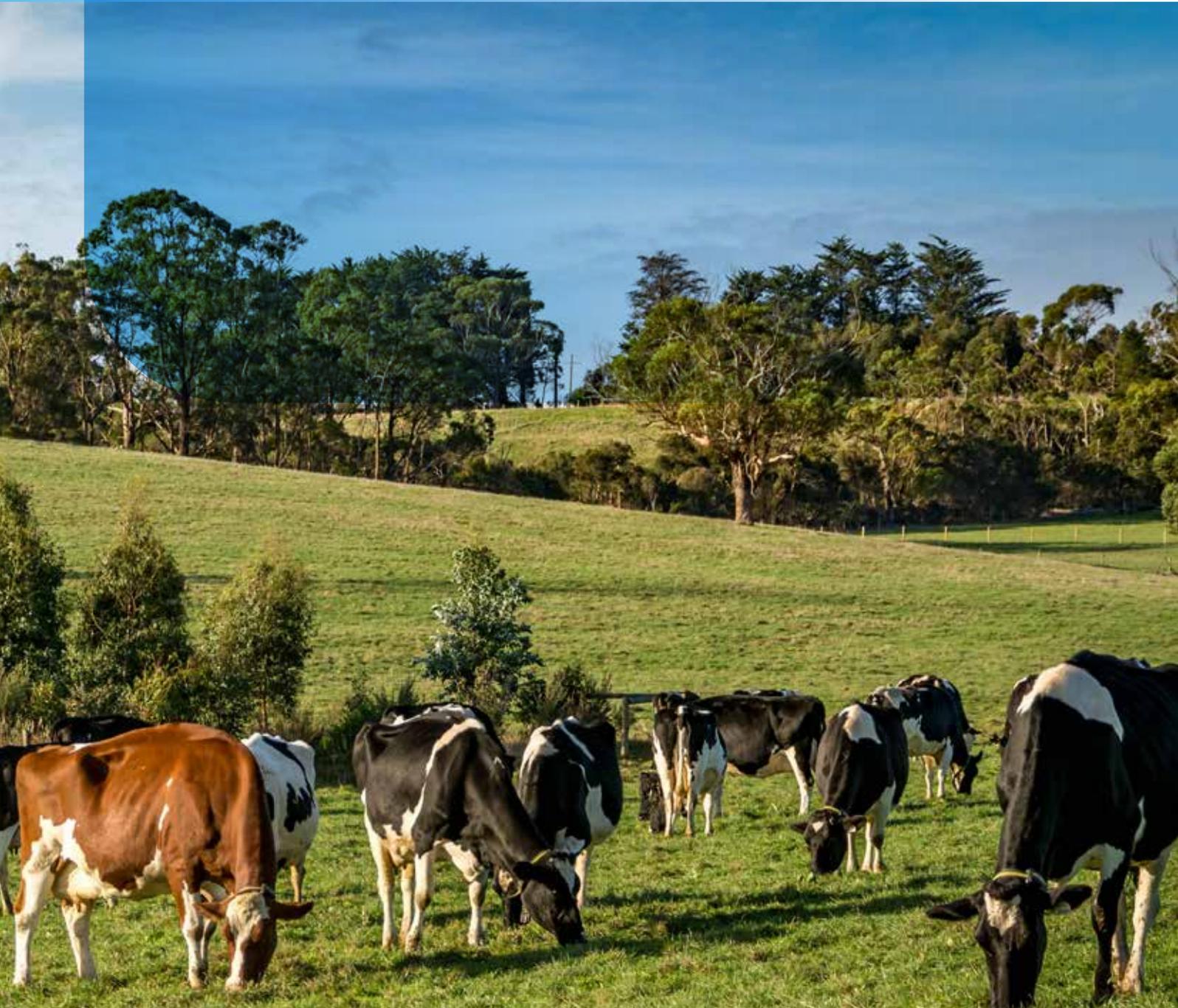


# Ginfo project report



Australia's genomic information nucleus

## Key points

- Doubled the size of Holstein reference population
- 50% increase in Jersey reference population
- Reliability improvements in all three Australian breeding indices
- Reliability improvements in all traits, especially daughter fertility and overall type



Mary Abdelsayed, Project Manager, Health Data Healthy Cows project (left) with Liz Weaver, Member Services Officer, Holstein Australia



Figure 1 Herds participating in *Ginfo* came from all Australian dairying regions



Con Glennen, *Ginfo* herd participant and project ambassador

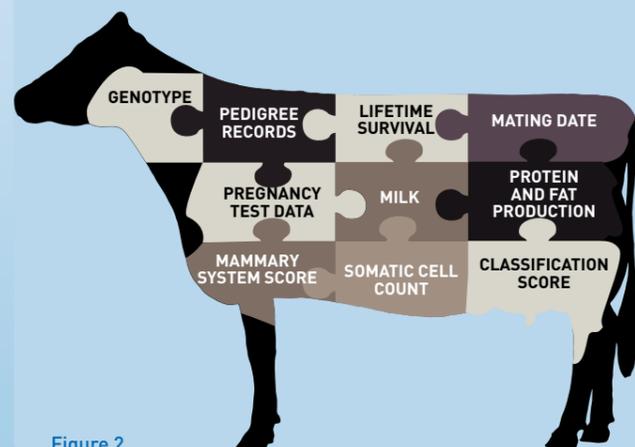


Figure 2 Predictions of a cow's genetic merit are more accurate when they are based on data from multiple sources



Dr Coralie Reich, Research Scientist, Biosciences Research Division, DEDJTR

## Increasing the reliability of ABV(g)s

*Ginfo* was a large-scale genotyping project to increase the reference population of Australian dairy cattle to achieve more reliable genomic Australian Breeding Values – ABV(g)s. A major delivery of Dairy Futures CRC, *Ginfo* ran from 2013–2016 and involved genotyping more than 30,000 cows in 100 herds with excellent records.

