Utilisation of the ovine HD SNP chip for meat quality traits in NZ composite terminal sire breeds

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• www.farmiq.co.nz

• a joint New Zealand government and industry Primary Growth Partnership programme

• Bringing farmers and consumers together
  – Farmers understand how to produce animals that meet consumer preferences and receive payments based on meat quality.
  – Consumers are offered premium-branded red meat that consistently meets their eating quality preferences.
THE FARM^{10} PROGRAMME

PRODUCT DEVELOPMENT
Extensive market testing is providing better insight into consumer preferences.

PROCESSING FEEDBACK
Electronic tracking and extensive measurement in plants is providing data on key parameters and supporting process improvement.

FARM^{10} SYSTEM
New tools integrate data from all sources to support farm decision making.

FARM PERFORMANCE
Best-practice production systems using data capture and analysis to better align with the value chain, are being developed.

GENETICS
Advanced genomics techniques are being used to help farmers select breeding animals with the best meat eating quality traits.
Genetics programme in FarmIQ

- deliver high-quality genetic and genomic breeding value predictions
  - growth, meat yield and eating quality in terminal sire flocks
- no real selection for meat quality in New Zealand sheep previously
- Lamb is a premium-priced product and should be a good eating experience
  - Develop tools to tailor products to consumer specifications
- Concentrated on terminal sire breeds (~80 percent of the leading industry sires)
- Deliver increased profitability for each of the value chain participants (farmer, processor, retailer)
Four phases

- **Phase 1**: HD SNP chip development
- **Phase 2**: Identify and measure eating quality and carcass yield traits in progeny of terminal sires.
- **Phase 3**: Genotyping individuals and prediction equation development
- **Phase 4**: Beta test results in commercial terminal sire breeding flocks to ensure the system is accurate, practical and cost-effective
Phase 1: HD SNP Chip development

1. Genomic Selection
   - increased marker density ensures better marker – trait association
   - increased prospect for successful across breed prediction
   - part of tool kit (+ GWS + SNP50 + 5K + imputation) to drive genotyping efficiency

2. Broader Experimental Possibilities
   - Loss of function SNPs
   - facilitates merging with gene expression studies: eQTL
   - rare SNP
Reference genome:

Sequencing
HiSeq 2000 2x100 paired end:

Mapping (BWA):

SNP identification:

SNP filtering:
Sheep HD SNP chip

SNP category:
- Equal spacing
- Functional
- GBS
- Literature
- 50k Chip

~SNP #:
- 564 k
- 55 K
- 19k
- 0.3k*2
- 48k
- 685k
- 695k

Total probes

Equally spaced across genome 564,309 80.62%

Literature 608 0.09%

ChrU 1,088 0.16%

Space for add-on content 5,875 0.84%

Accessible by GBS 19,118 2.73%

Functional MAF >0.1 26,077 3.73%

Functional MAF >0.02-0.1 34,355 4.91%

50K SNP chip 48,570 6.94%

Total SNPs 685,231
Sheep HD SNP chip

- Repeatability of the call rate was 99.9978

- Mendelian inheritance
  - Ave 651 failures out of 600,500 SNPs called for each of the 128 trio comparisons available in the QC set i.e. 99.89% of SNPs passed this criteria.
  - Failed SNPs
    - lower call rates (would have been excluded anyway).
    - most common reason: homozygote calls when in fact it was a heterozygote.
    - usually caused by a nearby variant on one allele interfering with oligo binding.

Oligo probes for 685,734 SNPs

606,006 SNPs passed manufacturing QC (87%)

NZ populations: 603,350 SNPs
Mean call rate of 99.75% across SNPs and animals.

NZ populations: 589,630 SNPs
Threshold >98% of animals have to have a genotype.
• MAF in New Zealand populations.
  → 536,373 assayable SNPs (ie MAF>5%) for inclusion into genomic selection analyses
    ▪ similar or higher than those typically reported in cattle for GS
    ▪ considerably in excess of the predicted requirement of 350,000 SNPs for across breed prediction based on linkage disequilibrium
Use of HD chip in NZ

• **FarmIQ**
  – Concentrated on NZ Terminal sires & meat quality traits
    • No genomic predictions available from elsewhere
    • Meat quality really only viable in terminal sires

• **Beef + Lamb New Zealand Genetics**
  – dual-purpose traits affecting on-farm productivity

• **PGgRc-NZAGRC** (Pastoral Greenhouse Gas Research Consortium and the Agricultural Greenhouse Gas Research Centre)
  – investigating the genetics governing sheep methane emissions.
Phase 2: Trait Investigation

• Identify and measure eating quality and carcass yield traits in progeny of terminal sires.

• Animals processed through Silver Fern Farms plants; utilise the SFF system of automatically tracking carcasses based on the use of electronic identification (EID).

• Eating quality indicators: meat tenderness, pH, marbling, colour and colour stability.

