

Is there a genomic revolution going on?

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Introduction

It should be becoming clear to the global beef industry that DNA-based technologies are with us to stay.

While progress with genomics (genetics at the DNA level) in the beef industry has been slow, it has been strongly embraced by the global dairy industry where accuracies of 0.7 (accuracies range from 0 to 1.0) for traits are now common.

In dairy breeding genomic testing has nearly replaced progeny testing; so important because prior to genomics a breeder could not get good data on milk production traits until a bull's daughters were being milked. By cutting out progeny testing, global dairy industries have saved millions of dollars that previously went into annual progeny testing of young bulls.

It is now clear that some breeds or beef breeding groups will go forward with the genomic technology, while others will drop out of the race or not even start. That raises the question in my mind; will the breeds that embrace the DNA technologies go forward with strength while the breeds that ignore the technologies disappear over time?

DNA technologies are now used for the following purposes in beef:

1. Parentage verification
2. Genetic defect testing e.g. breed-specific defects
3. Genetic condition testing e.g. red/black colour, horn/poll
4. Branded beef verification/validation – e.g. Certified Australian Angus Beef
5. DNA traceability – relating a piece of meat to a carcass or a live animal
6. Tests for production traits – calving ease, birth and final weight, scan eye muscle area, scan intra muscular fat (IMF or marbling)
7. Tests for difficult to measure traits e.g. tenderness, temperament, tick resistance.
8. Tests for costly to measure traits – Net Feed Efficiency, longevity, female fertility e.g. age at puberty

Technologies 1–5 above will definitely go forward across the beef world as laboratory capacity grows to service the increasing demand for these tests.

My recommendation to beef seedstock producers and breed associations is to move forward quickly with technologies (1-5) and utilise them to increase the quality control of our genetic information systems e.g. if we don't have correct pedigrees on a sire then the DEPs will not be correct. DNA traceability and source verification of beef is also important for consumer faith in our products often substituted in former times.

The better the information we can glean on an animal's genotype for a particular trait or condition earlier in its life, the better will be the genetic improvement.

Early promise of genomics

It was the promise of being able to pull a tail hair, send it to a laboratory for testing of the DNA and to receive back a result to rank animals for traits that are hard-to-measure or costly to measure that attracted me in the first place to genomics. As a beef genetics consultant the potential of that tool seemed great when I first became involved with GeneStar in 2000.

That promise still holds for the technology, but as time has passed we have learned that success for many traits will be hard won and there is still a strong effort needed especially from the cattle producers.

The rest of this article deals with the research and development of DNA marker tests for those traits for which we have had Estimated Breeding Values (EBVs) or Expected progeny Differences (1/2 an EBV, the transmitting ability of the animal) for up to thirty years.

The Early Days

At the beginning of the genomics era, geneticists thought they were looking for a small number of genes of large effects on the genetic merit of an animal. This 'pot of gold' was chased for a few years but then came the realisation that the polygenic traits were under the control of many thousands of genes, each with a very small effect, with a few exceptions.

In the early research it was thought that tests would be developed for production traits that would work across-breed. Now we know that the tests are really breed-specific.

The research then moved from analysis of a few DNA markers with a small diagnostic chip to larger diagnostic chips to the point that today it is relatively common at the research level to sequence the entire genome of an animal.

Researchers now produce equations that weight the effect of each SNP (simply a type of DNA marker) in a 770K (K=1000) marker genotype and calculate its correlation or association with the traits of interest. They then combine the results into a single overall estimate of an animal's genetic merit for a particular trait measured in a breeding program. The equations are called prediction equations and the single estimate is known as a Direct Genomic Value (DGV).

This DGV can be used alone to rank animals for a trait or more commonly it is integrated into an existing EBV or DEP to increase the Accuracy of the breeding value.

How do you produce a DGV?

Fifteen years into the beef genomics era there now exists a recognised set of steps to achieve DGV's that have utility for successful beef breeding.

