Application of genomics in breeding schemes for the genetic improvement of sheep and goats

Learning from our experience in Australia

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Outline

• Evolution of breeding values in Australia
• Genomic reference population
• Linkage
• Value of information sources
• Key technical challenges
• Validation of benefits
• Breeding tools
Single Step Australian Sheep Breeding Values (ASBVs)

Animal performance

Resource flocks and ram breeders

Carcass measurements

Consumer eating quality

Genomic testing

LAMBPLAN ASBV

Animal performance

Carcass measurements

Consumer eating quality

Genomic testing
The multi-breed nature of Australian sheep

Three “breed groups” each with separate genetic evaluations (2M+ animals)

- Merinos
- Maternal breeds (Border Leicester, Coopworth, Composites)
- Terminal breeds (Poll Dorset, White Suffolk, Texel, ...)

Fine wool
Medium wool
Strong wool
Composite breeding is increasing

Trend in Breed Composition

- Maternal Breeds
- Terminal Sire Breeds

Proportion Crossbred

Year

### Scale of our Sheep Genetics evaluations (Aug 2018)

<table>
<thead>
<tr>
<th></th>
<th>Merino</th>
<th>Maternal</th>
<th>Terminal</th>
</tr>
</thead>
<tbody>
<tr>
<td>Pedigree</td>
<td>2.5M</td>
<td>2.1M</td>
<td>2.9M</td>
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<tr>
<td>Records</td>
<td>13.6M</td>
<td>5.1M</td>
<td>8.8M</td>
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<tr>
<td>Flocks</td>
<td>510</td>
<td>324</td>
<td>929</td>
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<tr>
<td>Av Flock size</td>
<td>460</td>
<td>358</td>
<td>210</td>
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<tr>
<td>Traits</td>
<td>76</td>
<td>46</td>
<td>45</td>
</tr>
<tr>
<td>Genetic groups</td>
<td>558</td>
<td>104</td>
<td>94</td>
</tr>
<tr>
<td>Genotypes</td>
<td>24K</td>
<td>7K</td>
<td>22K</td>
</tr>
<tr>
<td>% current drop</td>
<td>1.1%</td>
<td>0.5%</td>
<td>1.5%</td>
</tr>
<tr>
<td>Solver time (hrs)</td>
<td>13.2</td>
<td>3.5</td>
<td>6</td>
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### Number of genotyped sheep in the genetic evaluation

<table>
<thead>
<tr>
<th>Animal Group</th>
<th>Breed Analysis</th>
<th></th>
<th></th>
<th></th>
<th>Total</th>
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</thead>
<tbody>
<tr>
<td></td>
<td>Maternal</td>
<td>Merino</td>
<td>Terminal</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Industry progeny</td>
<td>5,014</td>
<td>15,175</td>
<td>10,782</td>
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<td>30,971</td>
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<tr>
<td>Industry sires</td>
<td>612</td>
<td>2,120</td>
<td>2,642</td>
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<td>5,374</td>
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<tr>
<td>Resource flock progeny</td>
<td>4,875</td>
<td>13,407</td>
<td>11,671</td>
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<td>29,953</td>
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<tr>
<td>Total</td>
<td>10,501</td>
<td>30,702</td>
<td>25,095</td>
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<td>66,298</td>
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</table>
Trends in genotyping
The Genomic Reference Population
Reference population design (INF 2007 – 2012)

- Eight sites across Australia
- Mostly Merino ewe base
- 100 sires mated annually
  - 40 Merino
  - 40 Terminal
  - 20 Maternal
- Comprehensive phenotyping of progeny
- 50K SNP genotypes + (15K, HD, Seq)
Reference population post 2012 (MLA Resource Flock)

- Two of the eight original sites (Armidale and Katanning)
- Focus on carcass and eating quality traits
- Of the other trait groups, reproduction is our biggest limitation:
  - Commenced genotyping recorded ewes in industry flocks to boost the repro reference → still need to boost numbers
- Exploring alternate structures to work with industry based flocks
Genetic linkage between flocks
Strategies for generating linkage

• Using sires from other flocks
• Entering sires into;
  • Resource flock
  • Sire evaluations
• Young sire programs / performance groups
• Dams and decedents or link sires help
• Need to be performance recorded for key traits
• Linkage need for all breeds, flock, years and groups
• Genomic testing will help
Flock x Flock genetic linkage
Dispersed Flocks
Genomic Linkage
Accuracy increase with relationship to reference

Average accuracy of yearling fibre diameter for pilot animals by flock

![Graph showing the relationship between relationship to reference and GEBV accuracy.](image)

**Accuracy**

- 35
- 40
- 45
- 50
- 55

**Frequency**

- 0
- 10
- 20
- 30
- 40

**Relationship to reference**

- 0.05
- 0.10
- 0.15
- 0.20
Value of information
Phenotype is still king

• Breeders seeing more value in;
  • Pedigree
  • Good quality phenotypes
  • Genomic tests

• Value of slaughter info from surplus ram breeding animals and progeny tests
Value of genotyping

Genomic selection most beneficial when EBV accuracy is low
ALM Tech: Advanced Livestock Measurement Technologies
Superiority of top 10% selected on Carcass+ and EQ