The logistics of collecting hair samples and phenotypic data on this scale involved a collaboration between the Dairy Futures CRC, Holstein Australia, Jersey Australia, the Victorian Government and the Australian Dairy Herd Improvement Scheme (ADHIS).

### *Ginfo* herds and data

*Ginfo* herds were located across Australia's eight main dairying regions (see map). To qualify for *Ginfo*, herds had to reach a minimum score based on the quality of their records contributed to the ADHIS database. Additional points were awarded for having mating and pregnancy test results. Overall, *Ginfo* herds had much more complete records than the national average, especially for fertility. In total, 103 herds participated in *Ginfo*, including 32,386 daughters of 2917 sires. The information they contributed represented the largest genomic reference project in the world.

In addition to accessing herd data already on the ADHIS database, the *Ginfo* team collected tail hair samples for genotyping and classified all first lactation heifers for the full range of type traits.

The team genotyped tail hair samples from *Ginfo* herds using a new technology, 'Genotyping by Sequencing'. This could offer another option for commercial genomic testing in the future.

*Ginfo* data was used to calculate genomic breeding indices (BPI, HWI and TWI) and trait ABV(g)s for each cow. Trait ABV(g)s included: Production, Type and Mammary, Workability, Survival, Cell Count, Daughter Fertility and Feed Saved.

## Outcomes

The reliability of ABV(g)s and indices for both sires and individual cows has improved significantly as a result of *Ginfo*.

The addition of *Ginfo* data doubled the Australian Holstein genomic reference population and increased the Jersey genomic reference population by 50%.

**Sires:** *Ginfo* resulted in an increase in the reliability of sire information in the April 2016 ABV release, including Australia's three breeding indices (BPI, HWI and TWI) and ABV(g)s for other traits, particularly daughter fertility and overall type (see Table 1 and 2). The excellent quality of fertility data (mating dates, pregnancy test data, calving intervals) provided by the *Ginfo* herds has had a particularly big impact on improving the reliability of Daughter Fertility ABV(g)s. For example, the reliability of young bulls' Daughter Fertility ABV improved from 41% to 46% for Holsteins and from 37% to 39% for Jerseys.

**Cows:** Dairy farmers who genotype their own animals will also see improvements in the reliability of results. For example the average reliability of BPI for Holstein cows in *Ginfo* increased by nearly 30% from 35% (without genotype) to 63% (with genotype) (see Table 3 and 4).

### Where to now?

*Ginfo* has confirmed that incorporating the genotypes from large numbers of cows into a reference population can achieve substantial improvement in the reliability of genomic breeding values. The ongoing collection of data is vital to ensure genomic breeding values remain current as new sire groups become part of our dairy genetic population.

Table 1 Holstein sires: average increase in reliability of young genomic bulls

	Reliability Pre <i>Ginfo</i>	Reliability Post <i>Ginfo</i>	Reliability Improvement
BPI	54%	59%	5%
Overall Type	42%	49%	7%
Daughter Fertility ABV(g)	41%	46%	5%

Table 2 Jersey sires: average increase in reliability of young genomic bulls

	Reliability Pre <i>Ginfo</i>	Reliability Post <i>Ginfo</i>	Reliability Improvement
BPI	49%	51%	2%
Overall Type	38%	41%	3%
Daughter Fertility ABV(g)	37%	39%	2%

Table 3 Holstein cows: average increase in reliability

Number of cows: 13799	Reliability Pre <i>Ginfo</i> (no genotype)	Reliability Post <i>Ginfo</i> (with genotype)	Reliability Improvement
BPI	35%	63%	28%
Type and Mammary ABV(g)	38%	52%	14%
Daughter Fertility ABV(g)	30%	52%	22%

Table 4 Jersey cows: average increase in reliability

Number of cows: 2555	Reliability Pre <i>Ginfo</i> (no genotype)	Reliability Post <i>Ginfo</i> (with genotype)	Reliability Improvement
BPI	34%	53%	19%
Type and Mammary ABV(g)	36%	38%	2%
Daughter Fertility ABV(g)	29%	43%	14%



Thank you to all the *Ginfo* herd participants for making your animals available for tail hair sampling and classification; and for keeping excellent herd records. This provided the foundation for the success of this project. Your contribution has improved the reliability of genomic breeding values which underpin the genetic improvement of Australian dairy cows.

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*Cover photo: Janine Clark, Harklaje Holsteins Gippsland.*



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