Beef cattle genetic evaluation in Australia ~ BREEDPLAN

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AGBU
Aims:

• Increase rate of progress in bull-breeding herds
• Bull-buyers have information (EBVs and $Indexes)
• Bull-buyers and users have knowledge and tools to harvest value from genetics
Australian beef industry:

• c. 10m commercial cows, c. 0.25m stud cows
• c. 50,000 commercial producers, c. 1,500 studs
• Very little AI in commercial herds
• Focus of genetic evaluation is on:
  – Selection of replacement sires (bulls to breed bulls) and heifers
  – Objective information on herd bulls, typically sold at 15-18 mths
• 2 broad production regions:
  – Southern Australia (cooler, higher rainfall, beef usually not main enterprise)
  – Northern Australia (hotter, dryer, beef usually only enterprise)
• 3 broad types or sectors:
  – Southern dual-purpose (British breeds eg Angus, Hereford)
  – Terminal sire (Charolais, Limousin, Wagyu)
  – Northern (Brahman, Tropical Composite)
AGBU

- Joint venture of UNE and NSW DPI, initiated in 1976
- 25 staff (17 PhDs, 3 students, 5 professional staff, + visiting scientists)
  - Beef team: 12
- Focus on genetic and genomic analysis and evaluation
AGBU Contribution:

• All the development work for BREEDPLAN (and Sheep Genetics, PIGBLUP, TREEPLAN)

• Ongoing support for BREEDPLAN delivery

• Ongoing R&D:
  – analytical software
  – Models, genetic parameters
  – New traits
  – Implementation (reference populations, breeder workshops)
Using BREEDPLAN

• Owned and developed by the Australian beef industry
• Used by all major breeds in Australia (and several overseas)
• 145,000 new animals evaluated each year
• AGBU conducts the R&D for BREEDPLAN
• ABRI delivers BREEDPLAN:
  – user pays, at c. $AUD7.50 per new animal
  – Provides breed services to breeds in Australia, and to some overseas
• Funding for R&D c. 50:50 industry (levies) and government
## Australian breeds conducting a BREEDPLAN Evaluation

<table>
<thead>
<tr>
<th></th>
<th>Breed</th>
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<tbody>
<tr>
<td>1</td>
<td>Angus</td>
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<tr>
<td>2</td>
<td>Shorthorn</td>
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<tr>
<td>3</td>
<td>Belmont Red</td>
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<tr>
<td>4</td>
<td>Blonde d’Aquitaine</td>
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<tr>
<td>5</td>
<td>Braford</td>
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<td>6</td>
<td>Brahman</td>
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<tr>
<td>7</td>
<td>Brangus</td>
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<tr>
<td>8</td>
<td>Charbray</td>
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<td>9</td>
<td>Charolais</td>
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<tr>
<td>10</td>
<td>Devon</td>
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<tr>
<td>11</td>
<td>Droughtmaster</td>
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<tr>
<td>12</td>
<td>Galloway</td>
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<tr>
<td>13</td>
<td>Gelbvieh</td>
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<tr>
<td>14</td>
<td>Hereford / Poll Hereford</td>
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<tr>
<td>15</td>
<td>Limousin</td>
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<tr>
<td>16</td>
<td>Lowline</td>
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<tr>
<td>17</td>
<td>Murray Grey</td>
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<tr>
<td>18</td>
<td>Red Angus</td>
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<tr>
<td>19</td>
<td>Red Poll</td>
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<tr>
<td>20</td>
<td>Salers</td>
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<tr>
<td>21</td>
<td>Santa Gertrudis</td>
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<tr>
<td>22</td>
<td>Senepol</td>
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<tr>
<td>23</td>
<td>Shaver Beefblend</td>
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<tr>
<td>24</td>
<td>Simmental</td>
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<tr>
<td>25</td>
<td>South Devon</td>
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<tr>
<td>26</td>
<td>Wagyu</td>
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## BREEDPLAN Traits

