# BRIEF COMMUNICATION: Genetic parameters for meat traits assessed in the Headwaters New Zealand Progeny Test

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

## Introduction

Producing and marketing a consistently high-quality lamb product within an integrated value chain is the aim of the Headwaters New Zealand Group (HWNZ). Johnson et al. (2011) demonstrated a large amount of variation exists in the lean meat yield of a carcass, as estimated by the VIAscan® system, for animals that graded the same under the traditional New Zealand lamb-grading system (based on carcass weight and GR - a measure of soft tissue depth). VIAscan® is a two-dimensional imaging system (Hopkins et al. 2004) that estimates the percentages of lean in the shoulder, loin and leg regions of the carcass. HWNZ have established a composite breeding programme based on Perendale, Texel, Finn and Romney genetics. HWNZ have been undertaking an annual progeny test of ram lambs since 2010, with generated progeny slaughtered to obtain carcass and meat quality data which are used to generate breeding values for the identification of elite sires for inclusion in the main breeding programme. This paper reports on genetic parameter estimates for the carcass and meat quality traits using this resource.

## Materials and methods

Data were available from four progeny-test cohorts, born between 2010 and 2013, representing 40, 50, 60 and 67 sires each year respectively. Carcass and meat quality data were available on a total of 4063 and 2612 progeny respectively. Progeny were assigned to sire using DNA-based parentage.

Carcass traits recorded on the day of slaughter included carcass weight (CWT), carcass length, buttock circumference and VIAscan® measurements of carcass fatness (VSGR) and the percentages of lean-meat yield in the leg, loin, and shoulder (described in more detail in Johnson et al. 2011). The day following slaughter, the *M. longissimus* from one side of the carcass was collected and sliced in half. One half was wrapped and frozen to -20°C at the plant and the tenderness measured as described by Campbell et al. (2011). The other half was chill aged for eight weeks and then further processed to assess colour stability as described by McLean et al. (2009); pH and visual marbling score were also assessed on these processed samples.

*Analysis of the data*

The weight of lean in the three carcass regions were estimated by multiplying the corresponding VIAscan® lean yield proportion by the CWT of the individual. The weight of total lean (VSTOTAL) was estimated by summing the weight of lean from the three cuts. Variance components were estimated using restricted maximum likelihood (REML) procedures fitting an animal model in ASReml (Gilmour 2006). Univariate models were used to estimate heritabilities for each trait and bivariate models 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*sex*birthgroup*slaughter-mob was fitted as a fixed effect. All lambs within a year were slaughtered on the same day; slaughter-mob represents different pre-slaughter grazing mobs not different slaughter dates. Except for CWT *per se* and the bi-variate analyses between CWT and the other traits, CWT was fitted as a covariate for the remaining traits. For tenderness, pH and $pH^2$ were additionally fitted as covariates (Campbell et al. (2011)).

## Results and discussion

A summary of the data collected from the HWNZ Progeny Test is in Table 1. Heritability estimates for the carcass- and meat-quality traits assessed are in Table 2. together with genetic and phenotypic correlation estimates between the traits and CWT, VSTOTAL and VSGR. The heritability estimates were all moderate to high and ranged

**Table 1** Statistics for un-adjusted for lamb carcass and meat quality traits assessed in the Headwaters New Zealand Progeny Test.

| | Average | Phenotypic SD | CV (%) | Min | Max |
|---|---|---|---|---|---|
| Carcass traits | | | | | |
| Carcass weight (kg) | 18.0 | 3.10 | 17.2 | 9.6 | 28.4 |
| VIAscan® leg lean (kg) | 3.9 | 0.68 | 17.4 | 1.9 | 6.3 |
| VIAscan® loin lean (kg) | 2.7 | 0.56 | 20.7 | 1.1 | 4.5 |
| VIAscan® shoulder lean (kg) | 3.1 | 0.60 | 19.4 | 1.3 | 5 |
| VIAscan® total lean (kg) | 9.6 | 1.83 | 19.1 | 4.7 | 15.5 |
| Butt circumference (cm) | 63.3 | 3.01 | 4.8 | 51.2 | 73.3 |
| Leg length (cm) | 38.9 | 1.70 | 4.4 | 33.5 | 45 |
| Meat quality assessed in the slaughter plant | | | | | |
| Loin pH | 5.8 | 0.23 | 3.9 | 5.4 | 6.9 |
| Meat quality assessed in the lab | | | | | |
| Marbling (Subjective 1-5) | 3.0 | 0.54 | 17.8 | 1.5 | 5 |
| Tenderness (kgF) | 8.3 | 2.72 | 32.8 | 2.8 | 21.3 |

**Table 2** Heritability and genetic and phenotypic correlation estimates for lamb carcass and meat quality traits measured in the Headwaters New Zealand Progeny Test.

