

Beef Bulletin

September 2011



Speed breeding in livestock species

Last weaning at Swan's Lagoon

Brahman and Tropical Composite female cattle recorded over nine years

Speed breeding
For genetic gains of 30%

Genomics, global warming and the demand for beef

'Beef industry must reduce input costs by 50 percent.'

Professor Mike Goddard

Australian poll gene marker test

- Results of industry trials across breeds
- Works well in Brahman



"We've always wanted to identify carriers of horns. At this stage the CRC test is working a treat for what I want."

Ian Locke, of Wirruna Poll Hereford stud in southern NSW



Report:

Value of genetic tools across the beef supply chain

Alison Van Eenennaam



Applied Genomics for Sustainable Livestock Breeding

Beef CRC Governing Board



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



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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.



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



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Dr Burrow has extensive research management experience and a quantitative genetics research background.



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



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



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



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Mrs Clubb has extensive financial, management and accounting experience as well as a strong rural background and operator of a beef 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.

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 through world-class gene discovery and gene expression research to improve profitability, productivity and animal welfare of beef enterprises.

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 discovery and gene expression research and accelerated adoption of beef industry technologies.

Genomics key for long-term productivity gains in the beef industry



Dr. Heather Burrow

Genetic improvement of cattle is a key method by which the beef industry achieves productivity gains. It is also a tool that directly addresses challenges in beef production systems.

The recent sequencing of the bovine genome now provides a very real opportunity to significantly increase the rate of genetic gain across Australia's beef herd.

In coming decades Australia has a great opportunity to increase our supply of beef to a meat-hungry world.

For the Australian beef industry, which currently exports ~65% of its product, this represents a major trade opportunity. However, the increased demand for food will lead to greater competition for inputs such as land, water, grain and labour, driving up the cost of beef production.

Climate change is predicted to add to this challenge requiring livestock that are productive under

hotter, and drier climates and, in the (sub) tropics, cattle that can tolerate significant increases in ecto- and endo-parasitic burdens and vector-borne diseases.

The Australian beef industry has a strong record of productivity growth over the last five decades. Over recent years, however, that growth has slowed dramatically, with consensus that current productivity gains are no longer sufficient to overcome major global challenges such as climate change and global food security.

At a national level, the decline in productivity growth is exacerbated by an ageing rural workforce and an urgent need for greater skills in the agrifood industries to meet the sector's economic and strategic potential.

Australian beef producers will not be able to capitalise on the opportunity to sell more beef unless they achieve very significant productivity gains. It is for that reason the Beef CRC chose to focus its research program very strongly on the use of very promising and entirely new genetic and genomic technologies to deliver productivity gains for the Australian beef industry.

The Beef CRC is now on track to deliver its key scientific output on this work – that is, validated genomic prediction equations for carcase and meat quality traits, feed efficiency and reproductive performance across the British and the tropically adapted breed types. Those validated prediction equations will be delivered to BREEDPLAN and genomics companies operating in Australia by April 2012.

These genomic prediction equations will be directly integrated with phenotypic measurements and pedigree information in BREEDPLAN and delivered as genomic EBVs and used in exactly the same way that cattle breeders already use BREEDPLAN EBVs to get the best overall estimate of the genetic merit of their cattle.

Current CRC research demonstrates we can use this method to account for around 15% of the genetic variation between animals within the larger breeds and for traits with sizeable numbers of records. This means the accuracy of the EBV will be about 40%, a level that is commercially useful for traits that are otherwise very difficult or expensive to measure.

For those breeds and traits with few performance records, we may need to wait until full sequence information can be incorporated in BREEDPLAN. Including sequence data in BREEDPLAN is the focus of our proposal for a five-year extension of the Beef CRC.

In addition to delivery of our major output early next year, the Beef CRC has already delivered significant new outputs to benefit the Australian beef industry. Results of our northern and southern reproduction research are now providing clear strategies for herd improvements across Australia.

We recently completed industry trials of the poll gene test specifically for Australian tropically adapted breeds but which has also been found to be useful for other *Bos taurus* breeds.

We will be presenting a summary of our genetics and genomics outcomes for the beef industry at Beef Australia 2012 in May next year.

PUBLICATION DETAILS

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Editor: Sarah Meibusch, Margaret Puls

Art Direction: Aaron Puls

The Beef Bulletin is a quarterly publication for the Australian beef industry.

Enquiries about the Beef Bulletin should be addressed to:

Beef CRC
CJ Hawkins Homestead
University of New England
ARMIDALE NSW 2351 AUSTRALIA
beefcrc@une.edu.au

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CORE PARTICIPANTS



SUPPORTING PARTICIPANTS



Genomics, global warming and the demand for meat

The beef industry must deal with potentially rapid climatic shifts in traditional production areas and with new parasites and diseases. Genomics is a key tool to meet these challenges.

The United Nations Food and Agricultural Organisation (FAO) predicts the world's population will increase by 50 per cent by mid century. Demand for food will grow even more rapidly.

Global demand for protein – particularly meat – will rise accordingly, even as the beef industry tries to adapt to global warming.

The beef industry must deal with climatic shifts in traditional production areas and to new parasites and diseases.

“A lot has been said about increasing world demand for meat, milk and other livestock products,” Beef CRC Chief Scientist Professor Mike Goddard said.

“But the big challenge lies in staying ahead of the rising cost of inputs – grain, water and labour – and the likely requirement to reduce methane emissions.”

It's not just a matter of increasing meat or milk prices to remain profitable: advances in biotechnology will make it possible in future to produce synthetic meat or milk from cell cultures in bioreactors.

“Ask the wool industry about competition from synthetics,” Professor Goddard said.

‘Beef industry must reduce input costs by 50 percent’

Professor Goddard says the beef industry needs to reduce its input costs by as much as 50 per cent. “If you think that can't be done, the chicken-meat

industry did it in less than four decades between the late '50s and early '90s.”

Professor Goddard believes the gains will come in four areas: genetic improvement, new animal management techniques – the two main areas of Beef CRC's research – new productivity boosters like bovine somatotropin, and development of transgenic livestock.

“In the past breeders selected on the estimated breeding value of animals. But the variation that underlies differences in breeding values is due to variation in the animal's DNA.”

“The logical solution is to select directly for the DNA-sequence variants we want in an animal. But it has been very difficult and time-consuming to identify the particular variants that influence differences in complex traits in cattle like growth rate, meat quality, feed efficiency or reproductive rates.”

Professor Goddard, who also works across dairy and human genomics, said the dairy industry has it easier, because a single breed dominates global production: the Holstein-Friesian.

Rapid productivity gains

The best strategy for rapid productivity gains, says Professor Goddard, is to focus on com-



What's in a 'Snip'?

Animal genomes are strewn with millions of single nucleotide polymorphisms, or SNPs (pronounced “snips”) that have accumulated over millions of years, wherever random mutations have substituted one DNA base for another.

With SNP chips, geneticists can rapidly scan the DNA of individual animals, and identify genetic variations that potentially contribute to each animal's unique combination of physical, behavioural and performance traits, and its responses to its environment.

A SNP may alter genetic expression

Most SNPs have little or no effect, but a SNP in a protein-coding sequence may alter the protein's shape and function. A SNP in control sequence may alter a gene's expression. A SNP in the control region of a master regulatory gene can cause changes to ripple through whole networks of subsidiary genes, altering multiple traits in the animal.

Natural selection drives species evolution by acting upon traits influenced by SNPs, retaining those that enhance survival and reproduction, and eliminating deleterious changes.

Human preference has radically changed livestock species from their wild progenitors by selecting traits arising from SNPs that contribute to docility, appearance, and productivity.

New technologies like ultra-fast sequencers and SNP chips have dramatically increased the ability of geneticists to link the presence of specific SNPs to commercially desirable traits in livestock.



mercially important traits, and to use genetic markers, such as SNPs, to explore the whole genome, and identify all genes with large and small effects on commercially important traits.

By identifying SNPs that flag the presence of the best variants of these genes, breeders will be able to predict the breeding value of each animal.

For example, just one of the 30 chromosomes of cattle carries dozens of genes that contribute to live weight. While most are only bit players, their aggregate effect determines the breeding value of each animal.

To locate the large number of anonymous

“By identifying SNPs that flag the presence of the best variants of these genes, breeders will be able to predict the breeding value of each animal.”

genes contributing to live weight, geneticists use a technique called a genome-wide association study (GWAS).

A GWAS compares chromosome segments from elite animals that gain weight rapidly, with corre-

sponding chromosome segments from animals that gain weight relatively slowly, to identify variants that turn up at high frequency in elite animals, but at low frequency in the mediocre performers.

In the hypothetical case that a particular variant occurs in 90 per cent of the fast-growing animals, but is absent from mediocre performers, it's odds-on that that chromosomal region harbours a gene that strongly influences growth.

