# Cooperative Research Centre for **Beef Genetic Technologies**




*Annual Report* **2007/2008**

CRC BEEF

**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 world-class gene discover and gene expression research and accelerated adoption of beef industry technologies.

**OUTCOMES**

The CRC for Beef Genetic Technologies is targeting an additional $179 million in gross revenue of the Australian beef industry from 2012 using emerging genetic technologies to:

- Improve capacity to deliver high quality beef to Australia's 110 global markets using cattle of know genetic merit for exacting specifications without compromising animal welfare or the environment.
- Enhance beef yield and herd reproductive efficiency, improve efficiency of resource use, reduce production costs, minimise methane emissions and avoid chemical and antibiotic residues through precise application of knowledge about the genes controlling these attributes in cattle, their rumen microorganisms and in parasites that affect cattle productivity.
- Ensure Australia is the number one supplier of beef to meet the growing demand by neighbouring Asian countries to 2020.

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# Chairman's Report and Executive Summary

**Dr Guy Fitzhardinge**
*(Chairman)*

**Dr Heather Burrow**
*(Chief Executive Officer)*

# Chairman's Report

*"The Australian and New Zealand beef industries can not sit by and do nothing with respect to genomic technologies. While considerable uncertainty remains about the precise value, and form of value, DNA markers will ultimately take, leaving the introduction of these technologies to multi-national companies would generate considerable risks to the beef industry ..."*

Undoubtedly, the highlight of the Board's activities over Year 3 was to formally approve (at a simultaneous meeting of the Beef CRC and MLA Boards) the Beef CRC's new international genomics collaborations with leading research and industry organisations from USA and Canada. The impact of these new collaborations will be very far-reaching, ultimately impacting on the way the global beef industries use genomics technologies to benefit individual beef businesses at every level of the breeding, growing, finishing and processing sectors. It is already clear that the impacts of the new collaborations will be to:

- significantly increase industry (and research provider) confidence in the accuracy of DNA markers and their ability to identify animals that will better meet market specifications or are genetically superior for economically important traits and therefore suitable for use in breeding herds;
- at least halve the time it would otherwise take Beef CRC alone to complete these phases and have confidence that the results will be of use to industry;
- provide additional information about the value of the markers in different environments that would not otherwise be available to any country in the absence of the collaboration; and
- transform the way industry uses the markers across the collaborating countries, where a uniform model of DNA marker commercialisation is being implemented to promote more effective sharing of germ-plasm and technologies across the countries. The uniform commercialisation model will also include an ability to demonstrate the economic impact of DNA markers in industry, thereby greatly assisting in uptake of the technology in all countries.

Another major highlight for the Beef CRC Board over the past year was oversighting the implementation, in industry, of the Beef CRC's commercialisation model for DNA markers aimed at maximising uptake and economic impact of DNA markers in industry. In March 2008, Beef CRC hosted a DNA marker commercialisation workshop, after which a joint MLA and CRC DNA Marker Commercialisation Committee was formed by the Boards of MLA and CRC, with the following terms of reference:

"The Working Committee is required to investigate and report on the feasibility of implementing new arrangements to enable the Australian and New Zealand beef industries to improve uptake of rapidly advancing genetic technologies and the capture of expected benefits from such technologies, taking account of the:

- Policies and processes that may create impediments to the efficient operations of the preferred DNA marker commercialisation model; and
- Scientific issues that require resolution to allow implementation of the preferred model,"

An important conclusion from the working group was that it is not possible for the Australian and New Zealand beef industry, including Beef CRC and MLA, to do nothing with respect to genomic technologies. While considerable uncertainty remains about the precise amount of value and form the value from DNA markers will ultimately take, leaving the introduction of these technologies (including their research, development, commercialisation and implementation) to multi-national companies or other countries or other industries would generate considerable risks to the beef industry, that include the loss of influence over how the technologies are offered, access to the technologies on sub-standard terms, and the potential to disrupt systems that currently operate in Australia (e.g. BREEDPLAN, Meat Standards Australia) and which are already delivering value. Hence, the Beef CRC Board was pleased to endorse the working group's recommendations and approve the implementation of the CRC's new DNA marker commercialisation model, in conjunction with MLA and our beef industry partners in Australia and New Zealand.

The Working Committee reported back to the two boards in June 2008, identifying three areas of work to achieve implementation of the CRC's commercialisation model. Those areas involved development of:

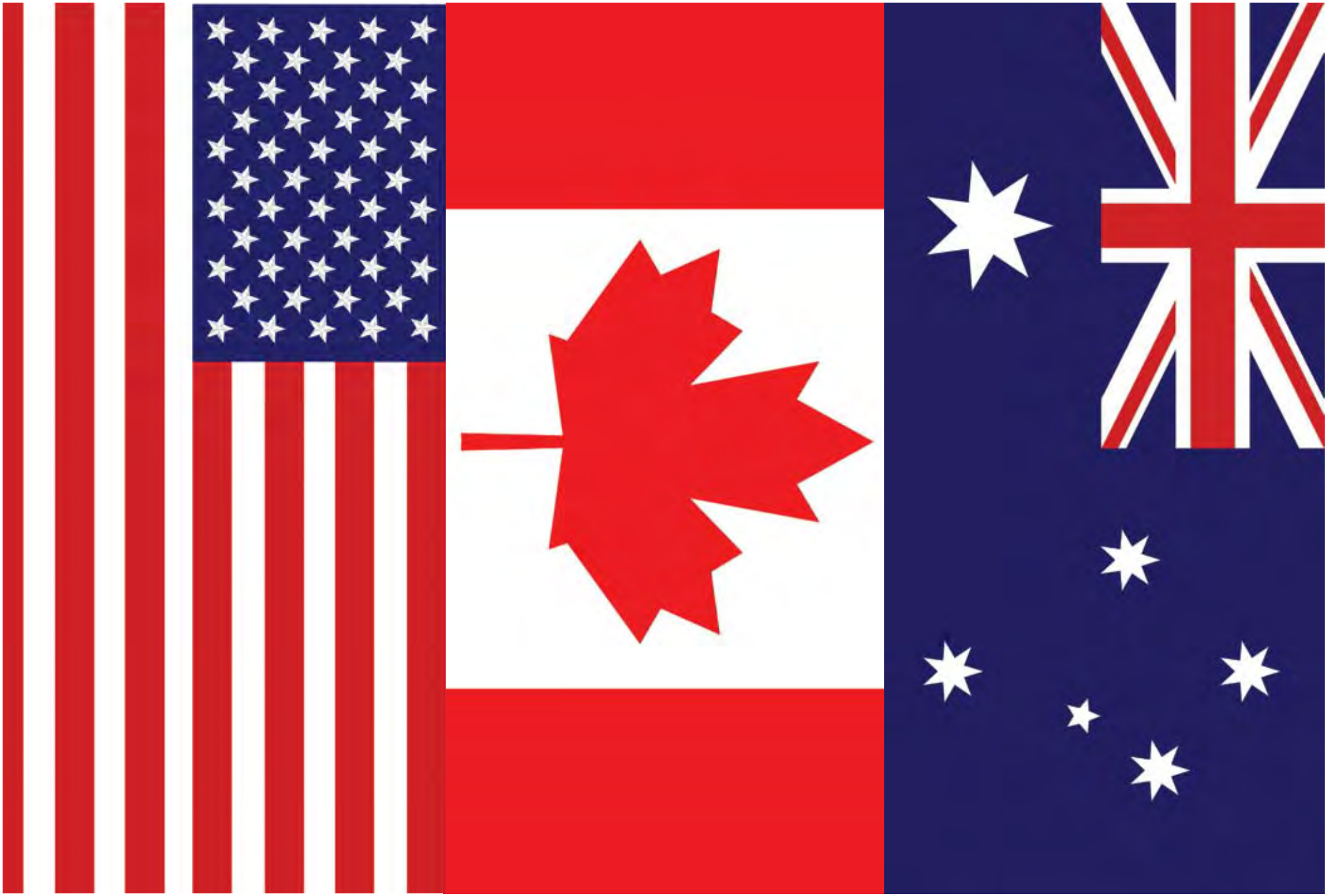
- a "National Database" (including data and software requirements, funding and governance arrangements) that is a pre-requisite for the new commercialisation model;
- a "Beef Information Nucleus" required by the Australian and New Zealand beef industries as an ongoing resource for discovery and validation of DNA markers; and
- an integrated education and training package across a number of organisations (Beef CRC, MLA, M&WNZ, AGBU, BREEDPLAN and a number of universities) relating to industry application of bovine genomics technologies.

There will ultimately be many applications of DNA technologies in industry, which in turn means that Beef CRC and MLA cannot have total influence over what is introduced and made available to industry. However, Beef CRC and MLA are committed to maximising industry's ability to make well-informed investment decisions about use of DNA marker technologies.

Other activities undertaken by the Board over Year 3 include:

- Completion of an externally-facilitated Board performance evaluation in November 2007;
- An externally-facilitated combined Board and Management Committee Strategy Workshop also held in November 2007;
- A combined meeting of the Boards of Beef and Sheep CRCs and Meat and Livestock Australia in March 2008;
- In my role as Beef CRC Chairman, I visited New Zealand in May 2008 and met with the Board and senior managers of Meat and Wool New Zealand, to consolidate the relationships between our two organisations; and
- Review of progress against milestones for Year 3 and consideration and approval of Year 4 budgets.

Guy Fitzhardinge
**Chairman**



# CEO's Report

*"Public or private research has yielded a number of markers of potential value to the beef industry. The value of these markers in differing production / marketing environment across countries needs to be confirmed for the common good ..."*

## HIGHLIGHTS

- International collaborations with USA and Canada around bovine genomics were unanimously approved by both the Beef CRC and MLA Boards in Australia and partner organisations in USA and Canada. Collaborative research is now underway, entirely with the aim of providing greatest benefits to the partners' respective beef industries. All project decisions are made on the potential benefit to industry, not on returns to research provider organizations or commercialising companies.
- Work is now underway in conjunction with the Australian and New Zealand beef industries to implement Beef CRC's preferred commercialisation model for DNA markers aimed at maximising uptake and economic impact of DNA markers in industry.
- As flagged in the 2007 Annual Report, Beef CRC's DNA marker discovery efforts were put on hold in mid-2007, pending availability of the new Infinium Assay (BovineSNP50) from Illumina. The new assay became publicly available in February 2008. Beef CRC was one of the first companies to use the panel. Genotypes were returned to the Beef CRC on 13 June 2008 and gene discovery data analyses are now underway.
- Beef and Sheep CRCs jointly hosted the new Minister for Primary Industries the Hon. Tony Burke, MP and the Member for New England, the Hon. Tony Windsor MP in Armidale in December 2007.
- Beef CRC post-graduate student, Emily Piper, was successful in winning an Early Career Scientist award at the 2008 CRC Association conference. Emily is a PhD student enrolled at University of Queensland who works collaboratively with UQ, QDPI&F and CSIRO scientists on the "Immunology of Tick Resistance in Cattle".
- The Boards of Beef CRC, Sheep CRC and Meat and Livestock Australia met jointly in Armidale over two days in March 2008.
- 90% (384 of 429) of 2007/08 tasks and milestones met on time, within budget, to the standard expected and risks associated with them appropriately managed. 45 tasks associated with analysis of data from the new Illumina 50K SNP panel and validation of significant DNA markers from those analyses were deferred to 2008/09.

## PROGRESS

Significant activities in Year 3 mainly revolved around developing new international genomics collaborations; progressing the CRC's preferred DNA marker commercialisation model with industry; validating existing DNA markers using the CRC's phenotypic databases in conjunction with Catapult Genetics/Pfizer Animal Genetics (now a wholly-owned subsidiary of Pfizer Animal Health) and Igenity (Merial); revising the CRC's "Path to Adoption" to provide a focus on CRC "products" rather than "projects"; and securing additional funds to support the CRC's core business of DNA marker discovery, validation and delivery to industry to achieve economic, social and environmental value-add.

### *A.* International Genomics Collaborations

Beef CRC's genomics research primarily aims to increase the profitability and competitiveness of the Australian beef industry by performing genome-wide association studies (GWAS) using SNP (Single Nucleotide Polymorphism) panels and phenotypic measures of production and adaptation to discover, validate and commercialise DNA markers associated with economically important beef production traits. Using these studies, Beef CRC plans to deliver DNA tests accounting for up to 50% of the genetic variation for each economically important trait.

In January 2008, Beef CRC organised a workshop in San Diego, USA, to scope areas of mutual public research interest around DNA marker discovery, validation and delivery to industry for beef cattle, to determine whether opportunities exist for new international collaborations that would speed up or enhance the quality of diagnostic DNA tests for use by the beef industries of the collaborating countries, and if those opportunities exist, to determine how best they can be captured. Workshop participants were from the US Department of Agriculture, US National Beef Cattle Evaluation Consortium, US Beef Improvement Federation, the Canadian Universities of Alberta and Guelph, AgResearch New Zealand and Beef CRC.

Five major areas of potential research collaboration were identified:

- Discovery of markers and their validation
- Validation of existing markers
- Coordinated resource populations
- Methods for delivering DNA markers to industry

› Development of larger SNP chips

i. *Discovery of markers and their validation*

This is the area with the greatest benefit to collaborators because it will lead to better panels of markers for commercialisation. The availability of the 50k SNP chip from Illumina is an opportunity to greatly improve the power to discover useful markers. For the foreseeable future, GWAS will be undertaken using the Illumina 50k chip. It was agreed that each country (Australia, USA and Canada) would undertake an independent GWAS (discovery phase) on ~1,000 animals for carcase and meat quality and feed efficiency in steers.

Once the independent GWAS are complete, the collaborating groups will meet to share the results, potentially in October 2008, and agree on a common panel of promising markers. Ideally, those promising markers will then be confirmed (confirmation phase) by each of the countries in a different ~1,000 animals each, using the 50k assay if economical and funds are available.

Thereafter prediction equations for use in each country will be developed based on these first two steps. A list of all markers that occur in any of the prediction equations will be drawn up and used in the industry validation phase by genotyping up to 5,000 animals for this list of markers to provide an unbiased estimate of the correlation between prediction and breeding value or phenotype. This will also allow validation of GxE discovered in the first two phases.

Traits included in the collaborations will be those traits common across countries. Traits available only to one organisation or country are exempt from the collaboration.

ii. *Across-country validation of existing markers*

Public or private research has yielded a number of markers of potential value to the beef industry. The value of these markers in differing production/marketing environments across countries needs to be confirmed for the common good. Sharing cattle phenotypic resources across countries will most efficiently accomplish this goal. This will be done by the group with the marker IP genotyping cattle belonging to the collaborating partner with the cattle phenotypes and DNA. (The genotyping could be done by either party). Results will be analysed by the group with the cattle and the results made available to the other party. The results will be made public. No transfer of IP will occur. This protocol can be carried out on a case by case basis.

iii. *Future resource populations*

Although existing resources are sufficient to conduct initial GWAS, they are insufficient for validation and, for economically important traits that are difficult to measure (e.g., efficiency of nutrient utilisation, fertility and disease resistance), they may even be insufficient for marker discovery. With rapid developments in genomics, the critical bottleneck in making use of these technologies is the lack of deeply phenotyped populations. International collaboration is most likely to overcome this gap and foster synergies previously not possible (e.g., GxG and GxE interactions). Each country will aim to establish fully pedigreed, diverse (ideally multiple breed) cattle populations relevant to their country, with a good sampling of animals from within each breed. Those cattle populations will then be measured for as many industry-relevant traits as possible and DNA will be collected and stored from every animal in the population. A common breed or breeds will be used across the countries (ideally two breed types e.g. one taurine and an indicine-derived breed if possible) to provide linkages. There may be benefits in also using common link sires. Trait definition will be very important as common measurement protocols will need to be applied across-country to evaluate Genotype x Environment and Genotype x Genotype interactions across-countries.

iv. *Delivery of marker technology to industry*

Results of the research in (i) and (ii) above will be published as soon as results are available. This might mean enough information is in the public domain so companies can provide a service without any agreement from the organisations who conducted the research. However, there is still likely to be some benefit to commercialisers to obtain information from the research organisations (e.g., the exact prediction equation for each trait). This information could be provided by a licence, trade secret or simple Material Transfer Agreement approach. The aim is to ensure genotypes derived from commercial testing are returned to the national database to allow generation of marker-assisted breeding values or commercial values.

The value of markers to cattle breeders will be maximised if they are used to calculate Expected Progeny Differences / Estimated Breeding Values (EPDs/EBVs) that are comparable to existing EPDs/EBVs and also comparable between companies providing markers. This implies national databases that contain phenotypes and genotypes and are used to estimate prediction equations and to calculate EPDs/EBVs. Under this model, genotypes derived from DNA testing simply provide additional data from which to estimate breeding values and commercial values. The aim is to incorporate DNA data into databases that are open to anyone with appropriate access authority. Thereafter, the organisation calculating the EPDs/EBVs or commercial values estimates the effect of markers within the analysis using all data in the national database. The research organisations will collaborate in research on methods of developing prediction equations and methods of using them in the calculation of EPDs/EBVs.

v. *Development of a larger SNP chip*

It is likely the current SNP chip does not provide dense enough SNPs to generate equations that predict breeding value in or across all breeds. Efforts will be made to enhance the 50k SNP panel to around 200-300k. Partners in this collaboration will be USDA-ARS, Beef CRC and

Illumina. Library construction will be done at USDA-Beltsville, with SNP discovery being done in both USA and Australia. Beef CRC will contribute by identifying new SNP specific to Australian cattle populations for use in the expanded SNP panel. Bioinformatics needs to develop the new panel may be done through the US Cancer Institute using high-speed, automated processes.

The impact of sharing results across countries and agreeing on confirmation and validation of a common panel of markers will be to:

- significantly increase the accuracy of the estimated markers' effects and the accuracy with which breeding values can be estimated by a panel of markers, thereby greatly enhancing industry confidence (and industry value) in their use;
- at least halve the time it would otherwise take to complete these phases and have sufficient confidence that the results are useful to industry;
- provide additional information about the value of the markers in different environments (i.e. GxE) that would not otherwise be available to any country in the absence of the collaboration;
- New cattle resources will help to close the "phenotype gap" especially for traits where current resources are inadequate e.g. health traits and feed intake;
- Shared research on methodology and industry structure to deliver marker assisted EPDs/EBVs will lead to adoption of better and more uniform methods in all countries;
- A 200-300k SNP chip will lead to panels of markers that can be used to predict breeding values across breeds; and
- The possibility of increased funding as a result of a more powerful project to put to funding agencies.

### *B.* Progressing Beef CRC's Preferred DNA Marker Commercialisation Model

Since the CRC's preferred DNA marker commercialisation model was approved by the CRC Board in February 2007, feedback on the model has been sought from a number of organisations, with the model formally presented and scoped at several industry forums. In March 2008, Beef CRC held an externally-facilitated DNA marker commercialisation workshop for relevant stakeholders. The workshop was designed to provide industry, commercialisers and research providers with an opportunity to examine the CRC's model, with a view to identifying problems and solutions to problems with the model.

Essential components of a new system were agreed as:

- A national database should be developed across breeds, covering seedstock and commercial sectors and also including research data;
- A new system must be able to communicate risks to the users with respect to use of technology in different genetic backgrounds, different environments and effects on other traits;
- A new system must recognise the system is dynamic and that the risk and degree of certainty changes as more information comes to hand;
- The system must have a process that provides high quality, well-structured phenotypic data on an ongoing basis. Currently an "Information Nucleus" is missing and should be established to feed straight into the national database.

### *C.* Validating commercially available DNA markers using CRC databases

In Year 3, Beef CRC was involved in two separate projects aimed at validating commercially available DNA markers for their use by the Australian and New Zealand beef industries. These markers are available through Catapult Genetics (Pfizer Animal Genetics) and Igenity (Merial).

The first project in conjunction with Catapult Genetics, AGBU, ABRI and MLA and co-funded by the Queensland Department of State Development was the "SmartGene for Beef" project, which aimed to develop marker-assisted EBVs for economically important traits and particularly for beef tenderness, a trait of crucial importance to Queensland. As part of the project, an analysis of genotypes (DNA markers) and phenotypes from Beef CRC-I and II and two industry datasets (Angus Progeny test and Durham R&D herds) with more than 8,000 animals was completed. A number of different breeds were included to determine gene frequencies and estimate individual marker effects of the twelve DNA markers for tenderness, marbling and feed efficiency (four per trait) commercialised by Catapult Genetics. The objective was to assess the utility of the markers as contributors for a new trait that could be included in BREEDPLAN, namely tenderness; or for traits that are already analysed in BREEDPLAN (intra-muscular fat and net feed intake) and to deliver trial Marker Assisted EBVs (MA-EBVs). Project results were presented to industry at an Australian Registered Cattle Breeders' Association (ARCBA) Forum in conjunction with the Brisbane Exhibition in August 2008.

The SmartGene results for tenderness were very consistent. 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. Depending on the specific cattle populations and management / processing treatments, the markers collectively accounted for between 8 and 16% of the genetic variation for tenderness. These markers will be the major components of BREEDPLAN trial Tenderness EBVs to be released in October 2008. Marker-assisted EBVs will allow producers to identify animals that are genetically pre-disposed to producing more tender meat. This will not only provide significant benefits to the Queensland (and the Australian) beef industry but also to our global customers.

*(L to R) Dr Heather Burrow, The Hon Tony Burke MP, Minister for Agriculture, Fisheries and Forestry, Prof James Rowe, CEO, Sheep CRC*

There were though, some unexpected results with respect to the marbling and feed efficiency markers. None of the four marbling markers had a consistent affect either individually or collectively on intramuscular fat or marble score. The extreme gene frequencies of these markers made it difficult to assess the difference between 0 and 2 star or 1 and 2-star genotypes in most breeds. Animals tested for these markers were grain-fed for up to 180 days but there were no very long-fed animals in these datasets. Similarly, the effects of the markers on feed efficiency traits were not significant for net feed intake or other traits associated with feed efficiency (e.g. daily feed intake and feed conversion ratio). Hence, when the markers were tested in totally independent populations, the estimated marker effects were neither consistent nor informative. The marbling and NFI markers were not Beef CRC markers, having been secured by Catapult Genetics from other research provider organisations.

The second project was in conjunction with Merial Ltd, USA. Merial commercialises DNA markers under the Igenity brand, mainly in northern and southern America, but intends to enter the Australian and New Zealand market in 2008/09. The company funded the genotyping of 5,000 Beef CRC animals with phenotypes for carcase and beef quality and NFI attributes, to validate associations between their markers and Australian phenotypes for the traits of interest. CRC provided coded DNA directly to Sequenom in the USA to undertake the genotyping using Merial's SNP panels. Data analyses were undertaken by Beef CRC through AGBU, in conjunction with Cornell University and the US National Beef Cattle Evaluation Consortium (NBCEC) to test the markers for the range of traits for which the markers are currently marketed. Results from this project have been published on the NBCEC website as well as being made available directly to Australian and New Zealand beef industry end-users.

### *D.* Revising Beef CRC's "Path to Adoption" model

Following the combined Board and Management Committee Strategy Workshop in November 2007, it was decided to revise the CRC's "Path to Adoption" document to clearly describe the path to market and adoption for each of the CRC's "products" (outputs) to assist both the Board and CRC Partners to more clearly identify progress towards achievement of those outputs. The changed focus provided much greater clarity for both the Scientific and Industry Review panels as well as the June 2008 Centre Forum meeting.

