Genetic parameters for meat yield and quality traits derived from the New Zealand Perendale progeny test

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Abstract

A catch phrase within animal genetics is that there is as much variation within a breed as there is between breeds. The New Zealand Perendale Progeny Test has been conducted on North and South Island sites since 2010 with the aim of investigating genetic variability for carcass traits. A total of 51 sires, from 27 studs have been assessed, with sires selected from the top 20% of the Perendale across-flock Dual Purpose Index SIL evaluation. Within each year/site lambs generated were born within a week (ewes naturally synchronised pre-mating), and slaughtered on the same day. A total of 2318 male progeny have been generated and slaughtered through Alliance with traits measured including weight traits, carcass dimensions, VIAscan® traits, carcass pH, carcass fat colour and, in some years, colour stability of chilled aged loins, subjective marbling score and meat tenderness. Genetic parameters were estimated with ASREML; carcass weight was fitted as a co-variate for carcass traits (excluding carcass weight). The heritability estimates for all traits were moderate to high, with the lowest of 0.22 ± 0.07 for VIAscan® GR, and the highest, for pH, of 0.44 ± 0.09, with the majority between 0.22 and 0.43. The high estimate for slaughter plant measured pH was supported by the 0.59 ± 0.17 estimate for pH measured in the laboratory on those samples which were measured for colour stability. The phenotypic correlations between traits were generally well estimated with small standard errors for the majority of trait combinations. The genetic correlations were not as well estimated with standard errors greater than 0.10 for most traits combinations, but despite the large standard errors some were still significant, and in general agreement with values the literature. The progeny test has therefore demonstrated significant genetic variability for the range of carcass traits assessed in this study within the Perendale breed.

Keywords: Perendale sheep; carcass traits; meat quality; genetic parameters

Introduction

Whilst historically dual purpose sheep breeds were bred with an emphasis on wool and meat, increasingly the emphasis is on increasing the number of lambs born and the subsequent growth and carcass characteristics of the lamb. The driver for the inclusion of carcass characteristics in breeding programmes is the result of the objective measurement of carcass merit being further developed and financial rewards being offered by some meat companies. One example is the introduction of the VIAscan® two dimensional imaging system introduced by Alliance Group Ltd in the mid 2000's, with commercial producers rewarded for carcasses which meet premium thresholds for the yield of lean in the shoulder, loin and leg primal regions. Given the difficulty in collecting whole carcass data on selection-candidate rams, with Computed Tomography scanning the only option, progeny testing is an alternate approach that involves carcass data collection on progeny of sires.

The New Zealand Perendale Breed Society has conducted progeny tests since 2010 that have generated data from progeny of 51 sires. Sires selected for inclusion must have been in the top 20% of Perendale sires in their across flock evaluation for the SIL Dual Purpose index which includes reproduction, wool, adult size and growth. Whilst some sires did have ultrasound or CT data available their ranking on the meat objective was not used in selection of sires because such data was not available for all sires. All sires had been used for at least one year in their home stud before they were used in the Progeny Test.

This paper reports on the genetic parameter estimates for carcass traits, based on the data generated on their progeny.

Materials and methods

New Zealand Perendale Progeny Tests have been carried out since 2010, the sites used have varied between years, but the use of a common sire between sites and years has generated genetic linkages. A summary of the number of sires tested per year and per site and the number of progeny measured for different traits (Table 1), sites changed in both Islands for the born 2013 year.

Table 1 Summary of the number of sires used per year, per site and the total number of male progeny measured for different sets of carcass traits from the New Zealand Perendale Progeny Test

Year of Birth	2010	2011		2012		2013	
Site[1]	SI 1	NI 1	SI 1	NI 1	SI 1	NI 2	SI 2
Number of sires	12	6	9	6	10	6	8
Number progeny measured:							
Carcass traits	435	237	336	262	490	209	349
Slaughter plant meat quality	428	237	340	72	119	213	249
Laboratory meat quality	427	229	332	72	118		

[1]SI 1=South Island Site 1; NI 1 = North Island Site 1; SI 2 = South Island Site 2; NI 2 = North Island Site 2.