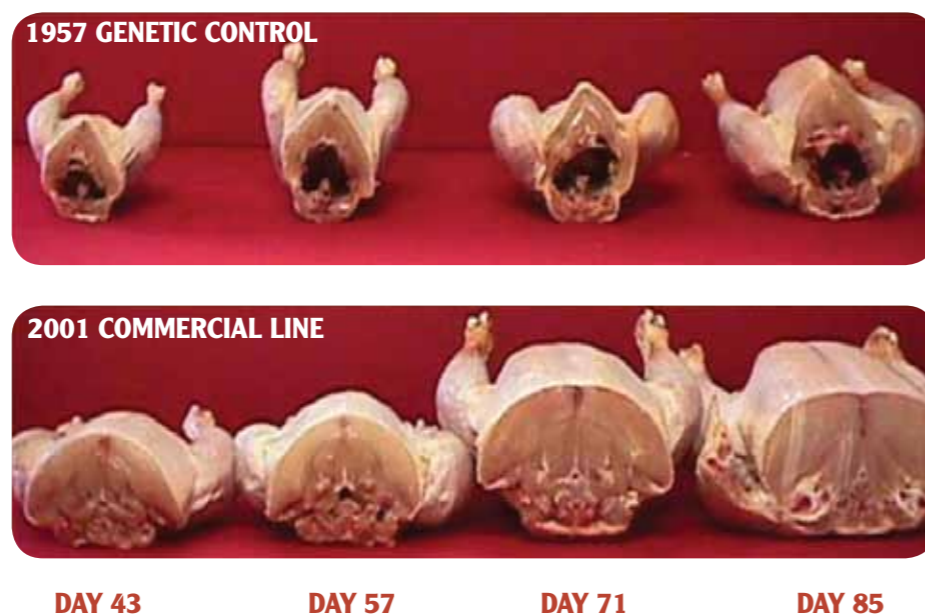
A SNP chip narrows the search, by scanning DNA sequences from multiple individuals, and identifying SNPs that occur at a high frequency in the elite animals.

Professor Goddard says early SNP chips that scanned only 10,000 SNPs (genetic variants) were superseded by the 50,000 SNP chip, which covered 10 different *Bos taurus* and *B. indicus* breeds. >>

Impact of genetic improvement in poultry

The poultry industry has raised productivity through genetic improvement, economies of scale and mechanisation in processing. The success of genetic improvement in the poultry industry is sometimes wrongly attributed to hormones.

Broiler Chickens



However even the latest 700,000-SNP chip falls short of capturing all genetic variation of potential importance to improving productivity.

Professor Goddard says the 50K chip works well in predicting a breeding value within animals of the same breed. It has, for example, been very successful in dairy cattle because of the heavy focus in that industry on a single breed – the Holstein.

“There are now datasets of tens of thousands of Holsteins and the industry is using this data to predict breeding values. AI studs are decreasing their progeny testing programs and basing their selection on genomic predictions.”

However, the problem for beef cattle is that industry data is spread across a large number of breeds – and the beef industry wants to be able to make predictions across all of them.

“So for us, the 50K chip is not dense enough,” Professor Goddard said.

“Because the association between SNPs varies from one breed to another, it is almost certainly the case that the variation between SNPs and real genes also varies from one breed to another.”

In fact, a SNP associated with increased productivity in Angus can actually have a negative effect in a Brahman and vice versa.

However, the recent release of higher density SNP chips of around 700K and 800K by Illumina and Affymetrix will provide chips that are dense enough to develop a prediction equation that will work across breeds.

“This is what the Beef CRC is currently working towards,” Professor Goddard said.

Breed specifications

In the final analysis, for geneticists to be able to predict which SNPs or combinations of SNPs will deliver the largest gains, it may be necessary to have breed-specific predictions.

“This means we would need experiments with many thousands of animals of each breed measured for the important traits and genotyped for the SNPs,” Professor Goddard said.

“However, by using very dense SNP chips, such as the 700,000 SNP chip, we may be able to develop a prediction equation that works for all breeds or at least for all the *Bos taurus* breeds or all the tropically adapted breeds.”

Even then, high-density SNP chips may still be slightly off target and miss the “ground zero” SNPs (the mutations or genetic variants that actually

produce the desirable genetic changes in the elite animals).

Professor Goddard believes it might just be simpler to use ultra-fast sequencers to produce complete genome sequences from many more animals, to zero in on the causal mutations in gene variants that provide the largest or most desirable gains.

Productivity revolution

Professor Goddard says new technologies have cut the cost of genome sequencing by a million-fold in the past decade. These technologies, in concert with the SNP chip, have laid the foundations for a productivity revolution in the beef industry.

Advanced breeding technologies will short-circuit the laborious and costly process of progeny testing, by allowing geneticists to rapidly aggregate “clouds” of gene variants for commercially desirable traits in breeding animals.

A pre-implantation scan of an embryo’s DNA will confirm whether it carries the right combinations of SNPs to produce elite progeny.

Professor Goddard says such advances are crucial for the industry to survive and prosper in the face of competing developments in food production. ■

Does the 50K chip work for beef?

Beef CRC Chief Scientist Professor Goddard says the 50k chip works well in predicting a breeding value within that same breed.

The 50K chip has been very successful in dairy cattle because of the heavy focus in that industry on a single breed – the Holstein.

“There are now datasets of tens of thousands of Holsteins and the industry is using this data to predict breeding values,” Professor Goddard said.

“AI studs are decreasing their progeny programs and basing their selection on genomic predictions.”

However, the problem for beef cattle is that data is spread across 7- 8 breeds and the beef industry wants to be able to make predictions across these breeds.

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“If the association between SNPs varies from one breed to another, it is almost certainly the case that the variation between SNPs and real genes also varies from one breed to another.”

A SNP associated with increased productivity in Black Angus can have a negative effect in a Brahman.

Professor Goddard said the beef industry had been stymied in delivering prediction equations to industry based on the use of the 50k SNP chips.

However, the recent release of higher density SNP chips of around 650k and 800k by Illumina and Affymetrix will provide chips of a high enough density to develop a prediction equation that will work across breeds.

“This is what the Beef CRC is currently working towards,” Professor Goddard said.

Beef CRC 3 is on track to deliver validated genomic prediction equations for carcass and meat quality traits, NFI and fertility to be transferred to BREEDPLAN and genomics companies in 2012.



Beef CRC’s measurement records legacy

When the Cooperative Research Centre for Beef Genetic Technologies (Beef CRC) began its term in 2005, the CRC was sitting on the largest beef cattle phenotypic databases for hard-to-measure traits of any research centre in the world – the legacy of the two CRC’s two previous incarnations.

“We had built up the world’s largest record of measurements of hard-to-measure traits in beef breeds like Hereford and Brahman,” Beef CRC CEO Dr Heather Burrow said.

“These measurements needed to be matched with information from the Bovine Genome Project, and at that time, we were confident we had enough animals to lead the world in discovering genes associated with these economically important traits.”

However, Dr Burrow said that when her research team accessed the Bovine Genome Project data in 2006, prevailing assumptions quickly changes.

“We thought that as few as five to 10 DNA markers would account for a large chunk of the variation for these traits in beef breeds and this was completely wrong. It turned out that we would need thousands more animals than we had in our databases, which meant forming partnerships with

other Australian and overseas groups studying the genomics of beef cattle.”

“The problem of getting DNA markers to work across the multiple breeds used by the beef industry is so much more complex than for a single dairy breed,” she said.

Genomic selection is working well in the dairy industry, whereas beef researchers had to first develop much larger panels of SNPs to provide the required density of coverage across their multiple breeds.

The dairy industry’s other significant advantage is its history of extensive use of progeny-testing to select bulls for milk production.

“As a result, they have very large numbers of bulls’ daughters with accurate measures of the economically important dairy traits. The beef industry has nothing to rival the dairy industry’s extensive progeny-testing programs.”

Where the dairy industry had highly accurate measurements from tens of thousands of animals of a single breed, Dr Burrow said the Australian beef industry only had limited measurements on perhaps 15-20,000 animals across multiple taurine and indicus breeds.



Should a Gene Test Decide Which Sport Your Kid Should Play?

By Bonnie Rochman, Time Magazine, June 8, 2011

Millions of kids play sports. But are they playing the right ones? Forget fun; this is about - to borrow a catchphrase from Charlie Sheen - winning. Now, at least two companies are marketing DNA tests that purport to help uber-competitive parents gain insight into which sports their progeny may be genetically built to excel in playing.

The companies say their DNA scans can help families decide which sports individual kids are most likely to win and hence - with an eye toward the future - which would be most likely to yield possible college scholarships. The tests can also suss out children who may be prone to health problems, such as heart problems and concussions, for example, that can be exacerbated by athletics, the companies say.

But the U.S. Food and Drug Administration (FDA) and other critics of the tests are calling foul. In May, the FDA wrote to one company marketing a sports-gene test, the Sports X Factor Test Kit, asking it to provide evidence that it should be allowed to sell its test without FDA clearance. Last year, similar FDA scrutiny prompted another direct-to-consumer DNA testing company to scuttle plans to sell its gene test in drugstores.

