Leading Breeder 2017
Proceedings

1st & 2nd March
Melbourne, VIC
# Leading Breeder 2017

Building on the Best – Improving Rates of Genetic Gain

## Wednesday 1st March
Registrations open at 12:00PM

### Session One: Improving Rates of Genetic Gain through Sheep Genetics

<table>
<thead>
<tr>
<th>Time</th>
<th>Session</th>
<th>Presenter</th>
<th>Affiliation</th>
</tr>
</thead>
<tbody>
<tr>
<td>1:00 pm – 1:30 pm</td>
<td>Welcome And Conference Opening</td>
<td>Hamish Chandler</td>
<td>Project Manager Genetics, MLA</td>
</tr>
<tr>
<td>1:35 pm – 2:05 pm</td>
<td>Development And Future Plans From AGBU</td>
<td>Daniel Brown</td>
<td>Principal Scientist, AGBU</td>
</tr>
<tr>
<td>2:10 pm – 2:40 pm</td>
<td>What The Good Do Well</td>
<td>Luke Stephen</td>
<td>Technical Specialist Sheep Breeding, DPI</td>
</tr>
<tr>
<td>2:45 pm – 3:00 pm</td>
<td>Managing Rates of Gain at Yalgoo</td>
<td>Jock Nivison</td>
<td>Yalgoo Merino Stud</td>
</tr>
</tbody>
</table>

### Afternoon Tea
3:00 pm – 3:30 pm

### Session Two: Improving Rates of Genetic Gain through Value Chain Initiatives

<table>
<thead>
<tr>
<th>Time</th>
<th>Session</th>
<th>Presenter</th>
<th>Affiliation</th>
</tr>
</thead>
<tbody>
<tr>
<td>3:30 pm – 4:00 pm</td>
<td>The Supermarket Outlook</td>
<td>David Bevis</td>
<td>Lamb Production Manager, Coles</td>
</tr>
<tr>
<td>4:05 pm – 4:35 pm</td>
<td>Linking Progress to Process</td>
<td>Mark Inglis</td>
<td>Farm Assurance &amp; Supply Chain Manager, JBS</td>
</tr>
<tr>
<td>4:40 pm – 5:10 pm</td>
<td>Technology and Innovation along the Value Chain</td>
<td>Sean Starling</td>
<td>General Manager RD&amp;I , MLA</td>
</tr>
<tr>
<td>5:10 pm – 5:25 pm</td>
<td>The End Product Starts With The Breeder</td>
<td>Tom Bull</td>
<td>Lambpro Prime Lamb and Maternal Studs</td>
</tr>
</tbody>
</table>

### Dinner Guest Speaker Kevin McDermott – Sheep Ireland
Drinks and canapes starting at 6:30 pm
Dinner served at 7:30 pm
Session Three: Improving Rates of Genetic Gain Through Genomics & New Technologies

8:00 am – 8:30 am  Using Genomics to Breed For Eating Quality  
Andrew Swan  
Principal Scientist, AGBU

8:35 am – 8:50 am  Getting your Measurement Strategy Right  
Tom Granleese  
Research Fellow, Sheep CRC

8:55 am – 9:20 am  Four Feet Closer To The Perfect Sheep  
Mark Ferguson  
Production Science Manager, NZ Merino Co.

9:25 am – 9:40 am  Tips and Tricks When Utilising New Technology  
Sally Martin  
Sally Martin Consulting

9:45 am – 9:50 am  Three Minutes on Weaner Mortality  
Daniel Brown  
Principal Scientist, AGBU

Morning Tea  
10:00 am – 10:30 am

Session Four: Improving Rates of Genetic Gain Through Business Development

10:30 am – 10:45 am  Genetic Tools Available To Improve Gain  
Caris Jones and Clara Collison,  
Development Officers, Sheep Genetics

10:50 am – 11:20 am  Improving Profit By Maximising Use of High Genetic Merit Sires  
Tim Byrne  
Consultant, AbacusBio NZ

11:25 am – 11:40 am  Breeding Objectives Under Climate Change  
Andrew Swan  
Principal Scientist, AGBU

11:45 am – 11:50 am  Three Minutes on Breeding for PP  
Tom Granleese  
Research Fellow, Sheep CRC

11:55 am – 12:10 am  Perception of Genetics – Survey Feedback  
Hamish Chandler,  
Project Manager Genetics, MLA

12:10 pm – 12:40 am  Getting Motivated and Driving Change  
Nathan Scott  
Consultant, Achieve Ag Solutions
Welcome and Conference Opening
Hamish Chandler, Program Manager Genetics - MLA

Sheep Genetics Index Trends

- MP+
- MCP+
- Lamb2020

Index Points (MP+ and MCP+)

Year

- 2004
- 2005
- 2006
- 2007
- 2008
- 2009
- 2010
- 2011
- 2012
- 2013
- 2014
- 2015
- 2016

112
110
108
106
104
102
100
115
120
125
130
135
140

0.00
0.05
0.10
0.15
0.20
0.25
0.30
0.35
0.40
0.45
0.50
0.55
0.60
0.65
0.70
0.75
0.80
0.85
0.90
0.95
1.00
1.05
1.10
1.15
1.20
1.25
1.30
1.35
1.40

www.sheepgenetics.org.au
Development and Future Plans

Daniel Brown + many others
Principal Scientist, AGBU

Outline

• Proposed changes to routine analyses
• Impact of the changes on ASBVs
• Current and Future R&D

Proposed changes to routine analyses
Summary of improvements to analyses

<table>
<thead>
<tr>
<th></th>
<th>Terminal</th>
<th>Maternal</th>
<th>Merino</th>
<th>Dohne</th>
<th>SAMM</th>
<th>Others</th>
</tr>
</thead>
<tbody>
<tr>
<td>Single Step in Main analyses</td>
<td>✓</td>
<td>✓</td>
<td>✓</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>New OVIS software</td>
<td>✓</td>
<td>✓</td>
<td>✓</td>
<td>✓</td>
<td>✓</td>
<td></td>
</tr>
<tr>
<td>Improved data changes</td>
<td>✓</td>
<td>✓</td>
<td>✓</td>
<td>✓</td>
<td>✓</td>
<td></td>
</tr>
</tbody>
</table>

Blended ASBVs v Single Step ASBVs

On farm pedigree and performance

Reference pedigree and measurements

Genomic testing

Accuracy = correlation

Blended ASBVs v Single Step ASBVs

On farm pedigree and performance

Reference pedigree and measurements

Genomic testing
**Benefits of Single Step**

- Simultaneous use of all information
  - No need for blending
- Actual genomic prediction accuracy used
  - Not an assumed population wide value
- All traits
- Genomic information flows through pedigree better
- Industry data contributes to reference population

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**raceMule: A new workhorse**

- The solver is the heart of OVIS
- To achieve full implementation of the single step analysis more efficient software was required
- Main benefits:
  - Better use of computer capacity
    - Multi-processing
    - Large virtual memory
  - More flexibility to fit different models
- Extensive testing has been conducted to demonstrate that this new software produces equivalent results

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**Which analyses?**

- Main
- WEC
- Visual

- Not reproduction (yet)

- Changes in ASBVs due to 3 main reasons
  1. Different methodology for fitting genetic groups
  2. Influence of genomic information
  3. Impact of correlated data (e.g., EQ data in main run)
Still some restrictions

- Still only using genotypes from major breeds
- Value of genomic tests still determined by;
  - linkage (genomic relationship) to reference animals
  - Other information sources available

Accuracy increase with relationship to reference

![Accuracy increases with relationship to reference](image)

Value of genotyping

![Value of genotyping](image)

- Genomic selection most beneficial when EBV accuracy is low
### Accuracy of 2016 drop from MERINOSELECT

<table>
<thead>
<tr>
<th></th>
<th>Non-genotyped animals</th>
<th>Genotyped animals</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Old</td>
<td>New</td>
</tr>
<tr>
<td>n</td>
<td>35,106</td>
<td>158</td>
</tr>
<tr>
<td>awt_acc</td>
<td>48.1</td>
<td>48.9</td>
</tr>
<tr>
<td>asd_acc</td>
<td>44.3</td>
<td>45.5</td>
</tr>
<tr>
<td>agfw_acc</td>
<td>40.8</td>
<td>42.9</td>
</tr>
<tr>
<td>acfw_acc</td>
<td>39.9</td>
<td>42.2</td>
</tr>
<tr>
<td>acfw_acc</td>
<td>39.9</td>
<td>42.2</td>
</tr>
<tr>
<td>acfw_acc</td>
<td>40.7</td>
<td>42.2</td>
</tr>
<tr>
<td>asl_acc</td>
<td>38.1</td>
<td>39.6</td>
</tr>
<tr>
<td>ass_acc</td>
<td>34.1</td>
<td>34.5</td>
</tr>
</tbody>
</table>

### ACFW of non-genotyped animals from 2016 drop from MERINOSELECT

![ACFW of non-genotyped animals from 2016 drop from MERINOSELECT](image)
How did our RBVs and Blended ASBVs go?

- The summary is very well
- Our expectation is not a correlation 1.0
  - Single trait compared to multiple trait
  - GBV analyses contained different sets of animals
  - Single step using all information

How did our RBVs go?

<table>
<thead>
<tr>
<th></th>
<th>infsire</th>
<th>Industry</th>
<th>valsire</th>
</tr>
</thead>
<tbody>
<tr>
<td>Infprog</td>
<td>2,495</td>
<td>108</td>
<td>1,154</td>
</tr>
<tr>
<td>awt</td>
<td>0.97</td>
<td>0.98</td>
<td>0.93</td>
</tr>
<tr>
<td>pemd</td>
<td>0.95</td>
<td>0.98</td>
<td>0.93</td>
</tr>
<tr>
<td>Merino</td>
<td>5,623</td>
<td>276</td>
<td>2,711</td>
</tr>
<tr>
<td>awt</td>
<td>0.97</td>
<td>0.98</td>
<td>0.94</td>
</tr>
<tr>
<td>pemd</td>
<td>0.97</td>
<td>0.98</td>
<td>0.95</td>
</tr>
<tr>
<td>sf5</td>
<td>0.98</td>
<td>0.99</td>
<td>0.96</td>
</tr>
<tr>
<td>lbwr</td>
<td>0.98</td>
<td>0.99</td>
<td>0.98</td>
</tr>
</tbody>
</table>

Let's take stock!

