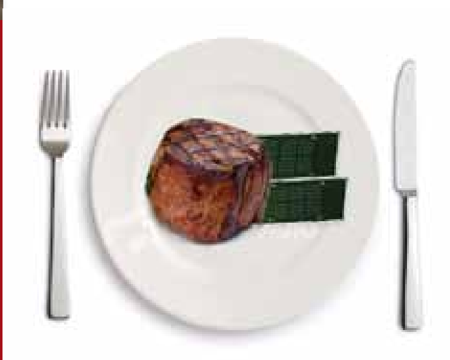
Beef Bulletin

July 2010

DNA markers for beef traits: do they work?

New Australian polled gene test



Beef and chips:

Key issues for the beef industry about DNA markers and gene discovery

Beef CRC photo competition

About the Beef CRC

The Co-operative Research Centre for Beef Genetic Technologies aims to add $179 million dollars to the value of the Australian and New Zealand Beef industries each year from 2012. Our focus is on world-class gene discovery and gene expression research to improve profitability, productivity and animal welfare.

MISSION

To capture the benefits of the human and bovine genome projects and the "Livestock Revolution" by improving the profitability, productivity, animal welfare and responsible resource use of Australian and global beef businesses through worldclass gene discover and gene expression research and accelerated adoption of beef industry technologies.

Dr Heather Burrow, Chief Executive Officer

Dr Burrow has over 30 years quantitative genetics R&D experience, specializing in genetic improvement of tropically adapted beef cattle.

Mr Neil Scholes-Robertson, Company Secretary

Mr Scholes-Robertson holds a Bachelor of Business and qualified as a Chartered Accountant.

Dr Greg Robbins, non-executive Director

Dr Robbins is General Manager of Animal Science for the Queensland Department of Primary Industries and Fisheries (QDPI&F) and former Director of the Queensland Beef Industry Institute.

Beef CRC Governing Board

Dr Guy Fitzhardinge, Chairman

Dr Fitzhardinge is a commercial cattle producer from NSW, a past member of the Boards of Meat Research Corporation and Meat and Livestock Australia.

Dr Keith Steele, Deputy Chairman

Dr Steele is a business advisor with beef R&D management experience, genomics knowledge and corporate governance and finance skills.

Mr Rob Backus, non-executive Director

Mr Backus brings northern beef sector and feedlot expertise and knowledge of the industry relevance of genomics to the Board.

Mrs Emma Robinson, non-executive Director

Mrs Robinson is a large successful beef producer in central Queensland and has extensive beef enterprise technology extension experience.

Mr Richard Rains, non-executive Director

Mr Richard Rains is the Chief Executive Officer of Sanger Australia Pty Ltd, an international meat trading business.

Mrs Robyn Clubb, non-executive Director

Mrs Clubb has extensive financial, management and accounting experience as well as a strong rural background and successful operator of a significant cattle enterprise in southern NSW.

Dr Jay Hetzel, non-executive Director

Dr Hetzel has worked for over 30 years in cattle genetics and genomics research and commercialisation.

From the CEO

DNA markers offer much promise for providing accurate genetic information about animals carrying important production traits, but what has been achieved to date?

This edition of the Beef Bulletin looks at DNA technologies now commonly used by industry, new products and the latest developments in research.

The first wave of genomic experiments to identify genes yielded some early success stories. Early research picked up genes that have a large size or effect, such as the genes influencing meat tenderness. The polled gene is another example of where just a few genes have a major effect. The 'big genes' enabled effective, accurate DNA tests to be developed for those traits.

However, what has emerged with ongoing research is that the incidence of these big genes is rare and important production traits like feed efficiency, growth rate, fertility and carcase and meat quality are influenced by hundreds, even thousands, of genes. These production traits have always been difficult to measure, as has understanding their biology.

Undoubtedly, DNA fingerprinting and DNA markers will play an important role in building the accuracy of our existing genetic and phenotypic knowledge base to improve breeding for hard-to-measure traits. But genomic science will not overturn all that has come before. Rather the new science will best be integrated into existing industry systems such as MSA and BREEDPLAN.

DNA technologies such as pedigree testing and screening for disease have been successfully implemented by industry over the past decade but the beef industry faces major challenges to keep up with the rapidly developing new DNA 'chips' that record vast numbers of DNA variants for important traits. They also face challenges validating this new information in unrelated cattle populations, and across breeds.

Although this job is not easy, it does not mean it should not be done, particularly when the likely benefits to industry are so great.

The beef industry has yet to reap the production gains from genetic improvements enjoyed by the dairy industry. Unlike dairy, beef genetic tools must work across different breeds. Some DNA tests and markers do this well but most do not.

The Beef CRC continues to undertake research in conjunction with its national and international partners to identify DNA markers for complex, hard-to-measure traits. Once these markers are located, virtually any measurable characteristic will be traced to a specific stretch of DNA. We anticipate that by the end of 2011, we will deliver DNA technologies associated with many complex traits and validated for industry use across Australia, USA and Canada.

On a personal note, I would like to advise readers that Alison Betts, former Editor of the Beef Bulletin, has resigned from the Beef CRC to devote time to raising her new-born daughter. I welcome livestock and technology communication specialists Rob Nethery and Margaret Puls to the team. Margaret has developed the content and new style of this edition of the Beef Bulletin. I hope you enjoy it.

Dr. Heather Burrow

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SUPPORTING PARTICIPANTS

A plain English guide to DNA technology for livestock

Over the millennia improvements in selective breeding of livestock have traditionally been based on studying the characteristics of animals that are easy to observe or measure, their phenotypes.

However, these traits ultimately depend on the information contained in an animal's DNA. It is DNA that is actually being "crossed" when animals bred.

Geneticists track phenotypic features such as fat content in livestock or milk production in dairy cattle to identify individuals whose offspring are likely to be superior for these traits.

Techniques to analyse DNA, developed over the last twenty years, are now enabling breeders to locate specific genes or chromosome regions (or DNA markers close to those genes or regions) that correspond to important production traits. Using these techniques, breeders can more quickly and accurately choose superior animals for breeding, speeding the overall process of genetic improvement.

DNA Fingerprinting

The characteristics of all living organisms, including humans, are essentially determined by information contained within the DNA inherited from their parents. DNA directs how cells develop and controls the way characteristics are passed on from one generation to the next.

Animals that have different characteristics also have different DNA sequences. DNA fingerprinting is a very quick way to analyse and compare variations in the DNA sequences of any living organisms.

DNA fingerprinting is now routinely used by animal breeders to identify parentage of seedstock animals, thereby allowing more accurate estimation of breeding values through genetic evaluation schemes such as BREEDPLAN.

It is also routinely used for identification or trace-back to better manage animals (e.g. to allocate sires to dams for breeding purposes) and/or to provide positive identification (e.g. in cases of stock theft or verification that products are true-to-label as required by some international markets).

Applications of Marker-Assisted Selection and Gene Mapping

A DNA marker is a piece of the DNA molecule that is close to a gene or chromosomal region. If the marker is found (through combined analyses of phenotypic or measured data and genotypic or DNA data) to be associated with an economically important trait of an organism, it can then be used to identify the genes that control those traits.

Marker-assisted selection is used with traditional genetic analysis of family pedigrees and breeding data to identify DNA markers associated with important traits.

In marker-assisted selection, a scientist who knows which piece of DNA is associated with a desirable trait can select animals that have that piece of DNA.

For example, if a DNA marker is often found in cattle that produce tender meat, it must be close to or include the section of DNA that controls meat tenderness. The more often the marker is found in animals that produce tender meat, the closer it is to the actual DNA segment that controls tenderness. A marker that is associated with a characteristic 90 percent of the time is closer than a marker found 60 percent of the time.