Some researchers are concerned that the information from sports-gene tests provide only a partial picture. Certainly, genes associated with energy, endurance, speed or strength - for which these companies test - play a role in athletic ability, but while they may be important, so are effort and drive.

"Genetic testing can't measure the passion a young person has for an activity," says Larry Lauer, director of coaching education and development at Michigan State's Institute for the Study of Youth Sports. "While someone might be predisposed to be successful in a certain sport, it doesn't mean they're going to enjoy it or want to work hard at it."

One of the biggest factors that influences how committed a child is to a particular sport over time isn't genetic or even physiological. "It's whether they develop a passion and an intrinsic motivation to train because this is what they enjoy versus doing it because their parents told them to," says Lauer.

The gene-testing companies are also playing into fears parents may have about their children's

What is a genome?

The word "genome" was coined in about 1930, even though scientists didn't know then what the genome was made of. They only knew that the genome was important enough, whatever it was, to have a name.

A genome is all of a living thing's genetic material. It is the entire set of hereditary instructions for building, running, and maintaining an organism, and passing life on to the next generation.

The genome is divided into chromosomes, chromosomes contain genes, and genes are made of DNA. Genes, packaged in chromosomes, affect specific characteristics of the organism.

Each one of earth's species has its own distinctive genome.

Genomes belong to species, but they also belong to individuals. Unless you are an identical twin, your genome is different from that of every other person on earth—in fact, it is different from that of every other person who has ever lived.

Although unique, your genome is still recognisably human. The difference is simply a matter of degree. The genome differences between two people are much smaller than the genome differences between people and chimpanzees.

Genome News Network: http://www.genomenetwork.org/resources/whats_a_genome/Chp1_1_1.shtml

American International Biotechnology Services, which markets Sports X Factor, tells parents it's a safety precaution. "We want to make sure [kids] are not out there blindly playing with one of these mutations and have a heart attack or a concussion," CEO Bill Miller told the Post. "It gives parents peace of mind that their kid is not going to drop dead in the middle of a workout."

And what about overzealous parents who may be wont to use test results to steer kids toward a sport they don't love and away from one they do?

As Lauer notes, there's a whole host of

"Some researchers are concerned that the information from sports-gene tests provide only a partial picture. Certainly, genes associated with energy, endurance, speed or strength - for which these companies test - play a role in athletic ability, but while they may be important, so are effort and drive."

factors that go into developing a successful athlete. Timing, for one: you have to perform great at the right time, so that that the coach plucks you from junior varsity or the college scout spots you in a crowd. You also have to stay injury-free and work hard consistently.

Read more: <http://healthland.time.com/2011/06/08/predicting-kids-athletic-skill-theres-a-dna-test-for-that/>



Nick Corbett from the Beef CRC ultrasounds a Brahman female as part of the 12-year project

Project delivers priceless fertility data

Beef Central online,
31 May 2011

One of Australia's longest-running cattle genetics projects, spanning 12 years of intensive recording, will complete its course on 31 May 2011 when the last group of No.3 cows have their calves weaned at Swan's Lagoon station in North Queensland.

The massive data collection exercise involved recording 2200 Brahman and Tropical Composite female cattle over nine years, their steer half-brothers over three years and 3500 of their bull calves over the first two years of their lives in a flagship project of the CRC for Beef Genetic Technologies.

A press release issued by Beef CRC said it had been a huge cooperative effort of science and industry, with the majority of the cattle having been run on five Queensland research stations.

Lead researcher, Dr David Johnston, from the Animal Genetics and Breeding Unit at the University of New England, praised the commitment of producers and the highly skilled technical expertise from CSIRO Livestock Industries, DEEDI and AGBU that led to the project's positive outcomes.

These collaborations had resulted in a world-first comprehensive understanding of whole herd profitability, with the key focus being the genetic basis of female reproduction in tropical cattle from puberty to six calvings, the press release said.

"I can't stress enough how important and rare this level of information is. Extensive measurements were performed on every cow many times, including ovarian scans, weight and condition scores, adapta-

tion scores and temperament assessments, with meat quality and feed efficiency measured in their steer half-sibs," Dr Johnston said.

Big spin-offs

The results promise big spin-offs for the northern beef industry. The data is already being used extensively in Breedplan, and new knowledge about genetic relationships between heifer puberty, lactation anoestrus in cows as well as indicators of female reproduction in bulls, all provide management recommendations for producers.

Many more genetic results will become available as the data continues to be analysed over coming



Tropical composite females under study as part of the 12-year project

months. DNA testing also means the genomics of tropical breeds and composites can be explored in these cattle.

The North Australian Pastoral Co has been involved with the Beef CRC since 1993 with the donation of cattle for the original crossbreeding program conducted at Duck Ponds near Comet in Central Queensland.

NAPCo's general manager, growing and marketing, Geoff Kingston, said since then, NAPCo had incorporated research outcomes into its own composite breeding programs.

"This has delivered a level of sophistication for our bull breeding programs unimaginable ten years ago," he said.

"Our animal selection has evolved from simple growth ratios to the use of EBVs and \$ Indexes incorporating many of the technologies and research findings from this genetic project," Mr Kingston said.

775,000 live animal records

To put the project into context, across all measures in total there have been 775,000 live animal records taken in the 2200 cows alone. This has provided an extremely powerful set of data.

It has not always been an easy task to accumu-

late the records, however, the CRC said. Since the project started in 1999, it had endured droughts, floods and cyclones which not only interfered with experimental timetables, but in some cases also forced the relocation of cattle. Most importantly though, stock losses were avoided.

"There were the inevitable difficulties in maintaining funding for the necessary time, but thanks to the commitment of the northern producers and our CRC staff we got through as planned, and we now have lifetime records on 2200 tropical cattle," Dr Johnston said.

"The value of the knowledge dataset should have long-lasting impacts for the Northern beef industry and prove to be an invaluable resource that allows future research to validated data for years to come," NAPCo's Geoff Kingston said.

Dr Johnston said genetics was a key factor for lifting reproductive performance in northern Australia.

"Producers need to focus particularly on their first-calf cows that are back in calf as three-year-olds and ensure they retain their progeny. There are

"Producers need to focus particularly on their first-calf cows that are back in calf as three-year-olds and ensure they retain their progeny."

tropical cattle out there that will calve every year - you just have to know how to look for them," he said.

Critically, the project would not have been possible without the long term financial commitment of the northern pastoral group of companies and individual breeders.

Ten long-term and very significant contributors have provided generous and crucial involvement: Australian Agricultural Co; Carolyn Briggs, Cona Creek, Springsure; Consolidated Pastoral Co; John and Sue Halberstater, Mandalay, Jambin; S. Kidman and Co; Tom Mann, Hillgrove, Charters Towers; Jennifer McCamley, Tartrus, Marlborough; MDH Pty Ltd; North Australian Pastoral Co; and Stanbroke Pastoral Co.

Collaborative Sequencing Project – “1000 bulls on the cloud”

Bovines in the cloud

“The database will be used by Beef CRC to impute sequence from SNP genotypes in research to find differences in the genome that are associated with economically important traits.”

With DNA sequencing now becoming cheaper, the time is near for ‘genome informatics’ to migrate to the cloud.

A proposed new project between the Australian beef and dairy industries and international partners, aims to assemble a database on 1000 cattle that have had their genome sequenced. Statistical methods will be used to correct sequencing errors, call genotypes at polymorphic sites and phase the genotypes.

The database will be used by Beef CRC to impute sequence from SNP genotypes in research to find differences in the genome that are associated with economically important traits.

The project will also maintain a public copy of the fully annotated bovine sequence, including all functional polymorphisms, as a unique resource for scientists and industry worldwide to use to develop new tools to better manage the biological differences between animals so they best meet market specifications.

The case for cloud computing*

Under the traditional flow of genomic information, sequencing laboratories transmit raw and interpreted sequencing information across the internet to one of several sequencing archives.

Users of sequence data typically download large datasets from the archives onto their local computer clusters for computationally intensive ‘number crunching’. Under this model, the sequencing archives, value-added integrators and users of the data all maintain their own computer and storage clusters and keep local copies of the sequencing datasets.

From 1990 to 2010, the cost of storing one byte of data has halved every 14 months. However since 2005, the cost of sequencing has halved every 5 months.

The cost of genome sequencing is therefore now decreasing several times faster than the cost of its storage. At some time in the not too distant future it will cost less to sequence an animal than to store its sequence information on a hard disk.

Genetic tsunami

‘Genome informatics’ systems face a potential tsunami of genomic data that will swamp storage systems and overwhelm computer clusters.