### *E.* Visitors to Beef CRC Headquarters

As in previous years, Beef CRC hosted a large number of high-level visitors and delegations, including the new Federal Minister for Primary Industries, the Hon. Tony Burke, MP, the Member for New England, the Hon. Tony Windsor MP and members of his entourage, including the CEO of Cattle Council of Australia, David Inall, at the CJ Hawkins Homestead in December 2007 (hosted jointly with Sheep CRC and MLA). Another highlight of Year 3 was a combined meeting of the Boards of Beef CRC, Sheep CRC and MLA in Armidale in March 2008.

*Risks, opportunities and responses to the above.*

As indicated in the 2007 Annual Report, discovery of Beef CRC's DNA markers is well ahead of schedule. But validation of those markers in totally new cattle populations (a pre-requisite for IP protection, commercialisation and industry utilisation) is proving more difficult, believed to be because a denser SNP panel (i.e. more than 50,000 SNPs) and more animal records are needed. By way of example, human geneticists are now using panels of 500,000 – 1 million SNPs and tens of thousands of experimental records. Livestock geneticists have some advantages relative to human geneticists because they are able to utilise DNA markers through selective breeding and/or culling of animals with unfavourable forms of genes, and they do not need to identify a treatment to "cure" unfavourable genetics. However, the outcomes of the "SmartGene for Beef" project outlined above strongly reinforced to Beef CRC the need for conservative approaches to industry release of its markers, to ensure they are not released prematurely before they are proven to add value to industry breeding and management programs.

Currently Beef CRC and other livestock genomics researchers have access only to a 50,000 SNP panel. Based on simulation in beef cattle and research results from dairy cattle, the 50k panel is likely to yield DNA markers that are useful within, rather than across, breeds. Beef CRC is working with the international research community to develop a larger (e.g. 200-300k) SNP panel, but the expanded panel is unlikely to be available before 2010 at the earliest. And because of the difficulty that Beef CRC has encountered in validating its DNA markers in totally independent cattle populations, it is also possible the targeted 50% of genetic variation for the traits targeted by the CRC may not be achieved either. Hence, Beef CRC has undertaken sensitivity analyses to determine the likely impact on targeted CRC outcomes (i.e. a potential value-add to the Australian beef industry of $179m per annum from 2012) of achievement of reduced amounts of genetic variation. The purpose of these analyses was to determine whether Beef CRC should request changes to the outcomes shown in the Commonwealth Agreement or to restrict the changes only to the outputs and milestones, as flagged in the 2007 Annual Report.

The sensitivity analyses were based on economic analyses presented in Beef CRC's Stage 2 Business Case, where "with-CRC" and "without-CRC" scenarios were compared. Results of the sensitivity analyses are shown in the table below. It is assumed the proportion of genetic variation explained by the markers is directly proportional to the accuracy of BREEDPLAN EBVs. The change in genetic merit per annum depends on the amount of underlying variation * accuracy * intensity / appropriate lags in adoption.

The change in genetic merit varies by trait and by breed, but the overall change in genetic merit per annum is directly proportional to the level of explanation of genetic variance. So if nothing else is done, the rate of productivity growth is directly proportional to the level of explanation of genetic variance from the markers. Therefore, as the level of explanation of genetic variance from markers falls from the 50% target, the overall rate of potential productivity improvement also falls from $179m per annum to $82m per annum if the amount of genetic variation accounted for by the markers reduces to 10%.

Although Beef CRC now concedes the stage of technology development may preclude it achieving its target of 50% of genetic variation across breeds within its life (i.e. by June 2012), the Beef CRC Board nevertheless agreed that a 50% target should remain. It also pointed out that even if only 10% of the available genetic variation is explained by the CRC's DNA markers, it still represents a very favourable return on the investment of Commonwealth funds. However, the difficulties of achieving this target will also be clearly explained to partner organisations and to the Australian and New Zealand beef industries to ensure false expectations are not generated.

Although Beef CRC now concedes the stage of technology development may preclude it achieving its target of 50% of genetic variation across breeds within its life (i.e. by June 2012), the Beef CRC Board nevertheless agreed that a 50% target should remain. It also pointed out that even if only 10% of the available genetic variation is explained by the CRC's DNA markers, it still represents a very favourable return on the investment of Commonwealth funds. However, the difficulties of achieving this target will also be clearly explained to partner organisations and to the Australian and New Zealand beef industries to ensure false expectations are not generated.

## KEY CHANGES OF A SUBSTANTIAL NATURE

In July 2007, Professor John Gibson was appointed as a Board Member of the Sheep CRC and also Acting Head of the School of Natural Resources and Rural Science at University of New England. These increased responsibilities prevented him from continuing as Manager of Beef CRC's Program 3. This responsibility has been assumed by Dr Drewe Ferguson of CSIRO Livestock Industries, Armidale from 1 July 2007.

## CONTEXT AND MAJOR DEVELOPMENTS DURING THE YEAR

Beef is Australia's most valuable agricultural export commodity, with the gross value of Australian beef production in 2006/07 being ~$8 billion (ABARE, 2007). There are 82,036 beef properties in Australia (ABARE, 2007). Based on value, Australia is the world's largest beef exporter. But with only 2.7% of world cattle numbers and 23% of world beef trade, Australia will only retain leadership through product differentiation based on quality and consumer specifications to deliver to exacting specifications of consumers in >110 diverse markets globally.

Beef CRC aims to improve capacity to deliver high quality beef to Australia's global markets using cattle of known genetic merit for exacting specifications without compromising animal welfare or the environment. This will be achieved by selecting cattle for specific markets based on the genes they carry, not through artificial modification of their genomes. New technologies derived from our understanding of gene networks will then be used to enhance cattle performance.

Use of CRC technologies to increase market share for Australian beef producers is supported by an industry economic model known as "The Livestock Revolution", which derives from "Livestock to 2020 – the Next Food Revolution" and is based on the International Food Policy Research Institute's global food model that uses data from 37 countries and country groups and 18 commodities. The model's baseline scenario predicts consumption of meat in developing countries will grow by 2.8% p.a. between the early 1990s and 2020. Corresponding developed-

*Sensitivity of benefits from the Beef CRC to level of genetic variance explained by gene markers*

| Level of genetic variance explained | Implied level of EBV accuracy | Overall rate of potential productivity improvement | R&D lag | Adoption lag | Adoption ceiling | Overall probability of success | Net Present Value over 25 years | Annual benefit at maximum adoption | When achieved |
|---|---|---|---|---|---|---|---|---|---|
| 'WITH CRC' CASE | | | | | | | | | |
| 50% | 70% | 9% | 5 | 2 | 35 | 80 | $1.93b | $179m | 2012 |
| 30% | 55% | 8% | 5 | 2 | 30 | 80 | $1.48b | $137m | 2012 |
| 20% | 45% | 7% | 5 | 2 | 30 | 80 | $1.29b | $120m | 2012 |
| 10% | 30% | 6% | 5 | 2 | 25 | 80 | $92m | $82m | 2012 |
| 'WITHOUT CRC" CASE | | 5% | 7 | 5 | 25 | 70 | $52m | $63m | 2017 |

world growth rates are 0.6% pa. By 2020, developing countries will consume 100 million metric tons more meat, dwarfing developed-country increases of 18 million metric tons. Australia is best placed to supply the expanded beef component of the Asian markets. A 2007 study by the Australian Farm Institute confirms these predictions for Australian agricultural sectors.

A ban on countries from northern and southern America exporting to north Asia (primarily Japan and Korea) due to cases of Bovine Spongiform Encephalopathy (BSE) and Foot and Mouth Disease (FMD) respectively continued over the past year, though re-entry to those markets by north America is imminent. American countries are Australia's major competitors in the global beef trade, meaning the demand for Australian beef in north Asia (where quality beef is essential) has continued over the past year.

The primary risk to Australia in the north Asian premium grain-fed markets is the ongoing combination of an unfavourable currency exchange rate (for Australia as a beef exporting nation), severe drought in many of Australia's grain-growing and beef-producing areas and the increasing use of feed grains to underpin the bio-fuel industry. As a result of these factors, the price of feed grain has risen dramatically in Australia, the number of cattle on feed remains at low levels and the price of Australian beef is now much higher for our trading partners. There is therefore an increasing need for cattle to perform off pasture to achieve the same, high-quality market specifications as can be achieved off grain. This combination of factors makes the need to achieve the Beef CRC's outcomes even more imperative.

## NATIONAL RESEARCH PRIORITIES - HIGHLIGHTS

Beef CRC's planned industry outcomes align precisely with each one of Australia's National Research Priorities as described below. Good progress was made in each of these areas over Year 3, though it is still too premature for outputs and outcomes to be delivered to industry.

- An Environmentally Sustainable Australia – Beef CRC is addressing this priority directly by developing technologies to reduce methane emissions from cattle, use feed resources more efficiently and minimise chemical and antibiotic use in beef production systems.
- Promoting and Maintaining Good Health – Beef CRC meat science research is contributing to this priority by providing beef producers with technologies that enable them to guarantee beef as a palatable, healthy and nutritious component of the Australian diet.
- Frontier Technologies for Building and Transforming Australian Industries - Beef CRC is transforming the Australian beef industry through application of genomics, proteomics and bioinformatics technologies to understand and exploit the genes controlling basic biological processes in cattle to profitably meet the exacting demands of our global beef markets. It is also "promoting an innovation culture and economy" in the Australian beef industry by using novel partnership and participative strategies to increase the uptake of technologies.
- Safeguarding Australia – Beef CRC outputs are contributing to this priority by developing genetic and non-genetic approaches that will enable beef cattle to resist invasive parasites (genetically) or to ensure the cattle are not exposed to the pests (e.g. by use of a CRC vaccine to control the parasites).

H. M. Burrow

Heather Burrow
**Chief Executive Officer**

*Table 1: National Research Priorities and CRC Research*

| NATIONAL RESERACH PRIORITIES | CRC RESEARCH (%) |
|---|---|
| **AN ENVIRONMENTALLY SUSTAINABLE AUSTRALIA** - Transforming the way we use our land, water, mineral and energy resources through a better understanding of environmental systems and using new technologies | |
| Transforming existing industries | 10 |
| Responding to climate change and variability | 10 |
| **PROMOTING AND MAINTAINING GOOD HEALTH** – Promoting good health and preventing disease, particularly among young and older Australians | |
| Preventive healthcare | 10 |
| **FRONTIER TECHNOLOGIES FOR BUILDING AND TRANSFORMING AUSTRALIAN INDUSTRIES** – Stimulating the growth of world-class Australian industries using innovative technologies developed from cutting-edge research | |
| Breakthrough science | 25 |
| Frontier technologies | 25 |
| Smart information use | 5 |
| Promoting an innovation culture and economy | 10 |
| **SAFEGUARDING AUSTRALIA** – Safeguarding Australia from terrorism, crime, invasive diseases and pests, and securing our infrastructure, particularly with respect to our digital systems | |
| Protecting Australia from invasive diseases and pests | 5 |


*Colorado State university students*

# Governance, Structure and Management

**Participants**

**Governing Board**

**Board Sub-Committees**

**Communication Strategy**

# Governance and Management



The Cooperative Research Centre for Beef Genetic Technologies is incorporated as Beef CRC Limited, a company limited by guarantee.

## PARTICIPANTS AND SUPPORTING PARTICIPANTS

Participants in the Centre are Department of Primary Industries NSW, Department of Primary Industries and Fisheries Queensland, Department of Primary Industries Victoria, Meat and Livestock Australia, Meat and Wool New Zealand, South Australian Research and Development Institute, University of Adelaide, University of New England and University of Queensland. There were no changes to the Participants in 2007/2008.

Supporting Participants are the Australian Lot Feeders' Association, CSIRO Livestock Industries, Cattle Council of Australia, Department of Agriculture and Food Western Australia, Murdoch University, National Livestock Research Institute (Korea), Northern Pastoral Group of Companies and The Ohio State University (USA).

These Participants and Supporting Participants give the Centre a national and an international, focus. The partnerships include R&D providers, commercialisers and industry organisations that enhance the CRC's ability to deliver outcomes to a wide range of end-users across Australia and New Zealand. In each state the outcomes are delivered by Participants with expert local knowledge and industry linkages.

## THE GOVERNING BOARD

The role of the Board is to govern the Company. In governing the Company, the Directors act in the best interests of the Company as a whole. Senior management manages the Company in accordance with the direction and delegations of the Board and the responsibility of the Board to oversee the activities of management in carrying out these delegated duties.

In carrying out its governance role, the main task of the Board is to drive the performance of the Company to achieve its research outcomes. The Board also ensures the Company complies with its contractual, statutory and other legal obligations, including the requirements of regulatory bodies. The Board has final responsibility for the successful operations of the CRC.

The entire Board meets at least 5 times a year. In addition the Board Committees meet several times a year as outlined in the Corporate Governance report in the financial section.

The Board comprises an independent beef industry Chairman, an independent Deputy Chairman, the CEO and 6 non-executive Directors appointed on the basis of the skills they can contribute to the Board. Board members, including the Chairman and CEO, are directly elected by the Participants. The planned mix of skills on the Board is such that at least 2 Directors are highly experienced in R&D management, at least 2 Directors are highly experienced in beef industry issues and the remainder of Directors have specialist skills required by the Company (e.g. financial, legal, commercialisation etc). Currently, six of the nine Board members are independent of the Participants. Six Board members are from the private sector. More details of the skills of individual Board members are shown below and in the Directors' Report in the financial report.

## BOARD SUB-COMMITTEES

### Finance and Audit Committee (FAC)

The FAC reviews the integrity of the Company's financial reporting and oversees the independence of the external auditors. Members of the Committee are Mrs R. Clubb (Chair), Mr HG Fitzhardinge and Dr KW Steele. The Company Business Manager and CEO are ex-officio members of the Committee. The FAC held three meetings in 2007/08.

### Intellectual Property and Commercialisation (IP&C) Committee

The IP&C Committee is responsible for providing guidance on IP management and commercialisation. Members of the Committee are Professor GR Sutherland (Chair), Dr KW Steele and Dr GB Robbins. The Company Business Manager and CEO are ex-officio members of the Committee. The IP&C Committee held four meetings during the year.

### Industry Impact and Adoption (II&A) Committee

The II&A Committee is responsible for providing guidance on strategies for industry uptake and adoption of CRC research. Members of the Committee are Mr RWK Backus (Chair), Mrs E Robinson and Dr DJS Hetzel. The Education and Training Manager is an ex-officio member of the Committee. The II&A Committee held four meetings during the year.

### Remuneration Committee

The Remuneration Committee assists the Board in fulfilling its responsibilities with respect to establishing appropriate remuneration levels and incentive policies for Directors and employees. Members of the Committee are Dr KW Steele (Chair), Dr HG Fitzhardinge, Mrs R Clubb and Professor GR Sutherland. The Remuneration Committee held three meetings during the year.

*Table 2.1 CEO and Governing Board Members*

| Name | Organisation | CRC Position / Role |
|---|---|---|
| Mr Guy Fitzhardinge | Thring Pastoral Company | Independent Chairman |
| Dr Keith Steele | Steele Business Solutions Pty Ltd | Independent Deputy Chairman |
| Mr Rob Backus | Private Feedlot Consultant | Independent Non-executive Director |
| Mrs Robyn Clubb (appointed November 2007) | | Independent Non-executive Director |
| Mrs Lucinda Corrigan (retired November 2007) | Rennylea Pastoral Company | Independent Non-executive Director |
| Dr Jay Hetzel | Byron Cattle Pty Ltd | Non-executive Director |
| Mrs Emma Robinson (appointed November 2007) | Caerphilly Pastoral Company | Independent Non-executive Director |
| Dr Greg Robbins | QDPI&F | Non-executive Director |
| Professor Grant Sutherland | Sutherland Science Pty Ltd | Independent Non-executive Director |
| Dr Heather Burrow | Beef CRC Ltd | Chief Executive Officer |

*Table 2.2 Programme Leaders*

| Name | Organisation | CRC Position / Role |
|---|---|---|
| Dr Heather Burrow | Beef CRC Ltd | CEO and Program 6 Manager |
| Professor Mike Goddard | DPI Victoria | Chief Scientist |
| Mr Geoff Allen | Beef CRC Ltd | Business Manager, CFO and Company Secretary |
| Mr Jim Walkley | Beef CRC Ltd | Chief Operating Officer and Program 4 Leader |
| Professor Dave Pethick | Murdoch University | Program 1 Leader |
| A/Professor Wayne Pitchford | University of Adelaide | Program 2 Leader |
| Dr Drewe Ferguson | CSIRO Livestock Industries | Program 3 Leader |
| Professor John Thompson | University of New England | Program 5 Leader |

*The Beef CRC Board - (Standing L-R) Dr Greg Robbins, Prof Grant Sutherland, Mr Rob Backus, Mrs Robyn Clubb, Dr Jay Hetzel, Mrs Emma Robinson, (Sitting L-R) Dr Heather Burrow, Dr Guy Fitzhardinge, Dr Keith Steele*

# Communication Strategy

Beef CRC's communication efforts function through a stand-alone project (Project 6.4 Communication and Public Relations) with the project leader directly responsible to CRC Management, but with very strong links with the Centre's research programs, vocational education, awareness and adoption projects. The project's aim during the 07/08 financial year was to build on the readily identifiable Beef CRC brand and to further foster the strong internal and external networks through which Beef CRC disseminates its distilled and targeted messages. The ultimate goal is to achieve widespread awareness and knowledge of the Beef CRC, while also re-enforcing the Centre's reputation as Australia's leading source of world class beef science and technology.

The communication plan includes objectives, strategies, implementation and evaluation methods to ensure outcomes foster and improve collaboration, deliver knowledge and build and maintain company activities with the CRC's key stakeholders. It promotes and encourages the sharing of information between CRC staff across Australia and internationally. The strategies in the plan provide a framework to deliver and aid the adoption of key messages and results of world class gene discovery and gene expression research to improve profitability, productivity and animal welfare for external and internal stakeholders and Australia's beef industry.

The Beef CRC brings together the interests of a range of international and domestic stakeholder groups, external and internal to the CRC. Stakeholders include staff, State and Federal governments, industry and research funders/ providers. To cater for their differing needs, and ensure the requirements of each group are addressed, key target audiences were identified each with its own specific objectives. Different strategies were then identified to deliver targeted messages and information for each target audience group.

The Communication Strategy is very closely linked with the Awareness and Accelerated Adoption projects. In particular, the Communications Manager worked with the extension and awareness teams to:

- generate publicity for field days and "roadshows"
- ensure accurate branding at CRC field days
- update the communication material outlining the main Beef CRC messages
- launch 'Science for Quality Beef' at the 2008 Feeder Steer School in Armidale

The Beef Bulletin, a magazine featuring the latest news and developments from the Beef CRC continues to receive positive feedback. During 07/08 financial year the Beef Bulletin was published within the Cattle Country Magazine (which has a circulation of around 15,000), leading to a potential 500% increase in readership. However, due to timeliness and circulation problems, Beef CRC will cease its contract at the end of September 2008 to concentrate on getting its messages out directly via its own industry circulation lists.

The Communications project also developed a CRC 'Products' book, an easy-to-understand booklet with a focus on the products, or outputs, from the CRC (as opposed to the projects). It describes the products, how industry will use them and gives a simple explanation of progress. The book was well received by the Board and partner organisations who provided new ideas to further enhance it.

Considerable progress was made during Year 3 in lifting the profile and recognition of the Beef CRC. Evidence includes an increase in the number of journalists approaching Beef CRC for information. The following table shows the major outputs from the Communications and Public Relations project.

*Table 6.4.1: Outputs at a glance*

| | 2007/08 (Year 3) | 2006/07 (Year 2) |
|---|---|---|
| Radio/Television | 2 hours 45 mins | 3 hours 9 mins |
| Print | 58, 930 sq cms | 47, 347 sq cms |
| Media Releases | 31 | 20 |
| Beef Bulletin | 3 | 3 |
| Annual Report | 1 | 1 |
| Communication Strategy | 1 | 1 |
| Events | 12 | 13 |
| Beef CRC Staff Newsletter | 6 (bi-monthly) | 12 (monthly) |
| Products booklet | 1 | 0 |


*Launch of the Orange Book "Science for Quality Beef"*

Besides receiving coverage in major rural and regional newspapers, radio and television we have also contributed Beef CRC materials to industry publications such as those produced by Meat & Livestock Australia (MLA), the Australian Lot Feeders Association (ALFA) and breed societies. This has meant major news stories for the Beef CRC are now receiving wider coverage than in 2006/07.

During 2007/08 a Beef CRC photo competition was launched to raise awareness about the Beef CRC and expand the database of photographs we can use in CRC publications. Around 238 non-copyright photos were received featuring cattle from entrants right across the country. The winners were selected by Rural Press journalists and each received a canvas print of their photograph.

Work is continuing to improve effective communication internally among staff throughout our very geographically dispersed network. The bi-monthly electronic newsletter has been well received and feedback has been overwhelmingly positive. The Communications Manager embarked on a road trip throughout Queensland in May 2008 visiting the northern CRC research stations. This not only helped create a closer working relationship with staff but was also a great source of stories for the Beef Bulletin and other CRC publications.