• Working with 11 New Zealand flocks that produce Texel terminal sires or composite-type genetics derived from the Suffolk, Texel, and Poll Dorset breeds; most of them part of the Focus Genetics network.
FarmIQ animals with meat yield (carcass weight, GR, Butt circumference) and quality measurements (pH, colour, tenderness, marbling)

<table>
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<th>YOB</th>
<th>Sires</th>
<th>Yield</th>
<th>Quality</th>
<th>NIR</th>
<th>EQ loins collected</th>
<th>StdSFF</th>
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<td><strong>Total</strong></td>
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<td>2014</td>
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<td>922</td>
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<td><strong>Total</strong></td>
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<td><strong>Total</strong></td>
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<td></td>
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<tr>
<td>Grand</td>
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<td><strong>839</strong>*</td>
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<td><strong>10,520</strong></td>
<td><strong>6,170</strong></td>
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Genetic parameters-Summary

• Traits are heritable (0.1-0.5)
• Meat quality and carcass traits especially
• Variation in growth CV ~14% of mean
• There are breed (or flock) differences
• Variation in meat yield and quality traits
  – Typically same or higher up to CV 30% (except pH)
**Phase 3: Genotyping, GWAS and mBVs**

- **Genotype resource**
  - ~10,000 animals born 2010-2012 (flocks A, B) genotyped HD chip (includes sires)
  - ~5400 animals born 2012-2013 genotyped LD & HD chip

- **Phenotype resource**
  - ~85 traits available
  - focused > 1,000 phenotype records
  - Meat quality
    - Tenderness (KgF)
    - Marble score (visual)
    - pH
    - Colour stability at 8 weeks (24, 48, 96, 168 h)

- **Model**
  - fixed effects: flock, year of birth, breed, mob and sex
  - covariate: carcass weight (only for meat quality)
  - Derived genomic relationship matrix (20,000 autosomal SNPs) and used to fit a polygenic model
  - Residuals used in a test for association with each marker with simple linear regression
Tenderness (Kgf)

Marbling-visual

Colour a (8 weeks 48 h)

Fat depth

Eye muscle depth

Carcass leg length
How big?

• **Tenderness**
  – mean 6.1 kgSF, SD 2.2kgSF, n=4798 animals
  – MAF =0.44, 1 copy =0.24, 2 copies 0.48 kgSF,
  – 6.2% genetic variation (r=25%)
  – Best variant located in middle of gene

• **Marbling Score**
  – Mean 3.1, SD 0.67, n =6011 animals
  – MAF =0.36, 1 copy 0.05, 2 copies 0.1
  – 5.5% genetic variation (r=23%)
Genomic Selection

100,000 SNPs were randomly selected from the 573,028 SNPs to investigate further for GS.
Accuracies of Genomic selection for lamb meat quality traits.

<table>
<thead>
<tr>
<th>Loin Trait</th>
<th>lbs group</th>
<th>h2</th>
<th>iterations</th>
<th>Training (n)</th>
<th>accuracy</th>
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<td>0.03</td>
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<td>9</td>
<td>507</td>
<td>0.16</td>
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<tr>
<td>Shear Force (KgF)</td>
<td>1</td>
<td>0.18</td>
<td>10</td>
<td>499</td>
<td>0.31</td>
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<tr>
<td>Marbling Score</td>
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<td>9</td>
<td>479</td>
<td>0.11</td>
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<tr>
<td>pH</td>
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<td>0.10</td>
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<td>504</td>
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<td>Colour (l8a168)</td>
<td>All</td>
<td>0.03</td>
<td>22</td>
<td>5605</td>
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<td>All</td>
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<td>12</td>
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<td>Shear Force (KgF)</td>
<td>All</td>
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<td>24</td>
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<td>Marbling Score</td>
<td>All</td>
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<td>5729</td>
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<td>pH</td>
<td>All</td>
<td>0.10</td>
<td>11</td>
<td>5623</td>
<td>0.09</td>
</tr>
</tbody>
</table>

GBLUP method used
Validation n=300
Correlations are the mean from resampled training and validation sets, 'iterations'-fold.

mBV accuracy = cor(tBV,mBV)= cor(Y, mBV)/sqrt(h2)
h2 is the estimated heritability
Phase 4: Testing in commercial flocks

- test results in commercial terminal sire breeding flocks to ensure the system is accurate, practical and cost-effective.

- Assisted by the 5K LD SNP (practical to use as part of an expanded parentage test)
  - new LD chip build underway ~15K SNPs

- Breeders will use the chip to assess their weaner ram lamb crop in early 2015.
  - ~2500 born 2014 ram lambs (as part of existing DNA parentage)
  - Used industry mating autumn 2015

- This work complements other approaches to improve eating quality, including enhanced pre and post slaughter management.
Summary

• Meat quality & eating traits heritable
• Genomic prediction accuracies from DNA up to 50%
• Looks like some loci with major effects
  – Can predict across breeds
  – Probably only explain moderate proportion of variation
  – May have to fix or discard if effects both positive and negative
Next steps

• Taste panel to “ground truth” physical measurements
• Create meat quality value index ranking animals
• Progeny test
  – Sires from new breeders (4 breeding groups)
  – More maternal sires (various)
  – Better linkage between flocks = better breed rankings
• Beta test in industry continued
**Timeframes**

- **Sequencing**
  - HD SNP chip creation

- **Genotyping**
  - 10,000 lambs for prediction equation

- **Beta Test**
  - 10,000 lambs + Prediction Eqn developed
  - Elite & Commercial Sires used with FARM IQ Eqn

- **Commercial use**
  - First crop FARM IQ lambs slaughtered

- **Meat trait measurement**
  - Manual
  - Auto

<table>
<thead>
<tr>
<th>Year</th>
<th>1</th>
<th>2</th>
<th>3</th>
<th>4</th>
<th>5</th>
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Acknowledgements

John McEwan
Michael Lee
Rudi Brauning
Wendy Bain
Rayna Anderson
Tracey Van Stijn
Ken Dodds
Animal Genomics Team