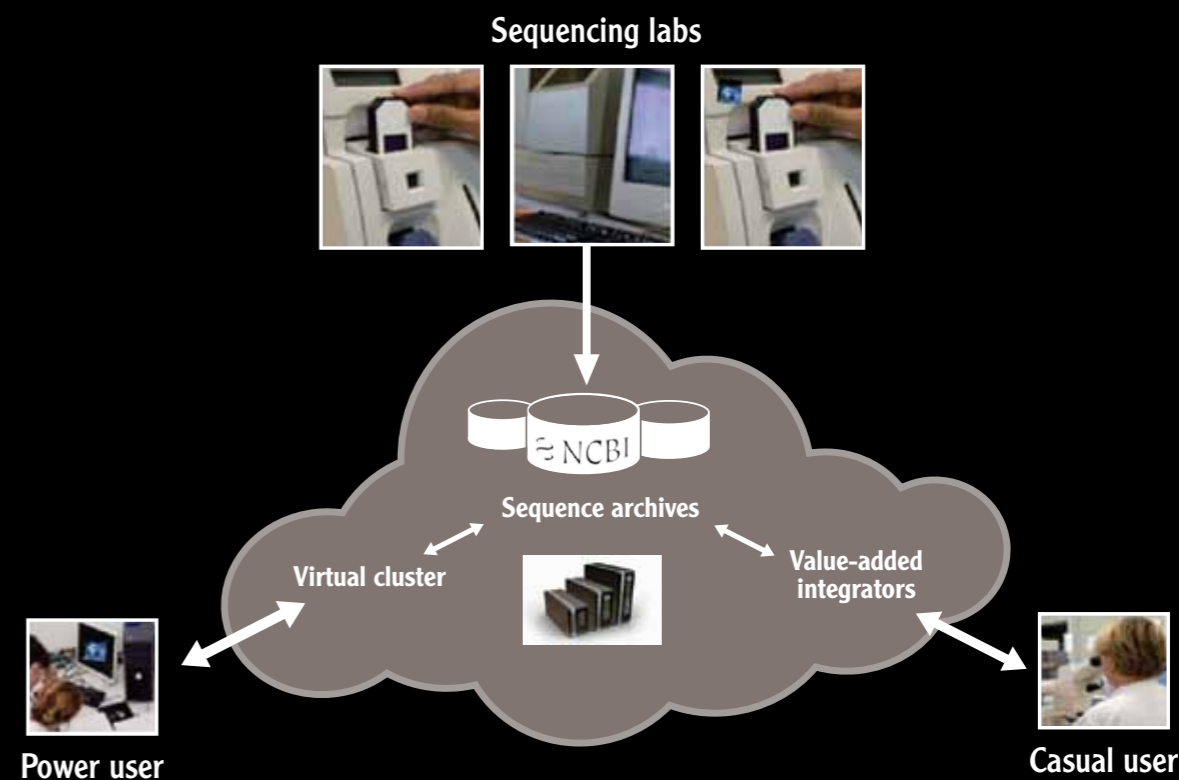
Consider this one statistic: The first big genome project based on next-generation sequencing technologies, the human ‘1000 Genomes Project’, which is cataloguing human genetic variation, deposited twice as much raw sequencing data into GenBank’s SRA division during the project’s first 6 months of operation than had been deposited into all of GenBank for the entire previous 30 years.

The 1000 Genomes Project is just the first ripple of the tsunami. There is no easy solution.

At some future point it will become simply unfeasible to store all raw sequencing reads in a central archive or even in local storage.

Genome biologists have to start acting like the high energy physicists who filter the huge datasets coming out of their collectors for a tiny number of informative events and then discard the rest.

CLOUD COMPUTING



Storing large datasets in the cloud

For the field of ‘genome informatics’, a key feature of cloud computing is the ability of service providers and their customers to store large datasets in the cloud.

These datasets typically take the form of virtual disk images that can be attached to linked computer networks as local hard disks

and/or shared as networked volumes. For example, the entire GenBank archive could be (and in fact is) stored in the cloud as a disk image that can be loaded and unloaded as needed.

There are some downsides to moving genomics into the cloud. An important one is the cost of migrating existing systems into an environment that is unlike the environment that exists today. Another issue is how

to handle potentially identifiable genetic data, such as that produced by whole genome association studies or disease sequencing projects. Network bandwidth is also an issue. And of course, guaranteed data security must be the number one consideration for potential users of cloud computing

*Adapted from The case for cloud computing in genome informatics by Lincoln D Stein in Genome Biology, 2010, 11:207.

Industry sire genotyping project

The Australian beef industry is building a database of DNA information (or 'genotypes') on its widely used sires.

A collaboration between the Beef CRC, Meat and Livestock Australia and nine breed societies, the 'Industry Sire Project' will soon deposit about 1300 DNA profiles from sires with BREEDPLAN accuracies above 60 per cent into a National Genotypic Database.

The purpose of the database is to provide the information required for independent calibration of genomic breeding value prediction traits developed by the Beef CRC and the genomics companies, so industry can be informed of the value of the tests in their own herds.

The Beef CRC's genomic prediction equations will be made available to BREEDPLAN by April 2012 so the extra genotypes can be used to increase the accuracies of estimated breeding values for hard-to-measure and economically very important traits.

Dr Hans Graser, Director of the Animal Genetics and Breeding Unit (AGBU) said the core role of the database will be to calibrate commercially available prediction equations for their effective use in BREEDPLAN.

Genomics is not a stand-alone silver bullet, Dr Graser observes. To get reliable outcomes from genomic predictions, they need to be used in conjunction with animal measurements ('phenotypes') and pedigree information.

The dairy industry, which has far fewer variables impacting on animal performance than the beef industry, collects thousands of phenotypes a week.

"In the beef industry, there is no parallel," Dr Graser says. "We have not implemented a process of systematic data collection for these hard-to-measure traits."

National Genotypic Database

Providing a critical resource for a number of Beef CRC projects, including the Industry Sire Project, the National Genotypic Database and matching DNA Banks collects, collates and stores DNA and the genotypes derived from the DNA from the elite industry animals.

The DNA Bank of stored DNA is maintained by the University of Queensland's Animal Genetics Laboratory. The National Genotypic Database is maintained by AGBU.

Genotypes from either Illumina's 50K or high-density SNP panels are generated from the DNA by a laboratory equipped to undertake the laboratory. This

could be in-house through one of the Beef CRC's partner laboratories (e.g. Victoria DPI or CSIRO) or it could be cost-effectively outsourced to a laboratory such as Geneseek.

Once the genotypes are available in the National Genotypic Database, they can routinely be used by BREEDPLAN in much the same way as phenotypic data and pedigree information is used.

With increasing information in BREEDPLAN analyses, genomic predictions will be continuously recalibrated to achieve greater accuracy, as already happens in BREEDPLAN for phenotypic information. The more animals in the dataset with phenotypes and genotypes, the higher the accuracy of the breeding values for these animals.

Breed societies recognise the importance of recalibrating the equations for use by their breeds to ensure the new genomic predictions are as accurate as possible and to achieve higher rates of genetic gain.

The value of genomic information "decays over time" as selection for favourable alleles fixes the genes.

It will be essential to continue to record animals and collect genotypes from successive generations of animals to ensure genetic progress can continue to be made well into the future.



Impacts of genomics on industry structures

To achieve value from the genomic revolution in beef cattle, it is critical that measurement and recording of animals remains a fundamental component of genetic progress. Who will carry the costs of recording in the future?

The Beef Information Nucleus (BIN) herds set up by several breed societies are an efficient way of collecting more esoteric genetic information, not least because of the genetic interlinking created through BIN breeding programs and the inter-generational links.

But it is another step to ask the breeds to continue to fund annual progeny tests over several thousand animals, "possibly permanently", in the view of Meat & Livestock Australia's Manager, R&D Strategy and Evaluation, Dr Rob Banks, the recent winner of the Helen Newton-Turner Medal awarded to practitioners engaged in the genetic improvement of productivity and product quality of livestock.

"At this stage, it appears that's what we'll need to do to keep genomic data relevant for ongoing

validation and calibration," said Dr Banks.

"And if a breed is to be confident in the test, they probably need to be doing the work itself."

Dr Banks said it was similar to having a stud dedicated to collecting genomic data.

"It's not cheap and breed societies don't normally do that sort of thing. Depending on the trait, maintaining the herd and collecting the data might cost a half million to \$1 million a year."

This raised the risk that the more costly genomic tools will only be available to the larger breeds with the resources to fund their development. As a result, the big breeds may increase their competitive advantage and the smaller breeds could shrink in numbers. The risk is that they disappear commercially.

Research in BIN herds is jointly funded by the breed societies and MLA and is currently underway with the Angus, Hereford, Charolais, Limousin and Brahman breeds.

New funding and collaboration options may be necessary to help the larger breeds maintain data collection independently, and to help small breeds contribute to the genomic footprint.

Rob plans to take this challenge to the beef industry over the next couple of years. It is, he says, "going to be a significant challenge to industry to work out how to do this."

The initial promise of genomics still holds true:

that breeders will be able to peer into an animal's genetic potential using a drop of blood or a few hairs.

But Rob thinks the true "disruptive" nature of genomics lies in how breeds will reorganise around the technology to best capitalise on it.

He foresees a time when cattle studs will split into two classes: the "multipliers" and the "nucleus".

The nucleus studs will be the BIN herds of the future: elite herds that contain the breed's reference animals, are deeply engaged with genetic data collection and management and effectively set the genetic directions for the breed.