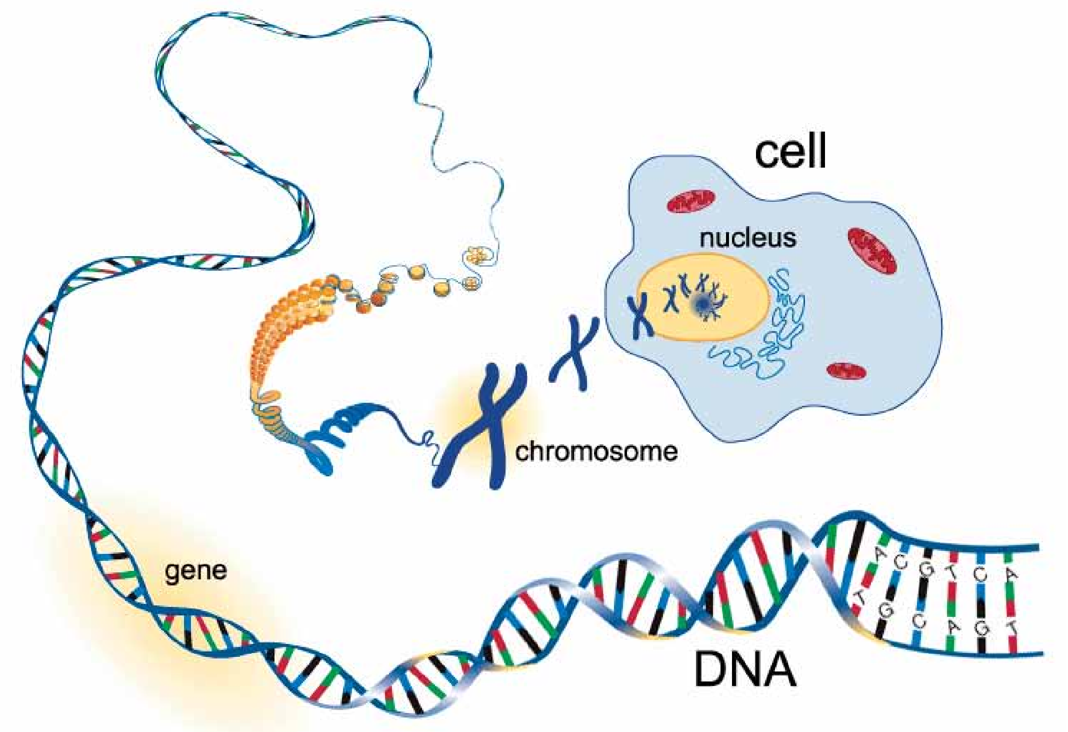
The goal is to locate markers at regular intervals along the DNA chromosomes, like the kilometre-markers along interstate highways.

Once markers are located, virtually any observable characteristic can be traced to a specific stretch of DNA by routine laboratory procedures.

Breeding

A breeder traditionally uses the appearance (phenotype) of an animal to judge the genotype (DNA) that animal has inherited.

DNA fingerprinting and marker-assisted selection can make the selection process more precise. They can also speed up the selection process and reduce the costs considerably. DNA tests can also be done at a very early stage, even in embryonic tissue.



DNA is carried in genes on chromosones from the nucleus of a cell
Image: http://elcamino.dnadirect.com/img/content/common/cellsToDNA.gif

DNA testing helps manage lurking recessive gene in Angus

DNA testing for the Angus recessive gene

Like the Trojan Horse, renown American Angus bulls GAR Precision 1680 (born 1990) and his son CA Future Direction 5321 (born 1995) came with a hidden surprise: recessive genes that shape curved hocks or big heads on calf foetuses, and then kill them before they are born.

Once, this genetic depth charge might have devastated the Angus industry.

Precision 1680 and Future Directions appear somewhere in the catalogues of most Australian Angus studs. The genetics of these bulls can take some of the credit for the roomy carcass that is powering the success of the breed today.

A couple of decades ago, the only way to root out the defective genes from the Angus breed would have been to stop using those sire lines. Angus Australia's chief executive Dr Peter Parnell says that's exactly what happened in the 1960s, when the lethal recessive gene Mannosidosis surfaced in the breed.

Fortunately, things had moved on when Precision 1680 and Future Direction were found in 2008 to be bearers of the lethal Arthrogryposis Multiplex (AM) and Neuropathic Hydrocephalus (NH) recessive gene conditions.

"Once this was identified as an issue, a scientist called John Beaver from the University of Illinois worked on a DNA test for both of those conditions, and was able to develop it in a reasonably swift time," Peter said.

"Our breeders have since tested tens of thousands of animals for that condition in the past 12 months."

> 'DNA testing helps us manage the problem of this recessive gene, whereas once we would have had to stop using those sire lines.'

Theoretically, DNA testing provides the ability to eradicate the lethal genes from the Angus herd. Practically, Peter says, the genes are now so widespread throughout the Angus herd that it is more sensible to manage the issue.

"The cow herds of many breeders will carry these genes, so it's impractical to try and eliminate all those carriers," he says. "But it is practical, through testing, to ensure you never use a bull that is a carrier. Eventually, they should become quite rare."

It's not mandatory for Angus Australia members to test for AM and NH, but the incentives are there to do so. AA publishes all testing on its website, and also calculates probabilities that animals are carriers based on their pedigrees.

Angus Australia's CEO Peter Parnell (right) with Rockdale's general manager Paul Troja and some grain fed scotch fillet. Image courtesy of Angus Australia.

Having a bull that is a carrier does not necessarily mean an expensive hamburger. Angus breeders who make full disclosure on a bull's carrier status often find a ready market in commercial producers wanting top genetics for a terminal crossbreeding program.

"The reality is, all animals and all humans carry at least some recessive genetics that can be either lethal or cause some major health problems. DNA testing means that for the first time, we can manage these issues and still maintain business pretty much as usual."

DNA marker FAQs

What is a DNA marker?

A DNA marker is a variation in the DNA code, mapped to a specific location in the genome. DNA markers can be genotyped and may be associated with one or more physical characteristics.

Are all DNA markers alike?

Markers can differ in mode of inheritance, physical size, functionality and how they are applied in genetic improvement. The prevailing type of marker now being used in DNA testing for traits is known as a single nucleotide polymorphism (SNP). SNP markers vary at a single base location in the genome, creating two different alleles (or forms) of the marker.

How accurate is an animal's marker genotype?

Modern genotyping technologies and applications are highly accurate. The techniques used to detect an animal's genotype are capable of identifying a change of a single base in an animal's genome at each DNA-marker location.

Will an animal's marker genotype change during its lifetime?

No, an individual's genotype is unique and fixed not long after fertilization of an egg by a sperm, and remains fixed throughout its lifetime.

Does a DNA marker only relate to one trait?

Many traits are genetically correlated to one another due to the fact that genes can impact multiple traits; for example, the effect of growth hormone on growth rate and carcass composition. Likewise, DNA markers that are either within these genes or linked to them are likely to have effects on multiple traits. It is also possible for a marker to have a positive effect for one trait and a negative effect for another.

Are economically relevant traits heritable?

Economically relevant traits vary in level of heritability, measured as the percentage of observed variation that is due to underlying gene effects that can be transmitted from one generation to another. While heritability may differ between populations, in general, traits such as fertility tend to be more lowly heritable than traits such as growth rate and tenderness, which exhibit moderate to high degrees of heritability.

Are the effects of DNA markers the same for different breed sub-populations around the world?

Often they are similar, although the more divergent or distant a population is from another, the greater chance there is for the effect of markers to vary. In beef cattle, the greatest expected differences are likely to occur between Bos Indicus and Bos Taurus sub-populations

The mother of 21st century cattle

A humble Hereford cow, known as Dominette 01449, has become the bovine genetic equivalent of Eve, by providing scientists with the first genetic blueprint for cattle.

Mapping the bovine genome has taken six years to complete and was only recently published in detail in 2009. The sequencing of the bovine genome was undertaken by an international team of scientists including CSIRO and AgResearch.

It turns out the bovine genome contains some 22,000 genes and 2,870 billion DNA building blocks and is much the same size of the human genome.

Dominette's genetic blueprint has been mapped a number of times to ensure detailed coverage, and compared to other breeds – Holstein, Angus, Jersey, Limousin, Norwegian Red and Brahman.

The bovine genome project data will underpin livestock research for the next 50 years. It will help identify animals that are better suited to a particular market or environment.

