AGBU
ANIMAL GENETICS AND BREEDING UNIT
A joint unit of NSW DPI and UNE

Development and implementation of genomic methods in beef cattle genetic improvement in Australia

Rob Banks (AGBU)
Alex McDonald (ABRI)

Background:

- Commercial population – 12m cows
- Stud sector – c. 0.25m cows
- Approximately half the cattle are in northern half of continent – adaptation challenges (heat, ticks, etc)
- 70% of product exported (US, north Asia, Europe are main markets)
- 20-25% of finished cattle have some grain feeding (feedlots)
- Large number of breeds – commercially relevant ones are:

Background:

- Large number of breeds – commercially relevant ones are:
  - South:
    - Angus, Hereford, Shorthorn, Murray Grey
    - Charolais, Limousin
    - Wagyu
  - North:
    - Brahman
    - Tropical composites (various combinations of Brahman pus Bos taurus)

Genetic evaluation:

- BREEDPLAN:
  - Multi-trait BLUP analysis
  - c. 25 traits
  - Breed-specific $Indexes for all breeds
  - All major breeds conduct regular (at least monthly) across-herd analyses
  - International data included in most major breeds where available

Genetic evaluation:

- c. 145,000 new animals evaluated each year
- This represents very high proportion of new bulls in south, and about 20% of new bulls in north (but very high proportion of sires to breed sires in north)
- Genetic trends similar on average to other countries (Amer et al, ICAR, 2012)
- Importation important in most breeds (mainly from US), but declining in significance

Genomics

- Single gene tests
  - Limousin muscle, horn/poll, deleterious recessives in Angus, etc
- Development of prediction equations through Beef CRC (2001-2012)
  - Dataset includes large number of breeds, not large numbers per breed x trait in most cases
  - Typical accuracy c. 30-35% accuracy
  - Now being delivered – major interest is for fertility traits in Brahman
    - Accuracy c. 0.30

Genomics

- Prediction equations approach
  - Cautious adoption to date (this includes for genomic values marketed by Zoetis and Igenity)

- Blending into BREEDPLAN EBVs
  - Tests are calibrated for accuracy of predicting the relevant BREEDPLAN traits in Australian data (this applies to Zoetis, Igenity and CRC tests)
  - In this approach, the genomic values are not extended out through the pedigree

Work in progress

- Single step
  - Being trialled now in single trait cases
  - Aiming to scale up to routine multi-trait datasets over next 3-6 months, to start trial implementation in BREEDPLAN in 2015
- Reference populations
  - Currently have/have had Beef Information Nucleus projects in several breeds (Angus, Brahman, Hereford, Wagyu continuing)
  - Co-funded by industry and Federal Gov’t

Challenges

- Maintaining reference populations – especially for breeds other than Angus
- Breeding program design incorporating use of genomics (what animals to phenotype, which to genotype, when to select etc):
  - All decision-making is at individual stud level, except for collective (breed) investments in reference populations
- How to make use of data collected on commercial cattle (concern re data harvesting and quality)
- Research into valuing phenotypes (so that individuals can make best investment decisions)

Opportunities

- How to interact with international populations
  - Keen to work together to understand genomic relationships across countries
  - Keen to work together to evaluate value of sharing phenotypes

- keen to contribute to development of tools