- Full implementation of single step is a massive achievement
  - Large multi-trait across breed analyses
  - 3m animals, 76 traits
  - Many genetic groups
  - MERINOSELECT: 543
  - Significant numbers of genotyped animals
    - MERINOSELECT: 10,840
    - Terminal: 12,570
  - Without compromising run time
- World leading achievement
Validation

- Past validation of single step RBVs
- Andrew’s recent work on EQ indexes
- More underway

Accuracy of genomic prediction from single trait analyses

<table>
<thead>
<tr>
<th>Trait</th>
<th>ABLUP</th>
<th>SSBLUP</th>
</tr>
</thead>
<tbody>
<tr>
<td>Birth weight</td>
<td>0.24</td>
<td>0.44</td>
</tr>
<tr>
<td>Weaning weight</td>
<td>0.20</td>
<td>0.40</td>
</tr>
<tr>
<td>Post-wean weight</td>
<td>0.19</td>
<td>0.32</td>
</tr>
<tr>
<td>Post-wean eye muscle</td>
<td>0.34</td>
<td>0.39</td>
</tr>
<tr>
<td>Post-wean fat</td>
<td>0.33</td>
<td>0.34</td>
</tr>
</tbody>
</table>

Accuracy of genomic prediction for carcass and E.Q. traits

<table>
<thead>
<tr>
<th>Trait</th>
<th>ABLUP</th>
<th>SSBLUP</th>
</tr>
</thead>
<tbody>
<tr>
<td>Carcass Eye Muscle</td>
<td>0.20</td>
<td>0.28</td>
</tr>
<tr>
<td>Carcass Fat</td>
<td>0.23</td>
<td>0.28</td>
</tr>
<tr>
<td>IMF</td>
<td>0.25</td>
<td>0.38</td>
</tr>
<tr>
<td>Shear Force</td>
<td>0.25</td>
<td>0.33</td>
</tr>
<tr>
<td>Lean Meat Yield</td>
<td>0.24</td>
<td>0.31</td>
</tr>
<tr>
<td>Dressing%</td>
<td>0.28</td>
<td>0.39</td>
</tr>
</tbody>
</table>
### Accuracy improvements (SSBLUP – ABLUP)

<table>
<thead>
<tr>
<th>Groups</th>
<th>Traits</th>
<th>Mean</th>
<th>Min</th>
<th>Max</th>
</tr>
</thead>
<tbody>
<tr>
<td>Within</td>
<td>Live</td>
<td>0.17</td>
<td>0.05</td>
<td>0.28</td>
</tr>
<tr>
<td></td>
<td>Carcass</td>
<td>0.09</td>
<td>0.08</td>
<td>0.13</td>
</tr>
<tr>
<td>Across</td>
<td>Live</td>
<td>0.05</td>
<td>0.03</td>
<td>0.11</td>
</tr>
<tr>
<td></td>
<td>Carcass</td>
<td>0.06</td>
<td>0.02</td>
<td>0.13</td>
</tr>
</tbody>
</table>

In summary:
- Single step always increases accuracy over ABLUP
- Single step mostly better than blending, but differences are small
- Benefits are higher within genetic groups → more relevant within flocks

### Reproduction data changes

- NLW records ignored for flock-drops with 100% survival in twins
  - Survival information not recorded properly
- Reproduction recorded added from INF followers

<table>
<thead>
<tr>
<th>Records Used</th>
<th>Maternal</th>
<th>Merino</th>
<th>Terminal</th>
<th>Dohne</th>
<th>SAMM</th>
</tr>
</thead>
<tbody>
<tr>
<td>Flocks</td>
<td>253,851</td>
<td>210,073</td>
<td>106,985</td>
<td>56,511</td>
<td>2,930</td>
</tr>
<tr>
<td>INF records</td>
<td>133</td>
<td>83</td>
<td>101</td>
<td>60</td>
<td>9</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>100% Twin survival records removed</th>
</tr>
</thead>
<tbody>
<tr>
<td>Records</td>
</tr>
<tr>
<td>Flocks</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Maternal</th>
<th>Merino</th>
<th>Terminal</th>
<th>Dohne</th>
<th>SAMM</th>
</tr>
</thead>
<tbody>
<tr>
<td>Records</td>
<td>15,765</td>
<td>6,631</td>
<td>5,046</td>
<td>5,723</td>
</tr>
<tr>
<td>Flocks</td>
<td>28</td>
<td>10</td>
<td>14</td>
<td>7</td>
</tr>
</tbody>
</table>

### Impacts on the analysis results
Terminal Genetic Trends

Terminal Flock Means

Terminal Top 150 sires (n=175 over 3 indexes)
Impacts on the analysis results: SAMM

• Very small changes for most traits
• Reproduction traits due to
  • Addition of INF follower data
  • Removal of nlw data for flocks with 100% survival in twins

Impacts on the analysis results: Dohne

• Very small changes
• Reproduction traits due to removal of nlw data for flocks with 100% survival in twins

Current and Future R&D
Current R&D

• Improved reproduction analysis
  • Components traits for reproduction
    • Fertility
    • Litter size
    • Ewe rearing ability
  • Single step (using genomics)
  • Correlated traits
    • Fat/EMD
    • Condition Score
    • Wrinkle
    • Face Cover
    • MBS
  • RBVs to come

Future

• Using genomic information from non-SG animals

• Improved use of genomic information
  • Weighting pedigree with genomics
  • Genetic grouping
  • Dealing with inconsistencies between pedigree and genomic information
  • Alternate models

• Using the data better
  • Eg more weights being recorded

Key Messages

• Enhancements to runs will improve ASBVs
  • Feedback appreciated

• Get your data in for new reproduction analysis
  • Joining details
    • Including weight and condition score
    • Pregnancy scanning data

• Ongoing R&D aimed at delivery of more accurate ASBVs for a wider range of traits
What the good do well

Luke Stephen
NSW DPI
1st March 2017
@lstevo9984

Today's Agenda

Evidence used
What impacts gain
Where to from here

The importance of gain

Required for sustainability
It needs addressing
There is significant variation
Just how big a range

Steps taken
- Get average data
- Filter accordingly
- Look at relationships
- Explain the variation

What has made the cut
- 3 years data minimum
- Members only
- International flocks included
Number of Flocks

<table>
<thead>
<tr>
<th>Breed Type</th>
<th>Number</th>
</tr>
</thead>
<tbody>
<tr>
<td>MERINOSELECT</td>
<td>200</td>
</tr>
<tr>
<td>TERMINALS</td>
<td>374</td>
</tr>
<tr>
<td>MATERNALS</td>
<td>132</td>
</tr>
<tr>
<td>DOHNE</td>
<td>60</td>
</tr>
</tbody>
</table>

The big result first
High Indexes - Faster gains

Index trend

Top 20
Bottom 20
Top 20
Bottom 20
Top 20
Bottom 20
Top 20
Bottom 20

MERINOSELECT
Terminals
Maternals
Dohne
So what impacts gain?

What is explained

<table>
<thead>
<tr>
<th></th>
<th>Relationship</th>
</tr>
</thead>
<tbody>
<tr>
<td>MERINOSELECT</td>
<td>0.28</td>
</tr>
<tr>
<td>TERMINALS</td>
<td>0.30</td>
</tr>
<tr>
<td>MATERNALS</td>
<td>0.30</td>
</tr>
<tr>
<td>DOHNES</td>
<td>0.27</td>
</tr>
</tbody>
</table>

The Key factors

- Sorting Pedigree
- Sorting Data Collection
- Using the information
Sorting Pedigree

Recording Full Pedigree = less assumptions

Increase pedigree depth = more valuable contributions

<table>
<thead>
<tr>
<th></th>
<th>MS</th>
<th>TER</th>
<th>MAT</th>
<th>DOH</th>
</tr>
</thead>
<tbody>
<tr>
<td>Top 20%</td>
<td>72.1</td>
<td>96.5</td>
<td>94.7</td>
<td>97.8</td>
</tr>
<tr>
<td>Bottom 20%</td>
<td>20.8</td>
<td>92.4</td>
<td>86.5</td>
<td>93.4</td>
</tr>
</tbody>
</table>

Record as much full pedigree as possible

<table>
<thead>
<tr>
<th></th>
<th>MS</th>
<th>TER</th>
<th>MAT</th>
<th>DOH</th>
</tr>
</thead>
<tbody>
<tr>
<td>Top 20%</td>
<td>47.8</td>
<td>88.0</td>
<td>83.9</td>
<td>95.8</td>
</tr>
<tr>
<td>Bottom 20%</td>
<td>14.8</td>
<td>73.7</td>
<td>73.9</td>
<td>91.2</td>
</tr>
</tbody>
</table>

Fill in missing Pedigree
Recording data

Record more traits = Improved index accuracy
Make progeny records count = more valuable record

Valuable records

<table>
<thead>
<tr>
<th></th>
<th>MS</th>
<th>TER</th>
<th>MAT</th>
<th>DOH</th>
</tr>
</thead>
<tbody>
<tr>
<td>Top 20%</td>
<td>67.0</td>
<td>63.4</td>
<td>67.8</td>
<td>57.8</td>
</tr>
<tr>
<td>Bottom 20%</td>
<td>51.2</td>
<td>50.0</td>
<td>66.6</td>
<td>61.0</td>
</tr>
</tbody>
</table>

Improve the accuracy of your groups
Index Accuracy

<table>
<thead>
<tr>
<th></th>
<th>MS</th>
<th>TER</th>
<th>MAT</th>
<th>DOH</th>
</tr>
</thead>
<tbody>
<tr>
<td>Top 20%</td>
<td>331</td>
<td>60.1</td>
<td>44.9</td>
<td>46.9</td>
</tr>
<tr>
<td>Bottom 20%</td>
<td>23.9</td>
<td>54.7</td>
<td>39.0</td>
<td>46.1</td>
</tr>
</tbody>
</table>

Measure the traits that impact your goal

Using the information

Using the data

Selecting Males = get the value of your investment

Selecting females = get the true value out

Using them earlier = faster turnover
Selecting animals

Ranked on index

Expressed along the bell-curve

Won’t always be perfect

---

Male Selection Efficiency

<table>
<thead>
<tr>
<th></th>
<th>MS</th>
<th>TER</th>
<th>MAT</th>
<th>DOH</th>
</tr>
</thead>
<tbody>
<tr>
<td>Top 20%</td>
<td>20.1</td>
<td>27.3</td>
<td>24.8</td>
<td>15.8</td>
</tr>
<tr>
<td>Bottom 20%</td>
<td>11.0</td>
<td>11.7</td>
<td>12.8</td>
<td>2.4</td>
</tr>
</tbody>
</table>

Don’t just sell your rams. Use it to select

---

Female Selection Efficiency

<table>
<thead>
<tr>
<th></th>
<th>MS</th>
<th>TER</th>
<th>MAT</th>
<th>DOH</th>
</tr>
</thead>
<tbody>
<tr>
<td>Top 20%</td>
<td>5.9</td>
<td>11.9</td>
<td>13.7</td>
<td>12.5</td>
</tr>
<tr>
<td>Bottom 20%</td>
<td>-1.7</td>
<td>1</td>
<td>4.3</td>
<td>7.8</td>
</tr>
</tbody>
</table>

Use the information on your females!!
### Male generation interval

<table>
<thead>
<tr>
<th></th>
<th>MS</th>
<th>TER</th>
<th>MAT</th>
<th>DOH</th>
</tr>
</thead>
<tbody>
<tr>
<td>Top 20%</td>
<td>3.0</td>
<td>2.7</td>
<td>2.5</td>
<td>3.1</td>
</tr>
<tr>
<td>Bottom 20%</td>
<td>3.2</td>
<td>3.0</td>
<td>2.7</td>
<td>3.4</td>
</tr>
</tbody>
</table>

Use younger rams where possible

---

### Female generation interval

<table>
<thead>
<tr>
<th></th>
<th>MS</th>
<th>TER</th>
<th>MAT</th>
<th>DOH</th>
</tr>
</thead>
<tbody>
<tr>
<td>Top 20%</td>
<td>3.3</td>
<td>3.3</td>
<td>3.3</td>
<td>3.8</td>
</tr>
<tr>
<td>Bottom 20%</td>
<td>*</td>
<td>3.4</td>
<td>3.3</td>
<td>3.9</td>
</tr>
</tbody>
</table>

---

**So where to from here?**
What to focus on

▷ Merinos - Pedigree and using info
▷ Terminals - Select your males
▷ Maternals - Improve index accuracy
▷ Dohnes - manage inbreeding

For you

Know where you stand
Identify areas to improve
Get maximum benefit for your investment

“You can write all the inspirational messages you want on your kids lunch box, nothing beats genetics”
Jock Nivison (He is the one on the left!!) is the current owner/operator of Yalgoo partnership. Yalgoo is a diverse seedstock and commercial livestock business. Situated north of Walcha on the northern tablelands and consists of 5 enterprises. All Yalgoo enterprises are managed with commercial discipline and genetic gain is driven by objective measurement and scientific enhancement.

Jock is a firm believer in maximising and capturing genetic gain in livestock enterprises in an effort to assist clients achieve target EBITs/DSE. This is one of the reasons he was nominated for NSW Farmer of the year in 2016.