"Multipliers" will focus on harnessing genetic information from the nucleus herds to produce the right animals in large numbers, and at low cost. The multipliers will be the breed's interface with the rest of the beef supply chain.

"It's going to be really interesting. For the Angus breed to get the data it uses today takes an investment of \$2-3 million a year. If 5-6 studs take on this job, how do they get compensated for their recording effort? Do they get to sell bulls as well?"

"I think genomics has the potential to change what it means to be a breed, as well as potentially changing the roles of the breed societies," he said.

The Australian Poll Gene Marker test

- Works very well in Brahman
- Shows promise in other breeds
- Needs more validation work in many breeds

What is the Australian Poll Gene Marker?

Industry testing of a new **Australian Poll Gene Marker** test developed for Australian herds has been completed.

The new gene marker was developed by the Beef CRC in partnership with CSIRO, MLA the UNE Animal Genetics and Breeding Unit and the University of Queensland Animal Genetics Laboratory.

The test aims to identify whether cattle are “true polled”. Some visibly polled animals may still carry a recessive gene for the horned trait and throw a proportion of horned offspring. This mixed heterozygous genotype is also associated with scurs – incomplete horns.

A true polled animal is “homozygous” – that is,

it carries a double copy of the poll gene and in most cases, will not throw horned offspring.

It is valuable for breeders and producers to have the tools to help predict the horned trait in their herds.

It is impossible to differentiate between true polled and polled carriers without genetic testing or pedigree information, such as extensive progeny testing.

Animals inherit half their genes from their sire and half their genes from their dam. The combination of these genes contributes to the animal’s horn status. In many breeds polled is usually dominant to horned, so even though an animal is polled it could still be carrying a horned allele.

How is the data presented to producers?

The poll gene test costs \$33 from the University of Queensland’s Animal Genetics Laboratory but is discounted if you order through a breed society or a bulk order. Currently the University provides a “one-

off” result certificate for samples provided. As with other poll gene tests, the Australian Poll Gene Marker test is not a test that identifies the poll gene itself, rather a marker linked to the poll gene. Therefore, a result cannot be 100% accurate.

A result certificate from a laboratory contains only an accuracy percentage which varies. The test generates the probability of the sample being one of three categories:

1. Homozygous PP (true-polled)
2. Heterozygous, PH (carrier of horns) or
3. Homozygous HH (horned animal)

Table 1 shows examples of test results that the University of Queensland Animal Genetics Laboratory would provide to producers and breeders who submit a DNA sample.

Please note: the Australian Poll Gene Marker test has been made available to commercial providers. Test results may be presented in different formats by different commercial providers.



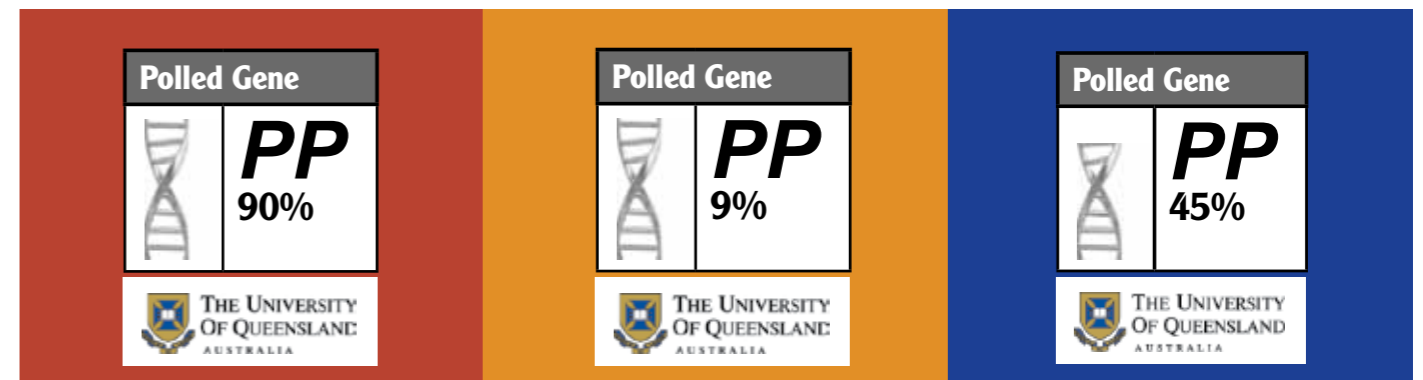
“In the last six years or so the breed has certainly seen premiums for polled bulls at auction sales and we get a lot of requests for polled bulls in our paddock sales. The frequency of the polled gene is still low in Brahmans, so I believe that anyone who wants to make genetic progress for polled will be valuing a homozygous poll. Without this test we have no confidence in whether an animal is a homozygote or a heterozygote.”

Sarah Streeter, whose family’s Fairy Springs Brahman Stud near Bowen, QLD, has been selecting for polledness for the past 15 years.

Table 1: Example results for the Beef CRC’s Australian Poll Gene Marker test

| Polled Bull 1 | | | Polled Bull 2 | | | Polled Bull 3 | | |
|---|-----------------|---------------|--|-----------------|---------------|--|-----------------|---------------|
| Homozygous PP | Heterozygous PH | Homozygous HH | Homozygous PP | Heterozygous PH | Homozygous HH | Homozygous PP | Heterozygous PH | Homozygous HH |
| 90% | 9% | 1% | 9% | 90% | 1% | 45% | 45% | 10% |
| The test identifies that the bull is “True-polled” with 90% accuracy. | | | The test identifies with 90% accuracy that although Polled Bull 2 does not have horns himself, he is a carrier of the horns. | | | The test does not provide a useful result. It informs you that while the bull is polled, there is equal probability of the animal being either true-polled or a carrier of horns | | |

The breeder will receive the following certificate from The University of Queensland Animal Genetics Laboratory:



Note: Other commercial providers may present the same results differently.

Table 2: Polled genotype and phenotype descriptions

| Genotype | 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. |

What are ambiguous results?

The Australian Poll Gene Marker test is based on a marker linked to the polled gene.

While some marker results are nearly always associated with polled and some marker results are nearly always associated with horned, there are also some ambiguous marker results for which the association between polled and horned cannot be determined.

This occurs when alleles, that is, one of a pair located at a specific location on a specific chromosome, are unable to be assigned definitively to either polled or horned status. The test returns these ambiguous alleles at different rates amongst different breeds.

In the research populations and industry trials in commercial populations, the Brahman samples tested recorded a very low frequency of ambiguous results (11%), which is a good result for the breed. It means that during the industry testing phase the new Australian poll gene test could provide a result 89% of the time for polled cattle.

How do I test my animals?

Contact your Breed Society or the DNA lab for a biological sample collection kit

1. Receive a Collection Kit
2. Collect hair sample
3. Complete the required forms
4. Mail form plus hair sample to lab
5. Wait for results to be returned.

Acknowledgements

The Beef CRC would like to acknowledge and thank all of those cattle breeders who provided samples and phenotypes for this research and in particular Mr Tom Mann of Hillgrove Station, Charters Towers for his long term commitment to this project. The research team of scientists who developed the test were led by Dr Kishore Prayaga and were awarded a prestigious Australian Museum Eureka Prize in 2009 for this work.

Further information:

Full Technical Report:
<http://www.beefcrc.com.au/Assets/785/1/PollGeneTechnicalReport27-6-11.pdf>

Beef CRC website:
<http://www.beefcrc.com.au/PolledGeneMarkerTest>

Beef CRC
 Tel: (02) 6773 3501
 Fax: (02) 6773 3500
 Web: www.beefcrc.com.au
 Email: beefcrc@une.edu.au

The University of Queensland
 Animal Genetics Laboratory
 School of Veterinary Science Building 8114 Level 2
 Gatton QLD 4343
 Ph: (07) 5460 1960
 Fax: (07) 5460 1565
 Email: cattleDNA@uq.edu.au
 Web: www.uq.edu.au/vetschool/agl

Australian test for polled gene: Case study in Brahman



The Streeter family

The recent release of the CRC polled gene marker test for industry validation prompted a keen response from Brahman breeders with 38 studs supplying 402 animals for testing. The Streeter family of White Kangaroo near Bowen were among the studs to supply animal samples and phenotypes for the study.

Sarah Streeter says her family's Fairy Springs Brahman stud has been selecting for polledness in their herd for the past 15 years, mainly because they value the fact that polls require less labour at branding and there is less stress imposed on the animal. "We recognized it as a beneficial trait to have in our herd," she said, "and I think dehorning will become more difficult in the near future because of welfare pressures."

The Streeters sell 80-100 bulls each year. "In the last six years or so the breed has certainly seen premiums for polled bulls at auction sales and we get a lot of requests for polled bulls in our paddock sales," says Ms Streeter. She believes the CRC marker test will be invaluable for their stud and for buyers wanting rapid genetic progress for the polled trait in their herds. "The frequency of the polled gene is still low in Brahmans, so I believe that anyone who wants to make genetic progress for polled will be valuing a homozygous poll. Without this test we have no confidence in whether an animal is a homozygote or a heterozygote," she said. Based on Brahman results from the validation study, if a bull tests homozygous polled you can feel confident that the result is about 90% accurate in predicting his status. A homozygous polled bull mated to a predominantly horned cow herd will result in the progeny being scurred or polled in the first generation.