By selecting for feed efficiency, for example, it may be possible to decrease the environmental footprint of the beef industry.

The gene sequence information yielded from the bovine genome also has direct application to sheep research, due to the close relatedness of the two species.

The DNA of this Hereford cow provides the blueprint for the bovine genome

Drilling into DNA

The complete DNA makeup of an animal is called its genome.

Breeding good cattle was once a craft, a combination of experience and educated guesswork. The craft is still there, but science is rapidly replacing the guesswork.

This is particularly true of DNA testing, a relatively recent scientific development that allows breeders to look into the physical animal and see the genetic patterns that form it.

DNA—shorthand for deoxyribonucleic acid—is life's instruction manual. Within its famous double helix are the on-off switches that describe all the nameable characteristics of living things: blue eyes, butterfly wings, horns or polls, white faces on red cattle, white faces on black.

In fact, the tendency of a bull to throw calves with either red or black coats is now one of a range of DNA tests that Australian breeders can use to peek "under the bonnet" of their breeding program.

Also available are DNA tests for the lethal Mannosidosis genetic deformation in Angus and Murray Greys; inherited congenital myoclonus in Poll Herefords; congenital myasthenic syndrome in Brahmans; myophosphorylase deficiency in Charolais; protoporphyria in Limousins and Pompes disease in Brahmans and Poll Shorthorns.

Once, discovering that a pedigree bloodline came with these built-in genetic defects meant throwing out the whole bloodline. DNA testing means that the advantages of the bloodline can be retained, but that the animals likely to pass on the defect can be screened out.

DNA testing is also taking much of the guesswork out of assigning parentage, revolutionising herd management at mating for stud breeders.

"We're talking about the ability of a test to properly exclude an incorrect animal. A breeder querying the parentage of an animal through DNA testing will find out for certain which animals or pedigree lines are not involved in the parentage of their animal."

Single-sire mating is still a guarantee of genetic purity, but DNA testing of calves from multiple-sire matings can do a similar job.

Dr Dianne Vankan, founder of UQ's Animal Genetics Laboratory, says the key to understanding DNA testing for parentage is to realise that it is a process of exclusion.

"When we talk about accuracy, we're talking about the ability of a test to properly exclude an incorrect animal," she explains. "It's more a matter of probabilities than finding an absolute 'yes/no' answer."

That means that a breeder querying the parentage of an animal through DNA testing will find out for certain which animals or pedigree lines are not involved in the parentage of their animal, but they can never be 100% certain that the qualifying parents were actually involved.

Some cattle populations have less genetic diversity than others, making the results less accurate.

DNA marker testing can also help researchers identify sequences of DNA that are highly correlated with certain production traits, such as beef tenderness. These traits result from the actions and interactions of many different genes.

Further complexity comes from the fact that the same DNA sequence can mean slightly different things in different breeds. In some, the sequence will indicate a definite impact on the trait whereas in other breeds there may be no impact. Many traits have either not been worked into a DNA test, or come from such a complex interaction of genes that it is difficult to accurately test for the trait's existence.

Some of this complexity is being addressed by the development of large SNP (single-nucleotide polymorphism – known as "snip chips") panels, which can contain a huge amount of DNA marker information that can be very quickly analysed. SNP panels can be used to asses for production traits as well as parentage.

Polled gene test: Industry feedback

Why I like polled beasts

"There are two main reasons why I like polled cattle. You can fit an extra two beasts on each truck deck; that equates to a considerable saving in freight costs. It's also much safer for people handling the cattle. You might get a few bruises from a polled bullock, but you won't get gored. I previously selected polled heifers and bulls in preference to cattle with horns. But that has meant a smaller pool of cattle to choose from. This could be why some people think breeding polled cattle negatively affects productivity. But you have to remember that Rome wasn't built in a day. If you try and eliminate horns over night by selecting only polled animals you could well be losing productivity in other areas. I welcome a test where a producer is told straight away whether a beast is going to produce a calf with horns or not. That will allow us to make our selections much earlier when we have bigger mobs of cattle to choose from."

-Tom Mann, Hillgrove Station, north of Charters Towers, is around 42,500 hectares and carries between 5000 and 8000 head of cattle.

Tom Mann

Northern Australian industry welcomes polled test

"The northern beef industry has long championed for research into an Australian test for horning. There are real welfare and productivity gains to be made from introducing more polled cattle into the herd. Because cattle in the North are often run in extensive production systems, you may not see a calf until it is 6-12 months old. Dehorning older calves involves greater welfare considerations and is more labour intensive. Now producers in Northern Australia can be confident of getting an animal homozygous for the polled gene and whose calves will be polled, which in the long-term will help breed out horns. The test enables you to make genetic progress more quickly by knowing if your animal is homozygous or heterozygous. There are a lot of breeders in Northern Australia making good progress on getting animals into polled herds. What the gene marker does is just provide an additional tool to speed up that process, and provide a higher level of confidence. But we need to know how well the test works in wider populations first."

- Wayne Hall, Manager Northern Production Research, Meat and Livestock Australia

Alex McDonald

The Limousin experience with polled gene testing

"Limousin breeders have now been using overseas horn/poll tests for about five years. Limousin breeders have tested over 300 animals because homozygous polled animals are worth significantly more than heterozygous polled animals. The cost of the test has varied from $88USto $120US and our experience is that it is not 100% accurate and we get an unacceptable level of "no results". We understand that the Australian test also will not be 100% accurate but we are looking forward to validating it for the Limousin breed. We need to know how accurate the test is but a test of above 90 percent accuracy will be very valuable for increasing the level of polledness in the Limousin breed."

- Alex McDonald, General Manager, Australian Limousin Breeders' Association

A genetic marker for polled Australian beef cattle

Breeding for polledness will boost welfare and profitability of the Australian beef industry

A new DNA test to screen for the genes associated with polledness in cattle will be available for industry to validate in cattle populations in August.

The test is being released at a discount rate during the validation phase of its efficacy, to confirm its accuracy in wider cattle populations.

A large proportion of the Australian beef herd is horned, and dehorning is routinely practiced to prevent bruising, hide damage and injury.

Dehorning is recommended at a young age but sometimes must be practiced on older calves, which costs more and can result in more pain and secondary infections for the animal.The value from reduced mortalities due to de-horning is estimated as $1.70 per weaner.

Using bulls tested to be true polled (homozygous) will allow rapid introduction of polled animals into Australian beef cattle herds and phase out the practice of dehorning.

The inheritance of horns is reasonably well understood in Bos taurus and European breeds.The Beef CRC and its partners (CSIRO, Meat and Livestock Australia and AGBU) wanted to develop a test that was accurate for Australian cattle populations and particularly for Bos indicus breeds.

The test was developed for Australian Brahmans and has already been evaluated in Brahman, Santa Gertrudis, Droughtmaster, Hereford, Limousin, Brangus and Belmont Red breeds.The test will be offered by University of Queensland's Animal Genetics Laboratory at a cost of $33.00 (including GST), which is further discounted if the tests are done through breed societies or in bulk. The aim is to validate the test's accuracy in greater numbers and different breeds of cattle, and to collect information on the frequency of the poll gene in those animals.

A polled bull may still carry the gene for horns

Because the poll gene is actually dominant over the horn gene in European breeds, a bull may look polled but still carry a single copy of the horn gene which can be inherited by his calves. **Table 1: Possible genetic combinations for the polled and horned phenotypes**

Genotype (test results)	Phenotype	Description
PP (homozygous) True polled	Polled	The animal carries two copies of the dominant polled gene alleles and throws predominantly polled calves.
PH (heterozygous)	Polled and scurred	The animal is polled but carries a copy of the recessive gene marker for horns and will throw a proportion of horned calves. This genotype is also associated with scurs.
HH (horned)	Horned	The animal possesses a double copy of the recessive gene alleles and will throw horned calves.

How well does the Australian poll gene test work across breeds?

Beef CRC trials with 1264 cattle over 15 properties across Australia shows the poll gene marker is strongly associated with polledness in beef cattle.