Jock has experienced different agricultural sectors across Australia and overseas including South Africa, Canada and New Zealand. As well as being involved with industry and technical groups for both the Merino and Hereford breeds.
Session 2
The Supermarket Outlook
David Bevis, Coles - Lamb Production Manager,
Chris Nicklin, Coles - Meat Business Manager

David Bevis
David Bevis is the Coles Production Manager for Lamb. He has been at coles for 25 years, all within the meat business across various roles from Supermarkets through to the Coles Meat ‘end to end’ supply chain. David completed his Butchers Apprenticeship in 1990 and has won a number of industry awards including Victorian Apprentice of the Year in 1992

Chris Nicklin
Chris is the Coles Meat Business Manager, covering beef, lamb, organics and sausages. Hi has 30 plus years of experience in Fresh Food retailing including in New Zealand, The UK and Singapore. Chris has been with coles for 7 years, also working within the Meat Business and has been a key contributor in the Coles ‘turn around’ after Wesfarmers acquired the supermarket.
Whats your market? What market do you produce rams for? If so what carcase spec are you and your clients aiming for?

- Domestic 45%
  - White Tablecloth
  - Butcher
  - Supermarket
- Export 55%
  - Middle East
    - Bagger Lambs 16-18kg Fat 1-2
    - Middle East Restaurant 18-24kg Fat 2-4
    - American Market 18-26kg Fat 2-4
    - EU 18 – 20kg Fat 2-3

Feedback How good is it?
Analyzing Data

- First lot of data requested for lamb 6 years ago
- Contact JBS IT
- Downloaded over a weekend

The Evolution of data collection

Palpation

Livestock Data Link
Weekly Mapping

Cobram: FA UMY and Compliance by Week (2016)

Overall Compliance %

Cobram: FA UMY and Compliance by Week (2016)

White Rose/Compliance (18-26kg) by Plant 71331 Grid
Cobram: Compliance by Month in Saleyard Lambs (2016)

<table>
<thead>
<tr>
<th>Month</th>
<th>Overall Compliance (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>57% Compliant</td>
</tr>
<tr>
<td></td>
<td>81% Compliant</td>
</tr>
</tbody>
</table>

FA Producers

1038 properties

Ave 2002 ewes / Farm

5.5% of Australia's breeding ewes
Producer Benchmarking

- Open to JBS Farm Assurance producers only.

**Weighting**
- 50% Carcase Spec
  - 25% Weight (18 – 26Kg)
  - 25% Fat Spec (Fat Score: 2, 3 & 4)
- 30% Number
  - 7.5% for every 500 supplied up to 2000
- 12% Spread of kill
  - 1% for each delivery
- 8% Loyalty
  - 2% per year up to 4 Years
- 100%

Benchmarking Producers

<table>
<thead>
<tr>
<th>Score</th>
<th>Name</th>
<th>Address</th>
</tr>
</thead>
<tbody>
<tr>
<td>95</td>
<td></td>
<td></td>
</tr>
<tr>
<td>94</td>
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<tr>
<td>93</td>
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<td>81</td>
<td></td>
<td></td>
</tr>
<tr>
<td>80</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

So why are we starting to analyze as much as we are?

Lamb Profitability for the Processor Based on Weight & LMY % (2015)

- 100%
- 90%
- 80%
- 70%
- 60%
- 50%
- 40%
- 30%
- 20%
- 10%
- 0%

- 1.5
- 2
- 2.5
- 3
- 3.5
- 4
- 4.5
- 5
- 5.5
- 6
- 6.5
- 7
- 7.5
- 8
- 8.5
- 9
- 9.5
- 10

<table>
<thead>
<tr>
<th>Weight Range (kg)</th>
<th>2005</th>
<th>2006</th>
<th>2007</th>
</tr>
</thead>
<tbody>
<tr>
<td>5.5 - 6.0</td>
<td>1.5</td>
<td>2</td>
<td>2.5</td>
</tr>
<tr>
<td>6.1 - 6.5</td>
<td>2.5</td>
<td>3</td>
<td>3.5</td>
</tr>
<tr>
<td>6.6 - 7.0</td>
<td>3</td>
<td>3.5</td>
<td>4</td>
</tr>
<tr>
<td>7.1 - 7.5</td>
<td>3.5</td>
<td>4</td>
<td>4.5</td>
</tr>
<tr>
<td>7.6 - 8.0</td>
<td>4</td>
<td>4.5</td>
<td>5</td>
</tr>
<tr>
<td>8.1 - 8.5</td>
<td>4.5</td>
<td>5</td>
<td>5.5</td>
</tr>
<tr>
<td>8.6 - 9.0</td>
<td>5</td>
<td>5.5</td>
<td>6</td>
</tr>
<tr>
<td>9.1 - 9.5</td>
<td>5.5</td>
<td>6</td>
<td>6.5</td>
</tr>
<tr>
<td>9.6 - 10.0</td>
<td>6</td>
<td>6.5</td>
<td>7</td>
</tr>
</tbody>
</table>
Thanks

• It's up to you to feed the world, but it won't be by your rules
As shown by the figure, there was no significant difference between score 1 and 2 lambs (1.02 ± 0.02) and (1.05 ± 0.019), respectively. Likewise, the mean time taken to reach score 3 lambs (1.12 ± 0.027) was similar to that of score 1 lambs. However, it took significantly longer (P<0.05) to reach lambs with scores 1.3 lambs than with score 1, and to reach lambs with scores 0.9 lambs with score 1.3 lambs. As a result, the mean time taken to reach score 1.3 lambs was significantly different (P<0.05). A model was developed which showed that carcass weight, sex, and their interaction and the batch all significantly (P<0.05) affected the batching time, as shown below.

<table>
<thead>
<tr>
<th>Technology</th>
<th>Algorithm</th>
<th>Correlation</th>
</tr>
</thead>
<tbody>
<tr>
<td>0.100 x 0.010</td>
<td>0.010 x 0.010</td>
<td>0.010 x 0.010</td>
</tr>
</tbody>
</table>

Why will processors encourage DEXA (and other tech) installations?
Technology and Innovation along the Value Chain

Sheep Genetics - Leading Breeder 2017
Technology and Innovation along the Value Chain

Processor processing segmentation

Using AUSMEAT registered plants as the starting point and utilising current public domain information, the following table was constructed to calculate the division of plants into species and throughput. Note some plants are multi-species and cell lines.

<table>
<thead>
<tr>
<th>Beef</th>
<th>Shoulder</th>
<th>Hind</th>
<th>Loin</th>
</tr>
</thead>
<tbody>
<tr>
<td>Small</td>
<td>10</td>
<td>20</td>
<td>30</td>
</tr>
<tr>
<td>Large</td>
<td>30</td>
<td>20</td>
<td>10</td>
</tr>
</tbody>
</table>

Aply estimated costs of installation for the range of solutions offered and required (i.e. different plants require different species and throughput) restated the budget required for the 50 processor of $150 million.

AUSMEAT, Calibration & Industry Standardisation

Intel inside® (industry standard) + O + q^p - \sum_{i=1}^{n} q_i x + Calibration block (industry standard) +
LEADING BREEDER
‘END PRODUCT STARTS WITH THE BREEDER’

LAMBPRO OVERVIEW
• Family owned and run
• 4910 Ewes to be joined in 2017
• Maternal and Terminal Breeding Program
• Estimate over 5500 rams in the industry from our breeding program

BREEDING PROGRAMS
• Primeline Maternal (18-24) (55% of ewes)
• Tradie (18-24) (31% of ewes)
• Poll Dorset (18-27) (12% of ewes)
• Hampshire/Southdown (Niche) (2% of ewes)
ESTIMATED MARKET BREAKUP

- Coles 36%
- Breakout 11%
- JBS 9%
- TFI 8%
- Other 36% (includes saleyards)

BREEDING PROGRAM

<table>
<thead>
<tr>
<th>Breed</th>
<th>Optimal Weight Range</th>
<th>Main Market</th>
</tr>
</thead>
<tbody>
<tr>
<td>Prerime Liner</td>
<td>18-25</td>
<td>All markets</td>
</tr>
<tr>
<td>Poll Dorset</td>
<td>21-27</td>
<td>All markets</td>
</tr>
<tr>
<td>Tradie</td>
<td>18-23</td>
<td>Coles, Breakout</td>
</tr>
<tr>
<td>Southdown/Hampshire</td>
<td>18-25</td>
<td>Specialist Retailers</td>
</tr>
</tbody>
</table>

MARKET CHANGE

- Markets have changed, genes changed with it
- 1995-2005 heavy focus 24+
- 2008 – 2017 18-24kg focus
PERFORMANCE V MARKETS

- Performance breeding without a market focus didn’t work for us
- High indexing doesn’t mean high buyer demand
- Trying to be all things to all people also doesn’t work
- Specialisation important to our business

DOMESTIC FOCUS

- Domestic market has become more specialised
- Export and domestic merging in specs
- More stringent demands, for muscle, adequate fat cover
- Two markets, whole carcase and retailers
- Both appear to be chasing similar lambs

QUANTIFYING CUSTOMER NEEDS

- Looked at retail yields of different breeding programs
- Understand the impact of PEMD
- Impact of fat
CONSUMER TESTING

• Commenced our own reference flock in 2015
• Tested 8 sires from three breeds
• All loins were tested for IMF, SF5
• All loins were consumer tested

CONSUMER RESULTS

• 20 point consumer difference
• Top sire was rated MSA 5 star
• Consumers would pay significantly more for top sire versus average

PRIME LAMB IMPROVEMENT COMPANY

• 28 sires to be tested in 2017
• Some on farm, some in a commercial operation
• Quick turn-around paramount (genetic gain)
• Good accuracy by end of 2017
PRODUCT BRANDING

- Our aim is to brand our lambs to buyers not consumers.
- Breeds are a poor mechanism to describe lambs.
- Key markets aware of research and enthusiastic about any improvements.
- Niche opportunity in top end retail for better genetics (fed well).
- Retailers looking to improve category as a whole.

FUTURE

- High accuracy outcomes for buyers of clients lamb subject to nutrition.
- Better market understanding of gene impact.
- Continued market demand on animals with known carcase characteristics.
- Monitor objective measurement technology.
Using genomics to breed for eating quality

Andrew Swan

Breeding to improve eating quality

On-farm data → Carcass measurements → Consumer eating quality → Genomic testing

Road testing the EQ index

- Highly accurate reference population sires:
  - What is the trait and index superiority of the leading sires?

- Validation of indexes using progeny in the consumer eating quality trial:
  - What is the impact of different levels of information on key traits?

