Breeding replacements from herd bulls

Genomics boosts genetic gain from natural sires

Key points

- Genetic gain is achievable when using genotyped natural sires to breed replacements.
- Australian Breeding Values (ABVs) of genotyped natural sires are directly comparable to those of AI sires.
- Genomic breeding values allow farmers to select natural bulls for traits that best suit their breeding objectives.
- Genomically testing natural sires provides pedigree verification.

To improve genetic gain from natural sires, look for high BPI genotyped bulls that meet your breeding priorities.

The ABVs of genotyped natural sires can be compared directly to an AI sire, giving farmers greater confidence in their natural breeding decisions. Look at the BPI and ABVs of genotyped natural bulls to identify those that meet your breeding priorities.

Tailoring a natural breeding program

Every dairy farmer has different breeding priorities that reflect their individual situation.

Management traits such as calving ease and temperament are often a priority in natural breeding programs due to the inability to selectively mate. Genomic breeding values provide reliable predictions on a number of important management traits that allow farmers to choose natural bulls according to their management priorities. The table below gives some examples of what to look for when selecting a natural bull.

Genomic breeding values

Genomic or DNA testing analyses a hair or tissue sample to predict an animal's genetic merit. Genomic Australian Breeding Values (ABVs) are calculated for more than 40 different traits, including production, conformation, health and management traits.

DataGene calculates three breeding indices - the Balanced Performance Index (BPI), Health Weighted Index (HWI) and Australian Selection Index (ASI). The breeding indices are calculated using a combination of traits with specific weightings to reflect a variety of breeding priorities.

To breed for…	Choose a team of bulls with…
Easier calvings	A Calving Ease ABV(g) of greater than 100
Improved temperament	A Temperament ABV(g) of greater than 100
Improvements in the traits that contribute to overall profitability	A high Balanced Performance Index (BPI) e.g. BPI of +300. On average this animal returns $300 more income over feed/herd costs than the national average.
Fast track genetic gain for fertility, mastitis resistance and feed saved	A high Health Weighted Index (HWI) e.g. HWI of +280. This animal is 280 units greater for the desired objective than average.
Genetic gain for overall production	A high Australian Selection Index (ASI) e.g. ASI of +200. This animal is $200 more profitable from production than average.

Reliability

Reliability is a measure of confidence in an ABV and improves as more information becomes available. The reliability of an ABV is expressed as a percentage (%). The reliability of ABVs of a genomically-tested natural sire with no milking daughters is the same as an AI sire with no milking daughters.

Table 1 shows the increase in reliability as more data is added - from parent average (no genomic test), to a genomic ABV (0 daughters) to a first crop proven sire.

The BPI and ABVs of genomically tested natural sires are directly comparable to AI sires. The table below shows that genomically-tested natural sires can have BPIs that are just as reliable AI sires.

Reliability of genomic tested Holstein sires: natural vs AI sires (April 2021)

Bull name	AI or natural	BPI	BPI reliability	# daughters
Carenda Jeronimo 862	Natural	487	63%	0
Moonarall a Kingdoc 8820	Natural	237	67%	0
Carenda Zone 811	Natural	464	64%	0
Ladys-Manor Big Orbitz	AI	544	59%	0
Kaarmona Diamond	AI	528	64%	0
Mr Super Contender	AI	450	91%	432(a)
Kaarmona Destined	AI	362	83%	70(a)
Calister Maebull	AI	363	94%	1,339(a)
Westcoast Perseus	AI	500	83%	77(a) & 2826(i)

(a) Australian milking daughters (i) International milking daughters

Pedigree verification

Natural bulls that have been genomically tested receive a verified pedigree. This can be used to:

- Reduce inbreeding (most herd improvement centres can use your herd recording data, along with verified pedigree data to produce inbreeding reports)
- Ensure breed purity and registration eligibility.
- Verify the parentage of offspring (useful when multiple natural sires are running simultaneously).
- Export eligibility for surplus progeny.
- More accurate identification of animals with superior and inferior genetic merit.

Cross-breeding

Natural sires are common in cross-breeding programs, with Jersey bulls often used over maiden Holstein heifers. Using genetically superior sires will provide additional genetic gain on top of the production advantage obtained from crossing strains which are genetically diverse (heterosis).

Genomic ABVs are available for cross-breeds (Holstein-Jersey cross and Jersey-Holstein cross), and will soon be published for Australian Red Breeds.

Genetic characteristics and defects

Genomic service providers are increasingly providing screening for a range of genetic defects, haplotypes affecting fertility and milk characteristics such as A2. By using genomically-tested natural sires you can take advantage of this and make better breeding decisions by avoiding bulls with defects or selecting positively for desirable milk characteristics.

How to select a natural bull

Most registered breed associations have online database where farmers can view, search and rank active registered bulls in their area.

To maximise the benefits of genomic testing in natural sire programs:

- Select herdbook registered bulls from a reputable breeder.
- Select bulls that have been genomically tested.
- Select bulls with a high ABV(g) for the production, health and management traits that are most important to your operation.
- Avoid bulls that carry recessive genetic defects.
- Ask your local herd improvement centre to run an inbreeding report to gauge the number of potential conflict matings.

Read more

DataGene resources: ABV pocket guide
DataGene Fact sheet: Calving Ease
DataGene Tech Note: Calving Ease ABV for Holsteins
DataGene Fact Sheet: Genomics for crossbreds

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More information

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