| | Heritability Estimate | Correlation With CWT | | Correlation with VSTOTAL | | Correlation with VGR | |
|---|---|---|---|---|---|---|---|
| | | Phenotypic | Genetic | Phenotypic | Genetic | Phenotypic | Genetic |
| Carcass weight | 0.19 ± 0.04 | | | | | | |
| VIAscan® leg lean[1] | 0.33 ± 0.05 | 0.92 ± 0.00 | 0.89 ± 0.03 | 0.91 ± 0.00 | 0.92 ± 0.02 | -0.47 ± 0.02 | -0.55 ± 0.08 |
| VIAscan® loin lean[1] | 0.33 ± 0.05 | 0.95 ± 0.00 | 0.93 ± 0.02 | 0.87 ± 0.00 | 0.90 ± 0.02 | -0.33 ± 0.02 | -0.39 ± 0.10 |
| VIAscan® shoulder lean[1] | 0.31 ± 0.05 | 0.95 ± 0.00 | 0.92 ± 0.02 | 0.77 ± 0.01 | 0.71 ± 0.06 | -0.24 ± 0.02 | -0.25 ± 0.11 |
| VIAscan® total lean[1] | 0.32 ± 0.05 | 0.95 ± 0.00 | 0.94 ± 0.02 | | | -0.42 ± 0.01 | -0.49 ± 0.09 |
| VIAscan® GR[1] | 0.44 ± 0.06 | 0.64 ± 0.01 | 0.35 ± 0.12 | -0.42 ± 0.01 | -0.49 ± 0.09 | | |
| Buttocks circumference[1] | 0.41 ± 0.06 | 0.89 ± 0.00 | 0.80 ± 0.05 | 0.39 ± 0.01 | 0.73 ± 0.07 | -0.16 ± 0.02 | -0.14 ± 0.1 |
| Leg length[1] | 0.44 ± 0.06 | 0.59 ± 0.01 | 0.37 ± 0.12 | 0.03 ± 0.02 | 0.08 ± 0.12 | -0.32 ± 0.02 | -0.58 ± 0.08 |
| pH measured in slaughter plant[1] | 0.19 ± 0.04 | -0.07 ± 0.02 | -0.25 ± 0.15 | 0.07 ± 0.02 | 0.04 ± 0.13 | 0.03 ± 0.02 | 0.06 ± 0.12 |
| Marbling score[1] | 0.40 ± 0.06 | 0.28 ± 0.02 | -0.28 ± 0.14 | -0.11 ± 0.02 | -0.20 ± 0.11 | 0.16 ± 0.02 | 0.22 ± 0.10 |
| Tenderness[2] | 0.24 ± 0.06 | -0.16 ± 0.02 | 0.11 ± 0.16 | 0.03 ± 0.02 | 0.06 ± 0.14 | -0.05 ± 0.02 | -0.07 ± 0.13 |

[1]For correlations with VIAscan® total lean (VSTOTAL) and VIAscan® GR (VGR), carcass weight (CWT) was fitted as a covariate in the model for both traits. [3]pH and $pH^2$ was fitted as a covariate for tenderness.

between 0.19 for CWT and pH to 0.44 for VSGR and Leg length. The standard errors associated with the heritability estimates were all 0.06 and below. The heritability estimates for the carcass traits are in general agreement with relevant estimates from the literature (Jopson et al. 2009; Payne et al. 2009; Mortimer et al. 2010; Johnson et al. 2015), although as discussed by Johnson et al. (2015) full comparison is difficult given different approaches to adjusting for carcass weight.

The genetic parameter estimates for the meat quality traits are similarly in general agreement with the literature (Payne et al. 2009; Mortimer et al. 2014; Johnson et al. 2015), although the trait definitions do differ between studies. The heritability for the trait of colour stability is not included in the table as methodology differences for the born 2013 animals meant the data could not be easily combined. Based on data from the first three years an estimate for colour stability of a* after 96-hours display was 0.20 + 0.05 which is consistent with other studies, although again, trait definitions vary amongst studies.

The three traits chosen for the correlation analyses (CWT, VSTOTAL and VSGR) were considered to represent relationships between the traits and growth, lean meat yield and carcass fatness, respectively. All phenotypic correlation estimates had associated standard errors of 0.02 or less. The estimated genetic correlations between CWT and the VIAscan® lean weight traits were very high with low standard errors as was expected given they were derived traits. Very high genetic correlations with low standard errors were also observed among butt circumference and CWT and VSTOTAL. The genetic correlations between VSGR and the other carcass traits were all moderately negative, although the associated standard errors were 0.09 – 0.11. No significant genetic correlations were observed among any of the meat quality traits and CWT, VSTOTAL or VSGR. In all cases these results are generally consistent with literature estimates (Payne et al. 2009; Mortimer et al. 2014; Johnson et al. 2015). As a result, there is potential to improve CWT and the meat quality traits in tandem given the traits are routinely measured and appropriate genetic selection objectives are developed.

The genetic and phenotypic correlations among the VIAscan® lean meat yield traits were also estimated, using a model with CWT fitted as a covariate. The genetic and phenotypic correlations between the lean weight in the leg and loin were 0.75 ± 0.01 and 0.83 ± 0.04 respectively, between the lean weight in the leg and shoulder 0.50 ± 0.01 and 0.44 ± 0.10 respectively, and between the lean weight in the shoulder and loin 0.52 ± 0.02 and 0.45 ± 0.10 respectively. These results suggest that there is independent genetic variability for these traits, and that differential selection pressure can be placed on the traits in selection indexes.

## Conclusion

These results demonstrate that for the carcass- and meat-quality traits of interest in the HWNZ programme, there is significant genetic variability, and that genetic progress can be made towards producing more consistent carcasses for an integrated supply chain.

## Acknowledgements

A number of Headwaters suppliers have been involved in the generation of, and finishing of, the progeny test lambs. Considerable assistance in data collection through the Alliance Meat plants has been provided by Gary

Macleanan, Sonja Linsday and Jo Phillips. Funding for the running of the progeny test has come from Headwaters New Zealand, Alliance and Beef + Lamb New Zealand Genetics (formerly Ovita).

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