Ms Streeter said they will definitely use the test as a marketing tool and intend to test all of their polled auction bulls, bulls retained for use in their herd and paddock sale bulls if requested. Ms Streeter adds, "Up until now we couldn't place any more value on one animal than another just on their polled phenotype. But now I would certainly expect to see a premium on a homozygous polled bull. Given that though, the animal still needs to be able to tick all the other boxes for reproductive soundness and have good carcass characteristics as well."

The Streeter family provided animals used in early research which led to the discovery of the poll gene test.

Australian test for polled gene: Case study in Hereford



Ian Locke, of Wirruna Poll Hereford stud in southern NSW

It was good news for Ian Locke when he learned the Beef CRC was developing a polled gene marker test for Australian cattle breeds.

Mr Locke, of Wirruna Poll Hereford stud in southern NSW, says he has always dipped into the horned Hereford gene pool because it's around 50% of the total Hereford population.

"I find it hard to sell horned bulls within my client base, and they generally prefer non-scurred bulls, but I've always been able to use horned bulls and use the dominance of the polled genes to our advantage," he says. "However we've had to be careful not to increase the frequency of the horn gene too much and we've always wanted to identify carriers of horns."

Mr Locke has been using the US based IGENITY horned/polled test for the past 5 years to test all sires he uses in his herd and donor cows for embryo transfer programs. He was able to offer about 80 test results from the US test, including samples and phenotypes for the test animals and their progeny, to help validate the CRC test. Results from both tests were 100% consistent. "At this stage the CRC test is working a treat for what I want," says Mr Locke.

Up until now Mr Locke has tested about 15% of his sale bulls. In his most recent sale a few buyers competed strongly for a number of tested homozygous polled bulls, and the premium paid was sufficient to pay for the next calf crop's tests. Mr Locke believes the amalgamation of the Poll Hereford and Hereford societies has increased demand for homozygous polled bulls. "The CRC test can give buyers the confidence to come in and buy a bull that will poll up everything in herds with horns."

Mr Locke has just tested his entire drop of 180 weaner bulls. He says he's committed to using the test for the next 4-5 years to determine the frequency of the polled gene in his herd and to minimise wastage associated with castrating horned bulls. Mr Locke is looking forward to having the results in hand to decide how to use them strategically for both breeding and marketing.



Applied Genomics for Sustainable Livestock Breeding

Conference Report

“Consensus was achieved the best way to use DNA information to improve rates of genetic gain was through integration of genomic data into existing genetic evaluation schemes such as BREEDPLAN, Sheep Genetics and the Australian Dairy Herd Improvement Scheme.

In early May 2011, the Cooperative Research Centres for Beef Genetic Technologies, Sheep Industry Innovation and Dairy Futures jointly sponsored a one-off international ‘Applied Genomics for Sustainable Livestock Breeding’ conference.

The principal sponsor was the Sir Mark Oliphant International Frontiers of Science and Technology Conference Series administered by the Australian Academy of Technological Sciences and Engineering and the International Science Linkages Scheme through the Federal Department of Industry, Innovation, Science and Research.

The aims of the conference were to:

- Develop stronger interactions between the research and livestock industry communities relating to implementation of genomics technologies in the beef, sheep and dairy industries;

- Present the most up-to-date results from genomics research groups around the world;
- Achieve consensus on the best ways to implement those results in the beef, sheep and dairy industries in Australia (and ideally for the international researchers participating in the conference to promote that consensus in their own countries and industries);
- Review genomics research progress to date and identify new opportunities to achieve additional benefits for the beef, sheep and dairy industries in future; and
- Strengthen existing and develop new research collaborations that are focused on delivering benefits for the livestock industries across all countries.

In total, more than 360 delegates from 23 countries participated in the conference, with most

delegates opting to participate in the entire conference.

Day 1 was strongly focused on genomic technologies and the way they are being developed for use by the livestock industries.

Day 2 focused on the application of those genomic technologies across a wide range of industries, including the beef, sheep, dairy, pork, poultry and aquaculture industries as well as for human medical applications.

The program for **Day 3** was very specifically developed with and for industry end-users from the beef, sheep and dairy industries, with the aim of assisting them with implementation of genomic technologies in their own businesses.

Feedback from conference delegates suggested the conference was very useful, with a number of delegates requesting an update in 1-2 years time. >>

Who attended?



Delegates from the following 23 countries attended the conference:

- | | | |
|-----------|---------------|--------------------------|
| AUSTRALIA | GERMANY | NIGERIA |
| BELGIUM | IRELAND | NORWAY |
| BHUTAN | JAPAN | PORTUGAL |
| CANADA | KENYA | SAUDI ARABIA |
| CHINA | KOREA (SOUTH) | SCOTLAND |
| DENMARK | MALAYSIA | SOUTH AFRICA |
| ENGLAND | NETHERLANDS | UNITED STATES OF AMERICA |
| FRANCE | NEW ZEALAND | |





Applied Genomics for Sustainable Livestock Breeding

Conference outcomes

For the Beef CRC, the conference exceeded our aim of effectively positioning genomics technologies for use by beef cattle breeders and assuring the Australian beef industry that Beef CRC was on par with the rest of the world in developing and using the technologies. The difficulties the Beef CRC had experienced with the early genomic research outputs had also been experienced by every other industry and laboratory world-wide.

The conference was also an excellent venue for developing new networks and collaborations and strengthening existing national and international collaborations amongst industry end-users, extension workers and consultants, genomics companies and

their service providers and key researchers from across the globe.

Remarkably, consensus was achieved across the beef, sheep and dairy industries that the best way to use DNA information to improve rates of genetic gain was through integration of genomic data into existing genetic evaluation schemes such as BREEDPLAN, Sheep Genetics and the Australian Dairy Herd Improvement Scheme. This approach was also strongly supported by international speakers from the poultry industry.

There was also strong agreement about the value of DNA information for identifying parentage and carriers of deleterious recessive genes, for reducing inbreeding and for optimising animal management strategies, in addition to predicting the performance

of breeding animals.

Synchronised video and slide presentations for the entire conference were made publicly available via the conference web-site. For the five-week period immediately following the conference, there were 5,818 access visits to this video site and visitors to the site were identified as being from 49 different countries. The average visit length was close to 30 minutes, creating unprecedented demand for the web host and indicating the content was of genuine interest to those accessing the site. ■

Conference website: <http://smogenomics.org/>
View webcast of conference presentations online (to May 2012) <http://www.mediavisionz.com.au/genomics/2011/>

Conference presentation:

How does genomics work in poultry?

The tools available to animal breeders for making selection decisions have never been more complex.

In beef, estimated breeding values (EBVs) that have traditionally combined pedigree and phenotypic information are now able to include genomic information for important production, reproduction and fitness traits to provide the overall best estimate of breeding values of animals being considered for selection in breeding programs.

However, an important difference in layer poultry is that all the genetic stock is owned by private companies and there is very tough competition amongst those companies. Companies do not share genomic information.

Dr Rudolph Preisinger, CEO of the German layer company, Lohmann Tierzucht GmbH, explained the complexity of layer breeding and the potential application of genomics in the poultry industry at the recent conference for Applied Genomics for Sustainable Livestock Breeding conference.

In the poultry breeding industry, pure layer lines are maintained by commercial poultry companies under high biosecurity in artificial environments so chickens can be exported. Cross lines are bred on commercial farms with direct genetic linkages to the pure lines.

All poultry companies have comprehensive phenotypic data recording in both pure and cross line birds. Genetic progress is generated from selection and reproduction within closed nucleus gene pools. Some layer gene pools have been closed for more than 50 generations.

"We rely on sibling testing to keep the generation interval limited and to run an all-in and all-out breeding program," said Dr Preisinger.

Reproduction of selection candidates occurs for 6-10 weeks with 4-6 progeny hatched per dam each week. Of those progeny, all females are retained. Only 1-2 males are randomly selected per full-sib family to keep inbreeding down. In total, the company keeps about 12-30 females and 2-3 males per dam which are the next selection candidates. Because the pure line farms are all-in and all-out, the majority of data comes from siblings of a similar age.

"With layers, you have to make selection deci-

sions on traits such as persistency before you have all the information available. We are looking for a precise, quick, economic way to get genotypes earlier," said Dr Preisinger.

Genomics offers the potential to achieve this.

Dr Preisinger sees the main advantage of genomics is being able to select the most promising males within full sib families earlier and more accurately, thereby substantially reducing generation interval. All layer companies are generating sequencing data from individuals or pools of individuals from pure lines with this aim.

"I see male selection as the major potential. Genetic information is combined with phenotypic data to achieve more powerful breeding values. Genomics is helping us to increase the chance of transmitting superior genetics to the next generation," said Dr Preisinger.