- Index accuracies for groups of animals with different levels of information
The development of eating quality ASBVs & indexes

<table>
<thead>
<tr>
<th>Year</th>
<th>Event</th>
</tr>
</thead>
<tbody>
<tr>
<td>2007-2017</td>
<td>Development of genomic reference population for carcass and eating quality traits (Sheep CRC, MLA)</td>
</tr>
<tr>
<td>2011</td>
<td>First RBVs for carcass and eating quality traits</td>
</tr>
<tr>
<td>2015</td>
<td>Eating quality breeding objectives developed combining economic and genetic data from reference population</td>
</tr>
<tr>
<td>2016</td>
<td>Multi-trait single step genomic ASBVs for carcass and eating quality traits, EQ and LEQ indexes released to breeders</td>
</tr>
<tr>
<td>2017</td>
<td>Single step analysis updated to produce genomically enhanced ASBVs for all traits - better ASBVs and indexes</td>
</tr>
</tbody>
</table>

The Sheep CRC consumer eating quality trials

- 2100 reference population animals have gone through consumer eating quality trials
- Data used to establish:
  - Economic breeding objectives and EQ selection indexes
  - Genetic correlations between consumer eating quality and other carcass and production traits
- These genetic correlations are critical to the indexes

The antagonistic relationship between yield and eating quality makes joint improvement difficult
Selecting the top reference population sires

<table>
<thead>
<tr>
<th>Trait</th>
<th>CPLUS</th>
<th>EQ</th>
</tr>
</thead>
<tbody>
<tr>
<td>PWT (kg)</td>
<td>2.4</td>
<td>1.2</td>
</tr>
<tr>
<td>CEMD (mm)</td>
<td>1.5</td>
<td>1.0</td>
</tr>
<tr>
<td>CCAT (mm)</td>
<td>-0.3</td>
<td>-0.2</td>
</tr>
<tr>
<td>LMY (%)</td>
<td>1.3</td>
<td>-0.1</td>
</tr>
<tr>
<td>DRESS (%)</td>
<td>1.0</td>
<td>0.6</td>
</tr>
<tr>
<td>IMF (%)</td>
<td>-0.2</td>
<td>0.7</td>
</tr>
<tr>
<td>SF5 (N)</td>
<td>1.3</td>
<td>-4.9</td>
</tr>
<tr>
<td>Consumer EQ</td>
<td>-0.5</td>
<td>3.5</td>
</tr>
</tbody>
</table>

EQ has lower response in growth, muscle and fat, but still in the desired directions.

Lower lean meat yield for EQ but consistent with goal of holding constant.

Positive consumer eating quality for EQ, negative for CPLUS.

Validation of indexes in consumer EQ progeny

• Subset of 316 animals with EQ data used as test set
• Four sets of ASBVs with different amounts of information:
  • Excluding/including genotypes, measurements on animals and relatives
  • Superiority of top 10% of animals selected on indexes based on ASBVs from each analysis
• Breeding values for actual consumer eating quality* from independent analysis available for comparison

* Consumer eating quality is scored on a 0 – 100 point scale.

Analyses and comparisons

<table>
<thead>
<tr>
<th>Analysis</th>
<th>Scenario</th>
</tr>
</thead>
<tbody>
<tr>
<td>No Geno</td>
<td>A flock with no genotypes</td>
</tr>
<tr>
<td>Geno Av</td>
<td>A flock with genotypes with average linkage to the reference population</td>
</tr>
<tr>
<td>Geno High</td>
<td>A flock with genotypes with high linkage to the reference population e.g. sires used in the reference</td>
</tr>
<tr>
<td>Measured</td>
<td>Hypothetical + i.e. if you could measure carcass traits on animals and then select and breed from them</td>
</tr>
</tbody>
</table>

Select on EQ index for each analysis

Evaluate against most accurate analysis
Using Gemonics to Breed For Eating Quality

Eating quality index superiority

Increasing information

Consumer eating quality and lean meat yield

We can improve eating quality even with less accurate information, but at the cost of LMY

Consumer eating quality and lean meat yield

With more information eating quality improves and we have better outcomes for LMY
Using Gemonics to Breed For Eating Quality

Live animal and carcass fat depth

With less accurate information the improvement in eating quality is coming from fat.

Live animal and carcass fat depth

With more information the outcomes for fat improve, especially carcass fat.

IMF and shear force

Outcome = desirable responses: positive for IMF, negative for shear force.
Using Gemonics to Breed For Eating Quality

**Growth and muscle**

As information increases we have less response in growth, but still positive

Increasing information = increased response in muscle

**Two key messages**

- It is now possible to improve eating quality in terminal sires
- Genomic information gives breeders the ability to better control traits they cannot easily record

**EQ index accuracies**

<table>
<thead>
<tr>
<th>Group</th>
<th>Accuracy</th>
<th>Level of Information</th>
</tr>
</thead>
<tbody>
<tr>
<td>Reference sires</td>
<td>70</td>
<td>Progeny tested for EQ traits</td>
</tr>
<tr>
<td>Reference progeny</td>
<td>57</td>
<td>Direct measurement of EQ traits</td>
</tr>
<tr>
<td>Industry genotyped</td>
<td></td>
<td>Genotyped by breeders Genomic linkage to reference</td>
</tr>
<tr>
<td>Contemporaries</td>
<td>37</td>
<td>... of animals genotyped by breeders</td>
</tr>
<tr>
<td>2015 drop (ungenotyped)</td>
<td>35</td>
<td>Animals in flocks with no genotypes</td>
</tr>
</tbody>
</table>

Substantial increase in accuracy in flocks who genotype → higher accuracy = higher response
Summary

• Industry investment in the genomic reference population for meat traits has enabled selection for eating quality

• Joint improvement with lean meat yield difficult due to the negative correlation with eating quality, but not impossible:
  • EQ indexes are the optimal tool to overcome this antagonism

• Increasing accuracy of information = better outcomes:
  • Breeders can improve eating quality without genomic testing but at the cost of increased fat and lower lean meat yield
  • With genomic testing breeders have better control over traits
  • There is value in improving genomic linkage to the reference population

Acknowledgements

Innovative research undertaken by the meat science and genomics programs of the Sheep CRC underpins this work
Getting your measurement strategy right (genomics focused)

Tom Granleese
Leading Breeder Conference – Melbourne - 2017

Quick overview of presentation

- Power of pedigree
- Power of measuring
- Power of genotyping
- Genotyping strategies

Sound breeding program design

- Correct, full pedigree
- Well managed groupings
- Measuring traits
- High selection intensity
Reminders are good but…

…this isn’t new news to you!

- So let’s run over some quick basics before delving into genotyping strategies

Simulations to estimate power of pedigree, phenotyping, genotyping

- Merino breeding program – MP+ index
  - Principals still apply to maternals & terminals (so don’t drift off!)
- Assuming correct groupings (so no noise)
- Assuming 100% selection efficiency

5 scenarios

1) No pedigree, basic measurements (ywt, yfd, ygfw)
2) No pedigree, yearling and adult measurements
3) Scenario 2 PLUS sire pedigree
4) Scenario 2 PLUS full pedigree
5) Scenario 4 + genotyping 20% of ram selection candidates

Go into more depth soon
Simulations to estimate power of pedigree, phenotyping, genotyping

<table>
<thead>
<tr>
<th>Scenario</th>
<th>2-stage GS</th>
<th>Sire ped</th>
<th>Dam ped</th>
<th>WWY</th>
<th>YWT</th>
<th>HWT</th>
<th>AWT</th>
<th>YGFW</th>
<th>AGFW</th>
<th>YFD</th>
<th>AFD</th>
<th>YSS</th>
<th>ASS</th>
<th>NLW</th>
<th>Gen gain ($/yr)</th>
<th>MP+ points / yr</th>
<th>Index Accuracy</th>
<th>sel. Cands</th>
<th>Gen Int</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>0 0 0 0 0 0 1 0 0 0 0</td>
<td>1.33</td>
<td>2.8</td>
<td>0.33</td>
<td>3.8</td>
<td></td>
<td></td>
<td></td>
<td></td>
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<tr>
<td>2</td>
<td>0 0 0 1 1 1 1 1 1 1 1 0 0 0 0</td>
<td>1.44</td>
<td>3.0</td>
<td>0.35</td>
<td>3.4</td>
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<td>2.63</td>
<td>5.3</td>
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<td>6.6</td>
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<td>2.6</td>
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</tr>
</tbody>
</table>

4 vs 3: Full ped 47% ΔG → maternal info + nlw

Simulations to estimate power of pedigree, phenotyping, genotyping

<table>
<thead>
<tr>
<th>Scenario</th>
<th>2-stage GS</th>
<th>Sire ped</th>
<th>Dam ped</th>
<th>WWY</th>
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<th>YFD</th>
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<th>ASS</th>
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</thead>
<tbody>
<tr>
<td>1</td>
<td>0 0 0 0 0 0 1 0 0 0 0</td>
<td>1.33</td>
<td>2.8</td>
<td>0.33</td>
<td>3.8</td>
<td></td>
<td></td>
<td></td>
<td></td>
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</tr>
</tbody>
</table>

5 vs 4: GS extra 19% ΔG → lower gen. int. @ similar acc.

Quick refresher on genomic selection

- Most benefit:
  - Late in life; hard to measure; sex-limited; low heritability
    - Adult traits; carcase traits; nlw → often high value traits!
  - Early in life; easy to measure; high heritability
    - Weaning, post-weaning; body weights, scanning, wool; yfd
Genomic selection provides more information and hence variation for traits which allows great gain for hard-to-measure traits.

ASBV spread without genomics

ASBV spread with genomics

More variation – gives more potential to get more genetic gain!

How can you leading breeders extract that last potential using genomic selection?

- Without ending up like this?
How can you leading breeders extract that last potential using genomic selection

- More simulations
- This time using a 2 trait index (pwt and IMF)
- Only pwt measured phenotypically
- pwt and IMF have equal weighting on $ value of SD of breeding objective
- Merino breeders pay attention (!)

How can you leading breeders extract that last potential using genomic selection

- 5 scenarios
  1) Genomic testing on ram candidates prior to pwt measurement e.g. sort best candidates on PA → genomic test lambs
  2) Genomic testing on ram candidates after pwt measurement i.e. sort on breeding → genomic test yearlings

Just start with 2 to begin with.

Genetic gain vs proportion of genotyped rams

![Graph showing genetic gain vs proportion of genotyped rams]
How can you leading breeders extract that last potential using genomic selection

- 5 scenarios
  1) Genomic testing on ram candidates prior to pwt measurement e.g. sort best candidates on PA → genomic test lambs
  2) Genetic testing on ram candidates after pwt measurement i.e sort on breeding → genomic test yearlings
  3) Genetic testing on ewe candidates (only) after pwt measurement i.e sort on breeding for natural mating only → genomic test yearlings
  4) Genetic testing on ewe candidates (only) after pwt measurement i.e sort on breeding for MOET matings only → genomic test yearlings
  5) Genetic testing on ewe lamb candidates (only) before pwt measurement i.e sort on breeding for JIVET matings only → genomic test lambs
Getting Your Measurement Strategy Right!

Genetic gain vs proportion of genotyped

Annual genetic gain (genetic SD of index) vs Proportion selection candidates genotyped

Late-stage genomic selection rams
Early-stage genomic selection rams
Late-stage selection genomic selection ewes - natural
Late-stage selection genomic selection ewes - MOET
Early-stage genomic selection ewes - JIVET

Remember zero is base result

Percentage of maximum benefit vs proportion of genotyped rams

Percentage of maximum benefit to genomic selection (%) vs Proportion of ram selection candidates genotyped

Even if you MOET or JIVET 10 ewes genotype 35 for MOET and 45 for JIVET to get most of the benefit
So what is best value for money here?

Cost of ped, pheno ($15), genotyping ($50), repro annually – 500 nucleus

Summing up...

- Measuring ntw will give major trait and index responses (where weighted)
  - applies for any trait

- Genotyping provides more variation for hard to measure traits which allows greater improvement

- "20-80" genotyping rule applies in rams only if some preliminary measurements included in ASBVs when sorting the best candidates to genotype

- Genotyping rams best “bang for buck”
4’ closer to the perfect sheep

Dr Mark Ferguson
@fergenetics

The world needs more protein...

