The Future Use of DNA Technologies in the Beef Industry

David Johnston

- DNA technologies have several potential uses in the cattle industry. In this paper, these are discussed in two groupings: **Genetic prediction** and **Phenotypic uses**.

- **Genetic predicition** eg improving genetics and predicting outcomes of matings

1. Parentage verification
2. Gene and gene marker assisted selection
3. Monitoring and avoiding inbreeding
4. Avoiding genetic disorders

- **Phenotypic uses** ie describing a current group of cattle

1. Predicting the characteristics of a group of cattle. Eg drafting at feedlot entry into groups for differential feeding according to their marbling potential
2. Trace backs on live cattle or meat
3. Transgenics. This is expected to first be used for production of pharmaceuticals. Transgenic animals may also be possible in the future, by introducing genes from other species eg for disease resistance

Introduction

The mapping of the human genome in 2000 signalled to the world a new era in scientific discovery called the "genetics revolution". In the 50 years since the publication of the structure of DNA molecular biologists have been unravelling the amazing properties of this molecule of inheritance at an exponential rate. Spin-offs have already occurred for the beef industry, including the development of new powerful tools (e.g. DNA finger printing) and the discovery of many hundreds of individual bovine genes. Gene discovery is now reasonably simple and well understood, however the latest hot area of research is gene expression and regulation (functional genomics) and this is where the beef industry could benefit in the next 5-10 years. Australia is well positioned to play a leading role in this emerging field. The CRC for Cattle and Beef Quality functional genomics project is researching the changes in gene expression (e.g. marbling genes) over time, treatments or in different tissues. Other CRC projects also exist that aim to "develop genetic marker technologies that enhance selection techniques and ensure the production efficiency, product quality and consistent supply of domestic and export cattle".

The challenge, and opportunity, is to move the technology from a research medium to putting dollars in a commercial cattle producers' pockets. Some benefits are already available to breeding sector, however the prediction is that in the future DNA based technologies will benefit the commercial sectors (cow/calf, feedlot) and even the processing sector of the beef industry. Several Australian groups have been set up in the last 10 years and are offering a range of DNA services and products to Australian beef producers. The aim of this brief discussion paper is to outline some of the potential uses of DNA information to enhance existing methods of selection or to manage commercial cattle more profitably in the future.

Using DNA Technologies

Genetic prediction

Breeding is about selecting/controlling who will be the parents of the next generation. In some beef herds this is achieved by simple culling whilst in others it involves identifying superior genetics. This has been achieved through a progression of tools over the past 3 decades such as contemporary ratios, estimated breeding values (EBV), selection indexes ($EBV) and more recently gene marker information. Development of sophisticated statistical techniques, coupled with an explosion of computer power and advances in performance recording (e.g. the use of real time ultra sound scanning) has increased the accuracy to predict the superior parents, and through selection has resulted in significant improvement a range of economically important traits over the past 2 decades. Constraints to this progress have been the low accuracy of some traits, primarily due to difficulties measuring the traits on large numbers of animals. EBVs are estimates, and the more information available, the better the estimate. The question is how will DNA technology help in animal breeding of the future with regard to genetic prediction.

(i) Parentage Verification

Using DNA fingerprinting technology it is now (and has been for almost a decade) possible to exclude, and therefore by inference, assign a sire and dam as being the putative parents of an individual. This has some very important uses in genetic prediction. DNA fingerprinting allows the progeny generated from multiple sire (MS) matings (i.e. more than 1 sire in a mating group of females) to be sire identified based on the exclusion of all other sires. This has implications for the genetic evaluation, particularly for more extensively managed breeds in Northern Australia.

Assignment of sires in MS groups allow the pedigree information to contribute optimally to the genetic analysis and 'sire identified' multiple sire mating create better genetic linkage across years and also increase the effective number of direct comparisons (i.e. more effective progeny numbers) thus improving the accuracy of the EBVs.

Sire identification using this technology also has benefits for progeny test programs (commonly for abattoir carcase traits) from commercial herds. More data from commercial herds may be captured for genetic evaluations but will require collecting key cohort information and will also require changes to the industry structure to then be able to use any superior sire identified back in the seedstock tier.

If DNA parentage verification was to be used on a more wide-scale basis across the seedstock industry it could lead to increased heritability estimates due to improvements from the current level of mis-identification of pedigrees in seedstock field data has been estimated to be 5-15%.

It should be noted that DNA fingerprinting does not currently give 100% assignment rates and often the results are accompanied with a probability. For sire assignment from multiple sire joining groups the task is dependent on the number of markers used and how polymorphic they are, how many sires are present and the relatedness of the sires, and whether the dam genotype is known. It is important that the accuracy of parent assignment continues to improve. Also if the industry is using this technology that they are advised on what they can do to optimise future assignment rate.

(ii) Gene assisted section (GAS) and Marker assisted selection (MAS)

The DNA technology has move beyond the DNA fingerprinting capacity (which generally relies on anonymous sections of the chromosome) to identifying specific regions of the genome that are associated with observed differences in a phenotypic traits.

These regions are called quantitative trait loci (QTL) or more commonly flanked by linked markers (an identifiable regions both sides of the QTL). The question is how can gene markers (MAS) and genes (GAS) be used in future selection decisions?

