How can genomic tools support breeding and genetic improvement in Vietnam?

Professor Ben Hayes
Centre Director, Animal Science
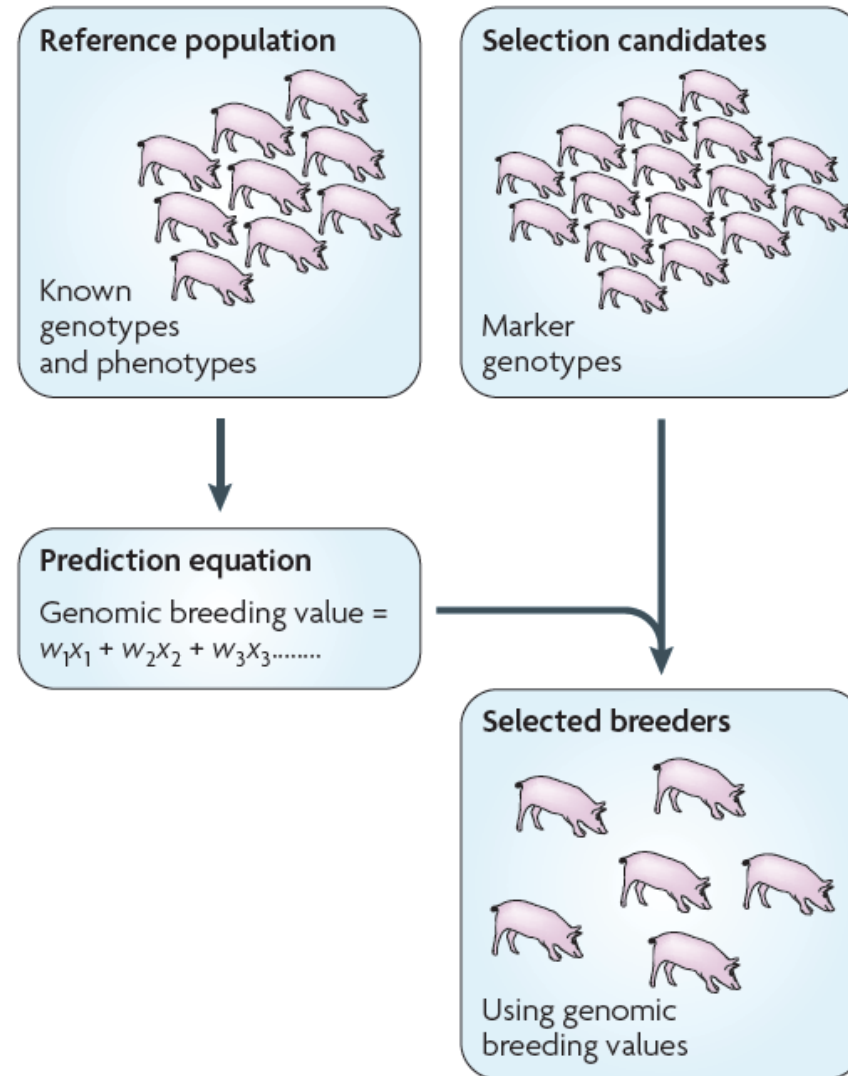Queensland Alliance for Agriculture and Food Innovation