However, the test is not 100% accurate. Research conducted on this marker to date suggests the test accuracy varies between breeds, though the numbers of animals tested is still relatively small.

Seven breeds have been tested: Brahman, Santa Gertrudis, Droughtmaster, Limousin, Hereford, Brangus and Belmont Red.

In these breeds, the accuracy of a homozygous polled animal being polled is approximately 90%. However, further data are required to validate these findings in wider cattle populations.

A full description of the data analysis is available from the Beef CRC and will be made publicly available.

Summary of results:

Of the animals found to be homozygous for the allele associated with polled (PP), or true polled, in most breeds all, or almost all animals, are polled.

By using bulls that have been tested and shown to be true polled (homozygous PP) in horned beef herds, these animals will produce either polled or heterozygous polled progeny.

In all breeds there will be a reduction in the proportion of horned calves, and in all breeds there will be an increase in the proportion of polled calves.

Over time, calves will be overwhelmingly polled.

Success for tenderness

Once dismissed as tough, more meat from *Bos indicus* cattle and their crosses is making its way onto butcher shop shelves across the country, courtesy of Beef CRC research.

"Tenderness markers work, and they work very well," says Dr Paul Greenwood of the New South Wales Department ofI ndustry and Innovation's Beef Centre in Armidale.

Dr Greenwood undertook research confirming earlier findings by the Beef CRC and others, which showed that cattle of predominantly *Bos taurus* genotypes tend to meet with consumer acceptance more often than those from *Bos indicus* genotypes.

"Part of the rationale behind our work was to look at whether there are other ways we can achieve a greater level of consumer acceptance of beef from *Bos indicus* cattle. Selecting cattle with tenderness markers is one way of doing that," he said.

> "DNA markers for tenderness have been successfully tested in large numbers of animals and in multiple muscles. They work well across breeds."

Dr Greenwood's team looked at two tenderness markers based on the calpain system, responsible for the breakdown of the muscle during ageing, therefore making the meat more tender if stored before consumption.

At the start of the experiment 2500 cattle from New South Wales, Queensland and Western Australia were sampled to find those with contrasting gene markers required for the experimental design. From those sampled in NSW and QLD, the selected animals were sent to Glen Innes while the selected animals from the WA steers were sent to Vasse Research Station.

"There were four groups in NSW: one group had two copies of the two favourable markers for tenderness, one group had the two copies of the two unfavourable markers for tenderness and there were two intermediate groups, each with two copies of one favourable and one unfavourable gene," Dr Greenwood said.

"The cattle in Western Australia had the extreme (favourable and unfavourable) genotypes but we also included other groups of cattle with one copy of the markers for tenderness."

The cattle were weaned, backgrounded and then finished in a feedlot. The cattle in Western Australia stayed on feed for 70 days; the groups in NSW were fed for 100 days.

At slaughter, the carcasses were subjected to different processing treatments. Some were hung the conventional way, by the Achilles tendon, others were tender-stretched. Ageing rates were also compared to determine whether the effect of the markers was consistent across the different lengths of ageing.

"If we compare the two sites, we found the cattle which had no copies of the two tenderness markers produced meat that was a full kilogram of shear force tougher than the meat from those that had copies of the two favourable gene markers," Dr Greenwood said.

Shear force is a mechanical measure of the amount of force needed to cut through a cooked piece of meat. The lower the shear force, the more tender the meat.

"The size of the marker effect was greatest in the traditionally-hung animals, aged for seven days. We still saw a significant difference in those that were tender-stretched, although the size of the effect wasn't quite as big."

Often, selecting for a particular trait can negatively influence other economically important production traits. The tenderness markers, fortunately, don't appear to have any negative impacts on the other traits that were examined in the study.

"We found across a range of production traits, including Net Feed Intake, growth, carcass characteristics and temperament, there were no adverse effects of the markers," Dr Greenwood said. "So generally speaking, the effects of the markers were quite specific to the tenderness of the meat."

Dr Greenwood said this work could have a number of potential spin-offs. "For producers, if one of their objectives is to produce more tender meat, then they can be confident these markers will have a favourable effect."

It could also mean greater efficiencies for the processing sector, Dr Greenwood added.

"Of course this would need to be examined in more detail but could lead to potential efficiencies due to improvements in the ageing rates of meat to achieve a required level of tenderness. If the aim is to produce meat of similar quality to current production systems then carcasses that have these markers, may not have to be aged as long as they are now."

This article was originally printed in the 'Beef Bulletin', Winter 2008. More recent research with tenderness markers undertaken by the Beef CRC has involved incorporating beef tenderness markers into BREEDPLAN, and into Meat Standards Australia (MSA), which has been achieved.

Snipping away at evolution

The genome of a one bovine is nearly identical to that of another bovine, but there is also a very important variation in small areas across the genome of different animals.

Single nucleotide polymorphisms, or SNPs, (pronounced "snips") 'mark' the location of a gene, although these markers often do not occur on, or in, the gene of interest.

SNP variations can be used to identify associations with differences for economically important traits between individuals within a population and across different cattle populations. A SNP association may change the function or the expression of a gene or genes of interest.

SNPs can account for biological variation between people and animals, which result in differences in a variety of traits.

SNP variations between animals are detected by screening animals using DNA marker panels to compare genomic data. The resulting 'genotypes' are analysed jointly with measurements of traits of interest, to identify areas of the genome that are associated with economically important traits in livestock.

DNA markers for tenderness work across beef breeds

The Beef CRC's 'SmartGene for Beef' project found DNA marker results for tenderness are very consistent across breeds. Of the four GeneSTAR tenderness markers examined in this project, T1 and T2 consistently showed significant effects in British breeds and T1, T2 and T3 showed effects in tropically-adapted breeds of cattle.

Meat from a range of cattle breeds was tested for the effect of increasing the numbers of "stars" on beef tenderness.

Tenderness was measured as longissimus dorsi (LD; loin muscle) shear force. Shear force is a mechanical measure that can be likened to how much force a person needs to chew a piece of steak. The lower the shear force value, the more tender the beef.

The effect of increasing numbers of "stars" was statistically significant ($P<0.05$) in each of the populations tested.

Beef CRC1	These data comprise seven pure-bred breeds, 4 temperate breeds (Angus, Hereford, Murray Grey and Shorthorn) (n=3,229) and 3 tropically adapted breeds (Brahman, Santa Gertrudis and Belmont Red (n=3,615)
Beef CRCII	These data are from the CRCII northern breeding project focused on tropically adapted cattle including purebred Brahman (n=2,039) as one breed and Tropical Composites (from various pastoral companies) as another (n=2,400)
Angus Progeny Test	Angus Australia progeny test program conducted using the NSW DPI Trangie Angus herd as dams (n=415)
Durham Progeny Test	The Shorthorn Beef progeny test program conducted in Durham herd (n=347), Orange, NSW

Table 1: SmartGene project summary results of GeneSTAR tenderness markers across different breeds

Key points in the tenderness results include:

•Of the four GeneSTAR tenderness markers examined, T1 and T2 consistently showed significant effects in British breeds and T1, T2 and T3 showed effects in tropically-adapted breeds of cattle.

•While the CRCI temperate population contained animals used in marker discovery; the results were also statistically significant in the independent CRCII populations.

•The markers identified variation in both normally-hung and tenderstretched carcases. However, as the tenderstretched carcases were more tender and had less variation for tenderness than normally-hung carcases, the effects of the tenderness markers were reduced under tenderstretch hanging.

•Although statistically significant, the total amount of phenotypic variation in tenderness accounted for by the GeneSTAR tenderness markers was only around 4% in temperate breeds and 6% in tropical breeds. While encouraging, it means many more markers are required in both breeds to account for a sizeable percentage of variation.

•For CRCI temperate breeds, results showed estimates were not accurate for Shorthorn due to the extreme gene frequencies and low numbers of animals. For Angus and Murray Grey, the T1 and T2 markers were significant, had modest effects on tenderness and acted additively, but T3 and T4 were not significant.

•For Herefords, only T1 was significant.