Theoretically it has been determined that QTL information for a trait that currently exists in a genetic evaluation (ie has and EBV) when included will increase the accuracy of the EBV for the trait, reduce the generation interval and therefore increase the genetic progress achieved. For further details see the review of Goddard and Hayes (2002).

In summary the current knowledge supports the view that DNA data will contribute relatively more to traits with low heritabilities and those expressed in one sex or late in life. This is because the genotyping can occur at a very early age and therefore removing the need for progeny testing and can be done before selection decisions are commonly made.

The larger the size of the effect of the QTL and the lower the initial frequency of the favourable allele (i.e. form of the gene) the larger will be the response. But of course we are rarely interested in improving just one trait so it is the effect of the QTL on the total breeding objective that needs to be established.

One of the current constraints with linked markers (MAS) is the need to establish linkage phase in each sire family through progeny testing. For large operations (e.g. pastoral companies) this may be possible but for the majority of cattle breeders it is likely that only direct markers will be of use.

Research into incorporating DNA information into exist BLUP genetic evaluations is underway (e.g. Fernando and Grossman 1989, Tier and Bunter 2003) but requires the ability to cope with different data structures (e.g. proportion of animals with genotypes), a population estimate of gene frequency, an accurate estimate of size of effect on all existing traits and lastly the availability of unselected genotypic data.

Several strategies have been proposed to optimise genotyping in populations to minimise the cost but maximise the benefits.

(iii) Monitoring and controlling inbreeding

Researchers, through the use of simulation studies have hypothesised that gene markers could be used to monitor and control inbreeding at the individual locus level.

Current methods of estimating the inbreeding level of an individual are based on the probability that two genes at any locus are identical by decent (i.e. came from the same ancestor). DNA technology offers a more precise method for assessing inbreeding, provided sufficient numbers of genes are tested.

(iv) Avoiding genetic disorders

DNA testing for genetic disorders provides a powerful tool to avoid the propagation of these harmful genes through breeding.

Commonly gene disorders are caused by single genes that are recessive and therefore difficult to determine without test matings. When a DNA test is developed for a particular genetic disease it could be used as a screening tool, particularly for animals that will be widely used in a population e.g. AI sires, ET donor cows.

Phenotypic uses

(i) Prediction

DNA technology is also being developed as a tool for determining the phenotypic potential of animals. It is proposed this will allow producers, feedlotter and even processor to sort and manage cattle according to their DNA profiles.

US company MMIgenomics is leading the way in the beef industry with an ambitious project involving the use of 600,000 single nucleotide polymorphisms (SNPs) where their aim is to use the technology to allow breeders and feedlotters to meet consumer demands for product consistency and tenderness.

For example it is hoped that cattle can be sorted into particular feeding regimes based on their gene profiles for traits such as marbling. The success of this technology will depend on the ability to find enough SNP's that explain a significant amount of the observed variation in the trait and is cost effective. It will also be possible for the SNP technology to be used to select seedstock with particular gene profiles.

(ii) Trace back (live animal and meat)

DNA testing is currently used as a failsafe method of traceability and are likely to increase in use in the future as a valuable tool for ensuring product quality and safety.

SureTRAK is a DNA product from the company Genetic Solutions that "allows complete traceability of meat through the production chain". The same DNA fingerprinting technique could be used as a "permanent" unique identification system of all live animals and may serve as a useful tool in the future to control stock theft.

Transgenics

DNA technologies also encompass the developing area of gene manipulation through the development of transgenics or via gene therapy. That is, introducing genetic material from one organism to another. Although the production of transgenic animals has been around since the 1970s, the advances in DNA technologies is certainly enhancing this field. I expect the greatest advantages from gene manipulation will come through the production of pharmaceuticals but in the future there may be applications in beef breeding and commercial production, possibly for traits associated with disease resistance.

Currently the cost of developing transgenics is extremely high (mainly due to the inefficiency of the current process) and there are several human and animal ethics issues will also need to be resolved.

What else is needed?

For DNA technologies to be adopted widely by the beef industry the increased gains from MAS or GAS must outweigh cost of genotyping. For this to occur it is likely that at least a couple of the QTLs affecting a trait are known and can be genotyped simultaneously on key animals.

Current limitations on the precision of DNA tests, and inaccurate estimates of the size of the effects must be considered.

Like all technologies we can almost be certain that the cost of receiving DNA information will decrease as the technology matures (i.e. move to SNPs technology and high throughput sequencers) but in the short to medium term it must be viewed as a constraint to the wide-scale adoption of the technology and its use in selection.

Conclusions

We are only in the early days of the DNA testing and application to the beef industry. The technology is likely to be most beneficial in increasing the accuracy of EBVs of traits that are difficult or expensive to measure, or are expressed later in life.

For beef, these currently include female fertility and longevity, feed efficiency and meat tenderness. However in the short to medium term there will be a need to collect phenotypic information on these traits both to provide data for the computation of EBVs but also data to test new direct or linked markers.

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References

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RANGERS VALLEY
1996 LOT FEEDER OF THE YEAR
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NATIONAL GRAIN FED BEEF COMPETITION 2000 JAPAN B3 + FEEDLOT CATEGORY WINNER
NATIONAL GRAIN FED BEEF COMPETITION 2000 JAPAN B3 + FEEDLOT CATEGORY RUNNERUP