Key drivers

- Fertility

  - maximise kg beef or lamb/cow or ewe

  - reduce methane/kg beef or lamb

- Meat Quality

  - High value markets

- Methane

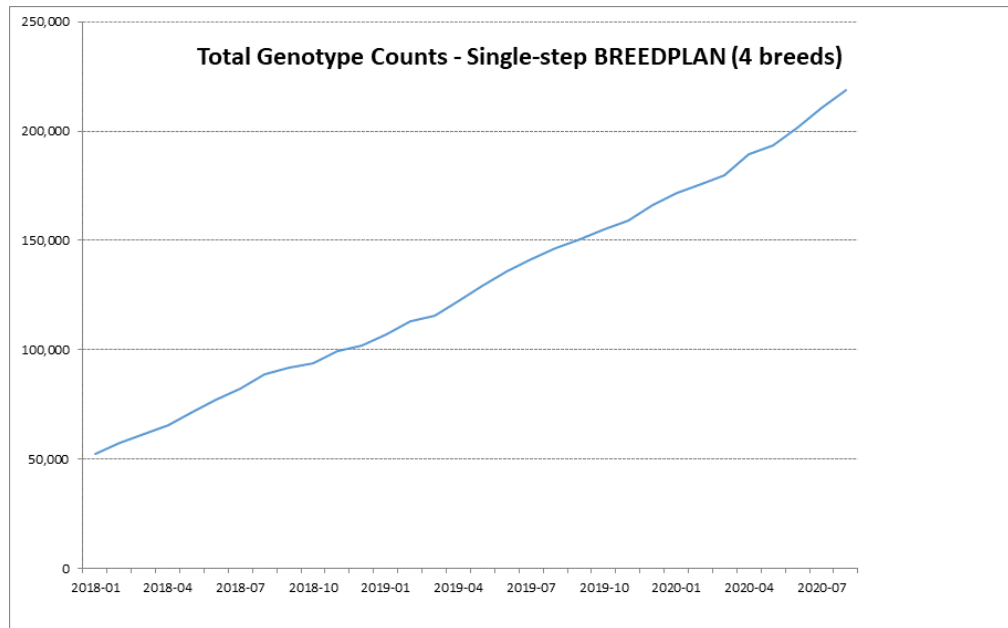 - Carbon footprint, access to markets

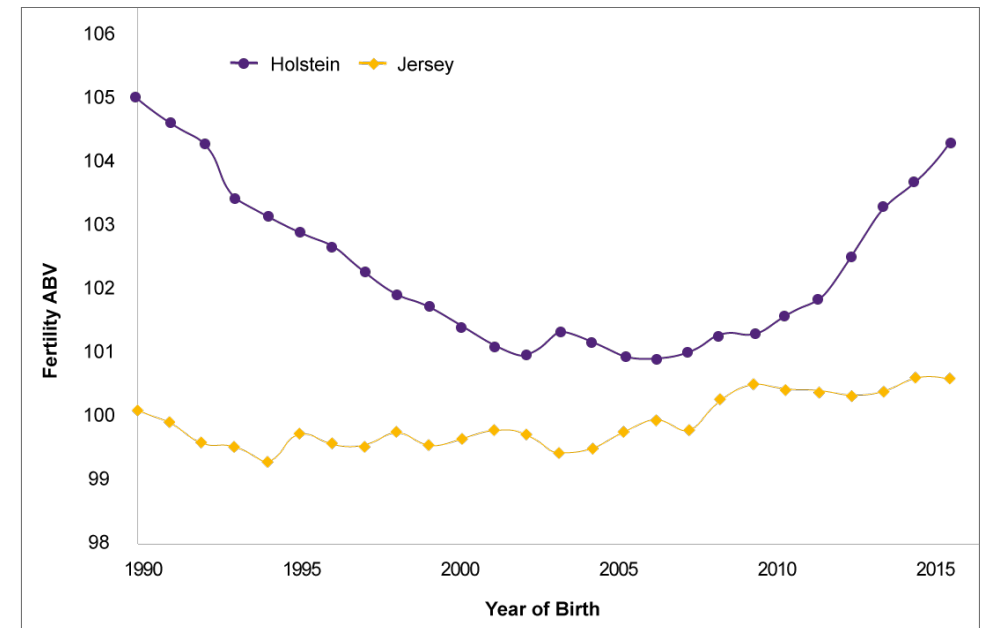- Adaptation

Genomic selection

>20 million animals genotyped

Reference population

Known genotypes and phenotypes

Selection candidates

Marker genotypes

Prediction equation

Genomic breeding value = $w_1 x_1 + w_2 x_2 + w_3 x_3 ....$

Selected breeders

Using genomic breeding values

Livestock genomics

Beef – uptake of genotyping

Total Genotype Counts - Single-step BREEDPLAN (4 breeds)
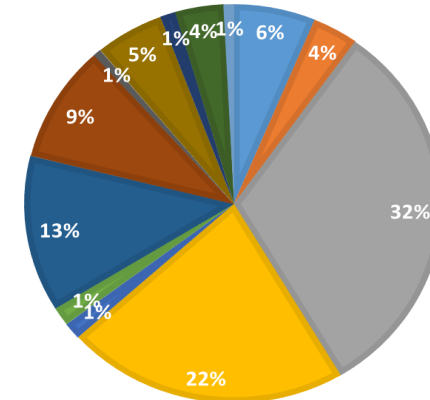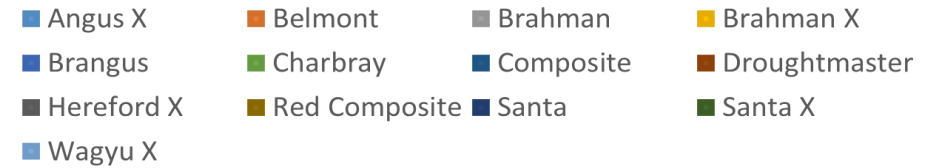
Dairy – Impact

Challenges for beef

- Large number of breeds, crossbreds, two sub-species (*Bos taurus* and *Bos indicus*)