The fundamentals

G + E
### Fleece weight, Micron, Scanning

<table>
<thead>
<tr>
<th>Breed</th>
<th>Fleece weight</th>
<th>Micron</th>
<th>Scanning</th>
</tr>
</thead>
<tbody>
<tr>
<td>Black Tag</td>
<td>2.5</td>
<td>16.5</td>
<td>117%</td>
</tr>
<tr>
<td>General</td>
<td>2.4</td>
<td>16.5</td>
<td>135%</td>
</tr>
<tr>
<td>Royal</td>
<td>2.4</td>
<td>16.4</td>
<td>154%</td>
</tr>
</tbody>
</table>

---

> “...assembling the ideal genotype for a particular task”

Professor Mike Goddard

---

> In **four** years...  
> ...what has changed?
Awareness & use of BVs to assist with ram selection

175 rams progeny tested

Understanding of sires resistant to footrot
Footrot Traits – Genetic Corr. With Production

<table>
<thead>
<tr>
<th>Trait</th>
<th>Average Footrot</th>
</tr>
</thead>
<tbody>
<tr>
<td>Weaning Weight</td>
<td>0.25</td>
</tr>
<tr>
<td>Birth Weight</td>
<td>0.10</td>
</tr>
<tr>
<td>Fleece Weight</td>
<td>-0.14</td>
</tr>
<tr>
<td>US Muscle Depth</td>
<td>0.13</td>
</tr>
<tr>
<td>Yearling Greasy Fleece Weight</td>
<td>0.35</td>
</tr>
<tr>
<td>Yearling Clean Fleece Weight</td>
<td>0.33</td>
</tr>
<tr>
<td>Yearling Fibre Diameter</td>
<td>-0.00</td>
</tr>
<tr>
<td>Yearling Fibre Diameter C.V.</td>
<td>0.14</td>
</tr>
<tr>
<td>Yearling Staple Length</td>
<td>0.17</td>
</tr>
<tr>
<td>Yearling Staple Strength</td>
<td>0.17</td>
</tr>
</tbody>
</table>

1. Weak unfavourable genetic correlations with weight (size of error could mean there really is nothing there)
2. Could be a moderate unfavourable relationship with fleece weight
3. Weak favourable link to fat and muscle (size of error could mean there is nothing there)
but the best is yet to come...
The potential of technology is exploding

Who will capture this opportunity?

From mobs on farms

To animals per m²
Ewe ID ZQ ID Paired with Certainty
120564 E3081wqau L6328fues 99%
120564 E3081wqau L7512zilm 97%
120564 E5273lacj L6872aoce 98%
120564 E6549kjbs L3482lwuc 98%
120564 E6549kjbs L6421xvug 93%
120564 E9134afeg Not yet lambed 100%
120564 E9134afeg L3819eity 94%
120564 E9134afeg L3819eity 94%

Live in awe of the power of genes
Use of new technology’s

- DNA Parent testing
  - Genomic project - what the findings are telling us
  - Parent testing - In a commercial ram breeding operation
  - Potential traps, things to consider

- Genomics
  - Genomic project - what the results confirmed

Acknowledgement

- Australian Wool Innovation
- MerinoLink Limited
- Moses & Son Wool Brokers
- Bluechip Livestock
Genomic validation project

- 10 rams - 2012 drop
- 300+ ewes - 2011 drop
- DNA; 50K; Progeny tested

Number of progeny per sire

<table>
<thead>
<tr>
<th>Ram ID</th>
<th>Number of progeny at Marking</th>
<th>% of Progeny</th>
</tr>
</thead>
<tbody>
<tr>
<td>120006</td>
<td>44</td>
<td>13.5%</td>
</tr>
<tr>
<td>120060</td>
<td>12</td>
<td>3.7%</td>
</tr>
<tr>
<td>120112</td>
<td>15</td>
<td>4.6%</td>
</tr>
<tr>
<td>120167</td>
<td>15</td>
<td>10.4%</td>
</tr>
<tr>
<td>120207</td>
<td>43</td>
<td>13.2%</td>
</tr>
<tr>
<td>120221</td>
<td>49</td>
<td>15.1%</td>
</tr>
<tr>
<td>120268</td>
<td>21</td>
<td>6.5%</td>
</tr>
<tr>
<td>120307</td>
<td>70</td>
<td>21.3%</td>
</tr>
<tr>
<td>121428</td>
<td>18</td>
<td>5.5%</td>
</tr>
<tr>
<td>Total</td>
<td>325</td>
<td></td>
</tr>
</tbody>
</table>

- Syndicate mating - Industry message
  - Over three years (2013, 2014, 2015 and 2016) similar results
  - Dominant ram each year (not always the same ram)
  - Range of progeny per sire - 4% to 30%
  - Sheep Genetics - down grade syndicates compared to single sire mates
  - This is a good example why!

Number of progeny per sire

<table>
<thead>
<tr>
<th>Ram ID</th>
<th>Number of progeny at Marking</th>
<th>% of Progeny</th>
</tr>
</thead>
<tbody>
<tr>
<td>122221</td>
<td>68</td>
<td>37%</td>
</tr>
<tr>
<td>130410</td>
<td>63</td>
<td>38%</td>
</tr>
<tr>
<td>140316</td>
<td>41</td>
<td>22%</td>
</tr>
<tr>
<td>Total</td>
<td>184</td>
<td></td>
</tr>
</tbody>
</table>

- AI Backup - similar message
  - Dominant rams
  - Range of progeny per sire - 1% to 58%
The twin story

- 2013 drop - 180 twins
  - 54% of the twins were half sibs - same dam different sire
- 2014 drop - 178 twins
  - 46% of twins were half sibs
- 2015 drop - 340 twins
  - 59% of twins were half sibs
- 2016 drop - 112 twins (AI Backup)
  - 21% of twins were half sibs

<table>
<thead>
<tr>
<th>Year</th>
<th>Total number of twins</th>
<th>Number of twins (1/2 sibs)</th>
<th>Number of twins (full sibs)</th>
</tr>
</thead>
<tbody>
<tr>
<td>2013</td>
<td>180</td>
<td>(54%)</td>
<td>(46%)</td>
</tr>
<tr>
<td>2014</td>
<td>178</td>
<td>(46%)</td>
<td>(54%)</td>
</tr>
<tr>
<td>2015</td>
<td>340</td>
<td>(59%)</td>
<td>(41%)</td>
</tr>
<tr>
<td>2016</td>
<td>112 (AI Backup)</td>
<td>(21%)</td>
<td>(79%)</td>
</tr>
</tbody>
</table>

Using DNA parent testing - ram breeders

- DNA parent testing provides a number of opportunities
- Sire pedigree vs Syndicate pedigree

<table>
<thead>
<tr>
<th>Syndicate</th>
<th>No. Sires</th>
<th># Progeny</th>
<th>Count of DNA Tested</th>
<th>% DNA</th>
</tr>
</thead>
<tbody>
<tr>
<td>15HAW001</td>
<td>2</td>
<td>66</td>
<td>32</td>
<td>48%</td>
</tr>
<tr>
<td>15HAW002</td>
<td>2</td>
<td>42</td>
<td>13</td>
<td>31%</td>
</tr>
<tr>
<td>15HAW003</td>
<td>5</td>
<td>130</td>
<td>52</td>
<td>40%</td>
</tr>
<tr>
<td>15HAW004</td>
<td>3</td>
<td>27</td>
<td>10</td>
<td>37%</td>
</tr>
<tr>
<td>15HAW005</td>
<td>4</td>
<td>71</td>
<td>14</td>
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</tr>
<tr>
<td>15HAW006</td>
<td>4</td>
<td>57</td>
<td>16</td>
<td>28%</td>
</tr>
<tr>
<td>15HAW007</td>
<td>5</td>
<td>69</td>
<td>19</td>
<td>28%</td>
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<tr>
<td>15HAW008</td>
<td>3</td>
<td>34</td>
<td>12</td>
<td>35%</td>
</tr>
<tr>
<td>15HAW009</td>
<td>7</td>
<td>68</td>
<td>11</td>
<td>16%</td>
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<tr>
<td>Totals</td>
<td>564</td>
<td>179</td>
<td>32%</td>
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**Tips and Tricks When Using New Technology**

**Sire and linkage profile**

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<th>Prog/Flk/s</th>
<th>2010</th>
<th>2011</th>
<th>2012</th>
<th>2013</th>
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<tbody>
<tr>
<td>070002</td>
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<td>44</td>
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<tr>
<td>050142</td>
<td>722:10</td>
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<td>35</td>
<td>35</td>
<td>35</td>
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<td>44</td>
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<tr>
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</tr>
<tr>
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<tr>
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<td>30:01</td>
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<td>30</td>
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<tr>
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<td>57</td>
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**Post DNA Testing**

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<tr>
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<td>245:01</td>
<td>57</td>
<td>113</td>
<td>75</td>
<td>75</td>
</tr>
</tbody>
</table>

**Industry messages**

- DNA parent testing is a great tool.
- If using in a syndicate situation be prepared to measure the whole syndicate.
- Understand the ramifications of “effective progeny” and how selecting small numbers out of different syndicate sire groups or management groups will affect your data quality.
Changes over time to Asbv's & Indexes

<table>
<thead>
<tr>
<th>Project Stage</th>
<th>30% Selection (rams selected for Genomic testing)</th>
<th>Mating (data selected based on the genomic test results)</th>
<th>Individual Ram data (Data shared by Sheep Genetics)</th>
<th>Progeny Weaning data</th>
<th>Progeny 1st Ass</th>
<th>Progeny 2nd Ass</th>
</tr>
</thead>
<tbody>
<tr>
<td>Data Available</td>
<td>Mid parent, rear type &amp; weaning weight data</td>
<td>Visual selection and Genomic test</td>
<td>Yoorting Fleece Data - yearling weight, fat &amp; muscle data</td>
<td>Progeny Weaning data - second stage on sisters</td>
<td>Progeny 1st Ass data</td>
<td>Progeny 2nd Ass data</td>
</tr>
<tr>
<td>Age of Ram</td>
<td>3 months</td>
<td>10 months</td>
<td>10 months</td>
<td>18 months</td>
<td>24 months</td>
<td>36 months</td>
</tr>
<tr>
<td>Age of progeny</td>
<td>3 months</td>
<td>11 months</td>
<td>22 months</td>
<td></td>
<td></td>
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</tr>
</tbody>
</table>

Changes over time to Asbv's & Indexes

<table>
<thead>
<tr>
<th>30% Selection</th>
<th>Mating</th>
<th>Individual Ram data</th>
<th>Progeny Weaning data</th>
<th>Progeny 1st Ass</th>
<th>Progeny 2nd Ass</th>
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</thead>
<tbody>
<tr>
<td>DP+</td>
<td>136.1</td>
<td>138.4</td>
<td>146.0</td>
<td>145.0</td>
<td>137.6</td>
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<tr>
<td>FP+</td>
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<td>134.1</td>
<td>137.6</td>
<td>134.5</td>
</tr>
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<td>MP+</td>
<td>139.4</td>
<td>139.5</td>
<td>140.8</td>
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<td>141.4</td>
</tr>
<tr>
<td>YFAT</td>
<td>-0.9</td>
<td>-0.9</td>
<td>-0.9</td>
<td>-0.9</td>
<td>-0.9</td>
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<tr>
<td>YEML</td>
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</tr>
<tr>
<td>YSS</td>
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<td>-2.6</td>
<td>-2.6</td>
</tr>
<tr>
<td>YCFW</td>
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<td>16.3</td>
<td>12.9</td>
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<td>YFD</td>
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<td>YWT</td>
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<td>27</td>
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<td>29</td>
<td>28</td>
</tr>
</tbody>
</table>

Index correlations

<table>
<thead>
<tr>
<th>Index</th>
<th>Fibre Production +</th>
<th>Merino Production +</th>
<th>Dual Purpose +</th>
</tr>
</thead>
<tbody>
<tr>
<td>Genomic / Sheep Genetics</td>
<td>0.82 (67%)</td>
<td>0.85 (72.85%)</td>
<td>0.78 (60.5%)</td>
</tr>
<tr>
<td>Genomic / AMSEA</td>
<td>0.72 (51.85%)</td>
<td>0.70 (48.61%)</td>
<td>0.24 (5.63%)</td>
</tr>
</tbody>
</table>

Sheep Genetics - Leading Breeder 2017
Conclusions

- There are changes amongst individual over time as more data becomes available.
- The overall “Ram Team Average” has remained stable.
- DNA parent test provides excellent pedigree; ewe efficiency and syndicate data.
- For the commercial breeder:
  - Be confident when purchasing rams using ASBV’s and indexes to achieve a breeding objective.
Session 4
Genetic Tools available to Improve Genetic Gain

Sheep Genetics Website Tools

Clara Collison - LAMBPLAN Development Officer
Caris Jones - MERINOSELECT Development Officer

Website Display

Tools Page
**MateSel in a nutshell**

1. Provide a list of eligible Males and Females.
   - Limited genetic gain is achieved if 'pre selection' is made
2. Set your index and desired parameters to improve.
3. Review the selection decisions that have been made.
   - Ideal for identifying and reducing coancestry and inbreeding levels within flock.
   - Perfect for AI / ET programs to identify most effective Sires pre purchase of genetics.