Generation of lambs

Commercial Perendale ewes were used to generate the progeny on each of the sites. All ewes were exposed to a teaser ram, and after 17 days they were randomly allocated into single sire mating mobs. The running with the teaser rams provided synchronisation and the ewes were only run with the rams for 7 days and then re-mixed with rams after 7 days to allow differentiation of lambing. At scanning only twin bearing ewes were retained for the trial and these continued to be run together until immediately prior to lambing at which point they were put in to their sire mobs and lambed down within a week. At the end of the lambing week, the lambs were tailed and tagged to sire, and the ewes re-joined and run together as one mob through to weaning. At weaning ram lambs (and in one year ewe lambs) were run as one mob until they were slaughtered on a single day. An average of 45 progeny per sire was slaughtered, with the minimum 16 and the maximum 65 within a year/site.

Measurements made

Lambs were weighed at weaning (Weaning Weight), and again prior to being trucked for slaughter (Slaughter Weight). Lambs were slaughtered at approximately five months of age, with all lambs slaughtered on the same day within a site. Traits measured post slaughter are described by Johnson et al. (2011) and included carcass weight (CWT), carcass length, buttock circumference (BC) and VIAscan® carcass measurements of the lean meat yield of the leg, loin, and shoulder expressed as a percentage of the carcass weight, together with their sum (total) and estimated carcass fat (VSGR). Dressing out percentage was calculated as the ratio between the carcass weight and slaughter weight. Approximately 24 hours post- slaughter pH was assessed by insertion of the pH probe into the *M. longissimus* in the lumbar region, and fat colour was also assessed in this region using a Minolta Chromameter as described by Payne et al. (2009). For a proportion of the animals, described in Table 1., the *M. longissimus* was collected and sliced in half, with a half frozen and measured for tenderness as described by Campbell et al. (2011) and the other half chill aged for 8 weeks at -1°C after which time it was further processed to assess colour stability using the method described by McLean et al. (2009), only the results for colour a* (redness) at 96 hours post further processing after the 8 weeks storage (LA96HR) are reported here.

Analysis of the data

The VIAscan® lean yield percentage data (as a proportion) was multiplied by the carcass weight of the individual to give the weight of lean for each of the three carcass regions and these were summed to give the total amount of lean in the carcass (VSTOTAL). 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 trait and bivariate analyses were used to estimate the phenotypic and genetic correlations between pairs of traits. The models fitted differed depending on the trait, however, for all analyses a contemporary group of year-of- birth*site*sex was fitted as a fixed effect. Carcass weight was fitted as a covariate for all traits except carcass weight and for bivariate analyses between CWT and the other traits. For colour stability, pH was additionally fitted as a covariate and for tenderness, pH and pH^2 were fitted as covariates (Campbell et al. 2011). Unlike other similar studies (Payne et al. 2009; Jopson et al. 2009) age at slaughter was not fitted a covariate, as all lambs within a contemporary group were born within seven days of each other and all were slaughtered on the same day and were therefore close to the same age.

Table 2 Statistics for un-adjusted carcass and meat quality traits assessed in the New Zealand Perendale Progeny Test