# End-user Involvement and CRC impact on end-users

*Beef CRC recognises a priority to achieve uptake of, and economic impact from, CRC outputs by a broad range of end users in the shortest possible time. End users include Participants and Supporting Participants, sponsors, beef producers, seedstock breeders, feedlots, beef processors, exporters and retailers, beef consumers and the community at large, students, scientists, other CRCs, red meat industry structures and agribusinesses. The CRC works with a wide range of agencies to achieve end-user uptake of outputs as outlined in the following table.*

| End-user name | Relationship with CRC | Type of activity and end-user location | Nature / scale of benefits to end-user | Actual or expected benefit to end-user |
|---|---|---|---|---|
| State Departments of Primary Industries (QDPI&F, NSW DPI, VDPI, SARDI, DAFWA) | Participants (QDPI&F, NSW DPI, VDPI, SARDI) and Supporting Participant (WA) | Delivery of CRC information to beef industry end-users throughout Australia and New Zealand | Beef CRC funds and equips staff from these agencies to use packaged CRC material for incorporation into their organisation's extension programs as well as delivering to industry directly on behalf of CRC | Access to valuable and unique information that is of direct benefit to their beef industry end-user clients |
| NT DPIF&M, Australian Association of Cattle Veterinarians (AACV), Beef Improvement Association of Australia (BIAA) and Cattle Breed Societies linked to 5,000 seedstock herds across Australia and NZ | Associates | Delivery of CRC information to specialist sectors of beef industry end-users throughout Australia and New Zealand | Tailored training packages for association members | Access to valuable and unique information that is of direct benefit to these beef industry associations |
| Meat and Livestock Australia (MLA) and Meat & Wool New Zealand (M&WNZ) | Participants and co-investors in Beef CRC activities | Partner in Beef CRC RDE&C activities throughout Australia and New Zealand | Direct access to Beef CRC information that is then merged by these organisations with their own industry-delivery packages and training materials | Access to valuable and unique information that is of direct benefit to their beef industry members |
| Red Meat Industry Organisations (Cattle Council of Australia, Australian Lot Feeders' Association) | Supporting Participants and co-investors in Beef CRC activities | Partner in Beef CRC RDE&C activities throughout Australia | Direct access to Beef CRC information that is then merged by these organisations with their own industry-delivery packages and training materials | Access to valuable and unique information that is of direct benefit to their beef industry members |
| Northern Pastoral Group of Companies and 3 individual seedstock breeders in northern Australia | Supporting Participants and co-investors in Beef CRC activities | Partner in Beef CRC RDE&C activities of direct relevance to these organisations in northern Australia | Advance access to Beef CRC information that is of direct relevance to their own beef businesses, with sufficient lead time to allow them to implement CRC results before the remainder of industry is informed | Advance access to Beef CRC information that is of direct relevance to their own beef businesses, with sufficient lead time to allow them to implement CRC results before the remainder of industry is informed |

| End-user name | Relationship with CRC | Type of activity and end-user location | Nature / scale of benefits to end-user | Actual or expected benefit to end-user |
|---|---|---|---|---|
| Seedstock breeders across southern Australia | R&D collaborators in Beef CRC's "Maternal Productivity" project | Collaborators in Beef CRC R&D activities of direct relevance to these businesses across southern Australia | First-hand access to Beef CRC results that are of direct relevance to their own beef businesses | Access to valuable and unique information that is of direct benefit to their own beef businesses |
| Australian Centre for International Agricultural Research (ACIAR) and Queensland Dept of Tourism, Regional Development and Industry | Co-investors in Beef CRC RD&E activities | Partner in Beef CRC RD&E activities primarily in Queensland | Beef CRC results are channelled through QDPI&F and MLA directly to beef industry end-users in Queensland. Research results are also available to ACIAR partner organisations in developing countries (primarily South Africa and the SADC countries) | Access to valuable and unique information that value-adds their own businesses of promotion and development of agricultural research in developing countries (ACIAR) and regional Queensland (DTRDI) |
| 34 Beef Profit Partnership (BPP) teams across Australia and New Zealand | Accelerated Adoption Partners | Technology adoption groups are located in all Australian states (except Tasmania and ACT) and New Zealand | Adoption of Beef CRC and other new beef technologies to improve profitability. Each BPP is made up of at least 7 SMEs. | Opportunity to improve profitability of beef business. |
| BREEDPLAN, Australia's and NZ's national beef genetic recording scheme | One of two primary "delivery vehicles" for Beef CRC results and DNA marker technologies | Commercialisation of beef genetic technologies including integration with DNA marker technologies across Australia and New Zealand | Genetic parameters derived from CRC results and information on CRC's DNA markers are transferred directly to BREEDPLAN for immediate integration into this system | Development of new BREEDPLAN traits, increased accuracy of BREEDPLAN Estimated Breeding Values and significantly increased confidence by BREEDPLAN users in the value of the predictions |
| Meat Standards Australia (MSA), Australia's unique beef grading scheme that guarantees beef eating quality based on consumer preferences | One of two primary "delivery vehicles" for Beef CRC results and DNA marker technologies | Commercialisation of Beef CRC results including possible integration with DNA marker technologies across Australia and New Zealand | Results relating to beef eating quality are transferred directly to MSA for integration in the scheme to increase the accuracy of prediction of beef quality | Enhanced accuracy of the prediction of beef eating quality, resulting in direct monetary benefits to suppliers of MSA beef and better value for money for consumers |
| Merial Inc and Pfizer Animal Genetics | Commercialisers of DNA markers and commercial research partners | Commercialisation of Beef CRC's DNA markers; Beef CRC also validates DNA markers developed by these companies for relevance to Australian production systems | Beef industry end-users have greater confidence in the value of the DNA markers developed by the commercial companies if those markers have been independently validated by Beef CRC scientists | Increased accuracy and therefore economic impact for Australian and NZ beef industry businesses |
| Community | Direct beneficiaries of Beef CRC RDE&C activities | 70,000 beef producers in Australia and millions of beef consumers in 110 countries world-wide | Increased prosperity of beef businesses and increased satisfaction of beef consumers | Increased prosperity of beef businesses and increased satisfaction of beef consumers |

# Research Programmes

Program1

Program 2

Program 3

Program 4

Underpinning Sciences

Commercialisation

Intellectual Property Management

Research Collaborations

# Program 1

# High Quality Beef for Global Consumers

**OUTCOMES (AS PER COMMONWEALTH AGREEMENT)**

- *From 2012, 10% of Australian beef sires will be evaluated for multiple DNA tests that account for 50% of the genetic differences in carcase yield, marbling and beef tenderness, increasing annual gross revenues in the Australian beef industry by $43 million for improved beef quality and a further $15.5 million for increased retail beef yield.*
- *By 2012, the compliance rate for cattle achieving market specifications will be increased by 20% with concomitant improvements in profitability due to improved operational, environmental and production efficiencies and increased throughput across the supply chain.*
- *By 2012, palatability prediction models, customised for international markets, will be developed and used by at least two of our key trading partners.*



## PROJECT 1.1.1/2 - FULL UTILISATION OF GENETIC MARKERS FOR IMPROVED BEEF QUALITY

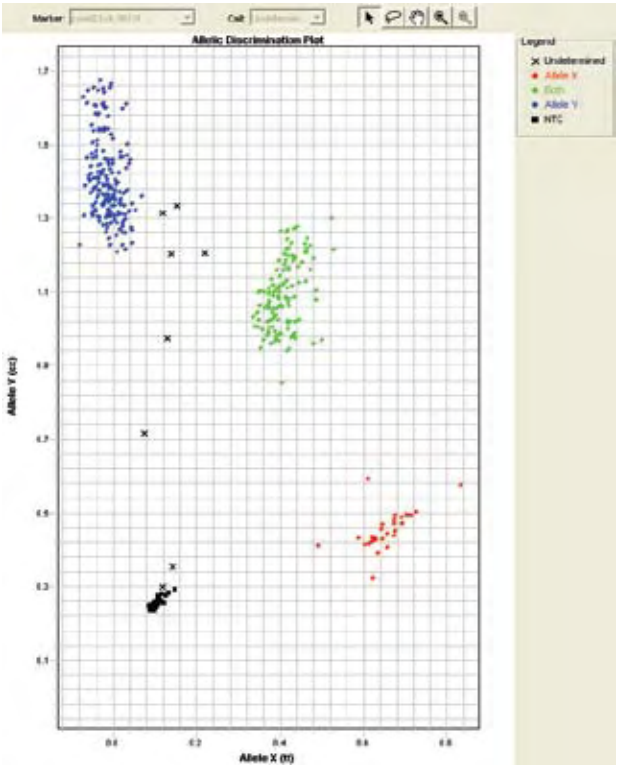
Improving the genetics of meat quality is difficult because the animals used for breeding are not directly measured for the trait. DNA testing is one way of understanding the genetics of meat quality.

All Commonwealth milestones have been met or exceeded. The emphasis of the project has shifted from what was originally outlined in the Commonwealth Agreement to now using methods that will reach the goal more rapidly. The team's main focus is to discover panels of genes/markers that explain as much of the genetic variance as possible. The team has set the challenging goal of explaining up to 50% of the genetic variance of the trait of interest. To achieve this, more than 1,000 animals with meat quality and yield measurements were genotyped for more than 50,000 gene markers representing sections from all the genomic regions of cattle.

During 2007/08, the team followed up the work from the previous year, where DNA markers had been identified in a pilot study using smaller numbers of cattle and gene markers. The team identified 20 DNA markers that passed the second round of screening in approximately 1000 animals from different breeds. Significant results were found in more than one breed or breed group for important meat quality traits such as intramuscular fat, tenderness and MSA grade scores.

Beef CRC has set stringent thresholds for markers to be commercialized. So before these 20 markers can be released they need to be confirmed in much larger populations of cattle. The team is currently in the process of evaluating these markers in several breeds of cattle important to the beef industry. At least 1,000 cattle per breed are being used. Prior to commercial release, the impact of each marker on meat quality characteristics will also have been validated in an additional several thousand cattle.

The CRC is not the only research organisation that identifies DNA markers associated with traits in beef cattle, so it is important to take research outputs from other countries to evaluate whether their markers work in our cattle. This year the team tested five DNA markers located in three genes that have been published as being associated with marbling score. These markers were tested in approximately 800 animals, from seven breeds, for associations to AUS-MEAT marbling score. One of the markers, in the gene carboxypeptidase E, showed significant additive effects in the Angus and Brahman breeds. Cattle with the blue genotype have higher average AUS-MEAT marbling scores in the Angus or Brahman breed than cattle with the red genotype, as seen below.




MILLI-Q
$H_2O$

In 2008/09, this marker will be tested in a sample of 1000 Angus and 1000 Brahman cattle to determine whether it would be useful to include it in a panel of markers for marbling.

The team takes its role in educating the next generation of scientists seriously. We have PhD students working on genes thought to affect meat and carcase quality. These researchers are examining the DNA and protein sequences of several genes to determine how they function to achieve the changes to traits such as marbling, tenderness and meat yield. These students have characterised the effect of the moderate myostatin mutation on meat quality found in the Limousin breed, showing the change in yield and marbling that occurs. This work has been published in a leading international publication. Several other genes affecting meat toughness are being investigated.

## PROJECT 1.1.3 - PROOF OF CONCEPT (GENE EXPRESSION)

The major emphasis of this Project in 2007/08 was to conduct an experiment to provide both industry assessment and biological understanding of gene markers of the calpain/calpastatin system that are associated with beef tenderness. Two herds of cattle selected for 'tough' and 'tender' genotypes were backgrounded and then feedlot-finished at research stations run by the NSW Department of Primary Industries and Agriculture WA.

The improvement in longissimus shear force for the cattle with the favourable calpastatin/calpain 3 alleles compared to those with the unfavourable alleles in normally (achilles) hung carcasses after 7 days ageing was 1.20 kilograms for the NSW herd and 0.93 kilograms for the WA herd (0*0* vs. 2*2* highlighted in Tables 1.1.3.1 and 2). Significant, or tendencies towards significant, differences between the 0*0* and 2*2* cattle were also evident for the longissimus of the tenderstretched sides of beef. Significant effects of the markers on other longissimus objective meat quality measurements or on semitendinosus (eye round) objective meat quality measurements were not evident.

Significant effects of the calpastatin and calpain 3 markers on carcase characteristics and MSA chiller assessments, growth, feed intake and efficiency measurements were not evident (results for NSW herd shown in Tables 1.1.3.3 to 5).

An MLA Donor Company project is now being established, where project muscle samples will be assessed for MSA eating quality to allow incorporation of the effects of the gene markers into the MSA model as an integral component of the path to adoption.

Calpain-calpastatin system protein abundance and activity and gene expression results are consistent with the phenotypic findings in relation

*Table 1.1.3.1. Effect of calpastatin (Cast) and calpain 3 (Capn3) markers on longissimus shear force (N, newtons) at 1 and 7 days ageing for normally (AT) and tenderstretch (TS) hung Brahman cattle (steers and heifers) from the NSW tenderness herd.*

| Cast_Capn3 | N | AT1 day | AT7 days | TS1 day | TS7 days |
|---|---|---|---|---|---|
| 0_0 | 38 | 80.8 | 78.5 | 42.8 | 47.3 |
| 0_2 | 26 | 81.9 | 71.3 | 47.9 | 46.7 |
| 2_0 | 45 | 78.4 | 73.8 | 46.7 | 45.1 |
| 2_2 | 41 | 79.5 | 66.5 | 45.4 | 44.6 |
| Sed | | 4.49 | 4.13 | 1.42 | 1.33 |
| 00-22 (N) | | 1.4 | 12.0 | 2.8 | 2.7 |
| **00-22 (kg)** | | **0.14** | **1.20** | **0.28** | **0.27** |

*Table 1.1.3.2. Effect of calpastatin (Cast) and calpain 3 (Capn3) markers on longissimus shear force (N, newtons) at 1 and 7 days ageing for normally (AT) and tenderstretch (TS) hung Brahman cattle (steers) from the WA tenderness herd.*

| Cast_Capn3 | N | AT1 day | AT7 days | TS1 day | TS7 days |
|---|---|---|---|---|---|
| 0_0 | 9 | 515.3 | 54.7 | 54.9 | 48.3 |
| 0_1 | 17 | 53.7 | 55.3 | 58.1 | 49.0 |
| 0_2 | 15 | 51.8 | 53.3 | 55.4 | 46.6 |
| 1_0 | 14 | 51.1 | 49.2 | 52.9 | 47.3 |
| 1_1 | 19 | 53.4 | 49.7 | 55.3 | 48.1 |
| 1_2 | 16 | 51.5 | 47.8 | 51.8 | 45.6 |
| 2_0 | 12 | 50.3 | 46.8 | 49.5 | 44.2 |
| 2_1 | 22 | 52.6 | 47.3 | 53.4 | 44.9 |
| 2_2 | 16 | 50.7 | 45.4 | 48.8 | 42.5 |
| Sed | | 2.82 | 2.34 | 3.09 | 2.34 |
| 00-22 (N) | | 0.58 | 9.34 | 6.13 | 5.79 |
| **00-22 (kg)** | | **0.06** | **0.95** | **0.63** | **0.59** |

*Table 1.1.3.3. Effect of calpastatin (Cast) and calpain 3 (Capn3) markers on carcass characteristics in Brahman cattle (steers and heifers) from the NSW tenderness herd*

| Cast_ Capn3 | *n* | HSCW | EMA | uOSS | HotP8 | RibFat | USlean (colour) | Temp at pH6 | pHu |
|---|---|---|---|---|---|---|---|---|---|
| 0_0 | 38 | 246 | 59.1 | 151 | 12.7 | 6.0 | 171 | 22.1 | 5.49 |
| 0_2 | 26 | 244 | 59.0 | 153 | 12.4 | 6.1 | 171 | 22.3 | 5.49 |
| 2_0 | 45 | 246 | 60.1 | 153 | 12.5 | 5.9 | 153 | 19.6 | 5.49 |
| 2_2 | 41 | 243 | 59.9 | 151 | 12.3 | 5.9 | 152 | 19.8 | 5.48 |
| sed | | 5.6 | 1.55 | 3.7 | 0.6 | 0.44 | 14.3 | 1.55 | 0.011 |

*Table 1.1.3.4. Effect of calpastatin (Cast) and calpain 3 (Capn3) markers on growth characteristics in Brahman cattle (steers and heifers) from the NSW tenderness herd*

| Cast_Capn3 | *n* | Background ADG (g) | Feedlot entry wt (kg) | Feedlot ADG (kg) | Feedlot exit wt (kg) |
|---|---|---|---|---|---|
| 0_0 | 38 | 737 | 322 | 1.22 | 441 |
| 0_2 | 26 | 752 | 318 | 1.20 | 437 |
| 2_0 | 45 | 719 | 321 | 1.14 | 439 |
| 2_2 | 41 | 734 | 317 | 1.13 | 435 |
| sed | | 21.2 | 7.2 | 0.054 | 10.2 |

*Table 1.1.3.5. Effect of calpastatin (Cast) and calpain 3 (Capn3) markers on feed intake and efficiency in Brahman cattle (steers and heifers) from the NSW tenderness herd*

| Cast_Capn3 | *n* | DMI | FCR | RFI |
|---|---|---|---|---|
| 0_0 | 35 | 8.4 | 7.0 | 0.148 |
| 0_2 | 26 | 8.3 | 7.2 | 0.235 |
| 2_0 | 45 | 8.0 | 7.6 | -0.147 |
| 2_2 | 40 | 8.0 | 7.4 | -0.060 |
| sed | | 0.27 | 0.48 | 0.176 |

to shear force and are helping to elucidate mechanisms responsible for the phenotypic effects. With respect to the CAST gene marker, we have shown that cattle carrying 2 copies of the marker (2*) show less calpastatin protein levels and 15% less calpain inhibitory activity ($p<0.001$; Figure 1.1.3.1). This suggests the CAST gene marker is associated with reduced calpastatin levels and subsequently, reduced calpain inhibition during the post-mortem period.

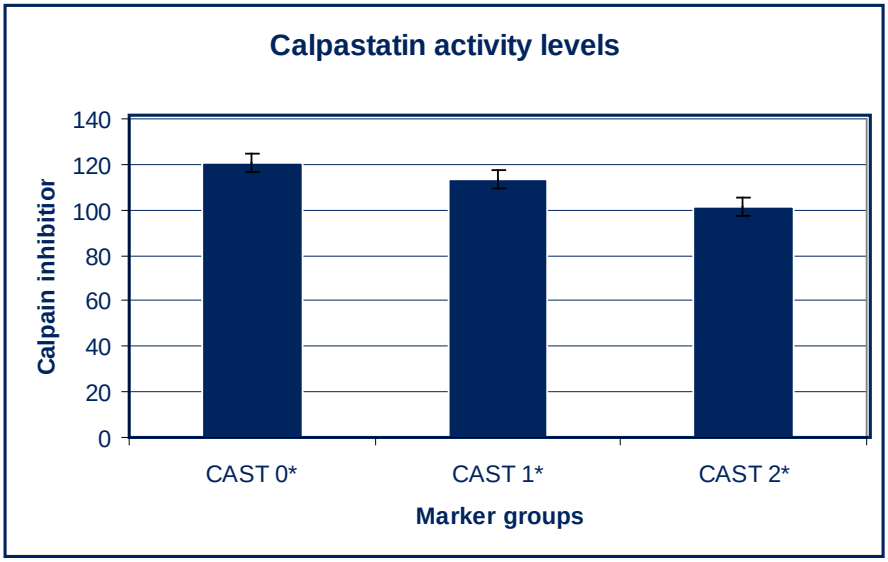



*Figure 1.1.3.1. Calpain inhibition by calpastatin within 0*, 1* and 2* groups of WA and NSW tenderness herds.*

Gene marker effects for CAPN1 were not significant at the protein amount level or at the activity level for calpastatin, calpain 1 or calpain 2 (P>0.05 for all). Gene marker effects for CAST did not influence protein amount level or activity of calpain 1 or calpain 2 (P>0.05 for all). Peptide sequences for synthesis of epitopes for production of monoclonal antibodies for CAPN3 have been investigated and opportunities for producing antibodies raised against these peptides have been identified.

Quantitative reverse transcriptase PCR (qRT-PCR) was employed to measure the mRNA levels of the calpain system genes (calpain 1, calpain 3 and calpastatin) and a variety of N-terminal calpastatin splice variants. The mRNA levels were measured in longissimus samples collected at slaughter from the NSW and WA tenderness herds (n = 409). Total calpastatin mRNA levels showed no relationship with the Cast3_84 DNA marker. However, the mRNA levels of calpastatin variant 2 were significantly associated with Cast3_84 (Figure 1.1.3.2). The association between calpastatin variant 2 mRNA levels and Cast3_84 bears striking similarity to the calpastatin protein levels measured in these longissimus muscle samples. This finding suggests the Cast3_84 polymorphism may be associated with the expression level of calpastatin variant 2.

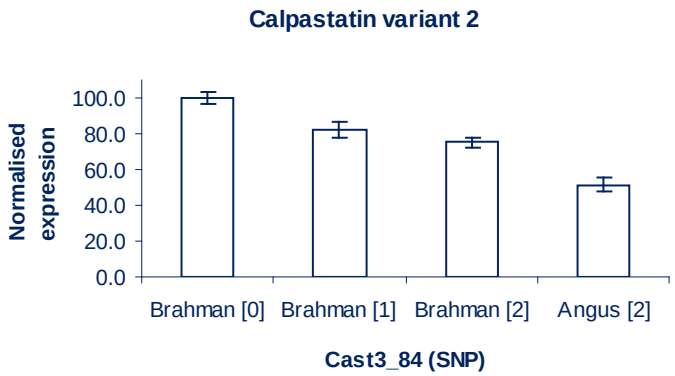



*Figure 1.1.3.2. Calpastatin variant 2 mRNA transcript levels in the LD muscle of cattle with 0, 1 and 2 copies of the GeneStar Tenderness DNA marker, Cast3_84 ($p < 0.0001$). The Angus cattle had favourable alleles for the tenderness markers and were used as a tender biological control.*

**Retail yield and muscling**

Eighteen polymorphisms in the myostatin gene and nine myostatin haplotypes were identified and association of haplotypes with indices of muscling and fatness determined in over 1,000 individuals in various cattle populations. Significant phenotypic differences between haplotypes in muscling and fatness were identified. Low muscle, high muscle and high muscle plus myostatin steers from the NSW DPI selection line herd have been examined in detail to understand their physiological response to anabolic and catabolic hormones and aspects of gene expression relating to muscle growth and development. We are also examining the commercial and financial feasibility of managing a loss-of-function myostatin mutation on-farm to increase lean meat yield and so profit, at least in supply chains where this can be measured and rewarded. Economic benefits of a Limousin myostatin mutation identified at the University of Adelaide are also being incorporated into this assessment.

**Marbling**

Project team members published a comprehensive review of marbling for the ISEP meeting in France in late 2007. This review on current understanding of regulation of marbling has highlighted potential for nutritional modification of marbling but this is only worth pursuing in cattle with the genetic potential to shift fat distribution to the marbling site i.e. high IMF in relation to other depots. As a result of these findings, we designed an experiment to study the development of marbling and fat distribution (and, by inference, retail beef yield) in elite and poor marbling genotypes that differ in their fat distributional characteristics. The experiment plans to also study effects of, and interactions with, industry production systems, namely pasture backgrounding or early-weaning coupled with concentrate feeding to feedlot entry, followed by feedlotting. The experiment will study in detail the biology of development of marbling and assess commercial phenotypic outcomes, with a view to identifying potential early predictors or markers of marbling and fat distributional characteristics, to refining beef production systems to enhance marbling. Subsequently the project aims to validate these outcomes in selected beef supply chains.

**Postgraduate students**

The Project has attracted 7 PhD students and 4 Honours students who have obtained scholarships to study various aspects of biology relating to beef tenderness, marbling and retail yield.

## PROJECT 1.2 – PREDICTION OF PHENOTYPE

All project milestones were met on or ahead of time. Major achievements include development and preliminary release of the "BeefSpecs" fat prediction tool following refinement of the growth model, development and testing of an "optimisation model" and initial work on an automatic live animal measurement system to improve inputs to the basic growth and steer performance prediction models.

A series of studies involving differing growth paths and varying types of cattle were conducted in the previous two Beef CRCs. Information generated from those studies allows us to confidently predict animal growth and carcase outcomes under different management scenarios. However the important extension of that work is to combine those findings with biological models. The Davis Growth Model (DGM) is the one that now underpins work in this project. The DGM describes the laying down of muscle and fat tissue, and the distribution into different depots like subcutaneous, intramuscular etc, at any stage of an animal's growth. We are using its ability to predict live and carcase fatness (P8 fat depth), given various growth scenarios, in relation to production targets and end-point specifications. Although the model itself is quite complex, it has been manipulated so that relatively simple input information about the animals and management systems can be used to drive it, and to deliver outputs that can be practically implemented for management decisions. The improvement in predictive value of the model will be examined when additional information like live or carcase trait EBVs (and ultimately genetic markers) is incorporated. The model enables beef businesses to predict cattle performance and final carcase characteristics, therefore allowing them to better manage beef production at all stages of production, from early growth to finishing and processing. It is a tool which can improve compliance to production targets and ultimately deliver better quality meat products to consumers. The model is under constant refinement with the testing of new inputs, as are the tools it has enabled the project team to develop.

