Genomics in beef breeding in Australia - 2014

Rob Banks
AGBU
Questions:

• What are the breeding units?
• What have people done to create reference populations, or what do they use as ref pop’ns?
• Are there any plan or visions on what to do next?
• Are there breeding groups (or AI companies) that have implemented new strategies, e.g. scanning lots of young bulls, or doing more JIVET or MOET?
Beef production & breeding in Australia I

Studs

Commercial producers

Feedlots & Processors

Domestic (via retailers) & export
## Beef production & breeding in Australia II

<table>
<thead>
<tr>
<th>Sector</th>
<th># Cows</th>
<th># Businesses</th>
<th>Typical turnover per business</th>
<th>Comment</th>
</tr>
</thead>
<tbody>
<tr>
<td>Stud (nucleus)</td>
<td>0.25m</td>
<td>1,500</td>
<td>&lt;&lt; $0.25m</td>
<td>8 main breeds&lt;br&gt;Average herd ~ 165 cows&lt;br&gt;Recording $25 per cow (up to $00’s)</td>
</tr>
<tr>
<td>Commercial</td>
<td>10m</td>
<td>50,000</td>
<td>&lt; $0.25m</td>
<td>60,000 bulls intake pa</td>
</tr>
<tr>
<td>Processing/Feedlots</td>
<td></td>
<td>5-10 processors 5-10 feedlots</td>
<td>Several million</td>
<td>Very small margins</td>
</tr>
<tr>
<td>Retail</td>
<td></td>
<td>2 main domestic with 80% market share; 67% exported</td>
<td></td>
<td>Limited brand differentiation to date</td>
</tr>
</tbody>
</table>
Genetic evaluation

• All major breeds use BREEDPLAN
• Across-herd multi-trait evaluation
• Importation significant in Angus, less so in other main breeds
• Genetic trend average $2.5-3 per cow joined per year (c. 3% of profit pa)
• gaps
Current recording effectiveness:

Recording effectiveness

0%
20%
40%
60%
80%
100%

Weight
Carcase
Fertility
Eating Quality
Efficiency
Fitness, Longevity

Trait Group
Current recording effectiveness:

Relative Importance and Accuracy

Marble score  Cow survival  SMY %  Dressing %  Cow weaning rate  Sale weight direct  Trait  CE maternal  CE direct  sale weight maternal  cow weight  Rump fat

IMPORTANCE

ACCURACY

0% 10% 20% 30% 40% 50% 60% 70% 80% 90% 100%
Value-adding in a beef breed:

Data and Selection Value-add

Selection value-add v data value-add
Genomics to date - I

• CRC 1 and 2 (pre-2005):
  – Focussed more on QTL or small number of markers
  – Lead to GeneStar products
    • Tenderness based on Calpain/Calpastatin
    • Other traits based on very small number of markers
    • Very limited market uptake
Genomics to date - II

- CRC 3 (2005-2012):
  - Aim to explain X% of variation for key traits
  - Applied GWAS to a number of projects based broadly around progeny tests
  - Multiple breeds
  - Developed strategy for implementation based around prediction equations
  - Moved to snp-based analysis in final stages – developed prediction equations (see later)
Genomics to date - II

• 2010 onwards:
  – In parallel, MLA and breeds developed Information Nucleus projects
  – Progeny test including hard-to-measure traits:
    • Individual feed intake
    • Some eating quality traits
    • Better measures of female fertility
  – Sires (and in some, progeny) genotyping
## Information Nucleus projects

<table>
<thead>
<tr>
<th>Trait group</th>
<th>Progeny per cohort</th>
<th>Sires per cohort</th>
<th>Growth, carcase and EQ Traits</th>
<th>Female Traits</th>
</tr>
</thead>
<tbody>
<tr>
<td>Angus</td>
<td>1,000</td>
<td>&gt;40</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Hereford</td>
<td>400</td>
<td>15</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Brahman</td>
<td>600</td>
<td>15</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Charolais</td>
<td>360</td>
<td>12-15</td>
<td>No</td>
<td></td>
</tr>
<tr>
<td>Limousin</td>
<td>360</td>
<td>12-15</td>
<td>No</td>
<td></td>
</tr>
</tbody>
</table>
Other related R&D projects

• Te Mania
  – Collecting data on commercial progeny of known high merit Angus sires (approximately 1,300 progeny) through feedlot and MSA traits, plus sire genotypes

• Wagyu
  – Collecting data on commercial cattle in feedlot plus genotypes
  – Aiming for 2,000 animals in 1st phase

• Northern Fertility
  – Collecting new fertility traits plus genotyping sires and grandsires (2-3,000 animals over 5 years)

