Beef cattle genetic evaluation in Australia ~ BREEDPLAN

Robert Banks

AGBU

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

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)

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- **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**

% Funding by Source - AGBU

- Partners — 23%
- Beef — 35%
- Sheep — 26%
- Pigs — 13%
- Other — 3%
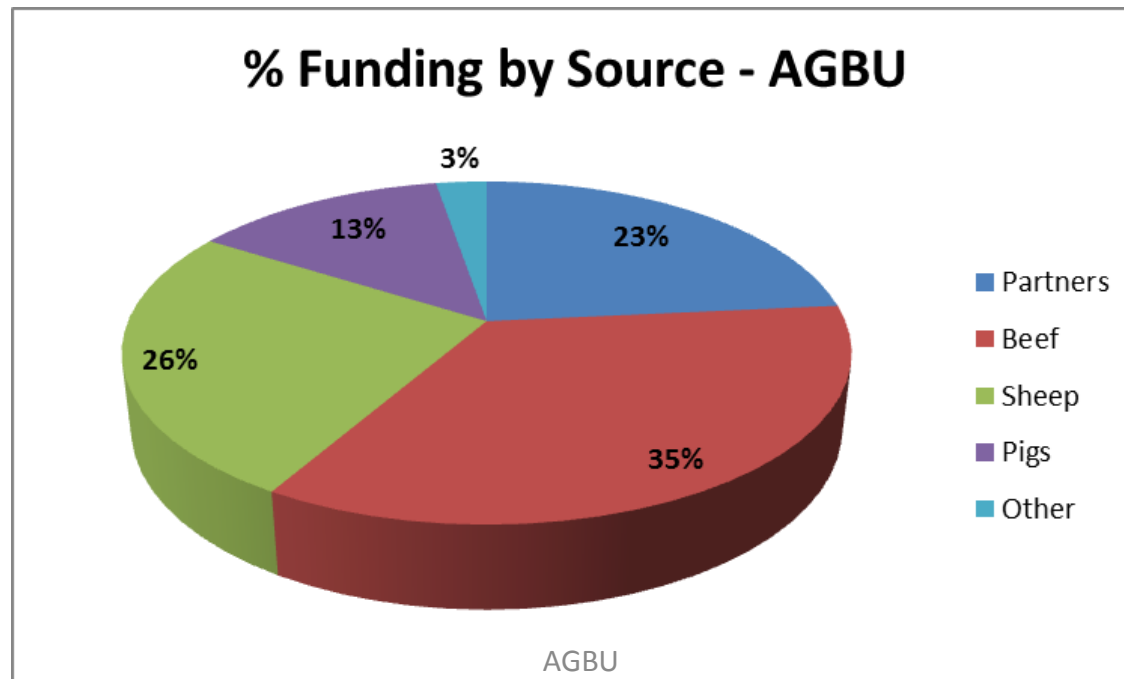
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AGBU Contribution:

- **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)**

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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

1. **Angus**
2. **Shorthorn**
3. **Belmont Red**
4. Blonde d'Aquitaine
5. Braford
6. **Brahman**
7. Brangus
8. Charbray
9. **Charolais**

10. Devon
11. **Droughtmaster**
12. **Galloway**
13. Gelbvieh
14. **Hereford / Poll Hereford**
15. **Limousin**
16. Lowline
17. Murray Grey
18. Red Angus

19. Red Poll
20. Salers
21. **Santa Gertrudis**
22. Senepol
23. Shaver Beefblend
24. Simmental
25. South Devon
26. **Wagyu**

BREEDPLAN Traits

Growth	Fertility	Carcase	Other
Birth Weight	Scrotal Size	Carcase Weight	Docility
Milk	Days to Calving	Eye Muscle Area	
200-day Growth	Gestation Length	Rib Fat Depth	
400-day Weight	Calving Ease	Rump Fat Depth	
600-day Weight		Intramuscular Fat %	
Mature Cow Weight		Retail Meat Yield %	