- Traits not routinely recorded

- Extensive conditions

- Northern Genomics project as an example

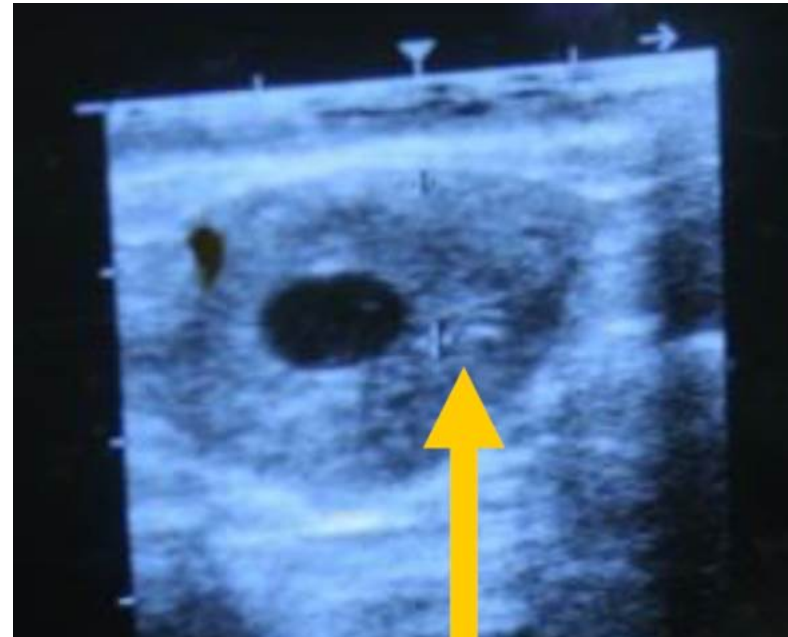# Northern Genomics Project

- 60 collaborator herds from across northern Australia

- 29,391 genotyped and trait recorded heifers

Legend:
- Angus X
- Belmont
- Brahman
- Brahman X
- Brangus
- Charbray
- Composite
- Droughtmaster
- Hereford X
- Red Composite
- Santa
- Santa X
- Wagyu X

Pie chart values: 32%, 22%, 13%, 9%, 6%, 5%, 4%, 4%, 1%, 1%, 1%, 1%, 1%

CRICOS code 00025B

QAAFI
Queensland Alliance for
Agriculture and Food Innovation

THE UNIVERSITY OF QUEENSLAND
AUSTRALIA

Queensland
Government

Northern Genomics Project - The data

- CLscore – cycling/not cycling at ~600 d of age (Heifer puberty)
- Genotypes: 35-50K TropBeef SNP Array → imputed 709K SNP

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Northern Genomics Project - The data