The visit by Professor Bob Sainz from the University of California (Davis) during February 2008 was very productive for the project. Professor Sainz worked with Dr Malcolm McPhee and Dr Hutton Oddy to refine the DGM to aid development of the fat calculator tool and the optimisation technique. He will also be involved in further refining the tool to allow its extension to Bos indicus cattle. Ongoing collaboration with the animal science group at UC Davis is a very useful component of this project.

The first tool to be produced from the DGM, now known as the 'BeefSpecs' fat calculator, is designed to predict fatness at a future point of growth. The calculator (Figure 1) reports final live and carcase weight and predicts P8 fat thickness, using inputs of initial liveweight, frame size, current P8 fat depth, expected average daily gain, feed type (grain or pasture), time on feed, whether hormone growth promotants have been used as well as an assessment of activity (feedyard, small or large paddock). This allows producers to better meet beef market specifications.

All inputs are derived from practical information that producers use every day. 'BeefSpecs' was developed using experimental data and then validated with commercial cattle, mainly pure British breeds but including some European crosses. The predictions generated agree closely to actual measurements in the Bos taurus animals examined. Modification and testing for Bos indicus groups is the next refinement. 'BeefSpecs' has already had considerable exposure to industry via demonstrations at major field days, the media, direct validation trials with commercial producers and other presentations. It has been well received and will be made available free to producers as a web-accessible tool in the MLA "More Beef from Pastures" program.

An "optimisation" module has also been developed and is undergoing further refinement. It uses predictions of performance from the DGM (initially P8 and carcase weight, as from 'BeefSpecs') and combines these with market specifications (like

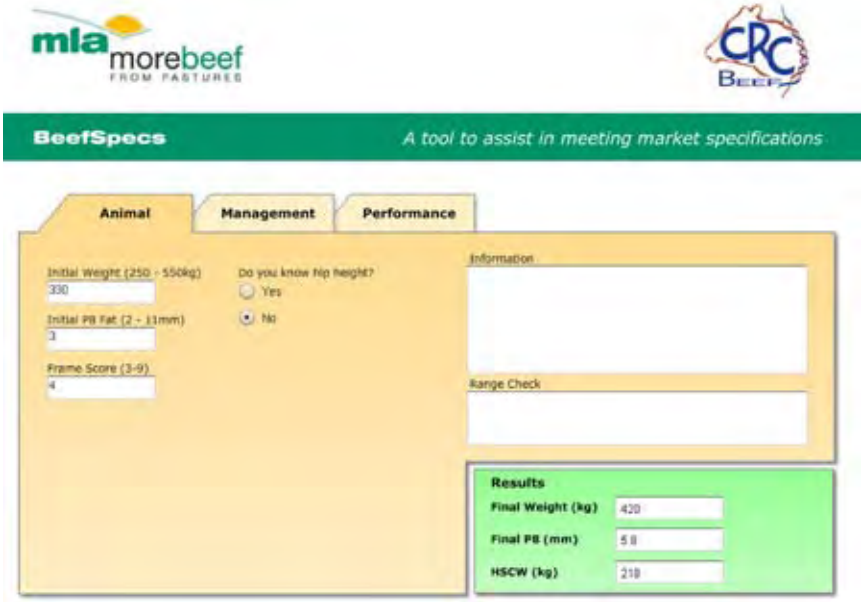



*Figure 1.2.1. Format of the BeefSpecs fat calculator, showing inputs and outputs.*

abattoir carcase grids) and costs of production to predict optimal time of finishing cattle to maximise market compliance and profitability. The "optimisation model" will have particular application for feedlot finishing, where it can predict the optimal time on feed for groups that have been drafted on carcase type or other specific criteria. Ultimately this project will combine all component growth, carcase and end-product quality predictions into a whole-chain optimisation model, encompassing production, finishing and processing phases, as well as associated market specifications, costs and returns.

The third tool to be produced from the growth modelling is a "steer performance model" that incorporates the function of the BeefSpecs calculator with other measurements of predictive value for performance and final carcase traits. The outputs will provide further refinement in predictions of carcase description and value relative to market specifications and meat quality. Additional live measurements required for inputs to this tool will be provided by a system still in the early stages of development in conjunction with Project 1.3. This is an automatic electronic measurement system, using laser beam technology, to capture body dimensions of the live animal, principally to allocate frame score, but also to describe muscularity and thus predict meat yield. Data will be automatically linked to animal ID and other information (e.g. liveweight) and will be used for both descriptive and predictive applications.

## PROJECT 1.3 - SUPPLY CHAIN VALIDATION AND PALATABILITY PREDICTION

On the recommendation of the Scientific and Industry Reviews and the Management Committee, this project has been revised by combining two previous projects, namely Project 1.2.2 - Supply Chain Validation and Project 1.3 – Palatability Prediction Models.

The key milestone in this project has thus far been to establish close relationships with beef processors to aid the delivery of Program 1 outputs using the principle of end-user engagement. There are currently five major processors participating in the project, including one in New Zealand. The project comprises a number of components common to each supply chain. The components are:

- Creating value by analysis of existing slaughter and production data;
- Testing and verifying phenotypic prediction models;
- Improving compliance to specifications through carcase feedback; and
- Other projects specific to individual supply chains.

Progress during 2007/08 with each processor is described below.

**Rockdale Beef, Yanco, southern New South Wales**

Rockdale Beef provided an historical dataset of 83,000 records comprising carcase and live animal data for the first component of the project. Beef CRC analysed the data and prepared a substantive report dealing with efficiency of beef cattle in the feedlot and compliance with carcase specifications. Feed efficiency was highlighted as an important factor affecting profitability of these cattle. Hence a feed efficiency 'demonstration' experiment was established. Rockdale is conducting a commercial evaluation of 3 lines of cattle (high, medium and low based on EBVs) that differ in net feed efficiency to assess the potential benefits to their operation. Results from this experiment will be available in late 2008.

**John Dee, Warwick, southern Queensland**

A dataset of 94,000 records was provided by John Dee for analysis. The report showed that profitability could be substantially increased by drafting cattle into groups targeting specific markets based on induction weight, frame, fat score and hormonal growth promotant status.

**Cargill, Wagga Wagga, southern New South Wales**

Cargill initially provided a dataset of 28,000 records for analysis. The data have been analysed and like the John Dee analysis, show there is scope to improve feedlot profitability by better selection of cattle prior to feedlot entry. Given these results, Cargill has indicated their strong support for establishment of Beef Profit Partnerships in cooperation with Program 5. Cargill has also indicated their desire to progress the development of a payment model based on yield (using VIAScan) and quality (using MSA grading).

**Harvey Beef, Harvey, Western Australia**

Two years of MSA grading data (some 60,000 records) from Harvey Beef have been analysed by a Beef CRC postgraduate student. Data analyses had two main focuses: (i) understanding the key factors which drive beef quality in Western Australian cattle (i.e. ossification, marbling and hormonal growth promotants) and (ii) understanding the distribution and frequency of boning groups throughout the year. This information is now being used to develop two new Harvey Beef brands (i.e. Platinum and Gold) underpinned by MSA boning group. Harvey Beef's next aim is to develop a payment system that rewards producers on quality parameters developed by Beef CRC.

**Auckland Meat Processors, Auckland, New Zealand**

A project has been initiated with Auckland Meat Processors with a focus on collecting data from a new 'smart stimulation' system that has recently been installed. The aim of the research is to test the ability to predict the incidence of high pH or dark cutting beef.

**Gene Marker validation**

The second milestone of this project was to collect MSA grading data and meat samples to quantify and validate the effects of gene markers for meat quality and meat yield. This aspect of the project was defined cattle populations with different attributes for validation. In lieu, meat samples from cattle in Project 1.1.3 will be taste-panel tested for beef eating quality as the first step in incorporating DNA markers into MSA. This work is being funded jointly by Pfizer Animal Genetics and MLA Donor Company.

# Program 2

# Feed Efficiency, Maternal Productivity and Responsible Resource Use

**OUTCOMES (AS PER COMMONWEALTH AGREEMENT)**

- *From 2012, feed costs for the national beef herd will be reduced by $15.5 million per annum without impacting on cattle weight gain, through genetic improvement of feed efficiency in seed stock cattle.*
- *From 2012, breeding herd efficiency (kg calf/MJ energy per cow and calf unit) will be improved on average by 0.5% per annum in at least 50% of specialist beef enterprises in temperate Australia.*
- *By 2012, commercial products and management strategies developed by the CRC will be used by 50% of feedlots and 20% of grazing enterprises to decrease methane emissions from beef cattle by 20% and increase the dietary energy captured for production by 5-10%.*

## PROJECT 2.1 – FEED EFFICIENCY GENE DISCOVERY AND GENE EXPRESSION

Research by the Beef CRC over the last decade has catapulted Australia to the forefront of research and development into feed efficiency of beef cattle with the outcome that the Australian beef industry has unique access to Estimated Breeding Values (EBVs) for feed efficiency, to the envy of our major international competitors. Achievement of just modest rates of adoption of genetic improvement in feed efficiency is conservatively estimated to have a net present value exceeding $200 million. However widespread industry adoption is hampered by the high cost of identifying genetically superior animals.

An affordable panel of DNA tests that explains up to 50% of the genetic variation in feed efficiency is required. These tests will become very valuable commercial property for use in Australia and internationally.

### Gene discovery

Net Feed Intake (NFI) is a trait where we expect to find many DNA markers, but each of modest effect. In Year 1, a whole-genome association (WGA) was conducted using the ParAllele 10k SNP genotyping system on high and low efficiency cattle from the original Trangie feed efficiency herd. Analysis revealed 100 Single Nucleotide Polymorphisms (SNPs) (at $P<0.001$), and many, many more SNP significant for NFI at $P<0.05$ and $P<0.01$. This year, multi-SNP re-analysis of the data found 13 SNP ($P<0.001$) and 72 SNPs ($P<0.05$) that together respectively explained 51.0% and 82.7% the total phenotypic variation in NFI. Multi-SNP analysis of the Trangie Progeny Test dataset found seven ParAllele SNPs were significant and together explained 9.3% of the variation in NFI in this dataset. In the re-created Trangie NFI-selection lines, 6 SNPs were significant and explained 18.8% of total variance. Four SNP were significant in the University of Adelaide Jersey x Limousin cross (JxL) herd and eight SNP in the Tropical Composite cattle tested for NFI in CRCII Project 2.3. However the SNP are not consistent across the different datasets.

To date, 61 candidate genes based on the JxL QTL and the Parallele data have been sequenced in the JxL sires. From the sequence data, 308 SNPs have been confirmed and 84 SNPs selected for genotyping. Based on association (linkage disequilibrium) analysis, 56 SNPs in 33 genes affected NFI related traits. 16 of the 56 SNPs were associated with NFI itself. These 16 SNPs were located in 14 different genes.

The 53 regions with significant SNP identified from the ParAllele scan of the Trangie cattle were searched for additional SNP even more closely linked to variation in NFI, and therefore, more suitable for a commercial test. Although both genotyping and data analysis is incomplete, one strong SNP has been found to be significant in both the Trangie Angus cattle and the CRC Tropical Composite cattle. The nearest genes appear to be CFTR_Bovin - Cystic fibrosis transmembrane conductance regulator and a novel protein coding gene with no information available yet from human datasets. This candidate gene approach forms part of the PhD research project of a CRC-funded student located in Melbourne with VDPI.

The ParAllele 10k SNP data were re-analysed against a newer version of the bovine genome map. This showed that our first WGA and consequent candidate gene searching has exposed less than one-third of the bovine genome to our scrutiny. It follows that two-thirds of the genome remains to be searched for new NFI SNP. At the end of Year 3 the new Illumina bovine genome 50k SNP chip became available and was used in a new experiment that, coupled with use of more cattle than screened in the first WGA, should provide the power to explore more of the bovine genome.

All milestones except 1.02 and 1.18 B (panels of NFI SNP for commercialisation) were achieved. These will be delayed until completion of the current WGA and validation.

### Industry implementation

The primary work this year has been the commercial-scale demonstration of the value of superior NFI-genetics to the feedlot industry. Three groups of Angus steers, each of approximately 80 head bred at Trangie and divided into high, medium and low NFI EBV groups, were sold to

a large commercial feedlot in southern NSW, to be evaluated for live weight gain, feed-intake and carcase and meat quality characteristics under their commercial conditions. The low NFI group consumed significantly less feed per day than either of the other two groups. Lower Feed Conversion Ratio (FCR) or NFI is more desirable and represents better feed efficiency. Over the duration of the feeding period the low NFI group had a 16% lower FCR than the average NFI group and a 12% better FCR than the high NFI group (Figure 2.1.1.1). The reason for the average group having the highest FCR from Day 1-35 may have been due to these animals having a heavier average start weight, which in turn led to a higher DFI.

The steers have been genotyped for SNP markers from Programs 1 and 2. They were slaughtered in July 2008. Abattoir carcase information, meat and tissue samples were collected and objective measurement of meat quality and a range of laboratory analyses (genotyping, proteomics, enzymes, expression microarrays) will be undertaken to check for associations with NFI EBV, NFI SNPs and meat quality SNPs. This work forms part of CRC-funded PhD student's (University of Adelaide) research on genes common to Programs 1 and 2 with a focus on protein turnover. It also contributes to an AusAid-funded PhD student's (University of Adelaide) research on the relationship between mitochondrial function and NFI. A CRC Summer Scholarship was awarded to a third student to allow her to analyse the feedlot performance of the steers for her 4th Year Honours project at UNE.

Ongoing review of the relationships between NFI EBV, NFI data and animal performance continued over the past year, resulting in two publications at the biennial conference of the Australian Society of Animal Production in Brisbane.

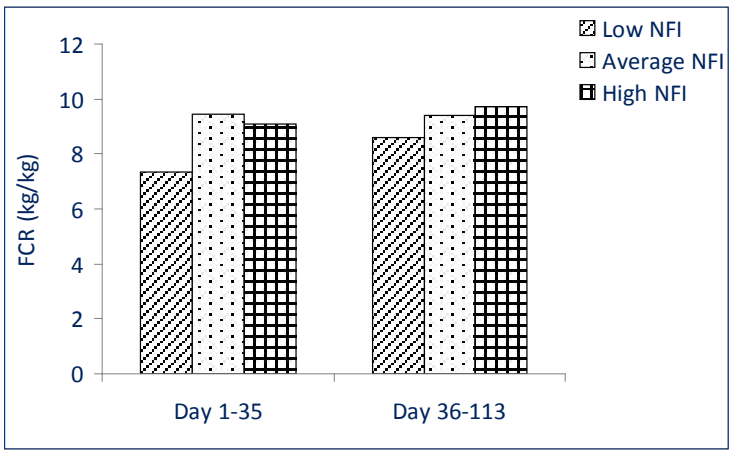



*Figure 2.1.1. Differences in FCR between the low, average and high NFI groups of steers.*

**Gene expression**

Knowledge of the mode of action of new gene tests and phenotypic and genetic associations with all commercially-important production traits will be needed to underpin adoption. In Year 3, a microarray gene expression experiment to identify differentially expressed genes between high and low Net Feed Intake (NFI) cattle was conducted by using liver biopsies from Angus bulls from the Trangie NFI selection lines. A cluster analysis with all 24,000 genes on the expression array shows low NFI animals and high NFI animals have distinct gene expression profiles. A list of 100 genes differently expressed was found with reasonable statistical support. Cluster

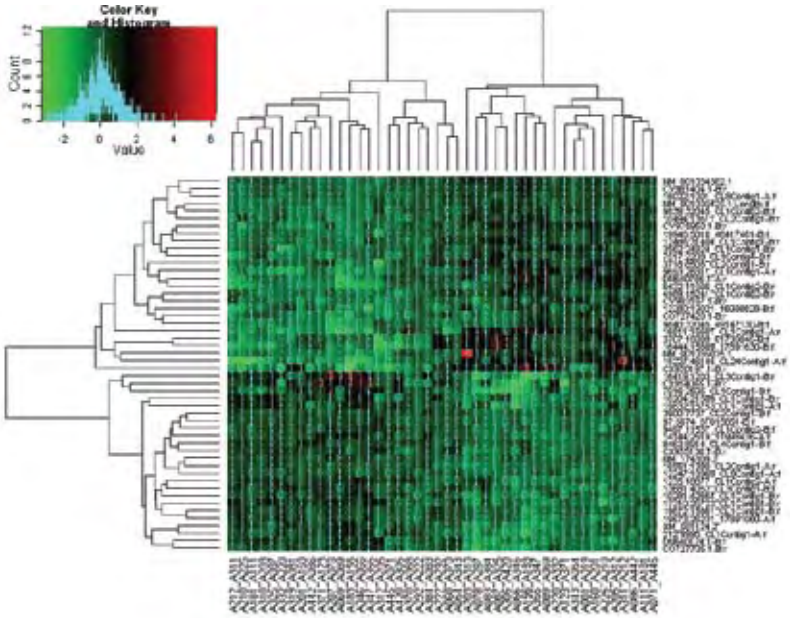



*Figure 2.1.2. Heatmap and dendrogram plots for samples and differentially expressed genes.*

analysis with the top 100 differentially expressed genes separated the high and low NFI animals into two distinct clusters (Figure 2.1.2), providing evidence that expression array profiles have potential to be predictors of phenotype, in this case, the expensive and difficult to measure trait of NFI.

181 probes were differentially expressed between cattle with high NFI and low NFI. They represented 163 unique genes, from which seven gene networks were derived. Their functions included cellular growth and proliferation, protein synthesis, lipid metabolism, carbohydrate metabolism, cancer, drug metabolism and small molecular biochemistry. Figure 2.1.3 shows one network down-regulated in high efficiency animals.

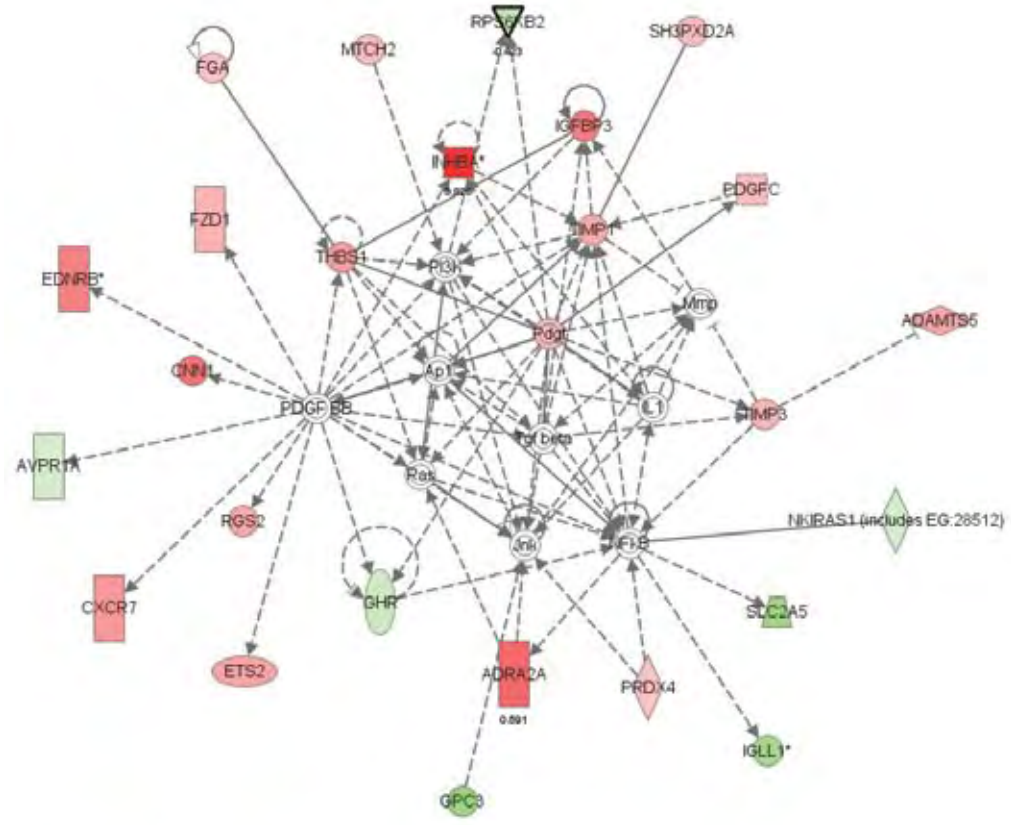



*Figure 2.1.3. Gene network down-regulated in high efficiency animal (the intensity of the colour indicates the difference between the two groups).*

*Struan Research Station*

## PROJECT 2.2 - SIMULTANEOUS IMPROVEMENT OF MATERNAL PRODUCTIVITY, FEED EFFICIENCY AND END-PRODUCT TRAITS

This project established genetically divergent Net Feed Intake (NFI) and fat lines of breeding females at Vasse Research Station, Western Australia and at Struan Research Centre, South Australia, to examine differences in maternal efficiency and productivity. These cattle are being run at high and low grazing pressures to examine how divergent lines behave under differing levels of nutrition. First weaning of both lines has occurred at Vasse, and first calving of the fat lines at Struan. Cattle at both sites are being rotationally grazed using a simple leader follower rotation at Vasse and the Techno GrazingTM System at Struan. Pre- and post-grazing pasture mass is assessed to estimate pasture intake. Intake estimates indicate that the high NFI (less efficient) females may eat more than the low NFI (more efficient) group when on a high level of nutrition but there was little difference at lower feeding levels. However low NFI females tended to wean heavier calves than the high NFI females when on a lower level of nutrition.

There was a tendency for the low NFI females at Vasse to have lower pregnancy rates (87%) than the high NFI females (95%) and longer days to calving. It is too early to determine whether the trends observed to date are real.

*Weaning weights of the calves derived from the fat and NFI lines*

| Vasse | Lean | Fat | Low NFI | High NFI |
|---|---|---|---|---|
| Low nutrition | 255 | 262 | 224 | 215 |
| High nutrition | 267 | 277 | 236 | 237 |

The Struan fat line cattle grazed the Techno system from August 2007 to late January 2008 and were subsequently fed silage based rations over the summer dry period. They are now clearly divergent for liveweight and condition score. Both the fat land NFI lines at Struan were joined in June/July 2008 for autumn 2009 calving and will graze the Techno system from August 2008.

This project also involves repeated measurements of body composition and reproductive performance of heifers in co-operator Angus and Hereford herds to examine changes in body composition (fatness, eye muscle area (EMA), intra muscular fat (IMF), live weight and hip height) from yearling age through to their second calving. To date over 7,000 body composition and performance records on ~4,000 heifers have been recorded. These heifers will be subsequently monitored for their maternal performance (i.e. reproductive performance, progeny value, structural soundness, longevity, salvage value). Heifers included in this study represent a wide range of Estimated Breeding Values (EBVs) for the key traits recorded on BREEDPLAN. The data will allow additional maternal traits to be estimated, to enable producers to predict likely maternal performance at weaning age.