•For tropically adapted breeds, results for T1, T2 and T3 fitted jointly showed significant and additive effects, except for T2 in CRCII Brahmans. However when T4 was added to the model, it had inconsistent effects, ranging from negative in CRC1 Brahman (that includes the discovery animals), to no observed effect in CRCII breeds, to positive in CRCI Santa Gertrudis and Belmont Red.

•T1, T2 and T3 in tropically adapted breeds were significant for tenderness in normally-hung carcases and had consistent effects on Meat Standards Australia (MSA) consumer taste panel scores. The marker effects appear to be additive in their effects on tenderness. . The effect of T3 was not consistent in British breeds and T4 does not appear to be a useful marker for tenderness in these breeds.

This article is based on an article published in the Beef Bulletin, Winter 2008.

Beef and chips: the science of better beef

Dr Heather Burrow

The cost of mapping the complete set of DNA contained in every cell of an animal, its unique genetic fingerprint, is in freefall.

It originally cost in the order of USD $50 million to map the genome of the first bovine. These days companies are advertising on the internet for humans to sequence their own genomes for as little as $5,000.

"The price keeps coming down," says Beef CRC Chief Executive Dr Heather Burrow, "while the capacity of DNA panels (or 'chips') to identify variations (Single Nucleotide Polymorphisms or SNPs) across the genome of different animals is advancing so quickly that it is difficult for scientists to keep up."

Dr Burrow said that before the bovine genome sequence became publicly available in 2006, scientists predicted that five to ten DNA markers would collectively account for around 50 percent of the genetic variation for each economically important trait.

But research now shows that hundreds, even thousands, of genes have a small influence on complex traits that are important for production; including feed efficiency, growth, meat and carcase quality, reproductive performance and adaptation traits.

DNA marker panels with the capacity to screen for 10,000 SNPs became available in 2005. Panels with 50,000 SNP became available in 2008 and are now being used as a commercial product in dairy breeding programs. New high density chips will become available in the near future and they are likely to offer more than 800,000 SNPs on a single panel. These new high density panels will be used for research purposes in the first instance.

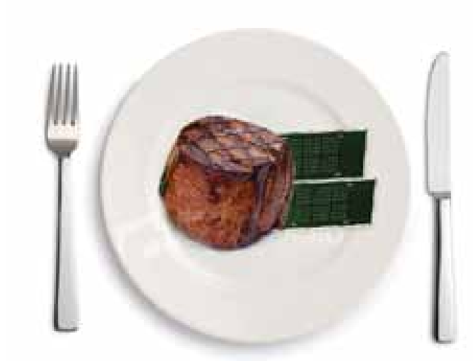
Testing each new panel of markers requires matching the 'genotypes' derived from the SNP panels with measured performance in animals (the 'phenotypes') to identify statistically significant associations between the genotypes and phenotypes. Those statistically significant associations then need to be independently evaluated or 'validated' across cattle breeds and beef production systems in totally unrelated cattle populations.

"In 2008 it cost Beef CRC around US$250 per animal to use the 50,000 SNP panel. We are now using that chip for less than AU$100 and we are expecting the cost to reduce even further once the new very high density panels become available."

Dr Burrow said the Beef CRC plans to use the new, denser SNP chips as soon as they became available. This research will be undertaken in collaboration with the United States Department of Agriculture, New Mexico State University and Iowa State University in the USA and the Universities of Alberta and Guelph in Canada.

The new collaborative research would continue and greatly enhance the existing international collaboration based on use of the 10,000 and 50,000 SNP panels.

The smaller SNP panels effectively identified genetic variation for economically important traits in animals within a breed. But the new high density panels are now offering an opportunity to develop predictive tests that work across different cattle breeds. This will be particularly important for the genetic improvement of smaller breeds that struggle to measure sufficient animals for the traits of interest.



"The new high density panels offer an opportunity to develop predictive tests that work across different cattle breeds. This will be particularly important for the genetic improvement of smaller breeds that struggle to measure sufficient animals for the traits of interest."

"Most critically though, we need to ensure the DNA tests are independently verified in appropriately-sized and independent cattle populations," Dr Burrow said.

"Industry needs independent verification of the genetic variation accounted for by DNA markers and an analysis of any trade-offs in production characteristics to ensure genetic progress is made as planned."

Based on results from its use of the 10,000 and 50,000 SNP chips, Dr Burrow said that Beef CRC expects to commercialise independently validated DNA marker tests accounting for at least 15 percent of genetic variation for a range of traits such as marbling, tenderness, saleable meat yield, feed efficiency and female reproduction by 2012.

"Accurate DNA tests and markers that account for 15 per cent of genetic variation for difficult- or expensive-to-record traits will provide effective ways of genetically improving cattle herds and better meeting beef market specifications," she said.

However, Dr Burrow said it was critical beef producers continue to record phenotypes of their cattle herds.

"It is the only way DNA markers will be properly evaluated in the future," she says. "It might not be overstating the case to say the future of Australia's cattle industry depends on the ongoing accurate recording and matching up of phenotypic and genotypic data."

Dr Heather Burrow
Heather.Burrow@une.edu.au

A look across the ditch – DNA markers in the dairy industry

Genomic breeding values for young breeding bulls

Up until a couple years ago, it took six or seven years to "prove" a sire, by gathering information. Now scientists can determine the genetic potential of a great sire while it is still a calf.

Dairy AI companies receive genetic information on the cow or bull. They can use this information to quickly select high calibre dairy animals for breeding.

The impact on the industry is enormous. Over the past 40 years, AI companies and dairy farmers have selected their breeding stock based on good traits and proven performance. AI companies traditionally start with a good cow, mate her with a good bull, and wait for a bull calf to be born. As soon as possible, the companies want heifers using the bull calf's semen. Next, the calves have to be bred and calved, and they have to begin milking to determine the success of the bull's semen.

Now the industry has lots of information on top quality bulls that are less than two years old. By the time a bull calf is six months old, DNA tests can accurately predict how good the calf is and if it has the right genetic makeup to come into the AI industry.

"The next quantum leap in productivity and profitability from using genomic information could translate into a $100,000 per annum lift in profit for a 300 cow herd. AI companies are already using DNA markers to select which bull calves will go onto progeny testing. The next major transition is to use bulls to breed cows at approximately two years of age based on their genomic breeding value (GEBV) only. This can lead to large increases in the rate of genetic gain due to the reduction in generation interval. It must be re-iterated that using bulls with reliabilities of breeding value of 0.55 rather than greater than 0.81 as is achieved with progeny testing does carry some risk - the chance of the performance of the daughters being lower than predicted is greater (as is the chance of the daughter's performance being higher than predicted). This risk can be mitigated to some degree by using teams of bulls rather than individuals."

-Dr Ben Hayes, Genomic Selection for Australian Dairy Cattle, Victorian Department of Primary Industries.

Dr Ben Hayes, pictured in Brasil during a recent visit, where he gave a course on using genomics in livestock breeding

"The next quantum leap in productivity and profitability from using genomic information could translate into a $100,000 per annum lift in profit for a 300 cow herd."

Beef industry should aim for dairy-style DNA model

The Australian beef industry should aim for a dairy genomics model where producers across the world share DNA information on their cattle.

That's according to genetic extension specialist from the University of California, Dr Alison Van Eenennaam.

"Pooling the evaluations from different countries into an international bull evaluation resource allows dairy producers to compare sires in Norway to sires in Australia," Dr Van Eenennaam said.

She said that the way individual beef breeds in the United States are charged with evaluating genetic data and producing genetic proofs is not an optimal model.

"In the dairy industry, a single USDA-funded group does all of the genetic evaluations," Dr Van Eenennaam said.

"This puts dairy in a more powerful position to get genomic data integrated into their genetic proofs whereas I think the beef industry is struggling to get that done."

The beef industry also faces greater challenges due to genetic tests needing to be developed for the different breeds used in beef cattle production, whereas dairy is made up of one or two predominant breeds.

Beef CRC photo competition winners

Jess Lang's 'Bullocks', won the inaugural Beef CRC photo competition 'Best Northern Cattle Photo'. Jess' photo was taken on "Wyora Station" at Winton in Queensland.