**Your frontier should Look like..**

- The frontier shape and structure, represents potential gain.
- End point distance from frontier represents amount of constraint you are imposing.

**What NOT to do:**

- Constraints of the above Matesel run:
  - Use all females and males provided.
  - All Rams had + or - usages of 5 (i.e.40-30 mating's). Sum of Max joining's was equal to sum of ewes being joined.
  - Plus many trait rules. [Maximum on BWT, Minimum on PWT, WEC, NLW..]
**When can you use MateSel?**

- Genetic Service provider Training in Melbourne included a MateSel training day.
- More training days available to service providers after Regional Forums
- Once all service providers train then some breeders
- Must have completed training before MateSel appears in your tools Page on Sheep Genetics.

**What it looks like**

**MATESEL at Sheep Genetics**

- Select analysis
- Analysis: [data chosen]
- Selecting sex: [data chosen]
- Create new run

**What it looks like**

- [Data table and options]
Genetic Tools available to Improve Genetic Gain

Advanced Run Parameters

The Frontier

Outputs
Genetic Tools available to Improve Genetic Gain

Sire Summary

Out Matings

RAMping up genetic gain

Project Aims
• Improve Breeding Program Effectiveness and Genetic gain:
  – Develop series of on farm reports
  – Identify potential barriers to genetic gain through benchmarks
  – Develop clear recommendations
• Develop training package that accredited Service Providers can use
• Reports available via Dashboard for SP and Breeder access
• Allow a more proactive approach
Genetic Tools available to Improve Genetic Gain

The ingredients of genetic improvement

<table>
<thead>
<tr>
<th>Selection intensity:</th>
<th>Select only the very best animals</th>
</tr>
</thead>
<tbody>
<tr>
<td>Selection accuracy:</td>
<td>Pick the best ones more often</td>
</tr>
<tr>
<td>Generation Interval:</td>
<td>Breed from them as soon as possible</td>
</tr>
<tr>
<td>Variation:</td>
<td>Different enough to pick from</td>
</tr>
</tbody>
</table>

RAMPing up genetic gain

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

Ramping Up Genetic Gain

Sheep Genetics - Leading Breeder 2017
Pedigree Analysis

1. Count animals submitted
2. Male to Female ratio *
3. Average Sire and Dam age
4. Pedigree breakdown - Graph and Table

Flock Performance

1. Percentage recorded
2. Average index accuracy
3. Index Gain
4. Male and Female Selection Efficiency

Data Summaries

1. Traits measured
2. Count of animals measured
3. Count of Contemporary Groups
4. Percentage of flock measured
5. Average Effective Progeny *
6. Average Percent Linkage
7. Average Age Variation
8. Average Birth Type Variation

* Conditional formatting used to highlight lower quality areas.
Sire Summaries

1. Sire IDs
2. Number of Progeny and Number of flocks
3. Count of progeny measured in each year*

Reproduction

1. Number of Preg Scans utilised in the analysis
2. Number of Dams identified
3. Yes or No for if the flock is in the Yearling NLB:NLW analysis
4. Fertility percentage
5. Number of Yearling Dams
6. Yes or No for if the flock is in the Adult NLB:NLW analysis

*Counts less than 10 highlighted red

*Headings to be made clearer with website update
Improving Profit By Maximising use of High Genetic Merit Sires

From farm to plate: AbacusBio

Making a difference to agriculture internationally using science & technology

AbacusBio

- Agri-science company with product and consultancy services
- 30 people incl. PhD students
- Strength in genetic improvement programmes
- We work with:
  - Organisations providing genetic improvement products and services for milk, meat, fibre, fish, honeybees
  - Bull/ ram/ buck breeders like yourselves
  - Commercial farmers
  - Meat companies
  - Technology providers
A case study of the value of better genetics
Leading Breeder Conference
1st and 2nd of March 2017
Tim Byrne

Bit of background – the Wharetoa flock

• Elite maternal and terminal genetics (1500 ewes fully recorded ewes in total)
• Excellent genetic merit for growth and meat (info on that to follow)
• Wanted to be able to show the value of their genetics to commercial farmers

Bit of background – genetic trends

• Genetic trends measure how the genetic merit of a recorded flock is changing over time
• Enable us to see what sort of differences exist between Wharetoa and the industry average flocks
• The units of the trend are in the units of the trait
  • Weaning weight is in kilograms per lamb
  • Lean yield is in weight of meat per carcase
Improving Profit By Maximising use of High
Genetic Merit Sires

The analysis

- Compare Wharetoa genetic trends with industry average for Maternal and Terminal flocks
- Focused on growth and meat – Wharetoa’s strengths
- Looked at the differences in genetic merit in 2015 born animals for weaning weight, carcase weight and lean meat yield
- Used Farmax (more later) to calculate the value of Wharetoa Maternal and Terminal genetics in a commercial flock

Maternal – Weaning weight (lamb effect)

- WWT
- eBV
- Year
- +0.41kg

Maternal – Weaning weight (ewe effect)

- WWT
- eBV
- Year
- +0.53kg
Improving Profit By Maximising use of High Genetic Merit Sires

**Maternal – Carcase weight**

- +0.63kg

**Maternal – Lean yield (kg extra meat/carcase)**

- +0.63kg

**Wharetoa maternal compared to industry**

- 0.94 kg more weaning weight from lamb effect/ milky ewes
- 0.63 kg more carcase weight (1.4 kg live weight at slaughter)
- 0.35 kg more lean yield (0.78 kg live weight at slaughter)

- Combine all these = 3 kg increase in lamb live weight as a result of Wharetoa maternal genetics over industry average

- 1.5 kg per lamb in the commercial flock
- Add the impact of bigger ewes = 3 kg more lamb live weight in Wharetoa maternal lambs compared to industry average

Sheep Genetics - Leading Breeder
Improving Profit By Maximising use of High Genetic Merit Sires

Terminal – Weaning weight

+0.38kg

Terminal – Carcase weight

+0.31kg

Terminal – Lean yield

+0.21kg
The differences

• 0.38 kg more weaning weight
• 0.31 kg more carcase weight (0.69 kg live weight at slaughter)
• 0.28 kg more lean yield (0.62 kg live weight at slaughter)
• Combine all these = 1.7 kg increase in live weight as a result of Wharetoa terminal genetics over industry average

• 0.85 kg per lamb in the commercial flock
• Combine the effect of hybrid vigour = 3 kg more live weight in Wharetoa terminal lambs compared to Wharetoa maternal lambs

Summary

• 3 kg more live weight (through growth and meat) in Wharetoa maternal lambs compared to industry average maternal
• 3 kg more live weight (through growth and meat plus hybrid vigour) in Wharetoa terminal lambs compared to Wharetoa maternal lambs
• Heavier maternal ewes means 8% increase in lambing percent
• Hybrid vigour means 3% increase in lamb survival in terminally-sired lambs
• Have modelled these through Farmax

Farmax modelling

• What is Farmax? – a bio-economic farm modelling tool.
• Feed supply, animal system, economic results and “biological fit”
• Start by building a model representing a farm as it is now – robust
• Can then look at any alternative systems to assess economic results and “bio-fit”
• Forecasts the results (profitability) of any development
The Base farm

- 300ha cultivatable land plus 50ha steep grazing
- Grows 15ha swedes, 6ha fodder beet and makes and feeds 300 bales of balage
- 3050 ewes, 70kg, mated 15th April, weaned 10th December, 141%
- 785 unmated hoggets
- 18.1kg average lamb carcass weight – all lambs finished
- All ewes mated to maternal sires

The alternatives

1. Base flock plus 10% or 40% Wharetoa terminal sires
2. Base flock upgraded to Wharetoa Maternals plus 10% or 40% Wharetoa terminal sires
3. Same as 2 but increase CWT to 22 kg for the terminal sire lambs

The assumptions

- Same feed supply for all models
- Wharetoa maternals lift ewe weights to 75kg, lambing % rises 8% to 149%, and average lamb live weight by 3kg
- Wharetoa terminals lift lambing % by 3% due to hybrid vigour, live weight by 3kg, and post weaning growth rates by 15% due to hybrid vigour and 20% due to Wharetoa genetic trends
Improving Profit By Maximising use of High Genetic Merit Sires

Impact of better genetics

- Significant shift earlier in the average kill date
- Earlier sales frees up summer/autumn feed for other uses
- Two methods looked at to use this feed:
  - Keep carcass at 18.1, increase ewe flock first, then finish store lambs with remaining available feed.
  - Increase lamb carcass weights to 22kg first, then increase ewe numbers if possible. No store lambs

Financial impact

- $ gains comes from incremental improvements to multiple factors
- Lambing %
- Weaning weight
- Lamb value higher/kg earlier in season
- Saved feed, more ewes, heavier lambs or finish additional store lambs

Copy of full report available from Wharetoa website (http://www.wharetoagenetics.co.nz/)

Performance summary

<table>
<thead>
<tr>
<th></th>
<th>Base flock</th>
<th>1. Base + 40% terminal</th>
<th>2. Wharetoa maternal + 40% terminal</th>
<th>3. Wharetoa maternal + heavy term lambs</th>
</tr>
</thead>
<tbody>
<tr>
<td>Additional Gross margin</td>
<td>$0</td>
<td>$27,000</td>
<td>$63,000</td>
<td>$66,000</td>
</tr>
<tr>
<td>Farm profit before tax &amp; drawings</td>
<td>$117,000</td>
<td>$141,000</td>
<td>$172,000</td>
<td>$178,000</td>
</tr>
<tr>
<td>% profit increase (of base flock)</td>
<td>0%</td>
<td>20%</td>
<td>47%</td>
<td>52%</td>
</tr>
<tr>
<td>Lambs on hand and March</td>
<td>1157</td>
<td>319</td>
<td>68</td>
<td>151</td>
</tr>
<tr>
<td>Average kill date</td>
<td>21 Feb</td>
<td>14th Feb</td>
<td>9th Jan</td>
<td>24th Jan</td>
</tr>
<tr>
<td>Number of ewes</td>
<td>1048</td>
<td>3134</td>
<td>1088</td>
<td>2962</td>
</tr>
<tr>
<td>No store lambs finished</td>
<td>0</td>
<td>413</td>
<td>0</td>
<td>0</td>
</tr>
</tbody>
</table>
Key messages

• An analysis can be done to quantify the $ impact of better genetics on commercial farms
• The impact of better genetics for growth and meat production are significant
• The same will apply to better genetics for wool and reproduction
• You can use these types of analysis to support the value generated from your breeding programme
• This is a key way to generate more demand for rams and/or higher prices

Creating more $ for commercial farmers
Merino breeding objectives under climate change

Andrew Swan and Phil Graham
AGBU and NSW DPI

Southern Livestock Adaptation 2030

Extensive modelling of climate change and livestock production at 80+ locations:
• Most climate scenarios to 2030 suggest higher temperatures and less rainfall
• Higher temperatures + less rainfall = shorter growing seasons
• Small temperature and rainfall variations significantly affect profits
• Lower rainfall areas hardest hit – cold, wet, elevated areas may benefit
• Adaptations can help reduce impact