Trait	Number	Heritability
Weight	26,724	0.29
Hip height	26,724	0.39
Body condition score	26,724	0.22

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Body condition score	26,724	0.22
Heifer Puberty	29,391	0.22
Pregnant 4 months after calving	8,477	0.11
Temperament	3,234	0.37
Tick score	2,094	0.33
Buffalo fly lesion score	15,927	0.14

Herd Profiles

- Benchmark my herd against 60 herds across Northern Australia
- For fertility, growth, tick and fly resistance, temperament
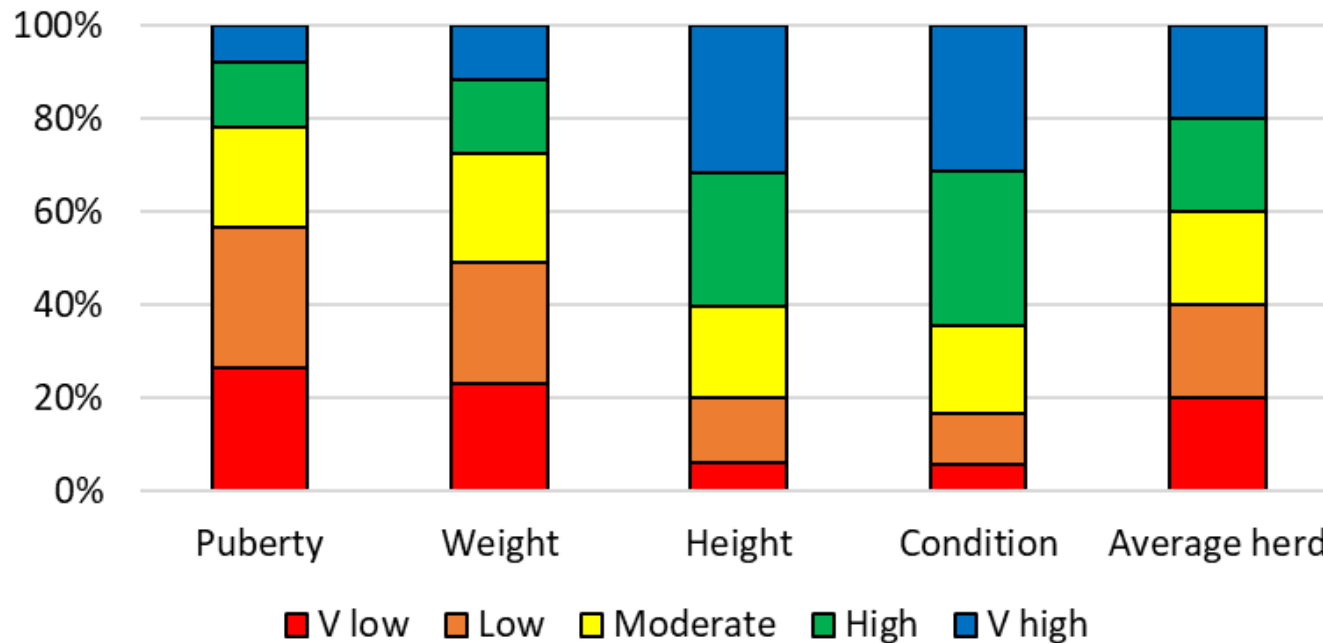

- Guide bull buying decisions – which traits to emphasise?

Genomic Breeding Value (GBV) from the Northern Genomics Project

- Collection of records in commercial herds enables GBV selection for fertility in multi-breed, composite, crossbred cattle

- Northern Genomics GBV useful for selecting bull teams, culling heifers

- Validated in a range of data sets, including for lifetime production

- Based on DNA only (from DNA + phenotypes)

Hayes BJ, et al. Multi-breed genomic evaluation for tropical beef cattle when no pedigree information is available. Genet Sel Evol. 2023 Oct 16;55(1):71.