	Average	Phenotypic SD	CV (%)	Min	Max
Weaning weight (kg)	31.3	4.54	14.5	16	50
Carcass traits					
Slaughter weight (kg)	42.0	5.69	13.5	22.5	65
Carcass weight (kg)	17.3	2.73	15.8	9.8	27.5
Dressing out percentage	41.1	2.60	6.3	34.0	55.2
VIAscan® GR (mm)	4.7	2.7	57.0	1	14.1
VIAscan® leg lean (kg)	3.4	0.29	5.2	3.6	5.6
VIAscan® loin lean (kg)	2.9	0.19	5.5	2.1	3.5
VIAscan® shoulder lean (kg)	3.4	0.19	4.6	2.6	4.1
VIAscan® total lean (kg)	10.8	0.55	4.4	8.6	12.6
Butt circumference (cm)	62.9	3.03	4.8	50.5	80
Leg length (cm)	28.1	1.62	5.8	23	34
Carcass length (cm)	81.8	3.63	4.4	69	96
Meat quality assessed in the slaughter plant					
Loin pH (24 hours post slaughter)	5.8	0.15	2.6	5.5	6.5
Fat colour b* (yellowness)	10.7	3.27	30.5	2.2	26.1
Meat quality assessed in the lab					
Marbling (Subjective 1-5)	3.0	0.54	17.8	1.5	5
Colour a* after 96hr retail display	12.0	1.51	12.6	7.2	18.7
Tenderness (kgF)	8.3	2.72	32.8	2.8	21.3

Results

A summary of the phenotypic data (Table 2) shows that for the majority of traits the co-efficient of variation ranged from below 6% for most carcass weight traits through to greater than 57% for VSGR. Whilst the co-efficient of variation for pH was lower at less than 3% it is a trait with a narrow range of values.

Table 3 Heritability and genetic and phenotypic correlation estimates for carcass and meat quality traits measured in the New Zealand Perendale Progeny Test.

		Correlation with carcass weight		Correlation with VIAscan® total carcass lean		Correlation with VIAscan® GR (measure of fat)	
	Heritability Estimate	Phenotypic	Genetic	Phenotypic	Genetic	Phenotypic	Genetic
Carcass Weight	0.35 ± 0.09			0.95 ± 0.00	0.94 ± 0.02	0.58 ± 0.02	0.59 ± 0.14
Dressing Out %	0.28 ± 0.08	0.32 ± 0.18	0.54 ± 0.02	0.02 ± 0.03	0.12 ± 0.19	0.19 ± 0.03	0.13 ± 0.22
VIAscan® leg lean[1]	0.36 ± 0.09	0.91 ± 0.00	0.90 ± 0.03	0.89 ± 0.01	0.96 ± 0.02	-0.52 ± 0.02	-0.56 ± 0.14
VIAscan® loin lean[1]	0.42 ± 0.10	0.95 ± 0.00	0.94 ± 0.02	0.84 ± 0.01	0.90 ± 0.04	-0.32 ± 0.02	-0.35 ± 0.19
VIAscan® shoulder lean[1]	0.26 ± 0.07	0.94 ± 0.00	0.95 ± 0.02	0.76 ± 0.01	0.76 ± 0.08	-0.28 ± 0.02	-0.46 ± 0.17
VIAscan® total lean[1]	0.43 ± 0.10	0.94 ± 0.02	0.95 ± 0.00			-0.46 ± 0.02	-0.51 ± 0.15
VIAscan® GR[1]	0.22 ± 0.07	0.58 ± 0.02	0.59 ± 0.14	-0.43 ± 0.02	-0.52 ± 0.16		
Butt circumference[1]	0.23 ± 0.07	0.86 ± 0.00	0.91 ± 0.03	0.23 ± 0.02	0.50 ± 0.16	-0.19 ± 0.22	-0.46 ± 0.17
Leg length[1]	0.26 ± 0.07	0.23 ± 0.02	0.19 ± 0.19	-0.07 ± 0.02	-0.39 ± 0.17	-0.28 ± 0.02	-0.14 ± 0.22
Carcass length[1]	0.22 ± 0.07	0.82 ± 0.01	0.85 ± 0.06	0.01 ± 0.03	-0.01 ± 0.21	-0.21 ± 0.02	-0.32 ± 0.21
Loin pH measured in slaughter plant[1]	0.44 ± 0.09	-0.07 ± 0.03	0.18 ± 0.18	-0.01 ± 0.03	0.21 ± 0.18	-0.06 ± 0.03	-0.39 ± 0.18
Fat colour b* (yellowness)	0.38 ± 0.11	0.22 ± 0.03	0.36 ± 0.19	-0.18 ± 0.03	-0.02 ± 0.20	0.17 ± 0.03	0.46 ± 0.21
Marbling score[1]	0.32 ± 0.10	0.27 ± 0.03	0.01 ± 0.25	-0.12 ± 0.03	-0.28 ± 0.21	0.27 ± 0.03	-0.01 ± 0.23
Colour a* after 96hr display[12]	0.28 ± 0.10	0.08 ± 0.03	0.37 ± 0.25	0.08 ± 0.03	0.07 ± 0.24	0.05 ± 0.03	-0.11 ± 0.26
Tenderness[123]	0.33 ± 0.10	-0.17 ± 0.03	-0.18 ± 0.25	0.11 ± 0.03	0.25 ± 0.22	-0.13 ± 0.03	-0.34 ± 0.22

