ABBA
Progeny Test/Beef Information Nucleus

Field Day
Banana Station, Banana
Tuesday March 24

An ABBA – MLA Donor Company Project
**What is BIN?**

- **Beef Information Nucleus**
- **Part of the Beef CRC/MLA Strategic plan for DNA Marker Commercialisation**
- **Provides for the systematic collection of accurate phenotypic information on economically important traits**
- **Originally – To facilitate the independent validation of DNA markers relative to Australian breeds and production systems**
- **Now – To contribute to improvement of Gene Marker predications and accuracy specific to the Brahman breed**
  - Technology changes mean there will be continuous updating and validation as new data is accumulated
  - Only breeds with good quality data will be able to take advantage of DNA marker technology
Structured progeny test

Will test 20-25 bulls annually for 3 years

Aim to produce approx 15 steers & 15 heifers per sire

All steer progeny will be slaughtered for carcase and meat quality data

Heifer progeny will be retained within the project to pregnancy test after the second joining
ABBA BIN – Major objectives

- To attract and evaluate sires which will influence the future of the Brahman breed for a range of economically important traits including:
  - Carcase & meat quality
  - Female reproduction
  - Growth traits

- To ensure ABBA members and the Brahman breed is able to take advantage of DNA marker technology

- To provide the resources to conduct other separately funded research into areas which would assist the future development of the Australian Brahman breed
The Project

- Evaluate 20-25 sires each year for 3 years
- Produce about 30 calves per sire in 3 Co-operator herds each year

  - Mark & Belinda Wilson, Banana Station, Banana producing calves by AI from high grade commercial Brahman heifers – AI 500-600 heifers plus 800 in Round 3
  - Rob & Annie Donaghue, Baradoo, Bauhinia producing calves by AI from high grade commercial Brahman heifers – AI 500-600 heifers plus 700 in Round 3
  - CSIRO – Belmont producing calves by AI and natural service from the Belmont registered Brahman herd – Rounds 1 & 2 – AI 120 plus natural service
The Project cont

- ABBA purchased steer progeny at weaning to finish on grass, grain feeding would only be used as a drought contingency

- Heifer progeny will be retained in the project until preg test following second joining within the co-operator herds

- Blood and hair samples from sires and all progeny will be collected for DNA extraction and storage as well as sire verification

- All data collected will be entered into the ABBA database and analyzed in Breedplan

- Analysis of DNA samples against marker panels in the future is not part of the project
Data to be collected

Growth traits

200, 400 & 600 day weight
Mature cow weight & condition score

Carcase & Meat quality

Ultrasound scan at 600 days
Eye muscle area
Rib fat
Rump fat
## Data to be collected cont

<table>
<thead>
<tr>
<th>Direct carcase data</th>
<th>Meat quality (at 14 days aging)</th>
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</thead>
<tbody>
<tr>
<td>Eye muscle area</td>
<td>Shear force</td>
</tr>
<tr>
<td>Rump fat</td>
<td>Meat Colour</td>
</tr>
<tr>
<td>Rib fat</td>
<td>Cooking loss</td>
</tr>
<tr>
<td>MSA grading</td>
<td>Extracted fat</td>
</tr>
<tr>
<td>Meat Colour</td>
<td>MSA taste test on some samples</td>
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<tr>
<td>Fat Colour</td>
<td></td>
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<tr>
<td>Ultimate PH</td>
<td></td>
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<tr>
<td>Intra Muscular Fat</td>
<td></td>
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<tr>
<td>Ossification</td>
<td></td>
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<tr>
<td>Hump height</td>
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</tbody>
</table>
Data to be collected cont

Female reproduction
  Days to calving
  Teat & udder scores on heifers

Other Data
  • Structural soundness scores
  • Flight Time
  • Ovarian Scans
    • 600 days
    • Into mating
### Progeny Details

**Sire Total 70 including 6 CRC link sires**

<table>
<thead>
<tr>
<th></th>
<th>Steers</th>
<th>AV/Sire</th>
<th>Range</th>
<th>Heifers</th>
<th>Av/Sire</th>
<th>Range</th>
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</thead>
<tbody>
<tr>
<td>Round 1</td>
<td>239</td>
<td>12.6</td>
<td>8-20</td>
<td>246</td>
<td>13</td>
<td>6-18</td>
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<tr>
<td>Round 2</td>
<td>295</td>
<td>12.3</td>
<td>6-17</td>
<td>315</td>
<td>14</td>
<td>7-20</td>
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<tr>
<td>Round 3</td>
<td>339</td>
<td>15.3</td>
<td>11-29</td>
<td>388</td>
<td>15.8</td>
<td>8-23</td>
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<td><strong>833</strong></td>
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<td></td>
<td><strong>949</strong></td>
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<tr>
<td>Event</td>
<td>Round 1</td>
<td>Round 2</td>
<td>Round 3</td>
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<tr>
<td>Steer turnoff</td>
<td>Completed</td>
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<td>May/June 2016</td>
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<tr>
<td>Heifer joining</td>
<td>Completed</td>
<td>Completed</td>
<td>Nov 2015</td>
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<tr>
<td>Preg test &amp; foetal age</td>
<td>Completed</td>
<td>Completed</td>
<td>Jan/Feb/Mar 2016</td>
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<td>Second joining</td>
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<td>Nov 2015</td>
<td>Nov 2016</td>
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<tr>
<td>Preg test</td>
<td>Completed</td>
<td>April/May 2016</td>
<td>April/May 2017</td>
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The Future

- Genomics will get cheaper
- Markers will explain more of the genetic variation
- Markers will have higher accuracy
- But to work they will require high quality phenotypes recorded across all traits
- BIN type data will continue to be required