Source: http://sla2030.net.au
Possible adaptations

- Strategies to reduce loss of ground cover (feed base):
  - Increase soil fertility
  - Add lucerne to feedbase
  - Reduce annual legumes
  - Improve pasture varieties

- Genetic improvement of livestock ➔ more efficient feed use

Breeding objectives and indexes for Merino sheep at a local level under predicted climate changes to 2030

GrassGro modelling of enterprise profitability

3 locations x Wool and Dual Purpose enterprises
Changes in profitability ($/DSE)

<table>
<thead>
<tr>
<th>Scenario</th>
<th>Woolbrook</th>
<th>Yass</th>
<th>Narrandera</th>
</tr>
</thead>
<tbody>
<tr>
<td>Current</td>
<td>16</td>
<td>30</td>
<td>21</td>
</tr>
<tr>
<td>2030</td>
<td>14</td>
<td>19</td>
<td>13</td>
</tr>
</tbody>
</table>

- Define location specific breeding objectives → indexes including:
  - Fleece weight (GFW)
  - Fibre diameter (FD)
  - Mature weight (WT)
  - Reproduction (NLW)
- Calculate gains from selection based on these indexes

### Index gains to 2030

<table>
<thead>
<tr>
<th>Trait</th>
<th>Woolbrook</th>
<th>Yass</th>
<th>Narrandera</th>
</tr>
</thead>
<tbody>
<tr>
<td>GFW (%)</td>
<td>1.4</td>
<td>8.0</td>
<td>1.3</td>
</tr>
<tr>
<td>FD (µ)</td>
<td>-1.7</td>
<td>-0.9</td>
<td>-0.5</td>
</tr>
<tr>
<td>WT (%)</td>
<td>-2.2</td>
<td>-2.2</td>
<td>4.1</td>
</tr>
<tr>
<td>NLW (%)</td>
<td>0</td>
<td>0</td>
<td>8</td>
</tr>
<tr>
<td>$ Profit ∆</td>
<td>+7</td>
<td>+4</td>
<td>+6</td>
</tr>
</tbody>
</table>

- GrassGro derived indexes highly correlated with MERINOSELECT standard indexes:
  - Woolbrook → Fibre Production
  - Yass → Merino Production
  - Narrandera → Dual Purpose
- But: larger reductions in mature weight for wool enterprises

### Capacity for adaptation

Genetic improvement → more efficient use of the feed base ($GM/DSE):

<table>
<thead>
<tr>
<th>Scenario</th>
<th>Woolbrook</th>
<th>Yass</th>
<th>Narrandera</th>
</tr>
</thead>
<tbody>
<tr>
<td>Current</td>
<td>16</td>
<td>20</td>
<td>23</td>
</tr>
<tr>
<td>2030</td>
<td>14</td>
<td>19</td>
<td>13</td>
</tr>
<tr>
<td>∆ index A</td>
<td>21</td>
<td>23</td>
<td>20</td>
</tr>
</tbody>
</table>

Adaptation also required to counter loss of feed base ($GM/ha):

<table>
<thead>
<tr>
<th>Scenario</th>
<th>Woolbrook</th>
<th>Yass</th>
<th>Narrandera</th>
</tr>
</thead>
<tbody>
<tr>
<td>Current</td>
<td>204</td>
<td>283</td>
<td>118</td>
</tr>
<tr>
<td>2030</td>
<td>134</td>
<td>186</td>
<td>39</td>
</tr>
<tr>
<td>∆ index A</td>
<td>186</td>
<td>223</td>
<td>49</td>
</tr>
<tr>
<td>Recovery %</td>
<td>74</td>
<td>38</td>
<td>13</td>
</tr>
</tbody>
</table>
Breeding Objectives Under Climate Change

Other livestock adaptations for climate change

- Methane emission reduction and feed efficiency

- Heat tolerance:
  - Resilience for production and reproduction

- Disease resistance:
  - Changes in disease epidemiology with climate change

Conclusions

- Predicted climate changes will lead to reduced productivity of sheep enterprises:
  - Lower pasture production → low rainfall regions worst affected
  - Adaptation necessary to recover lost production

- Genetic improvement is a key adaptation:
  - We looked at breeding objectives at the level of local enterprises
  - Index selection → some recovery of lost enterprise productivity
  - Reconcile reasonably well with current Merino indexes

- Genetic improvement is all about improving future productivity:
  - Livestock industries need to think more about matching breeding objectives to the production environments of the future

Thank you
Perceptions of Genetics - Survey Feedback

Perception of Genetics
Hamish Chandler

Market Research – Ipsos Survey
Survey both ‘Users’ and ‘Non-Users’ of the seedstock and commercial sectors in both the beef and sheep industries.
Specific Objectives:
• Explore & identify decision-making tools used when making genetic selections and how they are used.
• Establish what motivates producers to use genetic tools;
• Establish the barriers to using genetic tools;
• Explore what would encourage/ make Non-Users adopt genetic technologies in their business
• Measure the incidence of cited motivators & barriers

Stage One: Qualitative Exploration
Methodology
• 25 interviews with farmers
  Conducted via telephone and in-person; 90-20min durations
Sample Structure
NSW (6), VIC (4), QLD (5), SA (3), WA (4), NT (2), TAS (1)
A wide range of genetics knowledge and usage
M: Mixed sheep and cattle (6), sheep only (8), cattle only (11)
Use Genetics & Genomics tools and use BREEDPLAN / LAMBPLAN (8)
Use Genetics & Genomics tools don’t use BREEDPLAN / LAMBPLAN (12)
Don’t use Genetics & Genomics Tools, don’t use BREEDPLAN / LAMBPLAN (5)
Reporting
Full qualitative report delivered to MLA in September 2015
Perceptions of Genetics - Survey Feedback

Stage Two: Quantitative Survey

Fieldwork Dates & Method
09/11/2015 – 15/11/2015
Telephone interview

Sample Provider
Sample provided by MLA and Breed Societies

Sample Size
Total number of Producers (n=2,001)

Respondents by state:
- NSW 79%
- QLD 86%
- SA 67%
- TAS 67%
- VIC 82%
- WA 75%

Sample
1,031 Cattle Producers
794 Sheep Producers

Interview duration: 21.6 mins
Margin of error (total sample): 2.19%

Respondent Profile
Cattle and sheep producers responsible for making key breeding decisions across Australia.

Quotas used to ensure breeds were covered in proportion of stock numbers (not farm numbers).

Who was interviewed?

<table>
<thead>
<tr>
<th>Program</th>
<th>Segment</th>
<th>User</th>
<th>Non-User</th>
</tr>
</thead>
<tbody>
<tr>
<td>MERINOSELECT</td>
<td>Seedstock</td>
<td>81</td>
<td>13</td>
</tr>
<tr>
<td></td>
<td>Commercial</td>
<td>38</td>
<td>230</td>
</tr>
<tr>
<td>LAMBPLAN</td>
<td>Seedstock</td>
<td>95</td>
<td>22</td>
</tr>
<tr>
<td></td>
<td>Commercial</td>
<td>74</td>
<td>241</td>
</tr>
<tr>
<td>BREEDPLAN</td>
<td>Seedstock</td>
<td>544</td>
<td>28</td>
</tr>
<tr>
<td></td>
<td>Commercial</td>
<td>215</td>
<td>244</td>
</tr>
</tbody>
</table>

Genetic Progress

Q: All things considered, how satisfied are you with the genetic gains you have achieved in your animals over the last 10 or so years?

| Base: Cattle Stud – BREEDPLAN user (n=544), Cattle Stud – BREEDPLAN non-user (n=28*), Commercial Cattle – BREEDPLAN user (n=215), Commercial Cattle – BREEDPLAN non-user (n=244) |
| Base: Sheep Stud – LAMBPLAN user (n=95), Sheep Stud – LAMBPLAN non-user (n=22*), Commercial Sheep – LAMBPLAN user (n=74), Commercial Sheep – LAMBPLAN non-user (n=241) |
| Base: Sheep Stud – MERINOSELECT user (n=81), Sheep Stud – MERINOSELECT non-user (n=13*), Commercial Sheep – MERINOSELECT user (n=38), Commercial Sheep – MERINOSELECT non-user (n=230) |

Significant Gaps
Perceptions of Genetics - Survey Feedback

Genetic Progress - MERINOSELECT
Q: For what reasons are you less than fully satisfied?

<table>
<thead>
<tr>
<th>Reason</th>
<th>MS Seedstock non-user</th>
<th>MS Commercial User</th>
<th>MS Commercial non-user</th>
</tr>
</thead>
<tbody>
<tr>
<td>Slow rate of change</td>
<td>17%</td>
<td>13%</td>
<td>20%</td>
</tr>
<tr>
<td>Not the outcome I expected / want</td>
<td>17%</td>
<td>22%</td>
<td>9%</td>
</tr>
<tr>
<td>Always room for improvement</td>
<td>9%</td>
<td>15%</td>
<td>15%</td>
</tr>
<tr>
<td>Lack of understanding how to interpret, still a lot to learn</td>
<td>11%</td>
<td>9%</td>
<td>11%</td>
</tr>
<tr>
<td>Not the financial reward I was seeking</td>
<td>21%</td>
<td>6%</td>
<td>5%</td>
</tr>
<tr>
<td>Other</td>
<td>8%</td>
<td>6%</td>
<td>8%</td>
</tr>
<tr>
<td>Unsure</td>
<td>5%</td>
<td>6%</td>
<td>6%</td>
</tr>
</tbody>
</table>

Note: Sheep Stud – MS user not shown due to small base (n=5)

Genetic Progress - LAMBPLAN
Q: For what reasons are you less than fully satisfied?

<table>
<thead>
<tr>
<th>Reason</th>
<th>LP Seedstock User</th>
<th>LP Seedstock non-user</th>
<th>LP Commercial User</th>
<th>LP Commercial non-user</th>
</tr>
</thead>
<tbody>
<tr>
<td>Always room for improvement</td>
<td>11%</td>
<td>11%</td>
<td>11%</td>
<td>11%</td>
</tr>
<tr>
<td>Goal posts / financial reward</td>
<td>8%</td>
<td>8%</td>
<td>8%</td>
<td>8%</td>
</tr>
<tr>
<td>Issues with breeding stock</td>
<td>7%</td>
<td>7%</td>
<td>7%</td>
<td>7%</td>
</tr>
<tr>
<td>Lack of understanding how to interpret</td>
<td>7%</td>
<td>7%</td>
<td>7%</td>
<td>7%</td>
</tr>
<tr>
<td>Issues with technical data</td>
<td>7%</td>
<td>7%</td>
<td>7%</td>
<td>7%</td>
</tr>
<tr>
<td>Slow rate of change</td>
<td>7%</td>
<td>7%</td>
<td>7%</td>
<td>7%</td>
</tr>
<tr>
<td>High financial cost</td>
<td>5%</td>
<td>5%</td>
<td>5%</td>
<td>5%</td>
</tr>
<tr>
<td>Climate / environment / seasons</td>
<td>3%</td>
<td>3%</td>
<td>3%</td>
<td>3%</td>
</tr>
<tr>
<td>Not the outcome I was seeking</td>
<td>3%</td>
<td>3%</td>
<td>3%</td>
<td>3%</td>
</tr>
<tr>
<td>Breeding and management not satisfactory</td>
<td>3%</td>
<td>3%</td>
<td>3%</td>
<td>3%</td>
</tr>
<tr>
<td>Other</td>
<td>7%</td>
<td>7%</td>
<td>7%</td>
<td>7%</td>
</tr>
<tr>
<td>Unsure</td>
<td>3%</td>
<td>3%</td>
<td>3%</td>
<td>3%</td>
</tr>
</tbody>
</table>

Genetic Progress Summary

- Users of Genetic Programs more likely to have a clear Breeding Objective
- Users of Genetic Programs use a wider range of metrics, less reliant on basic assessments
- For most categories satisfaction with genetic gain not related to LP/MS use (excluding MS seedstock) – will impact on how to promote
Perceptions of Genetics - Survey Feedback

02/03/2017

Sheep Genetic - Leading Breeder 2017

Reputation Pyramid – LP & MS

Both Commercial & Stud Users have high levels of trust in LP & MS; Commercial Users are less familiar with the system & so their ‘Blind Trust’ will be more vulnerable to misinformation from other sources.