Libby Litchfield's 'Cows on a Hill' won the 'Best Southern Cattle Photo.' Libby's photo was taken at "Hazeldean" at Cooma, New South Wales.

Announcing the Beef CRC photo competition for 2010!

If you have access to both a camera and cattle, then the Beef CRC wants to hear from you.

Following on from a competition launched in 2007, the Beef CRC is hoping to uncover the best cattle photos in the country. The winners and some of the finalists from that competition are printed in this edition of the Beef Bulletin.

Whether your photo shows a mob of brahmans being mustered in the Top End, a cheeky angus calf playing hide and seek, or a dusty yard at the end of a day, as long as it's got cattle in it we want to see it.

But it doesn't have to be in the paddock. Processors and lot feeders are also invited to submit their favourite cattle or beef photographs as well.

The people who submit the two best photographs, one in southern Australia, one in northern Australia will each have their photo made into a canvas print to hang in their home or office. Each print measures 20 inches by 40 inches and is valued at $250. Everyone who submits a photo could also see their photos used in all major CRC publications.

So flick through the photo albums or start clicking today.

Please email your original photos as high resolution JPEGs to the Beef CRC:
beefcrc@une.edu.au

Entries close COB on Wednesday the 30th of August 2010.

The small print:

Anyone who submits a photograph to the Beef CRC agrees it's their own original creation and work, and does not infringe the rights (including copyright) of any other person. They understand the Beef CRC cannot return any physical materials (including any photographs). By entering the competition they authorise the Beef CRC to publish and use the photographs in all media, in Australia and internationally, without acknowledgment. The Beef CRC will not make any commercial use of the photograph without further negotiation with the photographer. They release and indemnify the Beef CRC, its assignees, and licensees from and against any claims arising from any breach of this warranty and the exercise of the rights granted herein.

Beef CRC photo competition finalists

Helen Commens, Windorah

Esther Glasgow, Victoria

Sharryn MacDougall, Dalby

John Walter, Pittsworth

Karly Picker, Armidale

Kym McMaster

Geoffrey Fordyce, DPI

Calling all Brahman studmasters

Brahman breeders set up the genetic evaluation framework for the future of their breed

The Australian Brahman Breeders Association (ABBA) is at the forefront of supporting research into gene marker technology, through its involvement in the Beef Information Nucleus (BIN) project, being conducted as part of the CRC/MLA Strategic Plan for DNA Marker Commercialisation. ABBA General Manager John Croaker said gene discovery technology was moving at a fast pace and offered great opportunities for the Brahman industry.

"The sequencing of the Brahman genome by the CRC is the first major work of this kind being undertaken in the word, as far as Brahmans are concerned," Mr Croaker said.

"Previous gene marker technologies, such as GeneStar and the SmartGene for Beef project have highlighted the need to have more independent validation and a database of phenotypes, as validation of results within the discovery population has proved not to be indicative."

A database of phenotypes not only enables gene marker discovery, but assesses and validate gene markers by breed within Australian populations and enables the combination of gene markers (MBVs) with pedigree and phenotypes to produce marker assisted EBVs which are potentially a lot more accurate than gene markers alone.

The BIN Project aims to facilitate the independent validation of DNA markers relative to Australian breeds and production systems.

Other aims include providing the resources to conduct other separately funded research into areas which would assist the future development of the Australian Brahman breed; and attracting and evaluating sires that will influence the future of the Brahman breed for a range of economically important traits including carcase and meat quality, female reproduction and growth traits.

"It will help identify young, proven Australian sires with a high accuracy for traits of interest to the Australian environment," Mr Croaker said.

"We hope that a by-product of this project would be separately funded research projects that might lead to a recalibration of the MSA model."

The project will involve evaluating 20-25 sires each year for three years, and their progeny of about 750 calves in three co-operator herds:

- Mark and Belinda Wilson, Banana Station, Banana: producing 250 calves by AI from high grade commercial Brahman heifers.
- Rob and Annie Donaghue, Baradoo, Bauhinia: producing 250 calves by AI from high grade commercial Brahman heifers.
- CSIRO Belmont: producing 250 calves by AI and natural service from the Belmont-registered Brahman herd.

All steer progeny will be slaughtered for carcase and meat quality data and heifer progeny will be retained within the project to pregnancy test after the second joining.

Mr Croaker said the ABBA would purchase steer progeny at weaning and finish on grass, only using grain feeding as a drought contingency, if required.

Blood and hair samples from sires and all progeny will be collected for DNA extraction and storage and all data collected will be entered into the ABBA database and analysed in BREEDPLAN.

Traits to be measured in the trial are:

- Growth traits – 200, 400 and 600 day weight, mature cow eight and condition score
- Caracase and meat quality – Ultrasound scan at 600 days and pre-slaughter for eye muscle area, rib fat, rump fat and intra-muscular fat
- Direct carcase data – Eye muscle area, MSA grading and carcase digital data analysis
- Meat quality – Shear force, compression, extracted fat
- Female reproduction – Days to calving, and teat scores on heifers
- Parentage verification of calves
- Structural soundness scores

The project will focus on joining in 2010, 2011 and 2012, looking at calves born in 2011-13, steer turnoff from 2014-16 and female heifer data from 2015-17.

'Studmasters are invited to nominate bulls for the BIN project. The bulls need to be Australian born, registered Brahman bulls aged less than five years.'

John Croaker, Managing Director, of the Australian Brahman Breeders Association, Rockhampton (far right), pictured at the DPI&F Beef Breeding Services semen storage and distribution complex at Rockhampton. Also pictured from left: Dr Brian Burns, DPI&F principal research scientist, Rockhampton; Professor Gabriel Bo, cattle reproductive specialist, Argentina; William Tucker, Garuda Brahmans, Bouldercombe.

Studmasters are invited to nominate bulls for the project for a fee of $1000. The ABBA will pay for the costs of health testing and collection of 200 straws of semen, and retains the right to sell 10 straws of semen.

To qualify, bulls need to be Australian born, registered Brahman bulls, aged less than five years, however preference may be given to younger bulls. They must have good temperament, good conformation and adherence to the Brahman phenotypic standard. Both reds and greys will be used in the trial, and any performance data including BREEDPLAN will be considered in the selection process.

Other considerations include the calving history of dam and grand dam, and performance of siblings and half siblings.

Mr Croaker said the project was being managed by the Association and was funded under the MLA Donor Company scheme which sourced funds from a pool of money set aside from the Federal Government as a percentage of exports.

Selections will be finalised by the ABBA Council in July 2010. Contact the ABBA for more details.

This article is reprinted from 'Brahman News', June 2010.

Securing the genetic future of Limousins

Alex McDonald

The Limousin breed was the first to commit to the development of a Beef Information Nucleus (BIN) herd, a $1.6 million, five-year project that is a key move in evaluating and developing DNA marker technology for the breed.

Alex McDonald, General Manager of the Australian Limousin Breeders Association, says that while producers are yet to experience the full benefits of DNA markers, he believes that the technology will mature rapidly.

The chips used to scan the genome to identify areas of interest are getting bigger, faster and cheaper. Human genome researchers already use chips that carry 500,000 DNA markers.

Chips carrying 50,000 marker sites are now available to the cattle industry (as compared to the previous 5,000 and 10,000 marker chips), and will greatly enhance the industry's ability to detect genetic variation and make profitable decisions around it.

The best way of employing the new genetic information will be to incorporate it into existing Estimated Breeding Values (EBVs), Alex says—but each breed will need to know how strongly the marker predictions correlate to actual results for their breed.

Enter the Limousin BIN herd.

"If you're not in the game, you have to go on blind faith that the tests work as the companies say," Alex says.

"We know there will be differences between breeds. The question is, how big will those differences be? If we don't have a Limousin database, we'll never know."

The Limousin BIN herd is designed around the joining of 10-15 young elite bulls to 300 commercial British breed cows each year for 3 years – meaning 30-45 bulls tested in all.

Calves will be weighed at birth and weaning, scored for docility, and after weaning will go through backgrounding and then grain feeding to 450 kilograms liveweight.