- Post-weaning weight
- Lean Meat Yield
- Consumer EQ
- Intramuscular Fat
- Carcass C fat
- EQ index efficiency

CPLUS, EQ, EQ+geno
### Relative to Basic scenario

<table>
<thead>
<tr>
<th>Scenario</th>
<th>Pheno</th>
<th>+Geno</th>
<th>+Short GL</th>
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</thead>
<tbody>
<tr>
<td>WWT</td>
<td>35</td>
<td>66</td>
<td>76</td>
</tr>
<tr>
<td>Basic</td>
<td>100</td>
<td>111</td>
<td>125</td>
</tr>
<tr>
<td>Plus</td>
<td>111</td>
<td>119</td>
<td>135</td>
</tr>
<tr>
<td>NLW</td>
<td>126</td>
<td>133</td>
<td>151</td>
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</table>

### Relative to NLW scenario

<table>
<thead>
<tr>
<th>Scenario</th>
<th>Pheno</th>
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<td>WWT</td>
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<tr>
<td>Plus</td>
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<td>95</td>
<td>107</td>
</tr>
<tr>
<td>NLW</td>
<td>100</td>
<td>106</td>
<td>120</td>
</tr>
</tbody>
</table>

- Massive improvement in gains by recording key Breeding Objective traits
- 5-10% increase in gain from genotyping alone
- 20-25% increase in gain if genotyping is combined with earlier joining
- 60% of gain from just a wwt, genotype and shorter GL
- Cost:benefit?
Technical Challenges
SS-GBLUP model

- H-1 matrix with G calculated ala Yang
  - allele frequencies across all genotypes within breed group

- Genetic groups fitted explicitly

- Lambda

- Accuracies as per Li et al (2017) AAABG
Lamba influences many aspects of EBVs

- Accuracy
  - Average correlation between adjusted phenotype and SS-EBV

A weight of 0.5 is being used in genomic evaluations for sheep as a compromise between accuracy and bias across traits and breeds.

- Genetic Trends
Breeds via GRM
Genotypes show breed structure

- Account for breed structure in $H^{-1}$:
  - Breed specific frequencies versus meta-founders?

- Obtaining sufficient genotypes to define a breed is a challenge

- Composites with missing parent breeds
Building the Multi-breed GRM
Validation
SS-GBLUP provides increased predictive ability compared to ABLUP

![Graph showing mean correlation for 5-Fold and Forward methods with analysis methods ABLUP and SS-GBLUP](Image)

Gurman et al. 2018
Genomic predictions for small breeds

• Little or no benefit from across-breed genomic prediction

• Need a relevant reference population for breeds of choice

• Progressive breeders with specialist breeds or composites would like to use genomic information

• But breeders not genotyping because they are not included

• And we don’t include them because there are not enough!
Small breed validations

- Including genotypes from small breeds improves empirical prediction accuracy by small amounts

- Accuracy improvements of SS versus pedigree EBVs are less than observed for the major breeds

- No impact on EBVs of animals from the main genotyping breeds (min r = 0.99)

- More impact from multi-breed G (min r = 0.97), but good reasons to use it

Inclusion of genotypes from small breeds needs qualification of benefits and advice on investment in reference populations
Breeding Program Tools
RAMping Up Genetic Gain

**Index Trend**

- **Top 20%**
- **Bottom 20%**

![Average Index Trend (points/yr)]

- **Analysis**
  - MS
  - TER
  - MAT
  - DOH
RAMping Up Genetic Gain

Flock based reports on three broad categories;

• Data Quality
  • Influences accuracy of selection

• Average sire & dam age
  • Indication of generation interval

• How well ASBVs are used to make selection decisions
  • As close as we can get to selection intensity
Set a breeding objective

Catalogue ranked for your needs
What’s my benchmark? Flock Profile Test

Flock Profile Genomic Test
- 20 randomly selected ewes
- Flock average estimates
- CFW, FD, SL, EMD, WT, CV, FAT, Curv, indices
Genetic Progress

- Merino - MP+
- Terminal - LEQ
- Maternal - MCP+

Year of Birth

Average Index
Impact on industry (genetic gain - index points/year)

- Summary of genetic progress since 2011
- 33 Terminal flocks with significant numbers of genotypes over last 5 years

<table>
<thead>
<tr>
<th></th>
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<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>Terminals (LEQ)</td>
<td>1.36</td>
<td>2.00</td>
<td>+47%</td>
</tr>
<tr>
<td>Terminals (C+)</td>
<td>3.85</td>
<td>4.29</td>
<td>+11%</td>
</tr>
<tr>
<td>Merinos (MP+)</td>
<td>1.57</td>
<td>2.19</td>
<td>+39%</td>
</tr>
</tbody>
</table>

Confounded with;
- Index development
- Genetic parameters (r_g)
- Industry awareness
- Reference population
Conclusions

• Single step analysis fully implemented

• Process of continual improvement
  • Traits
  • Models
  • Computational capacity

• Working with industry on breeding program design
Acknowledgements

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  • Andrew Swan
  • Phillip Gurman
  • Nasir Moghaddar
  • Sam Clark