<table>
<thead>
<tr>
<th>Growth</th>
<th>Fertility</th>
<th>Carcase</th>
<th>Other</th>
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<tbody>
<tr>
<td>Birth Weight</td>
<td>Scrotal Size</td>
<td>Carcase Weight</td>
<td>Docility</td>
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<tr>
<td>Milk</td>
<td>Days to Calving</td>
<td>Eye Muscle Area</td>
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<tr>
<td>200-day Growth</td>
<td>Gestation Length</td>
<td>Rib Fat Depth</td>
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<tr>
<td>400-day Weight</td>
<td>Calving Ease</td>
<td>Rump Fat Depth</td>
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<td>600-day Weight</td>
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<td>Intramuscular Fat %</td>
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<td>Mature Cow Weight</td>
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<td>Retail Meat Yield %</td>
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</table>

Trial EBVs: Net Feed Intake (x2), Flight Time, Structural Traits (x6), Shear Force
# Breeds and Traits

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<tr>
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<th>Growth</th>
<th>Number of traits</th>
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Using BREEDPLAN

- Identify the best animals to use as parents – both stud and herd bulls
- Breed better and better animals

Genetic Trend ~ $Index by Sector

$Index - per cow joined

Calving Year


Southern $Index
Euro $Index
Northern $Index
BREEDPLAN SOFTWARE

• Suite of programs designed to provide EBVs, Accuracies, Genetic Trends and many other results
• Many traits – Production, Reproduction, Carcase and others.
• One multiple trait analysis for all continuously distributed data
• Separate (single and multiple trait) analyses for categorical data.
• Selection Index (breed cases + customised)
• Diagnostic software
Multiple trait analyses

- Genetic effects (direct and maternal EBVs)
- Genetic groups for all EBVs
- Permanent environmental effects (maternal and repeat records)
- Sire x Herd interactions
- Heterogeneous variances
- Contemporary group
- Import overseas EBVs/EPDs
- Multiple breeds configuration
- Crossbred data
Multiple trait analyses

• Data (observations) are pre-adjusted:
  – To a standard age
    • Various methods including “intercept” method
  – To a standard age of dam
  – Carcase traits to constant weight
• Contemporary groups
  – Based on the history of the animals
    • Like are only compared (phenotypically) with like
  – Subdivided to minimise biases from correction and account for season (continuous update)
• Parameters
  – Estimated from the data
Categorical trait analyses

- Calving ease (difficulty)
  - With gestation length and birth weight in a multi-trait analysis

- Docility

- Structural Soundness
  - Intermediate optimum
Results

- **EBVs**
  - Blended with MBVs when available

- **Group solution & sire x herd fitted and estimated**

- **Accuracies**
  - Approximated

- **Summary results** – genetic trends, P & E trends
Future

- Incorporation of genomic information directly
  - “Single step” now under trialling
  - Using commercial carcase data with genomic pedigree (2014)

- Enhanced (faster) software
  - Exploit multiple cores
  - Re-parameterisation
  - Continuous evaluations

- Merging categorical analyses into main multiple trait analysis

- Continuing R&D into new traits, models and methods
Other activity

• $Index
  – Expanded modelling esp re feed costs
  – New traits incl methane and cow longevity
• Information Nucleus (reference populations)
• Improved procedures for immigrant information
• New estimation incl. SNP Bayes
• Genomic composition – genetic groups, inbreeding
Handling import animals:

- Animals that come with overseas estimated BVs of some sort
- Pseudo-progeny are generated:
  - Use O/S accuracy to estimate equivalent number of progeny
  - De-regress overseas BV to give pseudo-P for those progeny taking account of correlation between countries and between traits
  - This data (progeny pseudo-P’s) included in local analysis
- As domestic progeny and other relatives accumulate data, this contributes more and more of the local EBV
- Working on improved method now