<table>
<thead>
<tr>
<th>Sheep Stud (LP user)</th>
<th>Commercial Sheep (LP user)</th>
<th>Sheep Stud (MS user)</th>
<th>Commercial Sheep (MS user)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Advocacy</td>
<td>64%</td>
<td>65%</td>
<td>79%</td>
</tr>
<tr>
<td>Trust</td>
<td>81%</td>
<td>80%</td>
<td>90%</td>
</tr>
<tr>
<td>Familiarity</td>
<td>83%</td>
<td>81%</td>
<td>81%</td>
</tr>
<tr>
<td>Use</td>
<td>83%</td>
<td>51%</td>
<td>98%</td>
</tr>
</tbody>
</table>

Perceptions of LAMBPLAN

Never getting around to it is a key reason for LP non-use among both types of operations – indicates the benefit proposition is not known.

For What Reasons Does Your Sheep Stud Operation Not Use LP? (n=22)
- Cost is too much money 15%
- Never got around to it 23%

For What Reasons Does Your Commercial Sheep Operation Not Use LP? (n=241)
- Never got around to it 26%

For What Reasons Does Your Sheep Stud Operation Not Use MS? (n=13)
- Never got around to it 23%

For What Reasons Does Your Commercial Sheep Operation Not Use MS? (n=230)
- Never got around to it 28%

Perceptions of MERINOSELECT

Never getting around to using MS is a main reason for non-use, indicating that the proposition is not compelling enough.

For What Reasons Does Your Sheep Stud Operation Not Use MS? (n=15)
- Never got around to it 22%

For What Reasons Does Your Commercial Sheep Operation Not Use MS? (n=230)
- Never got around to it 28%
**Perceptions of LAMBPLAN & MERINOSELECT**

**Key Learnings: Trust & Perceptions of the Plans**

- Users trust LP & MS, but Commercial Users’ Trust is ‘Blind’. Non-Users seldom know enough to even start trusting.
- Users and Non-Users say similar things, just to different degrees: “A genetics database to aid decision-making.”
- Biggest complaints concern process hard to understand, issue with data capture and data accuracy / quality.
- Main reasons for Non-Use concern belief that many are too reliant on figures and financial costs. Most Non-Users could not cite any reason, so barriers to adoption may be low.

**Training & skills development – LAMBPLAN**

The most popular way for sheep meat Producers to gain genetics advice is through informal methods such as colleagues, agents & breeders.

<table>
<thead>
<tr>
<th>Sources Of Genetics Advice</th>
<th>Sheep Stud - LP user</th>
<th>Sheep Stud - LP non-user*</th>
<th>Cons. Sheep - LP user</th>
<th>Cons. Sheep - LP non-user*</th>
</tr>
</thead>
<tbody>
<tr>
<td>Informally through a colleague / other farmers</td>
<td>35%</td>
<td>42%</td>
<td>16%</td>
<td>20%</td>
</tr>
<tr>
<td>Livestock agent</td>
<td>3%</td>
<td>3%</td>
<td>4%</td>
<td>5%</td>
</tr>
<tr>
<td>Stud breeder / manager / owner</td>
<td>3%</td>
<td>3%</td>
<td>2%</td>
<td>2%</td>
</tr>
<tr>
<td>Own research / experience</td>
<td>3%</td>
<td>3%</td>
<td>2%</td>
<td>2%</td>
</tr>
<tr>
<td>Sheep genetics / LAMBPLAN people</td>
<td>3%</td>
<td>3%</td>
<td>2%</td>
<td>2%</td>
</tr>
<tr>
<td>Consultant</td>
<td>1%</td>
<td>1%</td>
<td>1%</td>
<td>1%</td>
</tr>
<tr>
<td>Other</td>
<td>3%</td>
<td>3%</td>
<td>2%</td>
<td>2%</td>
</tr>
<tr>
<td>Can’t get any advice</td>
<td>12%</td>
<td>15%</td>
<td>12%</td>
<td>15%</td>
</tr>
</tbody>
</table>

*Note: All data are weighted per producer / user.

**Training & skills development – MERINOSELECT**

The most popular ways for merino Producers to get genetics advice are through classers, breeders, agents & other informal methods.

<table>
<thead>
<tr>
<th>Sources Of Genetics Advice</th>
<th>Sheep Stud - MS user</th>
<th>Sheep Stud - MS non-user*</th>
<th>Cons. Sheep - MS user</th>
<th>Cons. Sheep - MS non-user*</th>
</tr>
</thead>
<tbody>
<tr>
<td>Classer</td>
<td>9%</td>
<td>6%</td>
<td>4%</td>
<td>4%</td>
</tr>
<tr>
<td>Informally through a colleague / other farmers</td>
<td>35%</td>
<td>30%</td>
<td>15%</td>
<td>15%</td>
</tr>
<tr>
<td>Stud breeder / manager / owner</td>
<td>3%</td>
<td>3%</td>
<td>2%</td>
<td>2%</td>
</tr>
<tr>
<td>Livestock agent</td>
<td>3%</td>
<td>3%</td>
<td>2%</td>
<td>2%</td>
</tr>
<tr>
<td>Own research / experience</td>
<td>3%</td>
<td>3%</td>
<td>2%</td>
<td>2%</td>
</tr>
<tr>
<td>Consultant</td>
<td>1%</td>
<td>1%</td>
<td>1%</td>
<td>1%</td>
</tr>
<tr>
<td>Breeder society</td>
<td>1%</td>
<td>1%</td>
<td>1%</td>
<td>1%</td>
</tr>
<tr>
<td>Sheep genetics / MERINOSELECT people</td>
<td>3%</td>
<td>3%</td>
<td>2%</td>
<td>2%</td>
</tr>
<tr>
<td>Other</td>
<td>3%</td>
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<tr>
<td>Can’t get any advice</td>
<td>12%</td>
<td>15%</td>
<td>12%</td>
<td>15%</td>
</tr>
</tbody>
</table>

*Note: All data are weighted per producer / user.
Training & skills development

Key Findings:

- The most popular way for sheep meat Producers to gain genetics advice is through informal methods such as colleagues, classers, agents & breeders.
- Sheep Genetics staff are the most common trainers, but there is a large number using alternative informal sources.
- Sheep Genetics are expected to provide training for Studs, while Commercial farmers expect to go to MLA.
- Those who have not had LP/MS training say it’s because they never got around to it or don’t have enough time – such reasons generally reflect general disinterest / motivation.

Achieving Desired Behaviour Change

Key messages / content have to address motivation:

- **Remove the mystery:** Explain how metrics are calculated – the more the better.
- **Ensure the system is easy and routine** to use.
- **Ensure that the genetic and financial payback** is easy to model and track.
- **Highlight the peace of mind** that comes from reducing the incidence of unwanted traits as much as achieving the desired ones.
- **Highlight the enhanced ability of these systems to enable Producers to make profits and progress towards business goals.**

Conclusions

Producers do ‘get’ the value of genetics-based breeding & purchasing

- This research has confirmed that Australian cattle and sheep Producers mostly:
  - DO value and track their genetic gains;
  - DO make breeding and purchase decisions based in large part on the desire to control the genetic quality of their stock;
  - DO generally have more positive than negative impressions of BreedPlan / LambPlan / MerinoSelect;
  - DO know where to go to get more information or training;
  - Are equally satisfied with their progress regardless of whether they use a Plan or not.
Conclusions
Despite Producers’ current usage of genetics-based buying / breeding, the Plans offer too little for the effort required

• The key problems for Producers using / considering BreedPlan / LambPlan / MerinoSelect are that:
  – The full range of traits that they value and record need to be included in BREEDPLAN / LAMBPLAN / MERINOSELECT.
  – The time, complexities and effort involved in data capture raise questions about data accuracies.
  – Trait management is seen more as a means to avoid unwanted traits than to breed specifically for others (i.e. is an insurance against negative outcomes instead of an investment into positive outcomes).

Recommendations
Changing the TOOLS
• Making data entry easier and more accurate (e.g. changing interface or processes, creating an input app).
• Enabling Users to record other user-defined / customised traits, even if they are not included in EBV / ASBV calculation (to enable a single data-collection point).
• Increasing the amount of financial modelling available.
• Add a ‘mythbusting’ section to acknowledge and address the concerns and misconceptions.

Changing the MESSAGES
• The industry standard, expected and used by more Producers.
• A proven way to help reach business goals and improve profits.
• Easy-to-see financial and genetic payback.
• Improved, easier and more efficient.
• Helps speed-up genetic gains.
• Increases the positive effects of improvements made throughout the farm systems.
• Gives peace of mind – reduces likelihood of unwanted traits.
• Understandable, transparent EBV / ASBV calculations.

Changing the INDUSTRY
• Make the improved Plans and tools measures ubiquitous – work to make them the norm in all sales, breed societies and related channels.
2017 & Beyond – Don’t waste your time!

Nathan Scott – Achieve Ag Solutions

The Australian Sheep industry is rich with knowledge, and technical information, but too often lacking in actual application. My challenge to you is to take up your role as an industry leader. Real leaders don’t need titles, they are those who have vision and demonstrate leadership through their actions.

As a “leading breeder” you are already part of the solution. Leading the industry into the future. With everything you have heard and learnt over the past 2 days, the opportunity now exists to go home and do something with that newly acquired knowledge. After all, knowledge is just taking up space in your head, unless it is actually applied in some way.

A big part of achieving success, applying your new found knowledge, and making change within your business is actually understanding yourself, and why you do the things you do. This session is designed to help you do exactly that. The following tasks will make considerably more sense once you have sat through my presentation, but each will play a role in helping you ACHIEVE. Use them to better understand yourself, better apply your knowledge, and lead through your own actions.

Don’t ask others to change,
Don’t beg others to change,
Don’t demand that others change.

*Inspire* them to change
Your things to do

Write down your current list of things you would like to get done in the next month –

• __________________________________________________________________________
  • __________________________________________________________________________
  • __________________________________________________________________________
  • __________________________________________________________________________
  • __________________________________________________________________________
  • __________________________________________________________________________
  • __________________________________________________________________________
  • __________________________________________________________________________

Now put them into the calendar and plan your month ahead

<table>
<thead>
<tr>
<th>SUN</th>
<th>MON</th>
<th>TUE</th>
<th>WED</th>
<th>THU</th>
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<td>29</td>
<td>30</td>
<td>31</td>
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</tr>
</tbody>
</table>
List your life goals –

Remember these are your goals only. Don’t show others. Don’t restrict yourself in what they are. Don’t think about the “how”, only simply what it is.

-__________________________________________________________________________
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-__________________________________________________________________________
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-__________________________________________________________________________
-__________________________________________________________________________

Stand Up!

Life is full of Challenges,
You can’t leave it all for someone else to do,
  Forget tradition, it’s time for change,
Life is too short, to wait for the slowest,
So stand up, and show some leadership,
  Stand up, and take some ownership,
  Stand up, this industry’s ours,
It’s not theirs, so come on and join me,
  Stand up, show some leadership,
  Stand up, this problem is ours.