*Weaning weights of the calves derived from the fat and NFI lines*

| Vasse | Lean | Fat | Low NFI | High NFI |
|---|---|---|---|---|
| Days to calving | 303.2 | 306.1 | 296.8 | 293.8 |
| ± se | 1.3 | 1.3 | 1.5 | 1.4 |

| Weight | IMF% | P8 Fat | Rib Fat | EMA |
|---|---|---|---|---|
| 0.81 | 0.63 | 0.63 | 0.55 | 0.55 |

Phenotypic correlations between pre-calving and weaning measurements for traits recorded on heifers in 2007/08 are shown below. Data from research sites and industry herds will be used to establish phenotypic relationships and a phenotypic prediction model. Once genetic and phenotypic relationships are established between key maternal productivity, feed efficiency and end-product traits they can be delivered through BREEDPLAN and BREEDOBJECT. All milestones for 2007/08 were met with the establishment of research herds at Vasse and Struan, commencement of estimated intake measurements in these animals and with more than half of the industry herd scans completed.

## PROJECT 2.3 - FEEDING AND MANAGEMENT STRATEGIES TO INCREASE DIETARY ENERGY CAPTURED AND REDUCE METHANE GENERATION

The overarching goal of this project is to identify and develop strategies to productively alter rumen microbiology and reduce methane emissions without adversely impacting feed utilization and growth efficiency of Australian beef cattle. A heightened awareness of how livestock contribute to Australia's greenhouse gas emissions has jeopardized the beef industries' "clean and green image", which may negatively impact product acceptability and management costs. For the economic wellbeing of Australia's beef industries, this problem needs to be addressed without deleterious impacts on livestock productivity. To that end, integrated studies in metagenomics, microbiology and animal genetics and nutrition are being employed to develop inoculants, bioactive agents and supplements that compromise methanogenesis and/or augment the (micro) biology and biochemistry that redirects rumen fermentation away from methane formation. All milestones for the 2007/8 year were achieved.

During the last year the project's research on methanogen diversity provided important insights for the long term milestones of the project. There is one type of methanogen (NT7-like) that was found in virtually all animals tested, but another type of methanogen (SM9-like) also appeared to be a major grouping in cattle with high methane output. The CRC-funded post-doc has already isolated several NT7-like strains. She has also spent considerable time during the last year working with other project scientists to isolate and stably propagate an SM9-like strain(s) from Australian cattle in pure culture, because only one isolate of this methanogen currently is available (from New Zealand). Unfortunately, while these "new" methanogen strains have been recovered from diluted samples of ruminal contents on more than one occasion, they have proved extremely difficult to maintain and propagate in pure culture. This is not uncommon in environmental microbiology and is generally a reflection that some microbes can't "live alone". It is obvious the growth of some of these microbes in their natural environment is much better than can be currently achieved in the lab. In that context, there is a positive benefit associated with continued efforts to successfully overcome the "lab-scale" problem. If we understand what is required to improve the growth of these strains under lab conditions, then we will know how to more effectively inhibit the growth of these microbes in the rumen. Project scientists will continue their efforts, because overcoming these problems should offer new approaches to inhibit methanogen growth in the rumen.

Finding ways to inhibit methane-producing microbes is another area of research being undertaken by the project. Work this year was based around the hypothesis that methanogens, bacteria and other archaea protect their niche within an ecosystem by secreting bacteriocins and archaeocins (bioactives that kill or inhibit other bacteria and archaea [methanogens], respectively), which should be biologically active against other ruminal methanogens. In addition, earlier work with Methanobrevibacter strains noted that as cells aged, many cells were killed by destruction of their cell walls. Research focused on developing challenge assays for these bioactives and screened for the presence of archaeocins from methanogens and selected bacteria. Methanobrevibacter YE286 was selected as the initial host strain on which archaeocins and autolysins were to be detected. Possible sources of archaeocins and autolysins that have been examined to date have been supernatants from culture fluids of late-log phase and stationary phase cultures of Methanobrevibacter ruminantium ATCC35063 (M1), Streptococcus bovis Sb15 and Butyrivibrio fibrisolvens YE44 (both rumen bacteria known to produce bacteriocins). After 7 days incubation the optical density of cultures and the methane production from the cultures was measured. To date, none of the culture supernatants have inhibited the growth or ability to produce methane of Methanobrevibacter YE286. Other supernatants from methanogens (particularly the NT7-like strains identified in both high and low methane cattle and other archaea (such as Sulfolobus spp.) will now be screened.

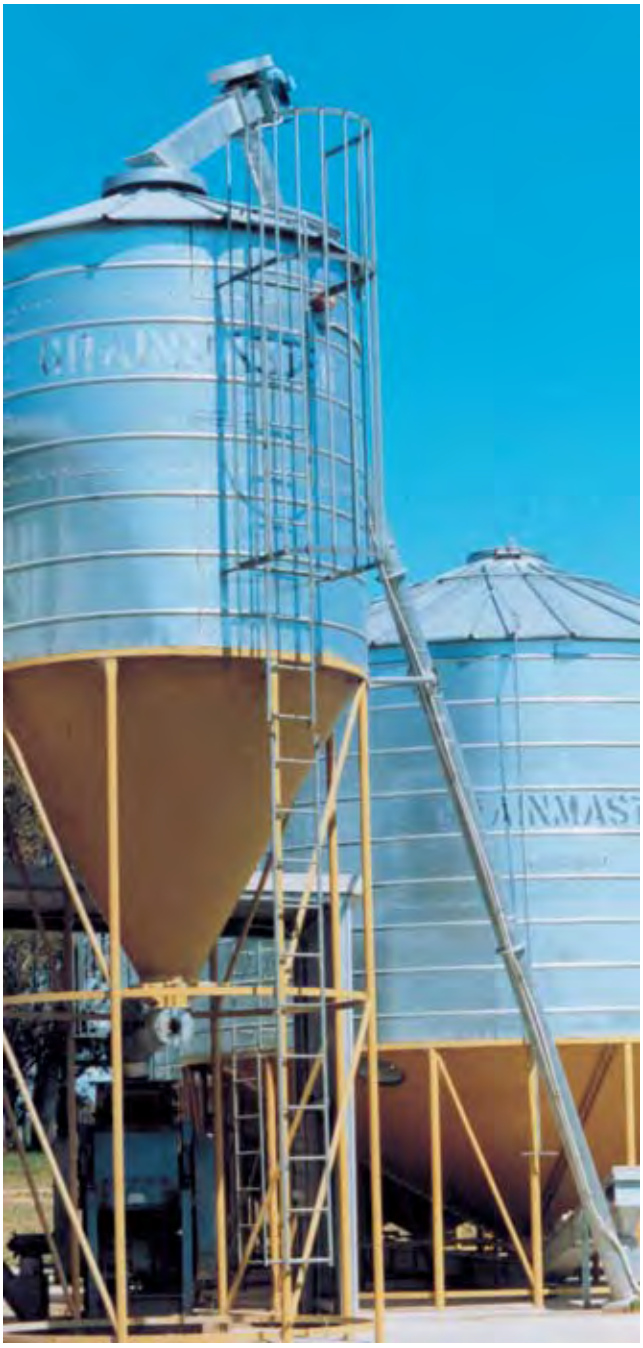
Progress has also been made in pursuit of candidate targets for inhibitors of methanogen growth, by producing proteomic maps for the two Mbb. NT7-like isolates obtained from the Trangie bulls. Proteomic profiles for two other methanogens (one from the rumen and the other not) have also been produced. Comparative analysis of these gels has helped identify proteins "specific" to the three rumen isolates. These analyses have been repeated and the protein "spots" of interest excised and subjected to mass-spectrometric analysis. They revealed the protein of interest is part of an essential enzyme in methane formation. As such, the combination of proteomics and genomic sequence data should identify and recover more "rumen-specific" targets, so bioactives designed to antagonize methanogen growth can be developed.

Strategies designed to inhibit the growth of ruminant methanogens are necessary but insufficient to bring about the outcomes sought by Beef CRC. Efficient feed utilization requires a reduction in methane output in combination with the capture of carbon and hydrogen in forms other than gases. To that end, an Australian Greenhouse Office / MLA-funded project through CSIRO and The Ohio State University used stable-isotope and enrichment studies to produce consortia of rumen microbes capable of coordinating carbon and hydrogen utilisation without methane production. The microbiology in some of these cultures was further manipulated with monensin. These consortia were shown to produce even greater amounts of propionate and

thus, consume more hydrogen without producing methane. Metagenomic libraries from all the enrichment cultures have been produced and the microbial diversity resident in the enrichments has also been established using 16S rrs-gene sequencing techniques. A "gene-centric" analysis of these enrichments is now being developed to identify the metabolic network(s) underpinning these alternative hydrogen-utilizing pathways.

Extensive animal experimentation was also conducted during the last 12 months, to establish whether there are links between methane emission, feed efficiency and genetic diversity of ruminal methanogens and alternate hydrogen-using species. Several meaningful outcomes have been achieved. First, the collaborative work between QDPI&F and NSWDPI scientists provided preliminary evidence for the SM9-like methanogens being more prevalent in animals considered to be high methane producers (relative to that predicted from feed intake measurements for the same animals). Second, animal trials conducted during the last year helped establish the "low methane phenotype" (LMP) may be a robust trait with potential for industry adoption, offering a long-term approach to reduce methane output. During the last year, NSW DPI has also concluded from their animal trials that the differences in methane emissions from cattle selected for NFI are only attributable to their differences in voluntary intake. Finally, and given the continued concerns of using the greenhouse gas SF6 to estimate methane emissions from livestock, some additional approaches for making methane measurements have been considered. The ratio of volatile fatty acids (VFA), and breath CO2: CH4 ratio, are now considered as possible markers of LMP.

Over the past year progress includes: i) isolation of targeted methanogens for genotyping and sequencing; ii) production of sequence data needed to support quantitative PCR measurements of these organisms in select animals; iii) identification of candidate rumen bacterial species that could provide an alternative hydrogen-utilizing pathway without methane production; iv) production of gene libraries needed to understand alternative pathways of hydrogen use by rumen microbes; and v) initiation and completion of some key animal studies that expands the scope of the NFI-methane axis to livestock consuming forages and pasture. We anticipate outcomes from these efforts will escalate during the next phase. Milestones for year 4 emphasize the use of genomic sequence data as a common theme for collaborative endeavours with New Zealand colleagues supported by the Pastoral Greenhouse Gas Research Consortium (PGgRC). Our goal is to broaden the scope and potential impact associated with the Beef CRC and PGgRC projects by pooling both genetic resources and expertise.



# Program 3

# Adaptation and Cattle Welfare

**OUTCOMES (AS PER COMMONWEALTH AGREEMENT)**

› *From 2012, the combined effects of reduced parasite control costs and improved productivity from use of well adapted cattle and improvements in animal welfare will increase the gross annual revenue of the Australian beef industry by $43 million per annum.*



## PROJECT 3.1.1 - GENETIC IMPROVEMENT OF TICK RESISTANCE

Ticks and other parasites add a significant cost to the northern cattle industry. The usual strategies to control parasites are pesticides, vaccines and genetic improvement. Beef CRC is currently focusing its research on two of these strategies: identification of novel candidates to develop a new tick vaccine and genetic improvement via delivery of DNA markers for tick resistance. With regard to genetic improvement, the Brahman and other tropically adapted cattle have traditionally been used to control or minimise the impact of ticks. But with industry moving towards taurine x indicine composite breeds into their herds to improve productivity, the animals are losing resistance to parasites.

The main aim of the project is to identify enough DNA markers for resistance to ticks to meet the challenging goal of identifying up to 50% of the genetic variance for tick burden. To achieve this, more than 600 animals of each of the Brahman and Tropical Composite breeds were genotyped with more than 50,000 DNA markers representing all regions of the cattle genome. This will complement our previous research where a sample of temperate, un-adapted dairy cattle, were genotyped for more than 9,000 DNA markers. Results are currently being compared.

During 2007/08, project goals were significantly altered to focus more effort on DNA marker approaches to tick resistance rather than on gene expression approaches. Over the past nine months, we have identified 14 DNA markers for tick burden from taurine cattle that also have effects in Brahmans or in tropically adapted composites. However before these DNA markers can be released for commercial testing, they need to be confirmed in larger samples of independent animals with tick counts or tick scores. Collecting animals with tick score data from large parts of the tick zone of Northern Australia will be an important part of future research in this project.

The project, although primarily focused on tick burden, also examines data on these cattle for other adaptive traits such as resistance to heat stress, worms, buffalo flies and droughts, as well as temperament. In Year 4, we plan to confirm markers associated with body temperature as this will increasingly become an issue associated with climate change.

## PROJECT 3.1.2 – NOVEL SOLUTIONS TO IMPROVE TICK RESISTANCE OF CATTLE

This project aims to elucidate the innate host pathways associated with tick resistance and susceptibility, to develop novel solutions to improve control of ticks. The main aims are to:

› Identify new tick vaccine candidates by:

1. understanding host mechanisms associated with tick resistance and susceptibility in divergent breeds of cattle both at the genetic and immunological level;
2. understanding the tick: host interface; and
3. screening all available tick gene sequences to identify immunogenic vaccine candidates (reverse vaccinology or genome based vaccine approach).

› Develop molecular rapid assays to detect ticks' resistance to acaricides.

Control of cattle ticks is vital to the continued success of the northern cattle industry in terms of compliance with regulatory protocols for intrastate, interstate and international livestock movement and to enhance cattle welfare by avoiding stress and debilitation. The cattle industry in northern Australia incurs ~$175 million in annual losses due to the impact of ticks. The cattle tick also transmits babesiosis and anaplasmosis and this tick-disease complex is the most important affecting world-wide livestock production losses estimated at $US2.5 billion due to losses in milk and beef production globally.

Chemical treatments (acaricides) are used to control ticks. However ticks have developed resistance to most existing acaricides and the current larval packet assay is time-consuming and inadequate. The implementation of fast and effective molecular acaricide tests will provide producers with an effective tool for the selection of appropriate acaricide treatment. In the long term, resistance to acaricides is increasing and new treatments are not forthcoming. The previously available TickGARD® Plus vaccine was not effective against all tick stages and required 3 or 4 booster shots per year. Thus the concept of a new tick vaccine with 12 month duration of immunity and 90% efficacy is considered a priority for industry.

This project is applying a 'reverse vaccinology' or genome-based approach to identify tick vaccine candidates. The project team successfully obtained additional funding from the Queensland Government's Department of Tourism, Regional Development and Industry (DTRDI) and also secured collaboration with the US Department of Agriculture to access their tick gene sequence resources

(13,643 sequences). Using bio-statistical computer analysis and predictive algorithms, the group is currently preparing 50 candidates for further scrutiny. Figure 3.1.2.1 provides an overview of the current status of activities.

Cattle are particularly vulnerable when they first encounter ticks. But in general, Bos indicus breeds develop stronger resistance after exposure than do British and European B. taurus breeds. To develop a successful vaccine which can initiate a protective immune response, this project has undertaken a comprehensive analysis of tick immunity and susceptibility using modern immunological and molecular genetic techniques of host cattle. This has also provided sera and cells which will enable screening of the 50 candidates currently under analysis (See Figure 3.1.2.1).

Two trials have been completed. The first pilot study compared the responses of tick-resistant Brahman and tick-susceptible Holstein-Friesian cattle after infestation with ticks (See Figure 3.1.2.2). The second study compared the development of tick resistance in naive Santa Gertrudis cattle following tick exposure. Santa Gertrudis cattle segregated into resistant and susceptible groups. Immune studies demonstrated that naïve resistant cattle may be innately 'prepped' with immune cells at the tick-host interface and thus are more ready to respond to ticks than are susceptible cattle.

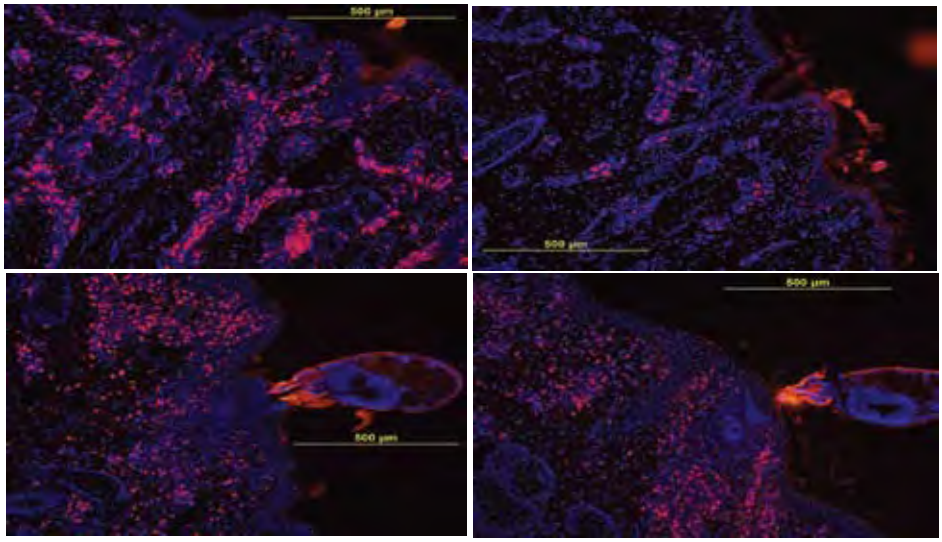


*Figure 3.1.2.2. Gamma-delta T cells (pink) in skin sections from a naïve Brahman (top left), a naïve Holstein-Friesian (top right), an infested Brahman (bottom left) and an infested Holstein-Friesian (bottom right)*

Microarray experiments examining gene expression in blood and skin of resistant and susceptible Santa Gertrudis cattle were undertaken. Analysis of results is underway and will provide data for correlation with immune phenotypic data collected from the Santa Gertrudis cattle and also the gene expression data from Brahman and Holstein-Friesian cattle in the first study. Completion of host studies is on track for late 2008.

Resistance against synthetic pyrethroid (SP) products for

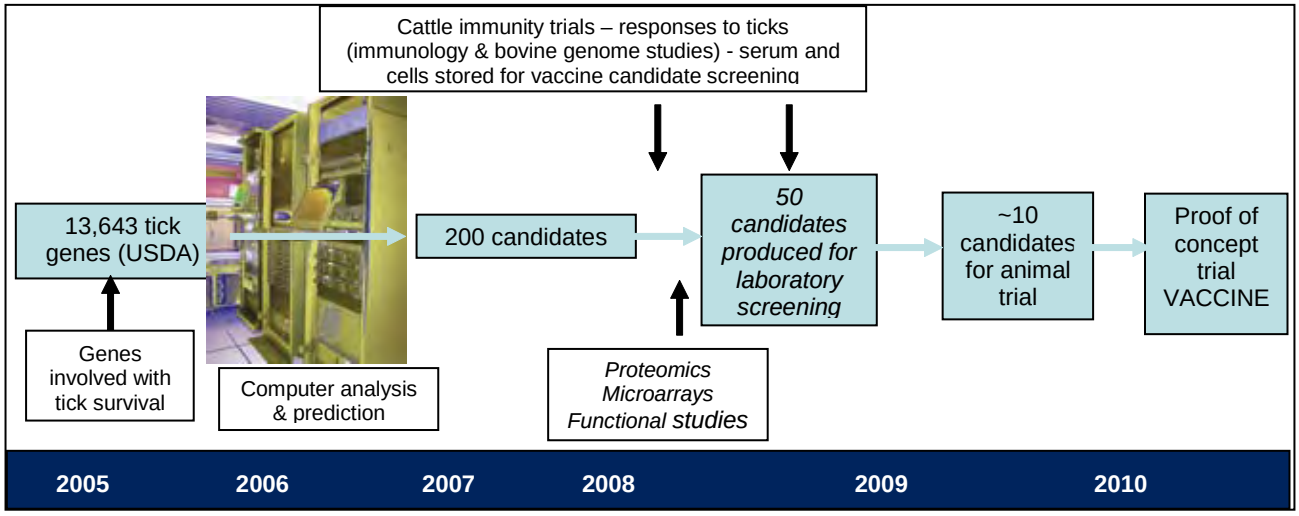



*Figure 3.1.2.1. Tick vaccine project progress. Currently the project is producing tick vaccine candidates for laboratory screening (activities highlighted in italics).*

the control of cattle ticks in Australia was detected in the field in 1984, within a very short time of commercial introduction. Researchers in the USA also reported a diverse pattern of resistance to SP products in Mexican ticks and identified a mutation linked to resistance within the tick sodium channel gene. No evidence of this mutation was found in Australian isolates of SP resistant ticks. We identified a different mutation in the sodium channel that is associated with resistance to SPs in cattle ticks from Australia. A diagnostic real-time PCR assay has been developed using allele specific Taqman MGB probes. Using the assay to screen field populations of ticks found that allelic frequencies correlated extremely well with percent survivorship at discriminating doses of Cypermethrin.

Another major achievement by the project over the past year was Emily Piper's success in winning an Early Career Scientist award at the 2008 CRC Association conference. Emily is a PhD student in this project, working collaboratively with UQ, QDPI and CSIRO scientists on the "Immunology of Tick Resistance".

## PROJECT 3.1.3A - OBJECTIVE MEASURES OF CATTLE WELFARE

To maintain future market access there will be an increasing requirement for assurance of the ethical standards of beef cattle production systems. The key pre-requisite of such standards in the context of animal welfare is the availability of reliable and objective indicators of welfare. This project forms part of a larger research initiative (Animal Welfare Objective Measures Program) being undertaken in Australia and New Zealand that aims to develop practical, objective measures of animal welfare.

This specific project has a more fundamental focus, where one of its primary objectives is to evaluate the utility of gene expression in the context of animal welfare assessment. In this instance, gene expression will be studied in leucocytes. Leucocytes were targeted for several reasons but most notably because of the known, but not necessarily well-understood, crosstalk between the immune and neuroendocrine systems. This will be investigated in cattle subjected to different stress challenges including chronic fear, weaning plus transport and under-nutrition.

The major focus of the project in Year 3 was completion of the chronic fear experiment by the Animal Welfare Science Centre in Victoria. Fear is known to be a potent stressor. When the occurrence of aversive stimuli is unpredictable and uncontrollable, it induces an enhanced or chronic stress response. From a practical perspective this can occur through repeated poor or negative handling of cattle. The aim was to apply a challenge model that facilitates development of chronic fear response in cattle. Young (10 mth) Bos taurus steers (n = 36) were subjected to 1 of 3 treatments over a 4 week period: (i) control, (ii) fear-provoking stimuli imposed over a period of 25 min (3 times/week) and (iii) fear-provoking stimuli imposed over a period of 25 min (5 times/week). There were three replicates of these treatments. The fear stimuli comprised sudden appearance of novel objects, flashing lights and mild electric shocks (via animal collars). These were initiated in a random manner over the 25 min period. Specific behavioural and physiological responses were measured. In addition, to validate that a chronic fear state had been achieved (i.e. HPA dysfunction), the response to a CRH/ACTH challenge was determined before and at the conclusion of the 4 week challenge. Blood samples for leucocyte gene expression were taken before, during and after treatment.

Results revealed a significant effect of treatment in several measures. The treatment means for average daily gain (ADG) over the 4 week treatment period, basal cortisol concentration and cortisol response to an exogenous CRH challenge at the conclusion of the treatment phase are presented in Table 3.1.3.1. These results indicate the challenge model has been effective. The increase in basal and peak cortisol concentrations, particularly in the animals subjected to the 5 times/week challenge, is indicative of a chronically stimulated hypothalamo-pituitary-adrenal (HPA) axis. This in turn has negatively affected nutrient partitioning in the animal, as manifested by the reduced growth rate.