Weight gain will be recorded, and a complete set of carcass measurements taken after slaughter including eating quality assessments.

The exercise will also help the breed assess the value of the unique Limousin F94L myostatin gene. The estimated beef yield of animals carrying a copy of the gene will be compared with those carrying none.

BIN herds

In genetics, breed matters. Beef Information Nucleus (BIN) herds are being put together to help us understand why.

BIN herds are the new testing ground for DNA marker technology. It has become clear that DNA marker tests do not result in the same outcomes across different breeds of cattle, and BIN herds are the industry's answer.

"For breeders to have confidence in the emerging DNA markers, they are going to have to calibrate the effect of those markers in their own cattle," says Dr Rob Banks, MLA's manager, Genetic Improvement.

"Let's say, as an example, that a DNA test has been developed in North America to allow Angus breeders to assess potential weight gain. Once, we might have thought it possible to use that test in Australia for all the breeds."

"Unfortunately, all the research to date is telling us that is not the case. If you want a DNA test for weight gain in Shorthorns in Australia, you'd better have some data on that breed in Australia to calibrate the tools against."

For breeds unable to put together BIN herds, there is the risk that DNA tests will be less relevant, "at least in the foreseeable future", Rob says.

"It's not that the tools won't work, but that you need to test them to assess how well they work."

"If you don't know how well they work, you don't know how much to spend on them. It's a matter of assessing the efficiency of the test for your particular needs. Only then can you make a considered decision on how much to spend on it."

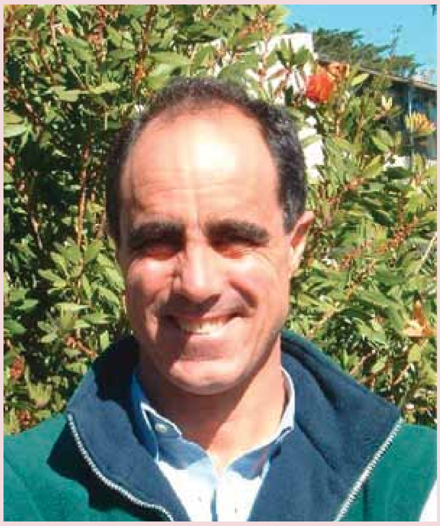
The Limousin, Hereford and Charolais breeds already have BIN herd projects in place.

The Angus and Brahman breeds have proposals close to final approval. Work is well underway for tropically-adapted composite breeds like Droughtmasters, and Wagyus and Murray Greys.

Shorthorn is working on how to transfer the understanding gained from its long-running progeny testing program, the Durham Project, into the next phase.

A good design for a BIN herd is similar to that needed for a progeny testing program, Rob says, and with more cattle the better.

"It's a good idea for a BIN program to be testing bulls that are genetically diverse, and as broadly representative of the breed as possible. At the same time, it's a good idea to be testing young and elite bulls, because they are the animals most likely to contribute to the breed in the future."



Rob Banks

"It's also going to be important to measure as many of the traits that are important to supply chain profitability as possible."

"Progeny tests have tended to focus on carcass traits: these BIN projectsare looking at female reproduction traits as well, and they will go further than previous projects in looking at eating quality and consumer assessment traits as well."

These latter traits have so far proved difficult to test for. If DNA marker technology opens up the capability for reliable testing, breeders will be able to test animals well before they reach breeding age, allowing for much faster genetic gain.

Rob says the first BIN projects will start generating progeny data next year, and information will "really begin to flow" in 2012.

Some of the DNA tests currently being brought to market will arrive ahead of the capacity of the BIN herds to calibrate the tests.

"That means that the industry, researchers and the companies providing the test markers will have to work together to come up with a reasonable way of evaluating those offerings before they can be tested under Australian conditions."

"The situation reflects a lot of learning about DNA technology. We couldn't have got to this point without that learning—finding that there is a greater deal of breed specificity than people anticipated, for instance."

That hard-won experience has also generated greater collaboration between the research community and marker commercialisation companies, Rob says. "We're now having a lot of fruitful discussion that's taking this whole issue forward."

Brahman genome sequenced

The unique DNA of a popular Australian Brahman bull will soon be added to the international cow genome databank.

Beef CRC CEO Dr Heather Burrow said the Beef CRC, in partnership with CSIRO Livestock Industries and the Victorian Department of Primary Industries, had now completed sequencing of the Brahman genome, along with the genomes of an Africander and Tuli bull.

It is the first time Australian cattle adapted for tropical conditions have been sequenced, and the information will be included in new generation DNA markers that producers can use to identify important production traits in animals.

"It's critical Australian producers can use DNA markers that incorporate the genetic variation that occurs in tropically adapted cattle – over half of Australia's beef production is based in the tropics," Dr Burrow said.

"To date, most of the data used to make DNA markers have been based on breeds which are suited to a temperate climate."

But the Beef CRC project identified over four million DNA variants unique to the Australian Brahman genome, demonstrating the variation that can occur across breeds.

CSIRO Livestock Industries' senior principal research scientist Dr Bill Barendse, a pioneer in the identification of new gene markers for economically important traits of cattle, said the project would help geneticists determine what "makes a Brahman a Brahman".

"The Brahman bull we sequenced was chosen because he has been widely used in Australia and it will ensure that Northern Australian cattle variation is captured in future selection tools," Dr Barendse said.

Brahman and Brahman-cross cattle comprise over half of Australian beef cattle population.

Brahmans were introduced to Australia in the early 1930s and proved well suited to the harsh climate and pests of the northern Australian rangelands. Over the past 40 years, Brahmans are estimated to have contributed over $10 billion to the Australian beef industry.

But Brahman and other tropically adapted cattle are not as significant for the beef production systems of other developed countries.

Dr Burrow said the sequencing of the Australian Brahman bull's genome, along with sequencing of the Tuli and Africander breeds, was particularly important for Australian production.

The inclusion of information about the DNA of these animals will ensure producers can be confident of using future new DNA marker panels in Australian beef production systems.

Livestock genomics masterclass

A genomics masterclass organised by the Beef CRC in Armidale in March bought together genomics experts and industry leaders from across the livestock industries.

Following the masterclass, a reference group was established to:

- Review policies and major issues as they develop in the two industries
- Ensure that educators and extension agents are given up-to-date information to deliver the appropriate message
- Be a source informed comment on genomic issues affecting the beef and sheep industries

The group advocates that information from DNA tests should be incorporated as part of the scientifically proven and industry accepted tools for communicating genetic merit – Estimated Breeding Values (EBVs) or Australian Sheep Breeding Values (ASBVs – derived from the national genetic evaluation systems currently operating for beef and sheep, BREEDPLAN and Sheep Genetics.

The group believes this approach is the best way to ensure maximum benefit for breeders and commercial producers.

Summary of technical Issues for livestock genomics across industries:

- Single genes of large effect are rare – therefore large populations needed for discovery, validation and calibration of markers that are of small effect – population needs to be relevant.
- Still just EBVs – traditional measures enhanced by genomics and best utilised as one analysis
- Genomic Breeding Values decay over time – prediction equations need to be regularly re-evaluated – need large data set of phenotypes and genotypes
- Biggest advantage from decreased gen interval and info on hard to measure traits
- Actual genotypes more valuable than MVPs especially in the long term
- Beef and Sheep need to restructure to capitalise on genomic selection
- Value of genetic testing is complex and depends particularly on market and position in supply chain

For more information contact Wayne Upton:
wayne.upton@beefcrc.com.au

New test to measure a heifer's puberty blues

This cow and calf above are part of a Beef CRC research program to improve the female reproductive performance of tropically adapted cattle.

New genetic tests expected to greatly improve the productivity of Australia's northern beef herd are close to being developed.

CSIRO research scientist Dr Rachel Hawken leads a collaborative project within the Beef CRC which focuses on the reproductive performance of female beef cattle.

Ideally, a beef cow produces one calf for every reproductive year of her life. However, in Northern Australia, cows have been selected for their ability to survive in harsh tropical and subtropical environments and may only produce a calf once every two years. Tropical heifers can reach puberty late and there is tremendous variation of age at puberty within herds – anywhere from 10 to about 40 months of age.

