

Genomics for Red Breeds

Technote 27

HIGHLIGHTS

- August 2021 is the first public ABV release to include genomics for Red Breeds.
- Initially, ABV(g)s are available for four traits in Red Breeds: milk, fat, protein and cell count; and three indices: BPI, HWI and ASI.
- The implementation of genomics for Red Breeds will see some re-ranking of animals.
- Genotyping more Red Breeds (bulls and females) will increase accuracy and expand the number of traits with ABV(g)s.

DataGene has used genomics in the genetic evaluation of Holstein and Jersey animals for 10 years.

It has been more challenging to implement genomics for Red Breeds due to the smaller population of the breed.

Test runs of genomic Australian Breeding Values – ABVs – for Red Breeds began in December 2020. This Technote provides information about the implementation process and what farmers can expect from the figures available initially.

Using female genomics

Female genomic testing can be used for parentage discovery and parentage confirmation as well as to provide an ABVg that can be used to predict the cow's future performance and breeding potential. Genomic testing can be done at a very young age, allowing decisions to be made long before a heifer enters the milking herd.

Parentage discovery and confirmation allows you to correct errors in pedigree recording and calf identification. This is particularly useful in larger herds or in herds where there is a large number of cows calving in a short period of time.

Female ABVs can be used to identify and determine:

- The best replacements to enter the herd.
- The lower genetic merit heifers to avoid bringing into the herd.
- Females to breed replacement heifers (e.g. candidates for sexed semen)
- Females to breed non-replacements (e.g. use beef semen).
- The herd's average genetic merit and monitor genetic progress over time.
- Females which bull companies select to breed the next generation of bulls.

Red Breeds

Genomic ABVs are available for genotyped animals where the breed of analysis is Aussie Red (U), Ayrshire (A), Illawarra (I), D (Dairy Shorthorn) or for cross bred animals sired by a bull from the U, A, I or D breeds.

Genomic traits

At this stage, genomic traits are available for four traits in Red Breeds:

- Milk (L)
- Fat (kg)
- Protein (kg)
- Cell Count.

These traits have the greatest amount of data because they are collected with every herd test activity.

The indices, Balanced Performance Index (BPI), Health Weighted Index (HWI) and Australian Selection Index (ASI) also include genomics as Milk, Fat, Protein and Cell Count ABVs contribute to the indices.

Reliability

Reliability is a measure of confidence in an ABV. The reliability of an animal's breeding values improves with age as more information becomes available, for example, genomics, performance records and herd test results (see table over page).

The reliability gain from genomics is greatest for young bulls and heifers as these animals have very limited performance records.

For bulls without daughters, the average reliability gain production traits improves from about 30% to 58% and from 24% to 54% for cell count.

For young females without their own performance records, the average reliability for production traits improves from about 27% to 52%. Cell count reliability improves from about 21% to about 48%.

The reliability of the SCC ABV(g) for a young heifer without records is as good as that for a cow with 10 tests. For production traits, 10 herd tests still gives a higher reliability than genomics.

Reliability of genomic ABVs: Red Breeds (July 2021)				
Trait	Reliability (%)			
	Protein kg	SCC	BPI	HWI
Young bull (no genomics)	43	40	37	34
Young genotyped bull	59	58	46	40
Young heifer (no genomics)	47	44	41	37
Young genotyped heifer	59	58	48	42
Cows with 3 or more lactations and no genomics	69	55	57	49
Cows with 3 or more lactations and genomics	71	60	59	51

Calculating Red Breed ABVs

Two modern tools underpin the release of genomics for Red Breeds: a new, high density chip and a single-step estimation of genomic breeding values (see next section).

The high-density chip contains 64% more DNA markers which contributes to improved reliability. The high density 'chip' is a combination of the Agriculture Victoria XT50 chip and the current 50K chip that has been the standard chip since the inception of genomics. All historic and new genotypes will be imputed up to this combined 'chip'. This means that chips used by genomic service providers that do not have a large overlap with the XT50 will be just as good as in the past, but addition of XT50 markers over time would increase accuracy, especially for small breeds (Red Breeds) and crossbreds.

Single-step analysis

DataGene uses a different method for calculating genomic ABVs for Red Breeds than other breeds.

Red Breed ABVs are estimated using performance records, pedigree and genotypes on an animal and its relatives in a single analysis. This is called single-step analysis.

In Australia, Red Breeds are the first ABVs to be calculated using single-step analysis.

Single-step is a more streamlined process compared with the traditional approach of calculating genomic and pedigree relationships separately and then combining them.

Single-step analysis is considered the international gold standard. Dairy genetic evaluation systems around the world are progressively moving to single-step processes over time.

The advantages single-step over the traditional multi-step model are:

- Accounting for selection bias (where the better animals are more likely to be genotyped).
- ABVs of ungenotyped animals can include a portion of genomics from genotyped relatives. For instance, the ABV for a young ungenotyped daughter of two genotyped parents will be the average of the parents' final ABV.
- Efficiency - it eliminates the step that combines multiple separate analyses.

Red Breed animals that receive ABV(g)s

Genotyped Red Breed bulls and females receive ABV(g)s. In addition, relatives of genotyped animals get a proportion of the genomics, for instance the parent average for a non-genotyped animal is the average of the parents' ABV(g). Red Breeds are the first in Australia to have parent averages calculated this way. It is one of the benefits of the single-step process.

Incorporating the genomics from relatives improves the reliability of an animal's ABVs but it is still less reliable than genotyping the animal itself. Therefore, there is no indication in reports if an animal's ABVs include genomics from relatives. Where reports state genomics included – ABV(g), this indicates an animal has been genotyped.

The data challenge

The table below shows the data sources used in DataGene's initial calculation of Red Breed genomics. It's based on 623 bulls and 7,015 females with genotypes. There are 143 herds with genotyped females.

Genotyping more Red Breed animals holds the key to improving reliability and expanding the number of traits with genomic ABVs.

Data sources for Red Breed genomics (July 2021)	
Data item	Size
Bulls with genotypes	623
Total number of bulls evaluated	28,390
Cows with genotypes	7,015
Number of herds with genotyped cows	143
Pedigree size (total animals evaluated)	775,466
Test day records used in the analysis	3,283,728
Cows with observations	246,787

Read more

[TechNote 6: Female ABVs](#)

[TechNote 13 Reading female ABV reports](#)

[TechNote 21 Genomic testing process](#)

[TechNote 23 Quality reports for genomic service providers](#)

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