[1]For correlations with VIAscan® total lean and GR carcass weight was fitted as a covariate in the model for both traits.
[2]pH was fitted as a covariate for Colour a*. [3]pH^2 was fitted as a covariate for tenderness.

The heritabilities for all traits and the genetic and phenotypic correlations between all traits and CWT, VSTOTAL and VSGR are given in Table 3. For the carcass traits which, with the exception of CWT itself, were adjusted for CWT, the heritability estimates for all traits were moderate to high, with the lowest of 0.22 for VSGR and the highest of 0.43 for VSTOTAL. The standard errors associated with the heritability estimates for the carcass traits were all 0.10 and less. For the meat quality traits the heritability estimates ranged from 0.28 for LA96HR through to 0.44 for pH measured in the slaughter plant. The standard errors associated with the heritability estimates for the meat quality traits were all 0.11 or less with the exception of pH which had a standard error of 0.15. The high heritability estimate for pH measured in the freezing slaughter plant was supported by the heritability estimate for pH measured from the same loins in the laboratory (data not presented) on those samples which had colour stability measurements made on them (albeit a smaller number (1163) of animals than were measured in the slaughter plant, see Table 1.) was 0.59 ± 0.16.

Three key sets of relationships were investigated in the bivariate analysis – between the range of carcass and meat quality traits and growth (using CWT as a proxy for growth rate as the lambs were slaughtered at the same age), lean meat yield (using VSTOTAL as a proxy) and carcass fatness (using VGR as a proxy). The same covariates and fixed effects as were used for the univariate analyses were used for the bivariate analyses. The phenotypic correlations between the traits were generally well estimated with small standard errors (<0.04) for the majority of trait combinations. The genetic correlations were not as well estimated in that the standard errors were greater than 0.10 for most traits, with the exception of those for genetic correlations between CWT and the majority of carcass traits which were less than 0.05. The genetic correlations between CWT and the carcass traits, with the exception of leg length, were all very high (>0.85). The only other significant (value more than two times the standard error) genetic correlations were between combinations of butt circumference, VSTOTAL and VSGR. For the remainder of trait combinations, although there were some that were up to 0.37, large standard errors were associated with the correlations making them non-significant.

Additional genetic and phenotypic correlations between the VIAscan® estimates of lean weight (adjusted for CWT) in the leg, shoulder and loin were also estimated. Between the leg and loin the estimates were 0.70 ± 0.02 and 0.84 ± 0.07 for the phenotypic and genetic correlations respectively, between the leg and shoulder 0.49 ± 0.02 and 0.62 ± 0.12 respectively, and between the loin and shoulder 0.51 ± 0.02 and 0.58 ± 0.13 respectively.