The test could be done on breeding females when they are very young calves or even as an embryo. The tests have been validated in an unrelated cattle population, and may represent the first such DNA tests to be commercialised for 'age at puberty' in the world.

Dr Hawken said the research aims to provide producers with DNA marker tests to help them select for two key traits – the age a heifer reaches puberty and the time it takes a cow to ovulate after calving.

"Management and the condition of livestock have an impact, but there is good evidence of genetic links to these traits," Dr Hawken said.

"New DNA markers now being developed will allow producers to genetically test their herds to find those heifers which mature more rapidly and can conceive calves earlier, without compromising on cow or calf survival rates."

Dr Hawken and her team are currently working with Central Queensland beef producers, collecting new industry data to validate the DNA markers they have discovered for post partum anoestrus, which can identify the cows that will ovulate during lactation.

The Australian team also recently compared the DNA markers they have discovered for age-at-puberty with markers identified in a study by colleagues at New Mexico State University in the United States.

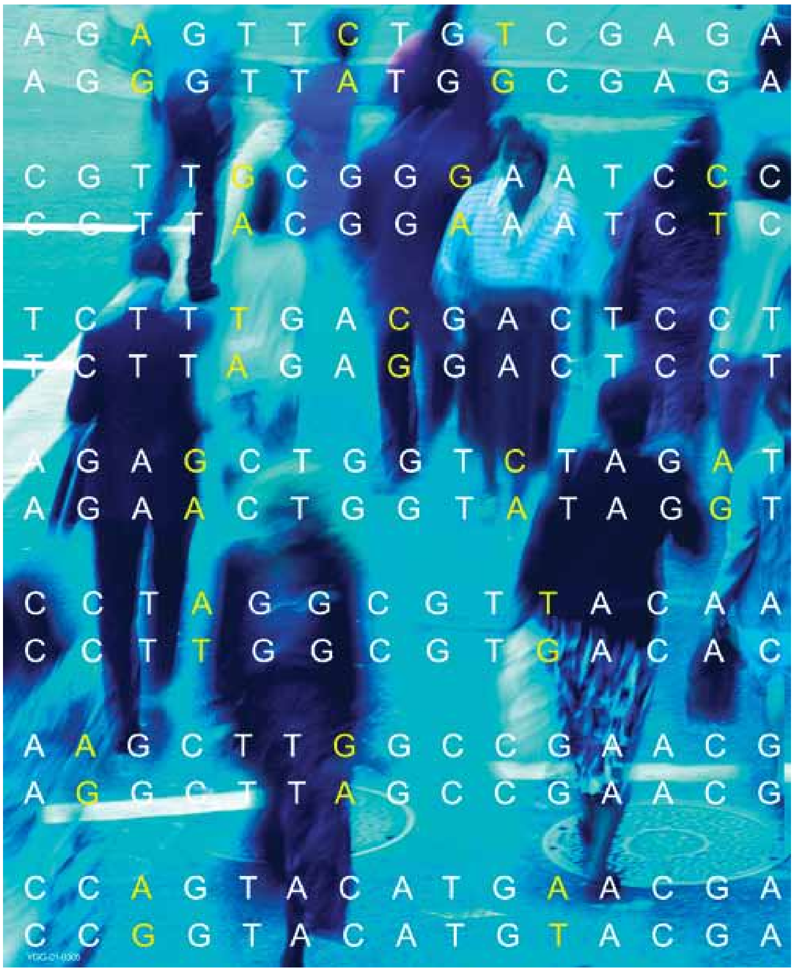
"Some of our DNA tests discovered in Brahman cattle validate those identified in Brangus cattle in the US, providing an independent confirmation of findings," said Dr Hawken.

Although DNA markers for reproduction in female cattle are close to being made available to industry, the big gains in productivity will ultimately come from identifying those bulls which will pass the desirable genotypes on to their daughters.

This research involves scientists and resources from the Beef CRC, CSIRO Livestock Industries, the Queensland Department of Employment, Economic Development and Innovation, the Animal Genetics and Breeding Unit at the University of New England and The University of Queensland in Australia and New Mexico State University and the United States Department of Agriculture in the USA.

Spit and SNP – marketing DNA tests for humans

Discoveries in the human genome have led to the development of individual DNA tests for health and disease in humans, using SNP panels with thousands of SNPs. However, recent debate has focused on the marketing and regulation of these tests. The US Food and Drug Administration is now moving to impose a regulatory framework for selling these tests direct to the consumer, as detailed in this recent *New York Times* article.



F.D.A. Faults Companies on Unapproved Genetic Tests
By Andrew Pollack, New York Times
Published: June 11, 2010

The Food and Drug Administration is cracking down on 23andMe and other companies that sell genetic tests directly to consumers.

The F.D.A. sent letters this week to five companies involved in that business, saying their tests are medical devices that must receive regulatory approval before they can be marketed.

"Premarket review allows for an independent and unbiased assessment of a diagnostic test's ability to generate test results that can reliably be used to support good health care decisions," Alberto Gutierrez, who leads diagnostic test regulation at the F.D.A., wrote in the letters.

The letters, posted on the F.D.A. Web site on Friday, say the companies must apply for approval or discuss with the agency why certain test claims do not require such approval.

But the letters stop short of saying the tests must be taken off the market until they are approved. Dr. Gutierrez said in an interview that it would be unfair to remove the tests from the market because the agency had not clearly told the companies that the devices needed approval.

23andMe and two other recipients of the letters, Navigenics and DeCode Genetics, sell tests that scan a person's DNA, looking at genetic variations that can suggest whether a person is at a higher or lower risk of getting diseases like cancer or diabetes. The most prominent of the companies, 23andMe, is backed by Google and run by Anne Wojcicki, the wife of Google's co-founder, Sergey Brin.

Illumina, which also received a letter, sells so-called DNA chips that are used by some companies to do the DNA scans. The fifth recipient, Knome, offers consumers a complete sequence of their DNA, which can be used to glean disease risk information.

The F.D.A. action is the latest salvo in a long-running debate about whether and how such tests should be regulated.

On one side are some doctors, geneticists and state regulators who say the tests should be regulated because the results might be used to make medical decisions. Some also say a doctor should be involved in ordering the tests and interpreting results.

On the other side are those, especially 23andMe executives, who argue that the services merely provide information, not medical diagnosis, and that consumers have a right to the information contained in their genes. At a time when consumers are taking more control of their health care, denying them such information would be, as one director of 23andMe recently put it, "appallingly paternalistic."

The companies have also said that their tests do not require F.D.A. approval because they have been developed and are offered by a single laboratory. The F.D.A. has typically refrained from regulating such tests, as opposed to test kits that are widely sold to laboratories, hospitals and doctor's offices.

The F.D.A. is now clearly deciding in favor of regulation, saying the tests of disease risk can have medical consequences.

"It is not unknown for women to take out their ovaries if they are at high risk of ovarian cancer," Dr. Gutierrez said. Some of the services are also offering consumers information that could be used to determine the doses they should get of particular drugs, like the blood thinners, warfarin and Plavix.

But Dr. Gutierrez denied that the agency was being paternalistic. "We really don't have any issues with denying people information," he said. "We just want to make sure the information they are given is correct."

In a statement Friday, 23andMe said it disagreed with the F.D.A.'s conclusion but was open to discussion on ways to regulate the personal genetics industry. "We are sensitive to the F.D.A.'s concerns, but we believe that people have the right to know as much about their genes and their bodies as they choose."

The Applied Genomics for Sustainable Livestock Breeding conference and workshops, will be a great opportunity for your organisation to build relationships with the beef, sheep and dairy breeding industries. The conference is sponsored by the Beef, Sheep and Dairy Futures Cooperative Research Centres (CRCs). Put in your diary!

2-5 May 2011, Melbourne

For more information, contact beefcrc@une.edu.au

From the 2007 Beef CRC photo competition: Photo of Amelia and Charlie by Nola Bruton

CRC
BEEF