Gene expression studies on the leucocyte samples have commenced with confirmatory RT-PCR assays to be followed by microarray analyses, which will be completed in 2008-09. The project will also commence the second animal challenge study examining the impact of different weaning treatments in young cattle. Weaning is perhaps one of the most stressful challenges cattle experience, which is why it was considered a good model to study in the context of animal welfare assessment.

*Table 3.1.3.1. Effect of chronic fear treatment on average daily gain (ADG) over the 4 weeks treatment period and basal cortisol and peak cortisol (following CRH administration) concentrations at the conclusion of the treatment period.*

| Measure | Chronic fear treatment | | | SE | P value |
|---|---|---|---|---|---|
| | Control | 3 times/wk | 5 tims/wk | | |
| ADG (kg/d) | 0.72[a] | 0.553 | 0.34[b] | 0.064 | 0.016 |
| Basal cortisol (ng/ml) | 3.5[a] | 4.2 | 8.0[b] | 0.61 | 0.004 |
| Cortisol CRH (ng/ml)* | 43.2[a] | 54.3[a] | 72.3[b] | 0.04 | 0.025 |

** Back-transformed means shown.*

## PROJECT 3.1.3B - GENETIC MARKERS FOR POLLED, AFRICAN HORN AND SCUR GENES IN TROPICAL BEEF CATTLE

Dehorning is routinely practiced in beef cattle, as horns are a leading cause of bruising, hide damage and other injuries, particularly in yards, feedlots and during transport. Although it is advisable to dehorn at a young age, because of routine management practices particularly in northern Australia, dehorning is carried out in older calves (between 3.5 and 10 months of age). Due to increasing animal welfare concerns about dehorning, breeding polled cattle provides a non-invasive welfare-friendly alternative. The aim of the project is to develop genetic marker tests for effectively introducing the polled condition to tropical beef cattle so the practice of dehorning can be effectively phased out.

The initial whole genome scan (WGS) was delayed to evaluate available options for WGSs. It was decided to proceed with a WGS of 88 unrelated Brahman (68) and Hereford (20) cattle to identify genetic associations between genetic markers (Single Nucleotide Polymorphisms, SNPs) and the genes of interest (poll and African horn). DNA from experimental cattle was submitted to a genotyping laboratory in California USA for whole genome amplification and genotyping with the Affymetrix GeneChip® Bovine 25K and 11.5K panels. Results were obtained in September 2007. Data analysis aimed to identify significant SNPs associated with horn status (polled or horned). Given the design of the experiment with an uneven distribution of number of animals in each phenotype-sex class and the confounding of sex with horn status (in Brahmans), data from each breed were analysed separately. Analyses for the Hereford dataset identified one SNP on chromosome 1 in complete agreement with the hypothesised mode of inheritance. In Brahmans, eight of the 12 most significant SNP were also located on BTA 1, confirming the importance of chromosome 1 in horn status inheritance.

A haplotype test allows determination of the genetic status of horns at the polled locus. This study represents the first attempt to evaluate the polled haplotype in Bos indicus cattle. Better understanding of the polled locus in Brahman cattle will facilitate mapping of African horn and/or scur genes. This research also intends to elucidate an understanding of scurs development in cattle by ruling out or implicating a separate locus.

The polled locus has been mapped to the proximal part of bovine chromosome 1 by several groups and was subsequently fine mapped to a 1Mb interval between two molecular markers. Our efforts were directed at evaluating the polled haplotype in Brahman (n=68) cattle and comparing it to a group of polled and horned Herefords (n=20). Published microsatellite markers in the region were ordered and genotyped. Additional SNP information for markers in the region was used to supplement the microsatellite markers, giving a total of 32 microsatellites and 37 SNP across a 4.9 Mb region.

One interesting microsatellite marker has been identified and is being investigated further. In the original experimental population, all polled animals were predicted to be polled by this marker (see Table 3.1.3.2). Although 2 out of 40 horned cattle were predicted to be heterozygous polled, it could be argued they were actually scurred, which is plausible in the heterozygous polled status. Encouraged by this result, two sets of validations were conducted. Results are promising. It is expected the use of this marker in a haplotype test in conjunction with other informative markers in this region will improve predictive ability. The parallel improvement in resolution of the confidence interval containing the polled gene would greatly assist in identifying potential candidate genes and in eventually identifying the causative mutation.

Sequential tissue sampling from the skull region of new-born horned (6), potentially polled (9) and potentially scurred (8) calves was conducted for microarray experimentation to identify differential gene expression across the phenotypes. It was decided to concentrate on peri-natal samples i.e. samples taken between 1 to 9 days after birth. A total of 11 calves (6 males and 5 females) were available, including 3 horned, 4 scurred, and 4 polled. Additionally, for two individuals (one female scurred and one female polled) 'control' samples were also extracted from central regions of the head away from the horn site. The experimental design used 5 Agilent chips each containing 4 microarrays. There was a greater emphasis (i.e. more hybridisations) in the important contrast of horned versus polled.

Experimental design details and tissue samples were submitted to the commercial provider (SRC Microarray Facility, University of Queensland) for microarray services using the Agilent dual-array platform. Results were obtained and analysed to identify significantly, differentially expressed (DE) genes. Significance levels for identifying differentially expressed genes were determined based on model based clustering through mixtures of distributions. A total of 733 DE probes were identified across various contrasts of interest i.e. poll vs. horn, poll vs. scur and

*Table 3.1.3.2. Actual and predicted horn status phenotypes as assigned by the marker of interest*

| ACTUAL Phenotype | PREDICTED phenotype | | | |
|---|---|---|---|---|
| | Homozygous Polled | Heterozygous Polled | Horned | Total |
| Polled | 25 | 22 | | 47 |
| Horned | | 2 | 40 | 42 |

horn vs. scur. Currently, the biology underpinning these differentially expressed genes is being investigated. One pathway of significant interest relates to genes involved in cell adhesion (e.g. desmocollin (DSC), desmoglein (DSG) and related cadherins genes) that appear to be down-regulated in polled versus horned individuals. Both DSC and DSG are known to be involved in the epithelial-mesenchymal transformation that might control specialisation of mesenchymal cells into osteoblasts involved in horn formation.

During 2007, a breeding program was conducted on a collaborating breeding property, Hillgrove Pastoral Company, Charters Towers, to generate a resource population for the project. At June 2008, 287 calves (Table 3.1.3.3) were identified, bled and their horn status recorded. It should be noted the majority of the calves are still too young to definitively ascertain their horn status. Currently there are 56% polled calves and 44% horned and scurred calves. However there is a strong possibility that some calves identified as 'polled' may develop horns/scurs later and some scurs may be reclassified as horns at an older age. Thus, regular phenotyping will continue to accurately determine their phenotypes. Efforts are underway to select a subset of this population for a second whole genome scan analysis.

*Table 3.1.3.3. Number of resource population calves and horn status (June 2008)*

| Phenotype | Female | Male | Total |
|---|---|---|---|
| Horned | 16 | 25 | 41 (14%) |
| Polled | 82 | 79 | 161 (56%) |
| Scurred | 46 | 39 | 85 (30%) |
| Total | 144 | 143 | 287 |

# Program 4

# Female Reproductive Performance

**OUTCOMES (AS PER COMMONWEALTH AGREEMENT)**

› *A comprehensive genetic improvement package that incorporates genomic and other animal breeding technologies for the genetic improvement of female reproductive performance in breeding cattle resulting in an annual improvement of $46.5 million in the gross revenue of the Australian beef industry from 2012.*

## PROJECT 4.1.1 - GENE DISCOVERY FOR POST-PARTUM RE-CONCEPTION AND AGE OF PUBERTY

In the late 1990s, Delgado et al's "Livestock Revolution" papers predicted an increasing demand for animal protein in developing countries globally. Australia can capture part of this opportunity for beef protein by increasing the reproduction rate in northern beef herds. CRC studies (e.g. Fordyce, Burns and Holmes) have examined the biological and economic consequences of reducing two key components viz: age at puberty and days to re-conception post calving by 30 days. Banks (MLA 2005 Strategic Planning Review) identified 'turn off' and weight as key profit drivers for Northern Australian herds. These analyses, coupled with industry growth (live export trade and expansion of the feedlot sector), re-enforce the view that improving reproduction rate is critically important.

Although reproduction rate per se is lowly heritable, individual components are much more heritable, indicating it is possible to identify genetic options for its improvement. There are two issues of concern to participants in the northern industry:

i) re-conception rates of lactating cows, particularly those with their first calf at foot; and

ii) age/weight of puberty in heifers that increases age of first calving (by up to 1 year in northern Australia), spreads time of conception and hence calving dates over an unacceptably extended period, which impacts negatively on meeting market specifications and reduces lifetime reproductive performance of females.

These issues are common to tropically adapted beef and high-performing dairy cows and to a lesser extent, to cows grazed in temperate zones. Identification of genetic markers for reproductive traits will enhance the overall performance of breeding females, thereby substantially increasing both herd productivity and profitability. The aim of this project is to identify diagnostic DNA markers for reduced age at puberty and improved post-partum re-conception in lactating females. These DNA diagnostic markers can then be used to select favourable phenotypes for reproductive performance in future populations. To accomplish this task, a whole genome association strategy has been undertaken. The cattle population under investigation is the lifetime fertility population established in the CRC II and continued in CRC III. This population includes over 2000 Brahman and Tropical Composite cattle that have been deeply phenotyped for a number of reproduction rate component, adaptability and meat quality traits.

Age at puberty is the first trait examined in this study as collection of appropriate measures from the resource population is complete. Other reproduction rate phenotypes are still being collected and will be assessed later in the project. To date, two whole genome scans have been completed to identify genetic markers associated with reproduction rate traits. The first used a panel of 10,000 Single Nucleotide Polymorphisms (SNPs) on a selection of 565 Brahman females. Association analyses of the whole genome scan identified a panel of 199 markers with a significant effect ($P<0.01$) on age at puberty for either additive dominance or allelic substitution effect in this subset of Brahman females. Subsequent genotyping of 105 of these markers indicated that 90 have a significant effect on age at puberty in the whole Brahman research population, while 15 markers are also significant in the Tropical Composite research population for either one of the inheritance models.

Seven genome regions of interest have subsequently been identified for further fine mapping. Fine mapping involves identification of new SNPs in and around the original whole genome scan SNP of interest, and the identification of SNP in and around any positional candidate gene in that genome region. To date, more than three hundred new and novel SNPs have been identified in these seven genome regions. A small subset of carefully chosen new SNP have been genotyped on the entire Brahman and Tropical Composite female cattle to determine whether any of the new markers are more informative for age at puberty than the original whole genome scan SNP. In two regions for which data analyses are complete, eight of ten markers tested are significant in the whole Brahman research population, while three are also significant with the whole Tropical Composite research population.

Based on both the whole genome scan and fine mapping studies, there are 15 markers

with a significant additive effect on age at puberty in Brahmans and Tropical Composites. Ten display an effect on age at puberty in the same direction, and thus could represent the first panel of markers for commercialisation and delivery to the beef industry to reduce the age at puberty. However, prior to release to the industry, these markers must be validated on an unrelated population. Furthermore, the effect of reducing the age at puberty on the 'lifetime reproduction rate' of these cattle must be estimated before release, to ensure no compromise on commercial measures of reproductive performance.

A second whole genome scan using 54,000 SNPs was completed in June 2008. This scan contains more than a six-fold increase in informative markers relative to the 10K scan performed earlier. Analyses have not yet been completed to examine the association between SNP and phenotype. Phenotypes to be examined include age at first CL (puberty), post-partum anoestrus interval, days-to-calving and calving success. The latter two traits are current industry measures for reproduction rate and would provide industry with a demonstration of effectiveness of marker panels on traits for which they are familiar.

### PROJECT 4.1.2 - EXPRESSION OF GENES ASSOCIATED WITH POSTPARTUM RE-CONCEPTION

Female reproductive performance remains the major determinant of profitability in beef cattle enterprises. The proportion of breeding cows that yield a calf each year and the time at which calves are born in relation to annual cycles of feed availability are both components of reproductive performance. In northern Australia the major need is to increase the number of cows that repeatedly produce a calf each year whilst in southern Australia there is greater emphasis on optimising calving periods to feed availability. Irrespective of the need, the interval from calving to re-conception determines whether cows calve each year and also the time of calving. After calving, cows enter a period of reproductive quiescence during which ovulation does not occur and accordingly cows cannot re-conceive. This interval is known as post-partum anoestrus. The resumption of ovulation is hence critical to postpartum re-conception. The aim in this project is to identify changes in gene expression that are associated with, and which may underpin, the resumption of ovulation postpartum. Given the importance of the brain in regulating the function of the ovaries, the hypothalamic area of the brain which contains neuronal networks associated with reproduction was chosen for gene expression studies.

The preferred model to study postpartum gene expression would be groups of cows with a divergent genetic predisposition for days-to-calving (inter-calving interval). Unfortunately, this genetic resource is not available and a biological model was used in place of a genetic model. The biological model involved removal of the calf from groups of first-calf cows and comparing hypothalamic gene expression in these cows with gene expression in cows that continued to suckle a calf. Removal of the calf typically results in the resumption of ovulation and it was rationalised this would be associated with changes in hypothalamic gene expression.

Another aim in this project is to provide a biological context for the whole genome association studies related to heifer age-at-puberty and cow postpartum reproduction. This includes determining whether candidate genes for puberty and postpartum reproduction are expressed in the hypothalamus and also informing the fine mapping of candidate genes.

The gene expression studies in this project are the first comprehensive studies on hypothalamic gene expression in cattle. Gene expression has been determined by quantitative PCR (qPCR) for candidate genes and microarray to discover novel genes associated with weaning and ovarian function. The qPCR studies have demonstrated, for the first time in cattle, clear differences in gene expression in sub-regions of the hypothalamus (Table 4.1.2.1). The regional differences in gene expression observed to date have a morphological and functional significance and can therefore be regarded as "textbook findings" for cattle. Publication of the findings will stimulate interest amongst reproductive biologists and lead to other research that will build on the understanding of gene expression and postpartum re-conception in cattle.

Microarray studies on novel gene discovery have yielded an impressive list of potential genes previously unknown to be associated with reproductive function, and in particular postpartum reproduction. Microarray gene expression results can be presented as Venn Diagrams and an example is shown in

*Table 4.1.2.1. Differential gene expression in sub-regions of the hypothalamus (H1, H2 and H3) in post-partum cows. All the genes are associated in some manner with reproductive function. Values within rows for each gene without a common superscript letter are significantly different.*

| Gene Symbol | Gene | Sub-region of hypothalamus | | |
|---|---|---|---|---|
| | | H1 | H2 | H3 |
| GNRH1 | Gonadotrophin releasing hormone 1 | 350[a] | 1[b] | 46[c] |
| KISS1 | Kisspeptin | 44[a] | 2[b] | 894[c] |
| ESR1 | Oestrogen receptor α | 17[a] | 2[b] | 29[a] |
| NPY | Neuropeptide Y | 13[a] | 2[b] | 23[a] |
| LEPR | Leptin receptor | 67[a] | 9[b] | 146[a] |

Figure 4.1.2.1. In this analysis, 122 genes were differentially expressed in hypothalamic sub-region H1 between suckled and weaned cows, and 84 genes were differentially expressed in hypothalamic sub-region H3. Of significance, 41 genes were in common between hypothalamic sub-regions H1 and H3. Although the biological context and relationships to resumption of ovulation and postpartum re-conception is still being explored, this is the first time that differences in gene expression have been discovered between weaned and suckled cows and between cows with suppressed ovaries and cows that have resumed ovulation. Preliminary analysis of the microarray results has underscored the power of this approach in fundamental discovery science of genes and gene networks associated with postpartum reproduction.

This project is helping to inform the gene discovery and whole genome association studies (WGAS) in Program 4. A group of candidate genes that have emerged as significant for age-at-puberty from the WGAS can be generally classified as being associated with neuronal development and function or neuronal plasticity (Table 4.1.2.2). Other genes identified in the WGAS that are associated with general cellular interactions are cadherin 6 and integrin alpha 11. The latter genes, together with syntrophin gamma 1, have been shown to be expressed in hypothalamic sub-regions H1, H2 and H3. Furthermore, some of the genes show regional differences in expression across the hypothalamus.

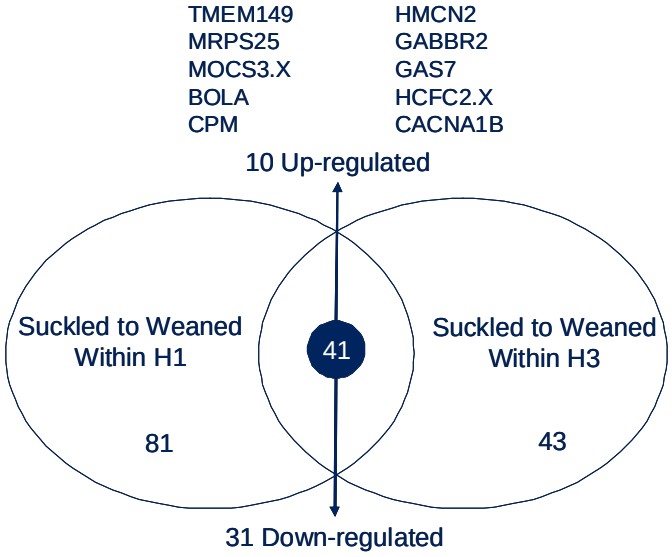



*Figure 4.1.2.1. Venn diagram for microarray results of genes differentially expressed in hypothalamic sub-regions H1 and H2 between suckled and weaned cows.*

*Table 4.1.2.2. Candidate genes potentially significant for age-at-puberty which are associated with neuronal structure and function.*

| Gene | Function |
|---|---|
| syntrophin gamma 1<br>hippoclacin like 1 | neuronal cell signalling |
| contactin 6<br>ankyrin 3 | neuronal cell surface interactions; cell morphology |
| axon guidance homolog 2 | neuronal axon guidance |
| lin-7 homologue a | neuronal synaptic vesicle |

Based on the discovery of genes for age-at-puberty that are associated with neuronal morphology and function, and which are expressed in the hypothalamus, it is proposed that a major reproductive event such as puberty is associated with changes in brain structure and function, or neuronal plasticity. If this is proven to be correct, then it would fundamentally change the understanding of endocrine and morphological events associated with reproductive function. A similar analysis is to be undertaken for the WGAS results for postpartum reproduction.

### PROJECT 4.1.3A – MALE INDICATOR TRAITS TO IMPROVE FEMALE REPRODUCTIVE PERFORMANCE

The objective of the project is to find better early-life predictors of female fertility in bulls, to improve reproductive performance of their male and female progeny and have this validated and commercialised by 2012.

Improved reproductive and growth rates have been identified as key drivers of profitability in northern Australia by MLA's livestock production R&D strategic plan (2006 -2011). In general, at least 60% of overall genetic gain in a beef herd derives from bull selection due to the higher selection intensities that can be achieved relative to those in young females. Given the relatively low branding rates in many northern herds, bulls are a major source of genetic improvement.

Except for scrotal size, there is little genetic information on male reproductive traits and their association with female reproduction. Predictors of lifetime reproduction rate and its component traits may be identified in blood or semen. New traits such as sperm morphology (particularly the percentage of normal sperm in an ejaculate) have been identified as important predictors of calf output of bulls in multiple-sire herds in northern Australia. Early life predictors of fertility in the male will greatly improve efficiency of selection of sires for reproductive performance of beef herds.

This project will determine whether there are traits in young bulls, either pre- or post-pubertal, that are indicative of superior reproductive performance in their female progeny. If so, this provides a selection method that can be applied in bulls for improving herd reproductive performance. The research will also establish whether there are adverse effects on male reproductive traits by selecting females on reproductive traits or males for meat quality traits. These genetic correlations are being established by using the male progeny from Project 4.1.3b in this project. As a by-product, the work will also establish whether it is possible to identify, early-in-life, bulls that have superior reproductive traits at 2 years of age which impact on their own calf-getting ability.

There are genetic and economic advantages in identifying new traits in the male to improve fertility of both male and female relatives. Identifying early life predictors of an individual's fertility would reduce the number of bulls required for breeding throughout northern Australia by up to 50%. Identifying new traits related to fertility of his progeny would allow opportunities to increase rates of genetic improvement for all traits and significantly increase the impact of using genetically superior bulls in commercial herds in northern Australia.

Approximately 3,500 bulls are being generated over six joining periods in Project 4.1.3b. The study commenced in April 2005 and will be completed in November 2011. Young bulls were produced by sires selected from BREEDPLAN herds recording reproductive data such as scrotal size and days to calving. The aim is to develop breed-specific (Brahman and Tropical Composite) heritabilities from about 80 sires with 20 progeny per sire per breed. Genetic correlations will be estimated using approximately 1500-2000 dam/son pairs per breed.

Weaner bulls are transferred to Brigalow Research Station or retained on Belmont Research Station. They are studied until 24 months of age and then returned to their owners or sold. Weight and scrotal circumference is measured at 3 monthly intervals with bull breeding soundness examinations (BBSE) conducted at 12, 18 and 24 months of age. A BBSE involves a physical assessment and collection of semen for morphology examination. At the time of BBSE, blood and semen samples are collected and stored for assessment as potential additional indicator traits for male and female reproductive performance.

Field collection of data from the third cohort of 620 bulls was completed in October 2007 with laboratory assessment of semen for morphology completed in February 2008. At both sites semen suitable for a laboratory estimation of morphology could be collected from 95% of bulls. Mean percent normal sperm of all bulls was 71% with little difference in raw statistics between breeds or locations. The fourth cohort comprises 736 bulls. The eighteen-month BBSE was conducted in April 2008. The fifth cohort was weaned from April to June 2008.

An analysis of data from the first three cohorts was undertaken. Traits included liveweight, body condition, flight time, fat depth and eye muscle area, physical traits such as feet, leg and sheath structure, semen traits and pre-pubertal hormones. The analysis was conducted within genotypes and, for bulls at Belmont, a comparison of Brahman and Composite bulls was made. Correlations between physical, scrotal and semen traits indicated there were some useful predictive relationships with early-life (12 months) and later-life (24 months) traits. For example, scrotal circumference at 12 months is highly correlated with scrotal circumference and percent normal sperm at 24 months.

Genetic parameters among male and female traits were estimated from the first three cohorts and included the fourth cohort to 12 months of age. Heritabilities of pre-pubertal hormones and scrotal circumference to 24 months of


BRIGALOW
RESEARCH STATION
Est. 1963
DPI
DEPARTMENT OF
PRIMARY INDUSTRIES
QUEENSLAND

age were generally moderate to high, but heritabilities of semen quality traits were generally low except for percent normal at 24 months. IGF-1 and scrotal size, particularly at 12 months, showed favourable genetic correlations with age at puberty in the females and was more pronounced in Brahmans. Percent normal sperm at 24 months and presence of sperm in the ejaculate at 12 months tended to be favourably associated with earlier puberty in females, but high standard errors (due to small numbers available for analyses) precluded any significance being placed on these estimates. The genetic correlations of LH, inhibin and flight time with age at puberty were generally low to negligible. Percent normal sperm in bulls was genetically associated with shorter post-partum intervals in females and was more pronounced in Brahmans, suggesting that selection for higher percent normal sperm in males would indirectly reduce post-partum interval. Body condition at 12 months and IGF-1 at weaning in the young bulls tended to be favourably associated with post-partum interval in the females. More observations are needed to confirm these associations.

