambs born and raised per litter, respectively) and age of dam could also influence some of the traits. Not including those effects in the models could supress the heritability estimates (increase the residual variance). However, for the flocks included in this study, this information was not available as dams were not recorded in most of the progeny-test flocks. The higher estimates obtained for LW6 compared to PRESLT could be due to the fact that maternal effects were not fitted for LW6. However, Pickering et al. (2012) also presented an estimate for live weight at 8 months of 0.35±0.001.

Table 2 Heritabilities of traits (diagonal), and phenotypic (above diagonal) and genetic (below diagonal) correlations among all traits for New Zealand sheep.

Trait[1]	LW6	PRESLT	CWT	EMD	EMW	FDM	CBUTT	CGRM	NRIB	LPH[2]	MARB[2]	LKGF[2,3]	A24[2,3]
LW6	0.32±0.02	0.86±0.00	0.88±0.01	0.62±0.01	0.66±0.01	0.51±0.01	0.76±0.01	0.39±0.01	0.04±0.01	-0.02±0.02	0.10±0.01	-0.06±0.01	0.19±0.01
PRESLT	0.97±0.01	0.22±0.02	0.92±0.00	0.54±0.01	0.58±0.01	0.44±0.01	0.81±0.00	0.47±0.01	0.03±0.01	0.07±0.01	0.13±0.01	-0.01±0.01	0.04±0.01
CWT	0.86±0.02	0.90±0.02	0.19±0.02	0.65±0.01	0.68±0.01	0.52±0.01	0.75±0.01	0.54±0.01	0.03±0.01	-0.10±0.01	0.29±0.01	-0.21±0.01	0.20±0.01
EMD	0.49±0.06	0.53±0.08	0.68±0.05	0.37±0.03	0.75±0.01	0.48±0.01	0.57±0.01	0.39±0.01	0.00±0.01	-0.04±0.01	0.03±0.01	0.02±0.01	0.07±0.01
EMW	0.58±0.05	0.58±0.08	0.71±0.05	0.88±0.02	0.27±0.03	0.50±0.01	0.60±0.01	0.35±0.01	0.01±0.01	-0.05±0.01	0.02±0.01	0.00 ±0.01	0.09±0.02
FDM	0.40±0.07	0.35±0.10	0.42±0.08	0.34±0.07	0.35±0.07	0.28±0.03	0.40±0.01	0.51±0.01	-0.01±0.01	-0.01±0.01	0.24±0.01	-0.10 ±0.01	0.12±0.01
CBUTT	0.76±0.04	0.72±0.03	0.73±0.04	0.55±0.08	0.60±0.08	0.09±0.12	0.25±0.02	0.41±0.01	0.01±0.01	0.01±0.01	-0.05±0.01	0.07±0.01	0.03±0.01
CGRM	0.30±0.09	0.34±0.07	0.46±0.07	0.51±0.09	0.41±0.11	0.94±0.05	0.22±0.07	0.21±0.02	0.02±0.01	-0.04±0.01	0.16±0.01	-0.06±0.01	0.05±0.01
NRIB	0.14±0.11	0.15±0.10	0.11±0.10	0.16±0.13	0.29±0.14	0.18±0.13	0.01±0.10	0.15±0.10	0.10±0.02	-0.01±0.01	0.01±0.01	0.06±0.01	-0.02±0.01
LPH[2]	0.21±0.16	0.20±0.12	0.06±0.13	-0.05±0.15	0.17±0.17	0.06±0.15	0.24±0.12	-0.06±0.12	0.27±0.14	0.09±0.02	0.15±0.01	0.08±0.01	-0.28±0.01
MARB[2]	0.16±0.11	0.15±0.08	0.28±0.08	0.09±0.11	0.04±0.12	0.38±0.09	-0.10±0.09	0.35±0.08	0.08±0.10	0.24±0.11	0.31±0.03	-0.14±0.01	0.05±0.01
LKGF[2,3]	0.02±0.11	-0.04±0.10	-0.17±0.10	0.07±0.10	0.12±0.11	-0.07±0.10	0.11±0.10	-0.12±0.10	0.20±0.12	0.41±0.12	-0.21±0.08	0.29±0.03	-0.05±0.01
A24[2,3]	0.17±0.13	0.14±0.11	0.29±0.11	0.02±0.12	0.19±0.13	0.42±0.11	0.01±0.12	0.41±0.10	-0.13±0.14	-0.36±0.12	0.27±0.09	-0.39±0.09	0.18±0.03

[1]Abbreviations are presented in Table 1. [2]Carcass weight adjusted, except for bivariate analysis including CWT. [3]LPH adjusted, except for bivariate analysis including LPH.

Saying that two traits are genetically correlated implies that selection applied to one of them will cause a change in the other which enables indirect selection of a trait. The genetic correlations among the traits were quite variable. They were generally positive and high among the weight traits (e.g., 0.97 ± 0.01 between LW6 and PRESLT), including live weight and carcass traits, indicating that selection for growth will also favourably impact the carcass weight and primal cuts. The genetic correlations among growth and meat-quality traits were low or non-significant based on their standard errors, indicating continued selection for growth will not have a large adverse impact on meat quality. CWT was favourably correlated to MARB, LKGF and A24. Number of rib pairs had a weak or non-significant genetic correlation with all traits indicating that selection for NRIB would have little impact on meat production or quality traits. However, little progress could be made by selecting for NRIB as it has both a low heritability and phenotypic standard deviation.

EMD, EMW and FDM are key traits used in sheep breeding programs to predict genetic merit for lean meat production. These traits were moderately to highly correlated with growth and other carcass traits and had low or non-significant genetic correlations with meat-quality traits, except between FDM and both MARB and A24 such that selection to reduce FDM would have a negative impact on marbling score and meat redness. The high genetic correlation between FDM and CGRM (0.94±0.05) indicates that genetic merit for the ultrasound measurement of fat depth is a good predictor of genetic merit for carcass fatness.

Meat redness is associated with freshness by consumers. It was favourably correlated with MARB and LKGF and unfavourably correlated economically with FDM and CGRM. Selection to improve meat redness would increase carcass fatness and produce more tender meat. LKGF had favourable genetic correlations with all meat-quality traits. Selection to reduce pH would reduce marbling score, increase meat redness and result in more tender meat. Selection to increase MARB would favourably affect tenderness and meat redness.

Parameter estimates from this study indicate that there are not many strong genetic antagonisms among growth, carcass and meat quality traits, except some moderate antagonisms among FDM and MARB (0.38) or CGRM and MARB (0.35) and LPH and MARB (0.24). The genetic parameters presented in this brief communication could be used to update the terminal sire genetic parameters in the Sheep Improvement Limited (SIL, www.sil.co.nz), genetic evaluation to provide more accurate breeding values, to inform selection indices in the future, and thus, improve the rate of genetic gain in the sheep industry.

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