Eating Quality Indexes - Welcome

- Webex should prompt you to setup audio

- Please **MUTE** your phone

- Having problems? Email drubie@mla.com.au

- Please ask Questions and Feedback through the chat

- Feedback can also be made in the survey after the webinar
  - Link will be emailed out with recording of the webinar ASAP
Eating quality indexes for terminal sires
Breeding directions for meat sheep

- Long term gains in growth rate and lean meat yield

Carcass+ = simple breeding objective, accurately assessed

- To remain competitive the industry also needs to address meat quality:
  - Selection for growth and lean $\rightarrow$ decreased eating quality
Ingredients of an eating quality index

Animal performance

Carcass measurements

Consumer eating quality

Genomic testing

Index = Trait economic values \times \text{ASBV}
DEVELOPING THE INDEX
How to value eating quality

Sheep CRC Consumer eating quality data

• Tenderness
• Juiciness
• Flavour
• Overall liking

Scores on a 0 – 100 scale in CRC slaughter animals

MSA retail grading system

• Higher eating quality score → higher MSA retail grade

Willingness to pay surveys
Large between animal variation in eating quality

<table>
<thead>
<tr>
<th></th>
<th>Ungraded</th>
<th>3 star</th>
<th>4 star</th>
<th>5 star</th>
</tr>
</thead>
</table>

... and therefore in MSA grade
If we could improve eating quality score...

... we would increase the proportion of meat in higher MSA grades → increase in value
The economic value of improved eating quality

An increase by 1 score translates to:

- An increase in carcass price of 15 c/kg*
- Economic value of $3.21 per ewe

(* If there was supply chain feedback)
### Economic weights based on carcass traits

<table>
<thead>
<tr>
<th>Trait</th>
<th>Economic value ($/ewe)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Sale weight (kg)</td>
<td>pwt</td>
</tr>
<tr>
<td>Lean meat yield (%)</td>
<td>lmy</td>
</tr>
<tr>
<td>Dressing %</td>
<td>dress</td>
</tr>
<tr>
<td>Carcass eye muscle (mm)</td>
<td>cemd</td>
</tr>
<tr>
<td>Carcass fat (mm)</td>
<td>ccfat</td>
</tr>
<tr>
<td>Eating quality (0 – 100 score)</td>
<td>tmsa</td>
</tr>
</tbody>
</table>

**Index variations:**

- **LMY** = carcass index *without* eating quality ($index equivalent to CPLUS)
- **LMYEQ** = carcass index *with* eating quality (as above)
- **LMYEQIMF** = extra emphasis on intra-muscular fat
The problem: unfavourable genetic correlations

<table>
<thead>
<tr>
<th></th>
<th>lmy</th>
<th>tmsa</th>
<th>imf</th>
<th>sf5</th>
</tr>
</thead>
<tbody>
<tr>
<td>Lean meat yield</td>
<td>lmy</td>
<td>1.00</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Eating quality</td>
<td>tmsa</td>
<td>-0.19</td>
<td>1.00</td>
<td></td>
</tr>
<tr>
<td>Intra-muscular fat</td>
<td>imf</td>
<td>-0.51</td>
<td>0.38</td>
<td>1.00</td>
</tr>
<tr>
<td>Shear force</td>
<td>sf5</td>
<td>0.42</td>
<td>-0.68</td>
<td>-0.55</td>
</tr>
</tbody>
</table>

Higher yield = poorer E.Q.

Higher yield from lower imf and higher sf5

but ... better E.Q from higher imf and lower sf5
Varying the balance between LMY and E.Q.
## Correlations between breeding objectives

<table>
<thead>
<tr>
<th></th>
<th>CPLUS</th>
<th>LMY</th>
<th>LMYEQ</th>
<th>LMYEQIMF</th>
</tr>
</thead>
<tbody>
<tr>
<td>CPLUS</td>
<td>1.00</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>LMY</td>
<td>0.88</td>
<td>1.00</td>
<td></td>
<td></td>
</tr>
<tr>
<td>LMYEQ</td>
<td>0.44</td>
<td>0.57</td>
<td>1.00</td>
<td></td>
</tr>
<tr>
<td>LMYEQIMF</td>
<td>0.30</td>
<td>0.36</td>
<td>0.92</td>
<td>1.00</td>
</tr>
</tbody>
</table>
Carcass and E.Q. ASBVs are needed for the index

- RBVs have been available since 2011:
  - Lean meat yield and dressing%
  - Carcass eye muscle and fat
  - Intra-muscular fat and shear force
- Single trait analyses
- Including genomic information via “single step”
- Limited in scope:
  - Resource population animals with measurements and genotypes
  - Animals genotyped by breeders in pilot projects etc
  - Some animals via pedigree

In 2016 we make the transition from RBV to ASBV
The new analysis for carcass and E.Q. ASBVs

- Full multi-trait single step genomic analysis:
  - Body weight and scan traits
  - Carcass and eating quality traits

- Data from all LAMBPLAN animals from 2000 year of birth

- All animals will have breeding values for all traits → reporting still subject to accuracy thresholds

- ASBVs from this analysis used to build eating quality index

- Post-weaning weight
- Lean meat yield
- Carcass eye muscle
- Carcass fat
- Intra-muscular fat
- Shear force