A pilot study was conducted at Belmont in January 2008 on pre-pubertal bull calves to determine peak responses and the length of the plateau of LH after injection with 3 dose levels of GnRH. Results of this study were then used to determine LH levels in pre-pubertal bull calves at Brian Pastures (85 calves), Brigalow (75), Belmont (257), Toorak (166) and Swan's Lagoon (138). At the same time, all bull calves were bled for inhibin and at weaning for IGF-1. A number of seminal plasma proteins have been linked, in other studies, to fertilisation and early embryonic development. Additional funding support of $150,000 for 3 years (from MLA) will allow progress in correlating the various seminal plasma proteins in semen as indicators of male reproductive traits such as percent normal sperm. This investigation will form part of a PhD project.

### PROJECT 4.1.3B – EARLY PREDICTORS OF LIFETIME FEMALE REPRODUCTIVE PERFORMANCE

The broad objective of this project is to identify early-life indicators of lifetime female reproductive performance. To achieve this objective, the reproductive performance of breeding females (Brahmans and Tropical Composites) located at a number of tropical northern Australian environments (Brian Pastures, Brigalow, Belmont, Swans Lagoon and Toorak) is being recorded for:

- Mating and calving information – pregnancy diagnosis, calving date, lactation status etc.
- Detailed death and disposal codes along with repeated measures of body weight, composition and linear type traits (e.g. teat and udder scores) to allow estimation of genetic parameters for longevity and early-life indicators.
- Reproductive tract scans (CL scans) to determine resumption of cycling in lactating females.

These observations allow determination of days-to-cycling after calving, days-to-pregnancy after calving and days-to-calving after mating. Although the focus is primarily to understand the genetics of new traits at the quantitative level and their relationships with traits measured in CRCII on these same females (e.g. age at puberty, age at first calving, calving history), opportunities will become available to undertake gene discovery and expression studies for new and existing traits towards the end of CRCIII.

During 2007/08, 1798 cows generated 1414 lives calves and weaned 1384 calves. Continuing the breeding strategy of the previous two years, Brahman and Composite bulls were mated together at Belmont to allow direct breed comparisons for a range of reproductive traits.

The genetic analyses of CRCII Project 2.3 data have been finalised and 5 research publications are ready for journal submission, reporting results on:

- Steer growth and feed efficiency traits
- Heifer growth traits
- Heifer pubertal traits
- Steer carcase and meat quality traits
- Heifer adaptive traits

All pubertal and post-partum data pertaining to the first two joinings were interrogated by the project's reproductive biologists to generate mating outcome information for each female. This was intended to accurately estimate and define traits such as age at puberty, age at post-partum oestrus, days from calving to post-partum oestrus, days from post-partum oestrus to conception and days from calving to re-conception etc. Phenotypic and genetic analyses of these traits are currently underway. Information on post-partum oestrus was further utilised to select animals for the second whole genome scan for project 4.1.1.

Industry engagement has been identified as a crucial factor for the ongoing success of this project. A plan to undertake economic analyses detailing the benefits and impact of research outputs is being implemented. A distillation workshop will be conducted in July 2008 in Brisbane with all the Project Leaders in Program 4 and key scientific personnel. During September 2008, all cattle owners (project co-operators) will be updated on the progress of the project through a program-wide initiative. Further, planning the phasing-out of project cattle resources annually over the next 3 years is important, as a sub-set of these cows will be completing their targeted 6 joining opportunities from 2009. This will be highlighted at cattle owner updates this year and options for their further utilisation to improve rates of genetic gain will be discussed.

# Program 7

# Underpinning Science

The Underpinning Science Program provides various genomic services to support research conducted by Programs 1 to 4, including database and DNA maintenance, coordination of genotyping and microarrays, coordination of analysis of QTL mapping and microarray experiments and bioinformatics support.

Beef CRC research is dependent on records of performance (phenotypes) and DNA samples collected during CRCI, II and III. Therefore, the maintenance of the database is a vital activity. A new database system is being developed and data uploaded so staff can input and retrieve data more efficiently.

DNA samples matching the phenotypic records of animals collected in CRCI, II and III are also vital for CRC research. University of Queensland Animal Genetics Laboratory (UQ-AGL) has been contracted to store the CRC's DNA collection and to process new tissue samples into DNA for long term storage. Buffy coat samples for approximately 11,000 cattle, representing 95% of the CRC1 cattle and 4,400 blood samples from CRC 2 animals was processed into DNA to maintain sample integrity for long-term storage.

The Underpinning Science Committee considered plans for genotyping for whole genome association studies (WGAS). The CRC elected to use the Illumina 50k assay because it gives better coverage, at a lower price, than the Affymetrix assay. Test samples of most available sources of DNA available were genotyped at Illumina and most samples were successful, indicating the DNA quality and quantity is satisfactory. Two GWAS have been undertaken, one for Programs 1 and 2 and the other for Programs 3 and 4. Genotypes were returned in June 2008 and data analysis is now underway.

Guidelines for design and analysis of WGS were prepared. Protocols and procedures for the approval of the design and the analysis of gene mapping experiments have been revised and staff undertaking such experiments are required to follow these protocols. As part of this revision we have analysed the value of call rate, minor allele frequency, departure from Hardy-Weinberg equilibrium and non-Mendelian inheritance in determining the quality of Single Nucleotide Polymorphism (SNP) data. We have tested methods of predicting the genetic value of animals from their SNP genotypes by setting aside a proportion of the data and using it to check the prediction derived from the rest of the data. This yields high accuracy if the test animals are a random selection of the full dataset (mirror prediction) but lower accuracy if the test animals are from different families to the rest of the dataset (future prediction). In assessing panels of markers in CRC studies, the 'future prediction' method will be used.

A simple forward-selection method to choose a panel of markers that predicts genetic value has also been developed and tested. We have shown that more significant SNPs are found in a GWAS when using haplotypes than when using individual SNPs. A new efficient method for haplotyping animals has been developed and programmed. This will be used in future to assess whether haplotypes give a more accurate prediction of genetic value than individual SNPs. Methods of estimating the relationship among animals from SNP data have been compared. This makes it possible to fit the polygenic breeding value of animals in an analysis, even if their pedigrees are unknown. This, in turn, reduces the number of false positives among the significant SNPs.

SNP data have been integrated and analysed with data on growth, carcase and meat quality, adaptation and female reproductive traits to discover hundreds of SNPs affecting these traits. A method of discovering SNPs that affect any one of several correlated traits has also been developed and tested.

A sub-committee of Underpinning Science considered alternative platforms for microarrays. The long oligo platform previously selected has been used but problems were encountered with the slides printed in Australia. New slides were obtained from the USA. Other platforms have also been used for specific experiments (e.g. Agilent) because they were better suited to the requirements of that experiment. Microarray and qRT-PCR experiments have been designed, analysed and reported. The Agilent array has been annotated. A document on guidelines for design and analysis of microarray experiments has been prepared and circulated.

A meeting was held in San Diego with representatives of United States Department of Agriculture (USDA), Canadian and USA universities, the US Beef Improvement Federation and AgResearch New Zealand to discuss collaboration. This resulted in agreement for collaboration in several areas of marker discovery and validation between the Beef CRC and USDA with other organisations possibly joining in the future.

A standard bioinformatics service is provided by CSIRO. This is based around their bovine genome sequence and annotation and is available to all CRC scientists.

A separate project known as "SmartGene for Beef" is also managed through the Underpinning Science program. It aims to integrate

BREEDPLAN EBVs and DNA diagnostic tests into a single genetic tool known as marker-assisted EBVs (MA-EBVs). The project is partially funded by the Queensland Department of State Development and Innovation. Partners include Beef CRC, Catapult Genetics, AGBU, ABRI and MLA in Australia and Cornell University in the USA.

Marker assisted EBVs (MA-EBVs) will allow beef producers to more easily use the complementary EBV and DNA genetic technologies to breed better quality beef. Specifically, integration of EBVs and DNA tests for tenderness will allow breeders of tropical breeds, in particular, to use MA-EBVs to improve selection for tenderness, which is the most significant characteristic in consumer taste panel assessments and is a major limitation for tropical beef breeds in meeting high eating quality standards. MA-EBVs will enable improvement of this characteristic in an efficient and natural way by identifying animals with genetically more tender beef, providing significant benefits to the Australian beef industry and its' global consumers.

The project is being undertaken in three distinct stages:

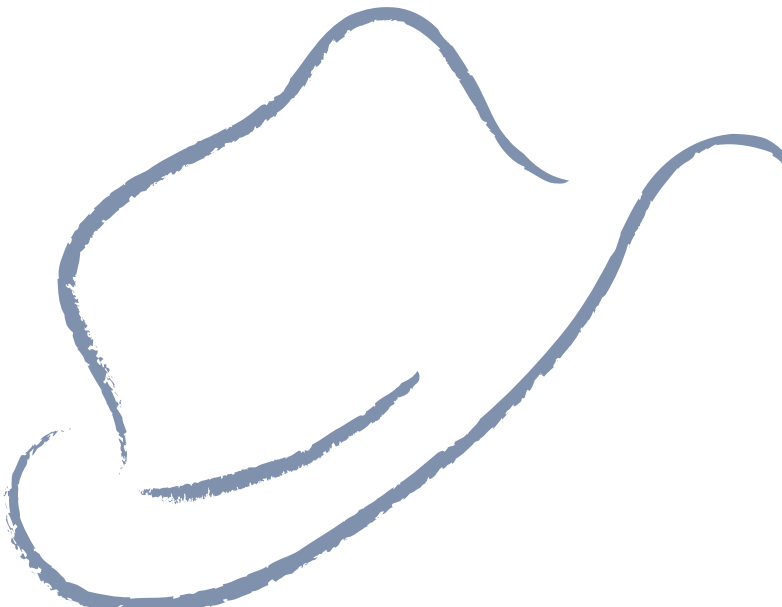
*Stage 1 Research by Catapult Genetics*: ~14,000 DNA samples from Beef CRCI and II animals were tested for the 12 commercially available GeneStar markers (4 markers each for Tenderness, Marbling and Feed Efficiency) and genotypes transferred to the Beef CRC database.

*Stage 2 Research by AGBU, through Beef CRC:* Joint analyses were undertaken of genotypic and phenotypic information to estimate the full range of genetic parameters needed to estimate MA-EBVs

*Stage 3 Research undertaken by AGBU in its own right:* develop trial MA-EBVs using genotypes (from Stage 1) and genetic parameters (from Stage 2).

In addition to these three distinct research stages, a series of four technical and industry workshops will be held over the life of the project, with the first technical workshop held in Brisbane in late May 2007.

Stage 1 and Stage 2 research was completed by December 2007. Since then, further rigorous analysis to confirm the results continued by AGBU and Catapult Genetics. MA-EBVs for Tenderness will be officially launched in October 2008, marking a major change in the way industry uses DNA markers to add value to their herds.



# Commercialisation and Utilisation



## COMMERCIALISATION AND UTILISATION STRATEGIES AND ACTIVITIES

The commercialisation strategy being used by Beef CRC (see flow chart diagram) recognises different types of products and processes arising from research, education and adoption activities and identifies appropriate pathways for their commercialisation (including IP and patent/trade secret protection where appropriate) and utilisation to achieve high value outcomes for industry.

The strategy is made up of three inter-related components:

1. ***IP identification, protection and management*** - This component is discussed separately below.
2. ***Commercialisation of IP*** – Complete "Paths to Adoption" were developed and documented for each potential Beef CRC "product" (including products based around an IP position as well as educational and knowledge packages developed by Beef CRC). Further work in Year 3 resulted in business plans for two of these products. Commercial consultants are used to assist with this process as required.

Over the past 12 months considerable effort was devoted to developing and implementing Beef CRC's preferred DNA marker commercialisation model. As flagged in the 2007 Annual Report, this model is aimed entirely at maximising uptake and economic impact of DNA markers in industry. In March 2008, Beef CRC held an independently-facilitated workshop designed to allow beef, sheep and dairy industry and relevant DNA marker commercialisation companies and research providers from Australia, New Zealand and the USA with an opportunity to examine the CRC's DNA marker commercialisation model and its proposed international genomics collaborations, with a view to identifying problems and solutions to overcome them. Workshop aims were to:

- describe, debate and refine the CRC 's model for DNA marker commercialisation aimed at achieving maximum uptake and economic impact in the Australian and New Zealand beef industries; and
- recommend to the CRC the next steps in implementing the refined commercialisation model.

Following the workshop, a joint meeting of the Beef CRC and MLA Boards recommended formation of a DNA Marker Commercialisation Working Group, responsible to a Steering Committee which comprised the Chairmen of MLA and Beef CRC and one Director with business experience from each of MLA and Beef CRC.

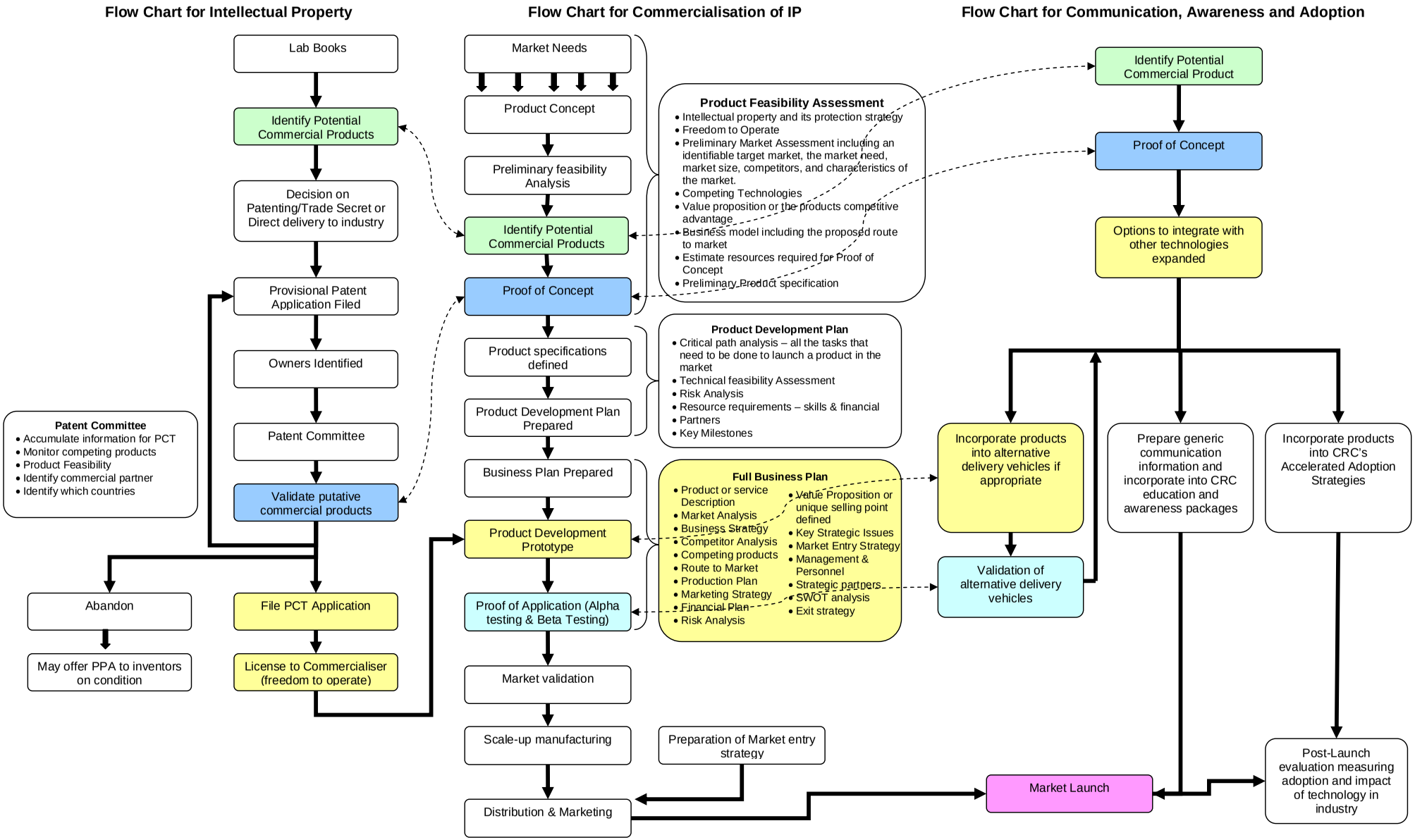
Subsequent widespread consultation by the Working Group across industry, BREEDPLAN and DNA marker commercialisers confirmed the CRC's model is technically achievable, and at least over the next 12-18 months, can be achieved largely with existing resources. Three specific development requirements to support the new commercialisation model were recommended, including:

i. Development of a "National Database" of genotypes (derived from DNA marker testing) and phenotypes (accurate measures of hard- or expensive-to-measure traits in research, commercial and seedstock cattle herds). This work will build on the existing Beef CRC database over the next year or so, with the aim of using the interim period to resolve governance and ongoing funding arrangements for the "National Database"; The final stages of the "SmartGene for Beef" project (see report in Program 7) were used to trial the estimation and reporting of marker effects, the potential/best approaches to prediction equations, and reporting to industry of marker values on commercial cattle and "augmented EBVs" for seedstock cattle, giving the Working Group confidence the National Database concept was the best approach to delivering integrated information derived from BREEDPLAN and DNA markers.

ii. Development of new educational and extension materials, training resources (at undergraduate, vocational and industry levels) and industry communication activities to support the new DNA marker commercialisation model integrated across Beef CRC, MLA, Meat and Wool New Zealand, BREEDPLAN and the DNA marker commercialisation companies to ensure a common message and most efficient use of resources.

iii. Development of a "Beef Information Nucleus" specifically aimed at significantly increasing the rate of genetic gain in the Australian and New Zealand beef industries by speeding up genetic progress within and across breeds, by:

- Providing a long-term resource for testing the effectiveness of genetic selection tools, using animals that are representative of the populations in which they are to be used;
- Intensively recording phenotypic information on a wide range of existing and new traits that are likely to impact on industry


Flow Chart for Intellectual Property
Lab Books
Identify Potential Commercial Products
Decision on Patenting/Trade Secret or Direct delivery to industry
Provisional Patent Application Filed
Owners Identified
Patent Committee
Validate putative commercial products
Patent Committee
• Accumulate information for PCT
• Monitor competing products
• Product Feasibility
• Identify commercial partner
• Identify which countries
Abandon
May offer PPA to inventors on condition
File PCT Application
License to Commercialiser (freedom to operate)
Flow Chart for Commercialisation of IP
Market Needs
Product Concept
Preliminary feasibility Analysis
Identify Potential Commercial Products
Proof of Concept
Product specifications defined
Product Development Plan Prepared
Business Plan Prepared
Product Development Prototype
Proof of Application (Alpha testing & Beta Testing)
Market validation
Scale-up manufacturing
Distribution & Marketing
Product Feasibility Assessment
• Intellectual property and its protection strategy
• Freedom to Operate
• Preliminary Market Assessment including an identifiable target market, the market need, market size, competitors, and characteristics of the market.
• Competing Technologies
• Value proposition or the products competitive advantage
• Business model including the proposed route to market
• Estimate resources required for Proof of Concept
• Preliminary Product specification
Product Development Plan
• Critical path analysis – all the tasks that need to be done to launch a product in the market
• Technical feasibility Assessment
• Risk Analysis
• Resource requirements – skills & financial
• Partners
• Key Milestones
Full Business Plan
• Product or service Description
• Market Analysis
• Business Strategy
• Competitor Analysis
• Competing products
• Route to Market
• Production Plan
• Marketing Strategy
• Financial Plan
• Risk Analysis
• Value Proposition or unique selling point defined
• Key Strategic Issues
• Market Entry Strategy
• Management & Personnel
• Strategic partners
• SWOT analysis
• Exit strategy
Preparation of Market entry strategy
Flow Chart for Communication, Awareness and Adoption
Identify Potential Commercial Product
Proof of Concept
Options to integrate with other technologies expanded
Incorporate products into alternative delivery vehicles if appropriate
Validation of alternative delivery vehicles
Prepare generic communication information and incorporate into CRC education and awareness packages
Incorporate products into CRC's Accelerated Adoption Strategies
Market Launch
Post-Launch evaluation measuring adoption and impact of technology in industry

# Intellectual Property Management

profitability, including traits that are difficult and/or expensive to measure; and

- Quantifying the effects and frequencies of DNA markers to allow new information to be evaluated and integrated into existing genetic improvement systems.

The Beef Information Nucleus will commence in the 2008/09 breeding seasons using a combination of Beef CRC seed funding and industry funds leveraged by MLA Donor Company co-investment. The aim is to develop a coordinated approach across southern and northern Australia and ideally also New Zealand over the next year or so, with the Beef Information Nucleus to be maintained in perpetuity on behalf of the beef industry (i.e. it will be developed and managed outside Beef CRC to ensure it is sustainable beyond the life of Beef CRC).

3. **Communication, Awareness and Adoption** – This component includes all areas of industry education, generic communication and awareness activities and also the CRC's "Accelerated Adoption" activities through Beef Profit Partnerships. It is described in greater detail in the Technology Transfer section.

In readiness for IP commercialisation activities, Beef CRC developed an IP management and commercialisation policy aligned with the National Principles of IP Management for Publicly Funded Research. In December 2006, a joint workshop was conducted with Sheep Genomics, MLA, CSIRO, Beef CRC and several patent attorneys to examine the issues around IP protection of whole genome scan data and develop a common approach aimed at maximising uptake of DNA markers across the beef and sheep industries. Since then, Beef CRC has worked closely with its new international genomics partners to develop an IP management position with respect to DNA markers. The collaborating organizations in Australia and North America have agreed the overall aim is entirely to provide greater benefits to their respective beef industries. All project decisions will therefore be made on the potential benefit to industry, not on returns to research provider organizations or commercialising companies.

It was therefore agreed that all project IP would be jointly owned by the collaborating organisations. But it will not be patented because it is impractical to patent large numbers of markers that individually have little value. Results could be kept as trade secrets. But that discourages further research to extend, validate or repudiate the findings. Hence, the project results will be published and no attempt made to protect them. Early publication of project results in high-quality, peer-reviewed scientific journals will provide transparency and increase industry and scientific confidence in the DNA markers, with the preferred approach being to publish initially by country, then collaborate on across-country publications.

Commercialising companies will have sufficient access to results to warrant their investments in further developing the technologies for market-readiness (e.g. they might be provided with prediction equations that apply specifically to one country or a particular region or production-marketing system within one country).

Each collaborating organisation will have the right to pursue further research based on the results and to own the IP developed. Traits available only to one organization or one country will be exempt from the collaboration and could still be licensed exclusively by that organization. Causative mutations will also be exempt, as they will most likely be identified by single research groups in one country.