All data into respective BREEDPLAN analyses, plus GBLUP and single step when available
As \( f(p) = \frac{k}{2p(1-p)} \) we have
\[
\int \frac{[2p(1-p)]^2}{2p(1-p) + \lambda_\beta / n_R} \cdot \frac{k}{2p(1-p)} \, dp = k \int \frac{2p(1-p)}{2p(1-p) + \lambda_\beta / n_R} \, dp
\]
\[
\int \frac{2p(1-p)}{2p(1-p) + \lambda_\beta / n_R} \, dp = \int \frac{2p(1-p) + \lambda_\beta / n_R - \lambda_\beta / n_R}{2p(1-p) + \lambda_\beta / n_R} \, dp = 1 - \frac{\lambda_\beta}{n_R} \int \frac{1}{2p(1-p) + \lambda_\beta / n_R} \, dp
\]
\[
2p(1-p) + \frac{\lambda_\beta}{n_R} = -\{2p^2 - 2p - \lambda_\beta / n_R\} = -\left\{2 \left( p - \frac{1}{4} \right) \left( 2 + \sqrt{4 + \frac{8 \lambda_\beta}{n_R}} \right) \right\} \left\{ p - \frac{1}{4} \left( 2 - \sqrt{4 + \frac{8 \lambda_\beta}{n_R}} \right) \right\}
\]
Let \( a = 1 + 2 \frac{\lambda_\beta}{n_R} \) then 
\[
2p(1-p) + \frac{\lambda_\beta}{n_R} = -\left\{2 \left( p - \frac{1+\sqrt{a}}{2} \right) \left( p - \frac{1-\sqrt{a}}{2} \right) \right\} \text{ thus } \frac{1}{2p(1-p) + \frac{\lambda_\beta}{n_R}} = \frac{1}{2\sqrt{a}} \left[ \frac{1}{p - \frac{1+\sqrt{a}}{2}} - \frac{1}{p - \frac{1-\sqrt{a}}{2}} \right]
\]
\[
\int \frac{dp}{p - \frac{1+\sqrt{a}}{2}} = \left[ \log \left( p - \frac{1+\sqrt{a}}{2} \right) \right]_0^1 = \log \left( -\frac{1-\sqrt{a}}{1+\sqrt{a}} \right) \text{ and } \int \frac{dp}{p - \frac{1-\sqrt{a}}{2}} = \left[ \log \left( p - \frac{1-\sqrt{a}}{2} \right) \right]_0^1 = \log \left( -\frac{1+\sqrt{a}}{1-\sqrt{a}} \right)
\]
\[
\int \frac{1}{2p(1-p) + \frac{\lambda_\beta}{n_R}} \, dp = \frac{1}{2\sqrt{a}} \log \left( \frac{-\frac{1-\sqrt{a}}{1+\sqrt{a}}}{-\frac{1+\sqrt{a}}{1-\sqrt{a}}} \right) = \frac{1}{2\sqrt{a}} \log \left( \frac{1-2\sqrt{a} + a}{1+2\sqrt{a} + a} \right)
\]
Finally 
\[
\frac{1}{n_Q} \sum_{q=1}^{n_Q} \frac{n_R \sigma_{xs(q)}^4}{n_R \sigma_{xs(q)}^2 + \lambda_\beta} \sim k \left[ 1 - \frac{\lambda_\beta}{n_R} \int \frac{1}{2p(1-p) + \frac{\lambda_\beta}{n_R}} \, dp \right] = k \left[ 1 - \frac{\lambda_\beta}{n_R} \frac{1}{2\sqrt{a}} \log \left( \frac{1-2\sqrt{a} + a}{1+2\sqrt{a} + a} \right) \right]
\]
Outcomes and questions I:

- Horn/poll test – UQ testing

<table>
<thead>
<tr>
<th></th>
<th>2010</th>
<th>2011</th>
<th>2012</th>
<th>2013</th>
<th>2014</th>
<th>Total</th>
</tr>
</thead>
<tbody>
<tr>
<td>BRAHMAN</td>
<td>135</td>
<td>248</td>
<td>705</td>
<td>701</td>
<td>10</td>
<td>1,799</td>
</tr>
<tr>
<td>SANTA</td>
<td>161</td>
<td>177</td>
<td>427</td>
<td>294</td>
<td></td>
<td>1,059</td>
</tr>
<tr>
<td>DROUGHTMASTER</td>
<td>2</td>
<td>70</td>
<td>174</td>
<td>273</td>
<td></td>
<td>519</td>
</tr>
<tr>
<td>LIMOUSIN</td>
<td>192</td>
<td>219</td>
<td>209</td>
<td>218</td>
<td>27</td>
<td>865</td>
</tr>
<tr>
<td>HEREFORD</td>
<td>35</td>
<td>108</td>
<td>336</td>
<td>361</td>
<td>11</td>
<td>851</td>
</tr>
<tr>
<td>CHAROLAIS</td>
<td>2</td>
<td>3</td>
<td>124</td>
<td>143</td>
<td>14</td>
<td>286</td>
</tr>
<tr>
<td>SIMMENTAL</td>
<td>25</td>
<td>22</td>
<td>16</td>
<td></td>
<td>4</td>
<td>67</td>
</tr>
<tr>
<td>XB</td>
<td>13</td>
<td>17</td>
<td>200</td>
<td>136</td>
<td></td>
<td>366</td>
</tr>
<tr>
<td>OTHER</td>
<td>166</td>
<td>656</td>
<td>679</td>
<td>293</td>
<td></td>
<td>1,794</td>
</tr>
<tr>
<td>TOTAL</td>
<td>706</td>
<td>1,523</td>
<td>2,876</td>
<td>2,435</td>
<td>66</td>
<td>7,606</td>
</tr>
</tbody>
</table>
Outcomes and questions 1:

- Genetic defects testing (Teseling and Parnell, AAABG, 2013)
- Link with analytical tools (in this case, GeneProb)

Figure 1. Frequency of carrier calves relative to birth years and the reductions in carrier frequency when DNA tests were made commercially available.
Outcomes and questions II:

• Calibration of CRC Prediction Equations:
  – Equations developed using CRC data and phenotypes (Bolormaa et al J Anim Sci 2013 91)
  – Calibrated against BREEDPLAN trait data, for inclusion of DGV into BREEDPLAN, where appropriate data exist
  – Calibration = correlation between prediction and observed adjusted phenotypes (Boerner and Johnston, AAABG 2013)
Outcomes and questions III:

• Calibration results:
  – c. 10 traits in Angus with accuracy > 0.2
  – Accuracy range of useful results 0.2-0.4
  – Some fertility traits in Brahman with accuracy > 0.2
  – Limited traits in other breeds

• Implementation:
  – 50k genotype, imputed up to 800k, apply prediction equation to produce DGV
  – Blend DGV with BREEDPLAN EBV
Outcomes and questions IV:

• How will genomics work for small breeds?
  – If < 1500 recorded animals per year, what is the benefit of genotyping – better control of inbreeding?
• How will it work for larger breeds?
  – How to handle different inputs – pedigree + phenotype, P + P + G, \textit{genotype alone}
  – Phenotypes from outside stud sector? Genotypes to non-stud customers?
  – Pay for phenotypes, sell EBVs?
  – How to preserve public information
• What about international links?
  – Needs reference data in each country
• Investment model in Australia – RDC role, studs, breed associations?

\textbf{Role of beef breed associations must evolve radically}
Questions:

• What are the breeding units?
  – Breeds? No (and never have been).
  – Motivated breeders? (Yes)
  – Alliances of motivated breeders plus data partners? (The future).

• What have people done to create reference populations, or what do they use as ref pop’ns?
  – BREEDPLAN data for calibration of prediction equations
  – Building BIN data to provide reference data for HTM traits. Industry data for other traits.

• Are there any plan or visions on what to do next?
  – Blending DGVs now available
  – Develop and implement single step for large-scale implementation (ie multiple herd or even breed)
  – Discussions starting around valuing data
  – R&D underway into tools to optimise recording and genotyping

• Are there breeding groups (or AI companies) that have implemented new strategies, e.g scanning lots of young bulls, or doing more JIVET or MOET?
  – Leading breeders already doing MOET ... JIVET, full scanning, capturing data from down the value chain, applying mate selection, some genotyping (likely already influencing ET programs)
I'm not very good with Excel, but I'm great at spreading sheets.

What beds are getting made?

<table>
<thead>
<tr>
<th></th>
<th>Made</th>
<th>Unmade</th>
</tr>
</thead>
<tbody>
<tr>
<td>Parent's Bed</td>
<td>48%</td>
<td>52%</td>
</tr>
<tr>
<td>Adults - no kids at home</td>
<td>55%</td>
<td>45%</td>
</tr>
<tr>
<td>Kid's Beds</td>
<td>24%</td>
<td>76%</td>
</tr>
</tbody>
</table>

Parent's Bed: 56% Unmade, 44% Made
Adults - no kids at home: 35% Unmade, 65% Made
Kid's Beds: 76% Unmade, 24% Made