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

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Breeds and Traits

Breed	Number of traits						
	Growth	Scan	Rep	Carc	NFI	FT	Total
• Angus	5	8	3	6	2		24
• Belmont Red	5	8	3	7		1	24
• Brahman	5	8	3	7		1	24
• Charolais	5	8	2	6			21
• Droughtmaster	5	8	1	6			20
• Hereford	5	8	3	6			22
• Limousin	5	8	3	6			22
• Santa Gertrudis	5	8	2	7		1	22
• Shorthorn	5	8	2	6			21
• Simmental	5	8	3	6			22

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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
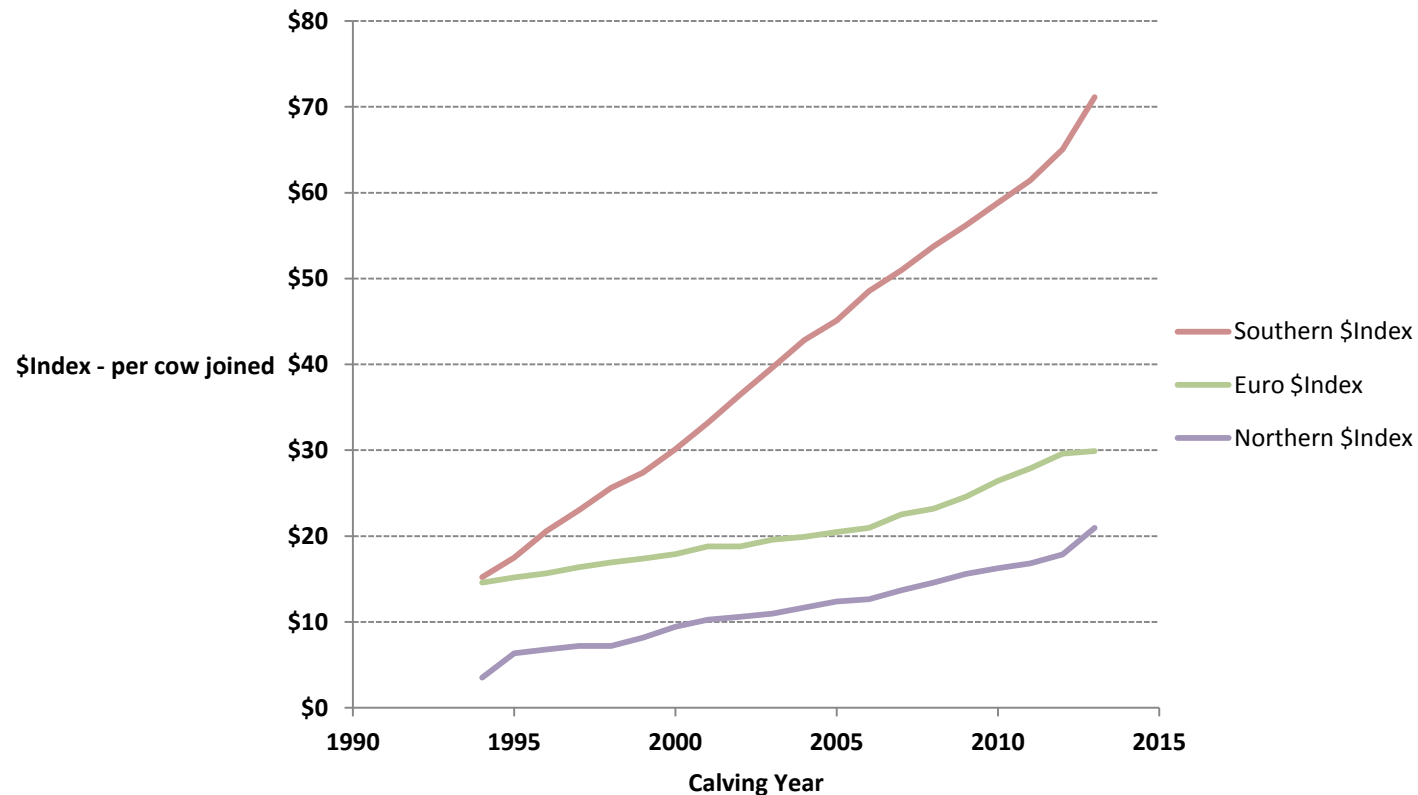
BREEDPLAN SOFTWARE

- **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**

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Results

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

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

- **Accuracies**
  - **Approximated**

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

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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**

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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**

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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