Undertaking a genomics program requires a large investment of time, physical and financial resources, and because of the nature of the poultry industry, is done entirely and independently by each of the companies. On the positive side, there is an abundance of reliable phenotypes available through established performance testing and generation intervals are short relative to other livestock industries.

Genome-wide selection in the poultry industry is still in its initial stages.

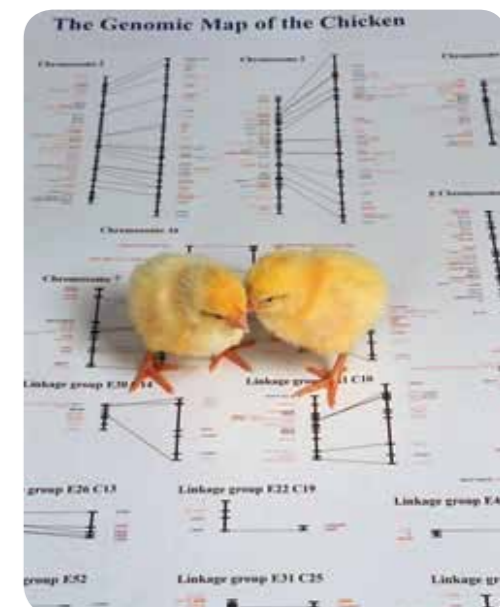
"There is the potential to increase the rates of genetic gain by up to 40% in layers and between 90% and 200% improvement in egg production and egg quality using SNP data. However for the initial several years, there is investment but no additional genetic progress," said Dr Preisinger.

However some costs of the program can be recouped.

During performance testing, phenotypic data is collected from the eggs of the pure lines. The eggs can still be hatched and the progeny sold to customers as parent stock or grandparent stock.

Genotyping an animal is costly, with Dr Preisinger's company currently allowing a cost of around 200 Euros (\$276) per bird for whatever density SNP

Applied Genomics for Sustainable Livestock Breeding



panel that will purchase. Initially 200 Euros would purchase a 50K SNP panel, but now that same amount will purchase a high-density SNP panel that is helping to increase the accuracy of selection.

The cost of genotyping 4000 birds in a 'training' (or discovery) data set using a high density chip, 10,000 application selection candidates using a low density chip, and 1000 parent stock using a high density chip, equates to about 5 million Euros.

This cost is borne by private companies and breaks down to a price increase of about 0.70 Euros per parent animal sold, which is a 10-15% increase in the current price of a breeder female. This means the genetic improvement in the sale animals needs to be sufficiently high to justify that price increase or the companies need to significantly increase their market share.

Genomics for the beef industry differs from the chicken industry in that for beef, the cost of genomics research is spread across the industry and not entirely borne by a few private companies. It is also the case that where a bull might be worth \$3000, a hen is only worth \$7.



Dr Alison Van Eenennaam explored that question at the SMO Livestock Genomics Conference in April, and arrived at some sobering conclusions.

An Australian-born cooperative extension specialist at the University of California, Davis, Dr Van Eenennaam told the conference that under current business models, the value of an individual genetic test is mostly reaped by processors.

The balance of benefit returns to seedstock producers, but it can be small - as is the value of a test to commercial producers.

With Beef CRC scientists Julius van der Werf and Mike Goddard, Alison used computer models to look at the returns to the seedstock sector of a hypothetical genotyping test.

The test was used in two scenarios: the expected returns from using a commercial sire sourced from a seedstock herd using DNA testing, and value of marker information in the selection of replacement stud males to be mated in a seedstock breeding program.

The model worked on assumptions of an

extremely powerful test, considerably more accurate than those currently on the market. Alison noted tongue-in-cheek that the modelling embraced "about 6000 assumptions" and bore no relationship to tests currently available.

In stud male selection, modelled returns to the seedstock sector in terms of improved selection response were impressive.

At the lower end, the models calculated that a single test of intermediate accuracy could return \$204 in value if used to select terminal sires for the grass-finishing domestic market.

Maximum value, calculated at \$1119 per test, was obtained when a theoretical high-accuracy test was used to select for a self-replacing herd aimed at the feedlot export market.

A different picture emerged when the model was used to break down how the value of genomic testing would accrue in the supply chain by aiding selection of commercial sires.

Processors stand to gain from genomic selection through increased accuracy of selection in traits like marbling score and yield. Seedstock producers gain from better selection toward traditional profit drivers like liveweight and maternal traits.

In the modelling,

producers only retained the lion's share of value from tests used to select terminal sires in grass-based systems; in all other scenarios, processors stood to gain the most.

For instance, a high-accuracy test to select ter-

"...genomic tools definitely have value in their own right, especially for the seedstock and processing sectors."

minal sires on grass-finishing indexes was estimated to return producers \$273 per test, and processors \$194.

But the other scenarios - maternal-focused selection on grass indexes, and terminal and maternal selection for the feedlot indexes - showed that genotyping delivered a clear win for processors and retailers, and a much more ambiguous result for the seedstock producers who traditionally do the testing.

At the upper end of the scale - selecting for maternal traits assessed on a feedlot index - producers gained \$191 in value per test, versus \$719 per test for processors.

(By comparison, an earlier presentation at the conference suggested the current generation of genomic tests deliver a low single-figure value for each animal tested.)

If producers are going to one day invest in a test of this calibre, with the associated expense, are they going to get that accrued value back from their supply chain? Alison asked.

Under the current model, no. "We have a market failure in beef that makes that hard to get, so it's likely the tests are worth a lot less than that," she told the conference.

So how does the industry place a value on genotyping, and on the cost of getting that information into BREEDPLAN?

Firstly, Alison said, genomic tools definitely have value in their own right, especially for the seedstock and processing sectors.

The technology has proved its worth in tackling the Arthrogyrosis Multiplex (AM) or "curly calf" genetic syndrome found to be rife through the Angus gene pool several years ago.

In three months in late 2008, the American Angus Association had used the technology to post the carrier status of 736 bulls; in the subsequent 11 months, it delivered results from more than 96,000 cattle, 20 per cent of them who proved to be AM carriers.

The testing costs racked up to US\$2.4 million - but more than 23,000 bulls and 53,000 heifers tested free of AM, a saving to the breed in the order of \$200 million.

The case for commercial producer use of genetic testing is less clear.

In the US, there is a push for commercial use of genetic technologies, but Alison is unsure of its current value for this sector.

Under a commercial situation, she said, "there is really a very small rate of improvement and a small return, because commercial heifers don't have that many descendants and you can't get the genetic amplification you can get in the seedstock sector".

As costs go down and accuracies go up, feedlots may find their own unique benefits from DNA testing for marker-assisted management.

There are signs that the value proposition is already there, Alison observed. US feedlotter Cactus Feeders is now using genotyping to sort select groups of cattle into different feed and growth promotant regimes.

But the beef industry still has a lot of work to do to determine who should bear the costs of genotyping, and who should reap the benefits.

"Ideally cattle would be genotyped once, early

in life, because there's a cost involved in extracting that DNA and it doesn't make sense for every sector to do it four or five times," Alison said.

If a test is done once, and early, then other players in the supply chain can use that information to assess critical parameters for their sector of the industry.

The future, Alison surmised, "belongs to those breeds or groups that can organise to do cost-effective genotyping and capture cumulative supply chain value by using information for multiple purposes".



Bigger not always the best

The United States beef cattle herd is three times the size that of Australia but US beef industry demographics suggest Australia may be able to embed genomics into its industry more effectively.

According to Dr Alison Van Eenennaam, speaking at the Applied Genomics Livestock for Sustainable Livestock Breeding conference, Australia has larger economies of scale which should enable more cost-effective access to genomics technology.

While the US has three times the number of breeding cows (31.4 million versus Australia's 12.9 m), it also has 20 times the number of beef producers:

- 90 per cent of US producers have herds of less than 100 animals
- Average herd size in the US is 122 animals, compared to 605 in Australia.
- The small producers own 49 per cent of the US beef industry.

"Australia has larger economies of scale which should enable more cost-effective access to genomics technology," Dr Van Eenennaam said.



Conference presentation:

Speed breeding in livestock species

Applied Genomics for Sustainable Livestock Breeding

A newborn Holstein-Friesian bull born today will not sire his first crop of heifers for five years. It will then be another three years before progeny testing confirms his potential to sire daughters that will be prolific milk producers.

But genomics expert Associate Professor Ben Hayes says milk yield can only be selected in heifers, and even with artificial-breeding technology such as embryo transfer, a long generation interval constrains the rate of genetic gain in cattle.

Dr Hayes from the Victorian Department of Primary Industries' Biosciences Research Division at Bundoora in Melbourne contributes to genomics research in each of the Beef, Dairy and Sheep CRCs.

Judging the genetic worth of embryos

He says genomic selection will soon allow breeders to confirm, even before a male embryo is implanted in its surrogate mother, that most of its daughters will be elite milk producers.

And genomic selection will allow breeders to take oocytes harvested from his three-month old

“With genomic selection, the accuracy of the breeding value is much higher at an earlier age than it is with traditional breeding.”

daughters, fertilise them in vitro with semen from another elite bull, and select female embryos with even higher milking potential than their mothers.