Year of birth:
- 2008
- 2010
- 2012
- 2014

Post-weaning weight (pwt) (kg):
- 2008: 8
- 2010: 9
- 2012: 10
- 2014: 11

Lean meat yield (lmy) (%):
- 2008: -0.29
- 2010: -0.28
- 2012: -0.27
- 2014: -0.26

Carcass eye muscle (cemd) (mm):
- 2008: 0.50
- 2010: 0.75
- 2012: 1.00
- 2014: 1.25

Carcass fat (ccfat) (mm):
- 2008: -0.25
- 2010: -0.26
- 2012: -0.27
- 2014: -0.28

Intra-muscular fat (imf) (%):
- 2008: -0.17
- 2010: -0.16
- 2012: -0.15
- 2014: -0.14

Shear force (sf5) (Newtons):
- 2008: 1.3
- 2010: 1.5
- 2012: 1.7
- 2014: 1.9
How to get ASBVs for carcass and E.Q.

- Need linkages to the genomic resource population
- Use sires who have been genotyped and progeny tested
- Enter sires for progeny testing
- Genotype your ram selection candidates
WHAT DOES THE INDEX LOOK LIKE?
Predicted trait gains over 10 years

<table>
<thead>
<tr>
<th>Trait</th>
<th>LMYEQIMF</th>
<th>CPLUS</th>
</tr>
</thead>
<tbody>
<tr>
<td>pwt</td>
<td>3.14</td>
<td>4.65  (kg)</td>
</tr>
<tr>
<td>lmy</td>
<td>0.87</td>
<td>1.91  (%)</td>
</tr>
<tr>
<td>dress</td>
<td>1.21</td>
<td>1.49  (%)</td>
</tr>
<tr>
<td>cemd</td>
<td>1.17</td>
<td>1.75  (mm)</td>
</tr>
<tr>
<td>ccfat</td>
<td>-0.40</td>
<td>-0.59 (mm)</td>
</tr>
<tr>
<td>tmsa</td>
<td>1.40</td>
<td>-1.40 (score)</td>
</tr>
<tr>
<td>imf</td>
<td>0.08</td>
<td>-0.35 (%)</td>
</tr>
</tbody>
</table>

Economic gain (%)
Sires of 2015 drop (n=1252, r=0.56)

Trait means of top 10% on each index

<table>
<thead>
<tr>
<th></th>
<th>LMYEQIMF</th>
<th>CPLUS</th>
<th>Mean</th>
</tr>
</thead>
<tbody>
<tr>
<td>pwt</td>
<td>1.39</td>
<td>3.14</td>
<td>13.29</td>
</tr>
<tr>
<td>pemd</td>
<td>0.86</td>
<td>1.03</td>
<td>1.94</td>
</tr>
<tr>
<td>pfat</td>
<td>0.26</td>
<td>0.20</td>
<td>-0.32</td>
</tr>
<tr>
<td>lmy</td>
<td>0.06</td>
<td>0.97</td>
<td>2.24</td>
</tr>
<tr>
<td>cemd</td>
<td>0.95</td>
<td>1.00</td>
<td>1.71</td>
</tr>
<tr>
<td>ccfat</td>
<td>0.08</td>
<td>-0.08</td>
<td>-0.28</td>
</tr>
<tr>
<td>imf</td>
<td>0.28</td>
<td>-0.13</td>
<td>-0.18</td>
</tr>
<tr>
<td>sf5</td>
<td>-2.16</td>
<td>1.87</td>
<td>2.56</td>
</tr>
</tbody>
</table>
Index comparisons: example 2

Trait means of top 10% on each index

<table>
<thead>
<tr>
<th>Trait</th>
<th>LMYEQIMF</th>
<th>CPLUS</th>
<th>tmsa</th>
</tr>
</thead>
<tbody>
<tr>
<td>pwt</td>
<td>-0.09</td>
<td>1.97</td>
<td>-0.29</td>
</tr>
<tr>
<td>pemd</td>
<td>0.34</td>
<td>1.09</td>
<td>-0.09</td>
</tr>
<tr>
<td>pfat</td>
<td>-0.05</td>
<td>0.08</td>
<td>-0.06</td>
</tr>
<tr>
<td>lmy</td>
<td>0.29</td>
<td>0.60</td>
<td>-0.02</td>
</tr>
<tr>
<td>cmd</td>
<td>0.86</td>
<td>1.11</td>
<td>-0.11</td>
</tr>
<tr>
<td>ccfull</td>
<td>-0.26</td>
<td>-0.07</td>
<td>-0.11</td>
</tr>
<tr>
<td>imf</td>
<td>0.49</td>
<td>-0.26</td>
<td>0.23</td>
</tr>
<tr>
<td>sf5</td>
<td>-3.20</td>
<td>1.57</td>
<td>-1.40</td>
</tr>
<tr>
<td>tmsa</td>
<td>1.04</td>
<td>-0.01</td>
<td>4.71</td>
</tr>
</tbody>
</table>

If we could select directly on eating quality
• Focussing on increased yield leads to a decline in eating quality
• The resource established by the Sheep CRC, its partners and MLA has given us the tools to improve eating quality
• Antagonistic relationships between traits means large gains in both yield and eating quality are unrealistic
• Joint improvement is possible, optimised through use of the index
• To get the most out of the index breeders need to be linked to the reference flock via genotyping and progeny testing