Training Step

1. **Record phenotypes (performance) records.** You have to record an animal's performance (phenotype) for a range of traits in a breeding program where animals (treated equally) are run together in well-recorded contemporary groups. Thousands of records are better than hundreds. EBVs/DEPs are preferred in this step.
2. **Extract DNA.** Tail hairs (or other tissues) are sampled from each animal recorded and sent to a laboratory so that a DNA sample is obtained.
3. **Genotype the DNA .** That DNA is then used to determine the animal's genotype using a 50K SNP chip, or for some animals a denser chip with 770K SNPs.
4. **Calculate the DGVs.** The set of genotypes and performance records (phenotype) for a defined group or population of animals is known as the "Training set" or "Discovery set".

This step is to establish the relationship between each individual SNP and measured performance for each recorded trait.

This step produces the prediction equations for this group of animals of one breed or sometimes representatives of more than one breed.

Validation or Integration Step

5. **Calibration step.** The DGVs are validated on an independent or a "Calibration set" of animals. EBVs/DEPs are commonly used in this step.
It is 'true' validation when the prediction equations are calibrated in a population totally independent of the original discovery population however, given the numbers required, a truly independent population of the breed may not be available. In this case the calibration is calculated on animals kept aside from the original training set.
This step then determines the correlation between the DGVs and EBV/DEP traits from the genetic evaluation scheme. The correlation calculated is the accuracy of the DGV in predicting the EBV/DEP trait.

Using the DGVs

6. Commercial tests are then developed in a laboratory that producers can buy. Results (DGVs) can be sent back to the producer or increasingly they are incorporated into an EBV or DEP – a "genomic-enhanced EBV or DEP".
7. Once some thousands of tests have been sold, the geneticists can then conduct a re-calibration (updating steps 4 & 5) to improve the correlations now based on many more thousands of phenotypes.

State of play in the Australian beef industry

The tenderness markers (calpain and calpastatin) were released early in the 2000s and are very effective and have positive effects on tenderness and palatability of beef for all breeds.

We also have a useful Horn/Poll test that caters quite well for the *Bos indicus* and *Bos-indicus* derived breeds.

The Zoetis (formerly Pfizer) Angus HD 50K test was released in Jan 2010 in US and April 2010 in ANZ. It shows accuracies of between 0.38-0.77 for 16 traits in US and 0.20 to

0.46 for 12 traits in Australia & New Zealand. A similar Angus test from the same company in USA has now been re-calibrated after c. 50,000 tests have been purchased and now has some traits approaching 0.8 accuracy. For other breeds there is little progress at this stage with accuracies lower than 0.2.

Beef Information Nucleus

To build up thousands of phenotypes for future genomic analyses, a number of breeds have developed designed progeny tests where over a five to seven year period they will collect many performance and carcass records on recorded animals of known pedigrees. A key trait to be recorded is individual net feed efficiency (residual feed intake), a trait of high economic importance and really difficult to measure by the seedstock industry

The Angus breed is leading this type of research in Australia just as it did in the use of EBVs and \$ Indices.

Genetic analysis

Australia's national beef genetic evaluation system BREEDPLAN has developed the methods to integrate genomic information into its EBVs/DEPs. They are well advanced in developing the 'single-step' method of developing EBVs directly from the genotype.

Not a silver bullet!

After 15 years of research and development around the world it is now clear that genomics is not a silver bullet. Nor does it mean that cattle breeders can give up measuring performance traits.

In fact the need for careful recording of performance is as important as ever and for the future of genomics for traits of low heritability it will require large databases with many thousands of records.

Conclusions

The global beef industry has lagged behind the dairy industry in the use of genomics. This is because the beef industry has not collected and does not have the thousands of phenotypes for many traits that the dairy industries have and the effective population size differs significantly.

Beef breeds or breeding groups must invest in many thousands of phenotypes if they want to obtain genomic tests that give accuracies over 0.5. This is vitally important for difficult to measure traits or traits that are recorded later in life (maternal traits) or those expensive to measure e.g. individual feed intake.

It is important to approach the validation phase carefully. Using an independent data set is important for specific breed tests. If not carefully approached the accuracy may be overestimated.

The revolution is just starting.....

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