Using small herd sizes as a reference?
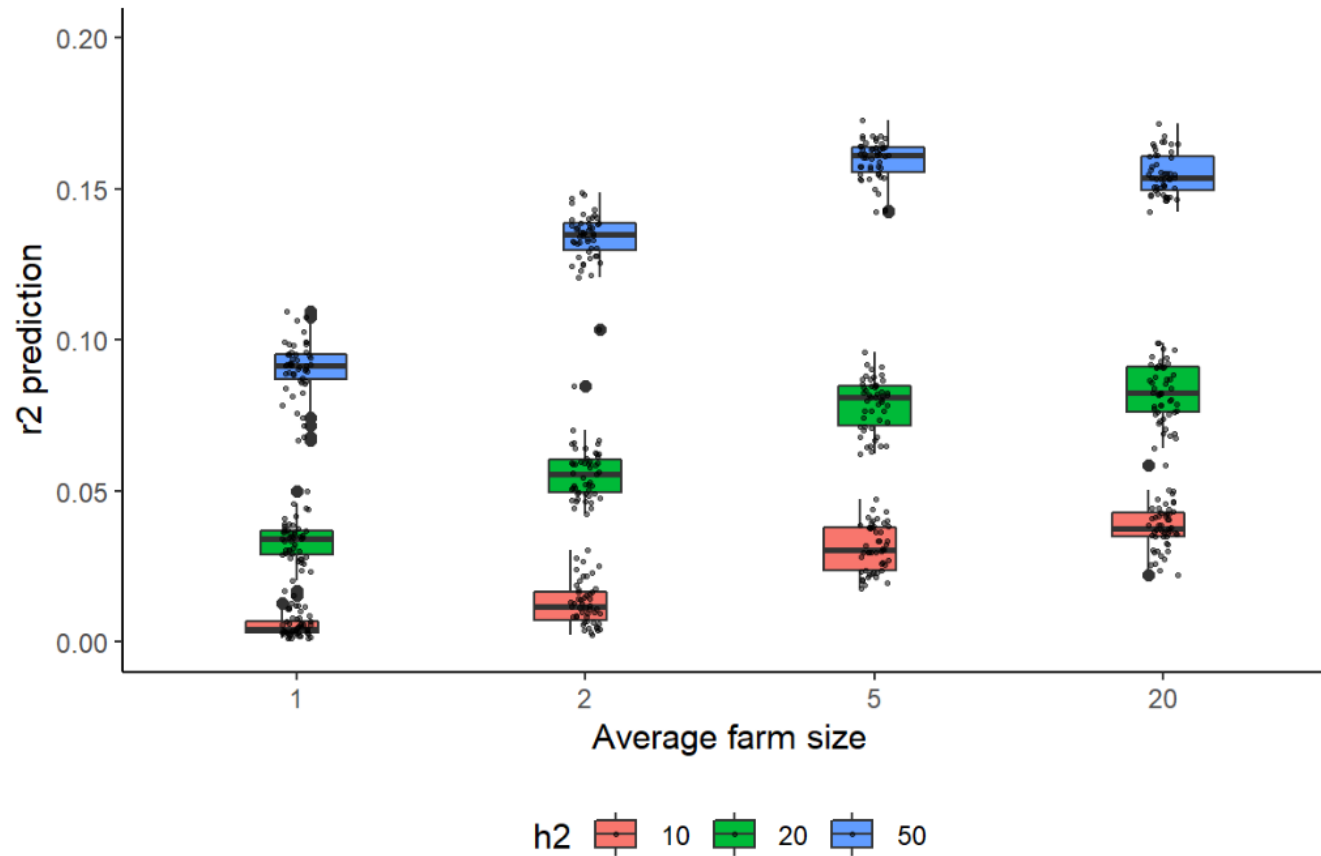
Costilla et al. Developing flexible models for genetic evaluations in smallholder crossbred dairy farms. J Dairy Sci. 2023 Sep 5:S0022-0302(23)00582-9

Conclusion

- Good genomic models now available to develop genomic tools for multi-breed/multi sub-species populations

- Accurate GBV for selection even without pedigree

- Use genomics to accelerate genetic gain by selecting and breeding from animals as early as possible

- Even relatively small herds can be used as a reference

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