At the Sir Mark Oliphant Livestock Genomics Conference in Melbourne in May, Dr Hayes described how genomic selection is already accelerating the rate of genetic gain for selected traits in livestock well beyond the incremental improvements from centuries of traditional breeding.

In the past, breeders have pursued improvement

by selecting visible or measurable traits, without knowing which genes contribute to traits of interest.

Different variants of the same gene determine whether an Angus will be red or black, or whether an animal will have horns or not. Simple rules govern the inheritance of single-gene traits.

But single-gene traits are the exception to the general rule that most important production traits are polygenic: that is, many genes - tens to hundreds, in some cases - acting in concert, contribute to a greater or lesser degree to commercially important production traits like weight gain, milk yield, beef tenderness or parasite resistance.

Superior genes

The aim of genomic selection is to identify superior variants of all the genes that contribute to important production traits, and bring them together in breeding lines in as few generations as possible. When combined with advanced reproductive technologies, genomic selection promises to deliver, over the next few decades, productivity gains that might

have taken centuries to achieve with traditional selection.

Dr Hayes said the accelerated genetic gains achievable through genomic selection depend on progress made through traditional selection, and how easily progress can be made for commercially important traits in the species of interest.

“If the only trait in your breeding objective was growth rate or ear length, then genomic selection provides little advantage over genetic selection,” he said.

Genomic selection valuable for complex traits

But for traits like female reproductive performance or food-conversion efficiency, genomic selection offers substantial advantages, including its unique power to assess male genetic potential for sex-specific traits like calving rates that can only be measured in females.

Dr Hayes said the dairy industry is the most advanced in applying genomic selection, because one breed, the Holstein Friesian, dominates production.

“With genomic selection, the accuracy of the breeding value is much higher at an earlier age than it is with traditional breeding. So in the dairy industry we can use accurate data for milk production even before heifers are ready to breed at two years of age.

Dr Hayes said it is more difficult to see where genomic selection can increase the rate of genetic gain in meat sheep breeds, where the main trait under selection is eye muscle area.

With traditional breeding methods, eye muscle area can be scanned before breeding age, and it is a fairly accurate predictor of eye muscle area at maturity. There is less opportunity to make gains by reducing the breeding interval. Yet genomic selection still offers the possibility of a 30 per cent extra gain.

“There are some other opportunities, such as number of lambs weaned, where you do not get very good information about breeding values until rams are much older.

“The other opportunity in meat sheep and beef cattle is to get into breeding based on objective traits - with eye muscle area, you’re actually trying to predict lean meat yield in sires and their progeny. The opportunity for genomic selection lies in being able to select directly for lean meat yield, which can be accurately measured.

Genetic gain increase of 30%

“There’s an opportunity to increase genetic gain by around 30 per cent, but you need to genotype

and measure a very large reference population to identify all the genetic variation contributing to lean meat yield.

Dr Hayes says the opportunity for increased genetic gain over traditional selection is around 40 per cent for wool sheep breeds. Because fleece weight in ram lambs is not a reliable guide to their fleece weight as adults.

The story is similar for beef cattle, with the rate of gain depending on the breeding objective. “For traits like feed conversion efficiency or intramuscular fat, which are difficult to measure, there is potential for genomic selection to deliver quite large gains.”

“In all these livestock species, we are trying to significantly increase our rates of genetic gain. To do that, we need more phenotypic data (i.e. accurate measures of traits on thousands of animals) so we can determine how particular genes, and different variants of those genes, influence the production traits that interest us.

“We need to present convincing arguments to each industry - especially the stud sector - about the value of genomics technology and measurements on their animals. To do that, we have to bundle pedigree and performance information with mate allocation options, and genomic breeding values.”

Breeding elite animals - faster

How it works:

Imagine that each of the 24,000-odd genes in the cattle genome is identified by a unique barcode, imprinted into the DNA strand in close proximity to each gene - or within the gene itself.

Unless they become separated when genes are reshuffled and repackaged in unique new combinations in eggs or sperm, each gene will be inherited with its identifying barcode, so geneticists can track commercially desirable variants of each gene as they are passed from parents to progeny.

A genome-wide association study (GWAS) scans the genome to identify bar codes that consistently occur in the fastest-growing animals, but not in slow-growing animals. These bar codes mark all gene variants that contribute to a gain in productivity, or some other desirable trait.

In a hypothetical example, the GWAS identifies 15 unique bar codes marking chromosomal “neighbourhoods” that harbour 15 as yet-unidentified genes that make important contributions to increased growth rate.

Progeny testing shows one of the genes - call it Gene X - is an important influence on growth rate. Genome scans identify 10 different alleles (variants) of Gene X in the beef cattle gene pool, of which three significantly boost growth rates.

In sporting terms, these are the gold, silver and bronze alleles of Gene X.

Geneticists can now design a breeding program to increase the odds that stud animals will inherit some combination of these commercially valuable alleles of Gene X.

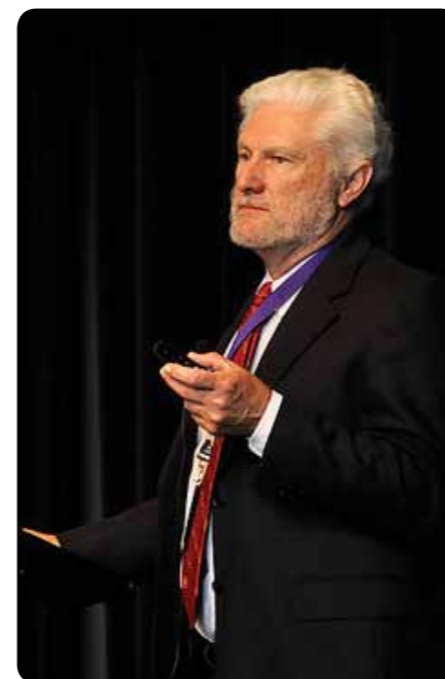
But the genome-wide association study has identified 14 other barcodes elsewhere in the genome marking genes that, in concert with Gene X, influence growth rate. Each gene has multiple alleles, but again, only a few elite alleles significantly boost growth rate.

The aim of the game of genomic selection is to design breeding programs that will bring together as many gold, silver and bronze variants of these growth-boosting genes as possible, in as few generations as possible.

By shortening the long generation interval in cattle, assisted reproduction technologies can carve decades off the time required to develop elite breeding lines.



Top honour for Beef CRC Chief Scientist



Beef CRC's Chief Scientist Professor Mike Goddard was one of seventeen of Australia's leading researchers to be honoured on 23 March by election to the Australian Academy of Science.

Mike is also a Professorial Fellow in Animal Genetics at the Faculty of Land and Food Resources at the University of Melbourne, where he holds a joint appointment with the Victorian Department of Primary Industries.

Election to the Australian Academy of Science recognises a career that has significantly advanced, and continues to advance, the world's scientific knowledge.

Professor Goddard FAA was elected for his distinguished work in quantitative genetics, with innovative use of genetic markers and statistical genetic methods to reveal the genetic architecture of complex traits for agriculture.

Congratulations Mike!

The bovine genome: as big as Australia



The instructions for assembling and operating a Hereford bull are written in approximately 3.5 billion bases or "letters" of DNA code.

Printed in letters 1mm wide, they would extend 3500km, from Melbourne to Perth.

Beefing up EBVs with genomics



Wayne Upton

Most cattlemen buy bulls the same way they have done for generations.

Generally speaking, they will buy the biggest, fattest animal at a sale, and use their experience as third or fourth generation cattleman or woman to visually assess the genetic worth of an animal by what it looks like.

While tradition plays its part in keeping the status quo, another factor is that many commercial breeders do not have a strong understanding of how to use Estimated Breeding Values (EBVs) to improve the profitability of their selection choices.

They are unsure what the difference is between tools like EBVs which have been around for some 30 years and the newer genomic markers and panels.

EBVs are calculated from information on the animal's performance and the performance of their relatives and progeny. Using this information, a prediction of the genetic worth of an animal can be made.

The newer genomic data is developed from an analysis of the genetic variants in an animal's genome sequence that may point to genes which impact on a desired trait.

When the newer genomic breeding value predictions have been tested and validated with new high density SNP chips, the Beef CRC will deliver genomic breeding predictions for carcase and meat quality traits, NFI and fertility to BREEDPLAN and genomics companies in 2012. These prediction equations will be incorporated into a single EBV for use by the beef industry, that is enhanced with genomic data.

The arrival of genomics has made the recording and measuring traits more important, not less.

Commercial breeders would like to have data on how well bulls perform for certain traits, however, they don't demand this information.

Collecting measurements on individual animals and their progeny is expensive. It is a significant issue for the Northern beef industry, where cattle run in extensive production systems and where cattlemen have learned to manage herds over generations without measuring the genetics of animals.

However, it is in these extensive breeder regions that a renewed focus on heifer management, breeder performance and bull selection based on inherent fertility is imperative.



Beef Bulletin