Discussion

Within maternal breeds such as the Perendale, although the emphasis of breeding programmes remains on maternal traits such as number of lambs born and the maternal influence on weaning weight, there has been interest in exploring their genetic variation for carcass and meat quality traits, which has been done through the establishment of the New Zealand Perendale Progeny Test. To support the desire for maintained maternal performance,

sires included in the progeny test must have been ranked in the top 20% of the Perendale across-flock evaluation for the SIL Dual Purpose Index which focuses on maternal and growth traits.

The results presented in this paper demonstrate significant genetic variability for all traits considered. The heritability estimates for the carcass traits are generally comparable to published estimates (Jopson et al. (2009) and Payne et al. (2009)) based on data collected from the New Zealand Central Progeny Test in which lambs are also slaughtered through Alliance and VIAscan® data is generated, and genetic parameter estimates of carcass traits based on data collected from the Australian Information Nucleus Flock (INF; Mortimer et al. (2010)). The exact analysis method for carcass traits is increasingly a topic of interest (Jopson et al. (2009), Payne et al. (2009), Mortimer et al. (2014b)) given adjustment for carcass weight, is adjusting for a correlated trait (Dodds 1991)). Additionally there is variation as to whether or not breed is fitted in the model. Alternate methods involve adjusting for the covariate post-analysis, however, the impact of this seems to be inconsistent with the study of Mortimer et al. (2014b) reporting inclusion of weight as a co-variate increasing the direct heritability, whereas between Payne et al. (2009) and Jopson et al. (2009), the models including carcass weight as a covariate decreased direct heritability estimates. Suffice to say, it is an area of research where further methodology investigation and development is required to optimise methodologies. Despite these differences in methodology the estimates are all in the "moderate" range, however, resolution of methodology is required for implementation in breeding objectives such that appropriate weightings are applied to the traits alongside others in the objective.

The genetic parameter estimates for the meat quality traits of fat colour b* are consistent with estimates by Payne et al. (2009) and estimates for retail loin colour a* and tenderness are consistent with estimates by Mortimer et al. (2014a), although the trait definitions do vary. In this study, a subjective estimate of intramuscular fat was made via assignment of a visual marbling score, the genetic parameter estimate for this subjective trait is comparable to first estimates based on the INF data (Mortimer et al. 2010 and Mortimer et al. 2014a). The trait that has the most disparate estimates compared to the literature is pH measured both in the slaughter plant and confirmed in the laboratory, with published estimates less than 0.12 (Payne et al. (2009) and Mortimer et al. (2014b)). The results from the current study suggest a high level of genetic variability in the data set studied, however, with less than 8% of animals exhibiting high pH (pH>6.0) which were predominately male, there is not a significant issue of high pH within the data set.

The significant genetic correlations observed between CWT and the VIAscan® traits were to be expected given they were derived from each other. The relationship between the lean yield for the different carcass regions after adjustment for carcass weight, although high was not unity; this also was observed by Payne et al. (2009) and Jopson et al. (2009), which indicates that differential selection pressure can be placed on the traits in selection objectives. Although there were some non-zero genetic correlations between CWT, VSTOTAL and VSGR and some of the meat quality traits, they were not significant due to high associated standard errors. Even in the studies of Payne et al. (2009) and Mortimer et al. (2010 and 2014a) based on significantly larger numbers of progeny and sires the standard errors associated with genetic correlation estimates between the carcass and meat quality traits were large enough to make any estimates non-significant. Cumulatively these results suggest that any relationships between carcass and meat quality traits are not strong, and that there is the ability to ensure any genetic selection programmes can achieve both improved growth, yield and meat quality, provided all traits of importance are measured and taken into account in the selection process.

Conclusions

These results demonstrate, that even within a breed where the majority of selection pressure has been placed on maternal traits, significant genetic variability does exist for carcass and meat quality traits. Further investigations will include measures of maternal traits of the half-sib sisters of the progeny slaughtered, which, together with data from the pedigree-related females in the studs from which the sires came, will allow the estimation of genetic correlations between carcass traits and maternal traits such as number of lambs born, body condition score and ewe longevity.

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