



## Genomics: An Australian perspective

Ben Hayes and many others





#### **Outline**

What are we breeding for?



Balance



#### Dairy

#### **Balanced Performance Index (BPI)**

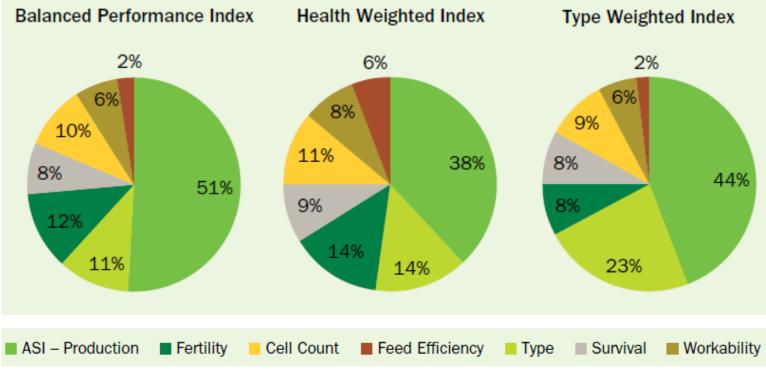
- · Economic index
- Blends production, type and health traits for maximum profit
- · In line with farmer preferences



#### Health Weighted Index (HWI)

· Fast track fertility and mastitis resistance





#### Type Weighted Index (TWI)

Fast track type





- Lamb
  - Growth, Fat depth, eye muscle area
  - Reproduction, worm egg count (WEC)



- Lamb
  - Growth, Fat depth, eye muscle area
  - Reproduction, worm egg count (WEC)
  - Lean meat yield
  - Eating quality index -> tenderness, intra-muscular fat, taste panel



Beef

- Southern Australia
  - Growth, carcass, reproduction, intramuscular fat, feed efficiency
- Northern Australia
  - Growth, reproduction
  - Feed efficiency, meat quality on the horizon







#### **Outline**

What are we breeding for?





- Genomics offers the (only?) opportunity to breed for better balance between easy to measure traits and hard to measure traits
- Need large populations animals that have traits measured and are genotyped

Different industries have tackled this in different ways













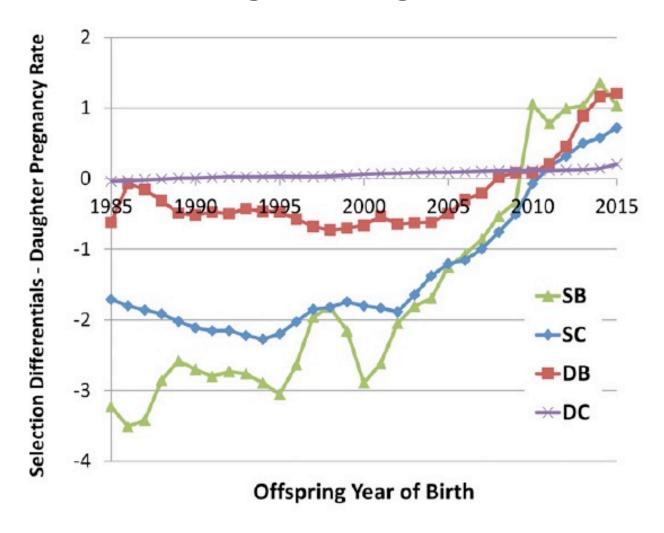
- Dairy
  - Ginfo project genotype 60,000 cows in commercial dairy herds (main emphasis good fertility records)
  - Accuracies genomic breeding values for young genomic bulls now quite high

Trait	Accuracy
BPI	79
Production	87
Survival	69
Fertility	69
Feed efficiency	54



#### **Genomic selection and Al**

Double rate of genetic gain



García-Ruiz et al. Proc Natl Acad Sci U S A. 2016 113(28):E3995-4004



- Lamb
  - Information nucleus (industry rams used on large research stations)
  - >30,000 genotypes
- Genomic breeding values for
  - Lean meat yield and dressing%
  - Carcass eye muscle and fat
  - Intra-muscular fat and shear force
- Multi-trait single step analyses (AGBU team)





- Beef
  - Beef Information nucleus for carcass traits, feed efficiency
    - Combination of industry funding and MLA
  - Large fertility projects, one on research stations, another on commercial properties
  - Multi-trait single step for some breeds (AGBU team)
  - Days to calving ~0.3-0.5 accuracy



Two big challenges for the future

1. How to maintain genomic selection reference populations? We will always need them.

- 2. How to make genomic breeding values work across breeds?
  - Otherwise enormous reference population needed for each breed/composite



• Current 50K works well strictly within breeds

Does not work across breeds

Composites?

Accuracy erodes rapidly with generations







Sequence data -> causal mutation in data set

## 1000 bull genomes Run6

- 2703 Sequenced Animals (Taurus, Indicus), 11x
- ~55 Breeds: Dairy, Beef, Dual Purpose, Crosses, Composites























#### Sheep catching up!

 Run2 of SheepGenomesDB contains 935 diverse sheep yielding >50 million variants!!

 James Kijas, Rudiger Brauning, Shannon Clarke, Alan McCulloch, Noelle Cockett, Gary Saunders, Marina Naval Sanchez, Sean McWilliam, Hans Daetwyler















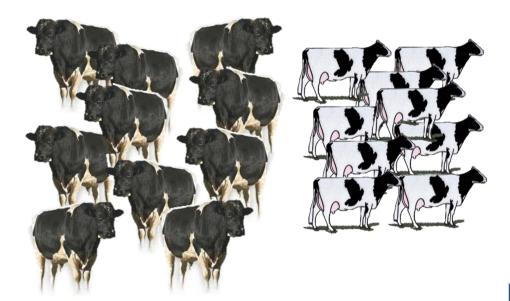








Sequence data -> causal mutation in data set



Holstein 14,055 Individuals



Jersey 5,259 Individuals



Reds 1,012 Individuals

Impute sequence data into all individuals

# **Across breed prediction**

	Fertility	Temperament
50K SNP	0.06	0.10
630K SNP	0.22	0.24
Sequence data	0.28	0.26

#### Conclusion

 Most industries now aiming for breeding goals which balance production, fertility, meat quality, feed efficiency and disease resistance



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- Genomic breeding values opens the opportunity to breed for these traits



#### Conclusion

- Most industries now aiming for breeding goals which balance production, fertility, meat quality, feed efficiency and disease resistance
- Genomic breeding values opens the opportunity to breed for these traits
- Major challenges in the future
  - building and maintaining reference populations
  - Making genomic selection work across breeds
  - Integrating new sequence variants into single step



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