Background IP will remain the property of the organisation that currently owns it. For instance, the partners will each retain exclusive access to their own databases of phenotypes and stored DNA, although the results from the collaborative project will be jointly owned. These arrangements protect Australia's position, because control of existing IP is retained and there is complete freedom to use project IP for further research and commercial licensing in Australia.

As indicated above, these approaches to IP management are designed entirely to maximise benefits to Australia, New Zealand and the international partner countries by:

- significantly increasing end-user confidence in the value of the DNA markers in their own beef businesses through scientific peer review, public scrutiny and transparency about the size of effect of the markers on the traits of interest;
- generating competition amongst the genotyping companies to reduce the cost of commercial DNA testing by creating a high-volume, low-cost genotyping market (in Australia, genotyping is currently delivered via a monopoly situation); and
- generating competition amongst the genetic service providers to ensure industry has best access to advice about the range of different applications of DNA markers in their beef businesses.

## PATENTS AND SPIN-OFF COMPANIES

A provisional patent was taken out for MQ4 meat quality markers developed in Program 1 in September 2006 (Australian Provisional Patent Application No 2006905196 for Meat Quality Markers). The provisional patent was re-filed in September 2007 to ensure protection whilst further research on the DNA markers was undertaken. Now that agreement has been reached around the international genomics collaboration and placing the DNA markers in the public domain, this provisional patent will be allowed to lapse. No other patents are maintained by Beef CRC Ltd. Earlier Beef CRC IP is maintained by the previous partner organisations and has been licensed into CRCIII as Background IP.

Beef CRC has no spin-off companies.

# Research Collaborations

## NEW COLLABORATIONS

In Year 3, a major new international genomics partnership was developed between the US Department of Agriculture (USDA), the Canadian Universities of Guelph and Alberta, US National Beef Cattle Evaluation Consortium (NBCEC), AgResearch New Zealand and Beef CRC to undertake collaborative research and delivery to industry in five specific areas:

- Discovery of DNA markers and their validation;
- Validation of existing DNA markers;
- Development of new resource populations, coordinated across countries;
- Methods for delivering DNA markers to industry; and
- Development of larger SNP panels to assist with DNA marker discovery.

A March 2008 joint Board Meeting of the Beef CRC and MLA Boards unanimously approved the collaborations. The US and Canadian partners formally approved the collaborations in April 2008. Although New Zealand will not undertake DNA marker discovery activities in the next 2-3 years, it will contribute by providing access to New Zealand cattle resources that have been measured for the traits of interest. Once the collaborative model has been fully implemented the collaborations will be opened to other participants or countries, including the DNA marker commercialisation companies such as Merial and Pfizer, assuming they can work with the agreed collaborative model.

Each partner organisation will fund its own research within the collaboration. Initially each organisation will use existing funding. But in future, funding applications coordinated across countries will also be prepared to support the collaborations. Early publication of results in peer-reviewed scientific journals will provide transparency and increase industry and commercialiser confidence in the results. The preferred approach is to publish initially by country, then collaborate on across-country publications.

The agreed aim of the proposed collaborations is entirely to provide greater benefits to the beef industries of the collaborating countries (i.e. recommendations are being made on the basis of value-add to industry, not on potential returns to the research provider organisations or the commercialising companies). Hence there are unlikely to be patent claims over the traits that are researched collaboratively. Traits available only to one organisation or country will be exempt from the collaboration and can still be exclusively licensed. Causative mutations will also be exempt from this type of approach, as they will most likely be identified by single research groups. For instance, after joint results are shared, one organisation could fine map and attempt to identify a particular QTL without necessarily collaborating with the other organisations.

By sharing results across countries and agreeing on confirmation and validation of a common panel of markers, the impact will:

- significantly increase the accuracy of the estimated markers' effects and the accuracy with which breeding values can be estimated by a panel of markers, thereby greatly enhancing industry confidence in their use;
- at least halve the time it would otherwise take to complete these phases and have sufficient confidence that the results are useful to industry;
- provide additional information about the value of the markers in different environments (i.e. GxE) that would not otherwise be available to any country in the absence of the collaboration;
- help to close the "phenotype gap" through new cattle resources, especially for traits where current resources are inadequate e.g. health traits and feed intake;
- lead to adoption of better and more uniform methods in all countries resulting from shared research on methodology and industry structure to deliver marker assisted EPDs/EBVs;
- lead to panels of markers that can be used to predict breeding values across breeds as a result of the availability of a 200-300K SNP chip; and
- Possibly increase funding as a result of more powerful projects to put to funding agencies.

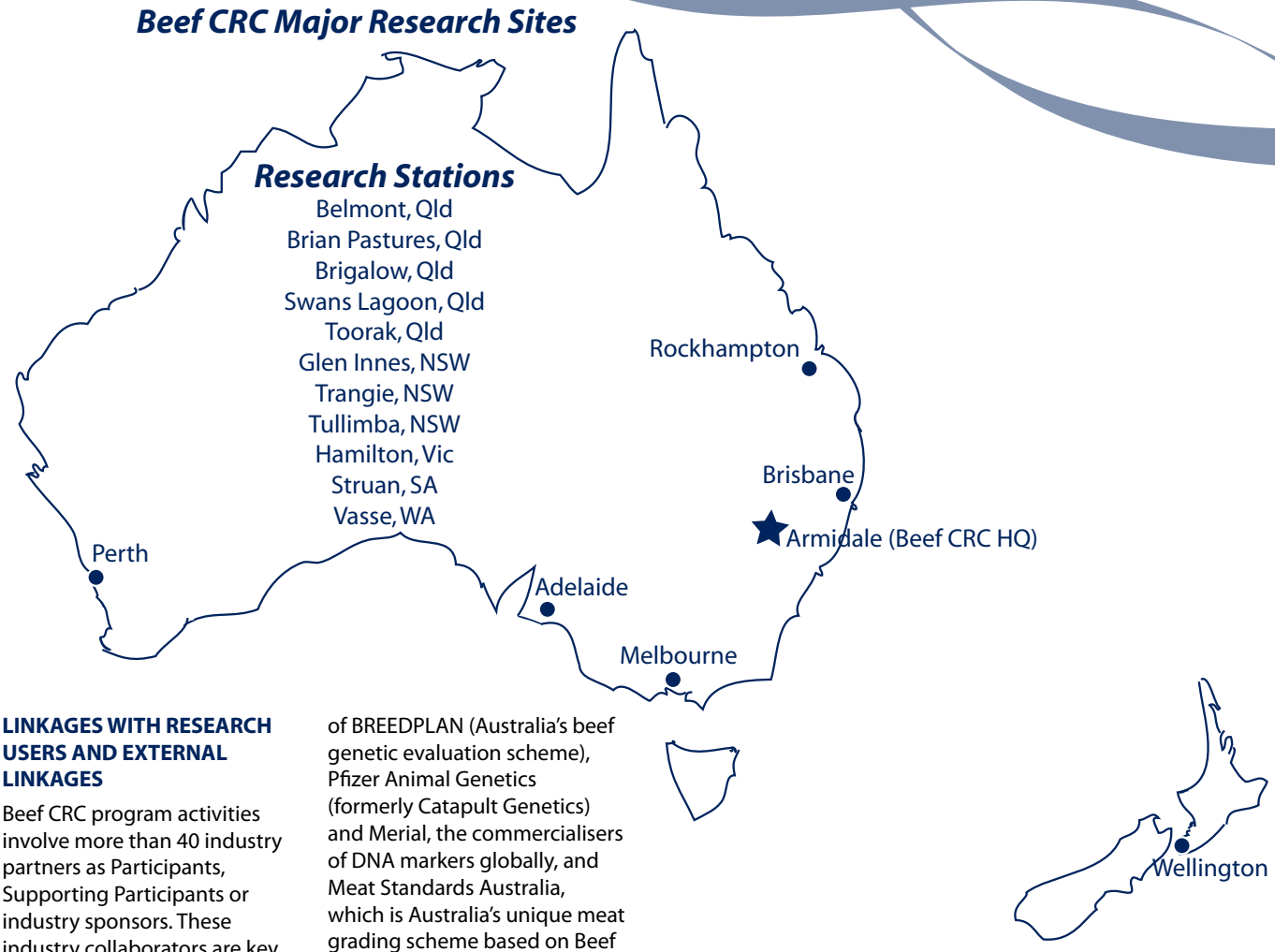
## COLLABORATIVE LINKAGES WITHIN THE CRC ACROSS ALL ACTIVITIES

Collaborative elements of the Beef CRC's research programs are illustrated in the diagrams below. The CRC's programs and projects cut across both site (see map) and institutional barriers and have linkages within and across programs. There are no serious constraints imposed by institutional boundaries. The Underpinning Science Program is linked to all research programs and provides across-program linkage in the coordination of research and sharing of genomics resources. The Education and Training

Program is also linked to all research programs and serves a similar role across programs in the provision of education, awareness and accelerated adoption services. Each of the projects undertaken in 2007/08 involved research undertaken at several locations and with staff from at least three participant organisations.

Over Year 3, the level of integration across all programs significantly improved relative to Years 1 and 2 with respect to both research and "path to adoption" strategies. The management-level Underpinning Science Committee continues to achieve strong collaborative linkages across the CRC's gene discovery and gene expression projects, using shared approaches and ready information-sharing. This integration is particularly evident through the combined analyses of 10K and 50K SNP data, under Professor Mike Goddard's leadership. In Year 3, the poorly-functioning Commercialisation and Adoption Committee was replaced, with Board agreement, by a number of "product teams" for each of the Beef CRC's products described in the CRC's "path to adoption" document. Each "product team" comprises a product champion and, depending on the nature of the product, a number of people with specialist expertise and interest in IP commercialisation, technical development, industry awareness and uptake of technology and/or communication. The product team is responsible for interacting with the product developers on a regular basis and for development of the commercialisation plan for that product. This approach is proving to be more effective at integrating CRC researchers with appropriate industry delivery specialists than previous efforts through the Commercialisation and Adoption Committee.

| P1<br>High Quality Beef | P2<br>Feed Efficiency and Responsible Resource Use | P3<br>Adaptation and Cattle Welfare | P4<br>Female Reproduction |
|---|---|---|---|
| **National Network Sites** | **National Network Sites** | **National Network Site** | **National Network Sites** |
| Brisbane, Qld<br>Glen Innes, NSW<br>Armidale, NSW<br>Melbourne, Vic<br>Adelaide, SA<br>Perth, WA<br>Vasse, WA | Traingie, NSW<br>Struan, SA<br>Vasse, WA<br>Melbourne, Vic<br>Camden, NSW<br>Adelaide, SA<br>Armidale, NSW<br>Hamilton Vic<br>Brisbane, Qld | Rockhampton, Qld<br>Brisbane, Qld<br>Armidale, NSW<br>Melbourne, Vic | Rockhampton, Qld<br>Brisbane, Qld<br>Millaroo, Qld<br>Gayndah, Qld<br>Julia Creek, Qld<br>Theordore, Qld<br>Armidale, NSW |
| **End-User Linkages** | **End-User Linkages** | **End-User Linkages** | **End-User Linkages** |
| ALFA Feedlots<br>Catapult Genetics<br>ABRI<br>Beef Improvement Assoc<br>John Dee Warwick P/L<br>Aust. Country Choice<br>Rockdale Beef P/L<br>Harvey Beef<br>Meat Standards Australia | Angus Society<br>Catapult Genetics<br>ABRI<br>Beef Improvement Assoc<br>Durham Shorthorn R&D Program | Catapult Genetics<br>ABRI<br>Northern Pastoral Group<br>Sheep Genomics<br>Beef Improvement Assoc | AgForce Qld<br>Northern Pastoral Group<br>Catapult Genetics<br>ABRI<br>Beef Improvement Assoc |




**LINKAGES WITH RESEARCH USERS AND EXTERNAL LINKAGES**

Beef CRC program activities involve more than 40 industry partners as Participants, Supporting Participants or industry sponsors. These industry collaborators are key partners in the development and implementation of the CRC's research, education and adoption strategies. For example, the CRC's research projects include breeding cows from industry herds that are used to generate specifically-designed experimental progeny to underpin research activities in the CRC's research programs. A strong feature of Beef CRC research is the very effective and close collaboration with private sector cattle businesses. Strong relationships also exist with the commercialising companies including deliverers of BREEDPLAN (Australia's beef genetic evaluation scheme), Pfizer Animal Genetics (formerly Catapult Genetics) and Merial, the commercialisers of DNA markers globally, and Meat Standards Australia, which is Australia's unique meat grading scheme based on Beef CRCI science that guarantees the eating quality of beef.

Beef CRC also collaborates with the Sheep CRC in a range of areas including running a shared post-graduate education program and a joint Livestock Library project. The Beef and Sheep CRCs share headquarters at UNE and are developing new areas of collaboration around industry adoption and economic impact assessment. Beef CRC continues to collaborate with SheepGenomics in the area of bioinformatics, particularly as applied to whole genome scan data.

# Glossary

| Abbreviation | Definition |
|---|---|
| ABRI | Agricultural Business Research Institute - based at UNE, ABRI provides a wide range of agribusiness information services, including delivery of BREEDPLAN |
| ACIAR | Australian Centre for International Agricultural Research, an Australian research funding agency that uses Australian research capacity to solve agricultural research problems in developing countries. |
| adipocytes | The cells that make up fat or adipose tissues |
| adipogenesis | The cellular developmental process that leads to fat |
| AGBU | Animal Genetics and Breeding Unit - based at University of New England (UNE), AGBU is a joint venture of UNE and NSW Department of Primary Industries |
| ALFA | Australian Lot Feeders' Association represents feedlots in Australia at every level, as the industry's national peak body |
| allele | One variant of a gene |
| ARC | Australian Research Council |
| AUS-MEAT | AUS-MEAT Limited is responsible for establishing and maintaining National Industry Standards for Meat Production and Processing. |
| Beef-N-omics | A decision support system developed by NSW DPI for southern beef production systems which combines herd dynamics, pasture availability and gross margin budgets |
| bioinformatics | The computational and mathematical backgrounds to modern biology and genomics; bioinformaticians can be database specialists, statisticians and/or computer programmers |
| biopsy | Removal and examination of tissue, cells or fluids from the living body |
| Bos indicus | Breeds of cattle originating from the Indian sub-continent; sometimes called Zebu breeds and includes Brahman and Sahiwal. |
| Bos taurus | Temperate British and European breeds of cattle e.g. Hereford, Angus, Charolais |
| BREEDOBJECT | A computer software package used to derive beef breeding objectives by weighting traits in the selection program for their relative economic values |
| BREEDPLAN | Australian's beef genetic evaluation system that estimates the genetic merit of animals for economically important traits |
| calpain | Calcium activated proteases believed to be important in the initial stages of breakdown of structural proteins in muscle. |
| candidate gene | Gene that is thought to be directly involved in a particular cell's, tissue's or animal's characteristics. |
| CCA | Cattle Council of Australia, the peak producer organisation representing Australia's beef cattle producers |
| cDNA | "Complementary DNA", a DNA molecule derived from RNA by the use of the enzyme reverse transcriptase; in this form, the molecule can be cloned and sequenced |
| cDNA library | A collection of cloned cDNAs |

| Abbreviation | Definition |
|---|---|
| cDNA microarray | An ordered array of thousands of cDNA inserts, printed as probes on a glass microscope slide |
| cloning | In context of tissue culture, establishment of a cell line from a single cell |
| cohort | See Management Group |
| collagen | An insoluble fibrous protein that occurs in vertebrates as the chief constituent of the fibrils of connective tissue and of the organic substance of bones |
| composite | A breed resulting from the matings of two or more existing breeds and animals are selected from within the progeny to continue the breed (e.g. Belmont Red, Santa Gertrudis) |
| confirmation | Confirming the significance and existence of an association between a DNA marker and an economically important trait in a totally independent cattle population. Beef CRC will confirm in at least 1,000 animals that are measured for the trait of interest and that are totally unrelated to the animals in the discovery population. |
| confounding | To correctly evaluate the performance of animals, all factors influencing performance must be able to be measured. Confounding occurs when some of the factors are not independent of others. For example, if all progeny of a sire are reared in the same paddock without representative progeny of other sires, then confounding of sire and paddock occurs and neither the effect of the sire nor the effect of the paddock can be determined. Confounding can be total (as in the above example) or it can be partial, where for example, only progeny of some sires may receive favourable treatment such as supplementary feeding because they are performing poorly relative to others under dry seasonal conditions |
| connective tissue | The sinuous material that runs between muscle cells and binds them together; in the concentrated and cooked form, it is the gristle in meat |
| CRC | Cooperative Research Centre |
| crossbreeding | Mating system in which two or more straight breeds are combined |
| CSIRO | Commonwealth Scientific and Industrial Research Organisation |
| discovery | The discovery phase of DNA markers occurs when an association between a DNA marker and an economically important trait is first identified in a population of cattle that has been accurately measured for the trait of interest. Beef CRC will undertake its discovery phase in at least 1,000 animals. |
| DNA | Deoxyribonucleic acid - contains the genetic information that is passed from one generation of animals to the next. It is a long double-stranded molecule made up of nucleotides A,T, G and C. |
| DNA fingerprinting | A method of determining the parentage of animals using DNA extracted from samples such as blood or tissue obtained from the animals. Each animal has a unique genetic makeup (DNA fingerprint). By comparing the DNA fingerprint of progeny with potential parents, it is possible to determine actual parentage. |
| DNA marker | DNA markers - stretches of DNA closely linked to the genes that underlie an economically important trait. They are used to detect different forms of genes. Tests based on DNA markers are used to predict the breeding performance (genotype) or the lifetime performance (phenotype) of animals for the particular traits. They use a wide range of tissue samples such as blood, skin, hair or muscle collected at any age after conception. |
| DPI | Department of Primary Industries |
| dressing percentage | Ratio of carcase weight to pre-slaughter live weight |
| EBV | Estimated Breeding Value – an estimate of an animal's genetic value for measurable traits such as growth rate, meat tenderness etc. EBVs are calculated from the measured performance of animals and their close relatives compared to other animals measured in an identical way. |
| EBVm | See MA-EBV |
| EMA | Eye muscle area |
| EST | 'Expressed sequence tag', a short (several hundred bases) nucleotide sequence derived from one end of a cDNA close; usually serves to determine the likely identity of the cDNA clone |
| expression profiling | The use of microarrays to study the gene expression profile of a particular tissue or cell |
| flight time | A measure of temperament in animals, it is the electronically recorded time taken (in tenths of a second) for an animal to cover a fixed distance (1.7 – 2.2 metres) after leaving a weighing crush |
| GxE | Genotype x environment interaction - GxE interactions occur when a breed or DNA marker (genotype) ranks differently in different environments e.g. British breed cattle grow well but Bos indicus breeds grow relatively poorly in temperate environments. In tropical environments, where levels of environmental stress are high, better adapted Bos indicus breeds grow much faster than British breeds. This same scenario could occur when DNA markers rank differently in different environments. |
| gene | The basic unit of heredity. Each gene has two or more forms which can be the same or different. |

| Abbreviation | Definition |
|---|---|
| gene expression | The process by which a gene code is transcribed into messenger RNA and exported to the nucleus for translation into proteins. Beef CRC uses this term to describe research aimed at understanding the function of the genes associated with expression of economically important genes and identifying non-genetic approaches (for example, changed management practices, modified diets, water medications, vaccines etc) that can be used to 'switch on' favourable genes or 'switch off' unfavourable genes in cattle where the form of the gene has been identified, so the cattle can be individually managed to better comply with market specifications. |
| gene marker | See DNA marker. |
| genetic correlation | Extent to which two attributes are determined by the same genes. Genetic correlations range from -1.0 to +1.0. A high negative relationship means an increase in one trait leads to a decrease in the other; a high positive relationship indicates an increase in one trait leads to an increase in the other trait. A low or zero correlation indicates there is little genetic relationship between the two traits. |
| genomic selection | Simultaneous selection for hundreds or thousands of DNA markers covering the entire bovine genome with the markers alone accounting for a significant proportion of the targeted genetic variation (i.e. selection will be based only on knowledge of the markers in the absence of pedigree and phenotypic selection as required to calculate MA-EBVs) |
| genotype | Genetic makeup of an animal, but is also sometimes used to indicate the breed composition of an animal. |
| heritability | Proportion of variation for a measurable trait attributable to variation in genetic factors and is therefore passed on to offspring. Heritabilities (h2) range from 0.0 to 1.0. A h2 = 0 means the trait is not controlled by genetic factors and h2 = 1.0 means the trait is under total genetic control. In general, traits that have h2 > 0.4 are considered to be highly heritable. |
| HGP | Hormonal growth promotant |
| homeostasis | The processes that keep a mammalian body metabolically stable in terms of temperature, energy supply, waste removal etc. |
| IGF-1 | Insulin-like growth factor 1, a factor that can be measured in blood and is associated with feed efficiency and fatness traits |
| IMF% | Intra-muscular fat percentage or fat within the muscle (marbling is a visually-assessed score of intramuscular fat) |
| inbreeding | A mating system in which mates are more closely related than average individuals of the population to which they belong |
| in vitro | Literally "in glass" and it refers to experiments that mimic life in a test tube or by tissue culture. |
| in vivo | Examining the reactions of life by experimentation with the living animal. |
| link sire | To validly compare the performance of animals across herds, it is necessary for those herds to be genetically linked. The usual method for linking these herds is to use a common (or link) sire in all herds where performance of animals is to be compared. |
| management group | A management group comprises a group of animals receiving identical treatment for the duration of the evaluation. For BREEDPLAN evaluations, this means that animals are born in the same paddock over the same time period and are exposed to the same management routines (supplementary feeding, weaning times etc.) throughout the period of the evaluation |
| metabolism | Processes of synthesis, degradation and transformation that occur within living organisms, and are responsible for all functions of that organism |
| microarray | An ordered array of thousands of gene probes, printed onto glass slides. |
| microsatellite | A genetic marker that is highly polymorphic, that is it has many alleles. |
| MA-EBV | Marker-assisted EBV – an estimated breeding value calculated using pedigrees and phenotypes for direct and indirect selection traits) and also DNA marker information |
| MLA | Meat and Livestock Australia a beef-industry owned company with responsibility for red meat industry R&D and for promotion and marketing of red meat within Australia and internationally |
| molecular techniques | Laboratory procedures that allow a researcher to investigate a scientific problem at the level of individual molecules. The term normally refers to nucleic acid techniques but is equally valid for protein techniques. |
| MSA | Meat Standards Australia, Australia's new meat grading scheme based on guaranteed beef eating quality |
| NFI | Net Feed Intake - a measure of feed efficiency that refers to variation in feed intake between animals after differences due to weight and growth rate have been accounted for. Low (more negative) NFI is desirable. |
| NPG | Northern Pastoral Group of Companies, a loose alliance of major pastoral companies operating in northern Australia |

| Abbreviation | Definition |
|---|---|
| ossification score | A visual scoring system to describe the development of bone in the bovine, and utilising the progression of calcification in the vertebrae. It is used to estimate maturity of the carcass. |
| P8 fat thickness | Fat thickness in mm recorded at the P8 rump site |
| PCR | Polymerase chain reaction, a technique to amplify DNA strands and used as a diagnostic tool to detect the presence of particular genetic sequences e.g. to identify a particular bacteria or a virulence factor in a bacteria |
| pH | pH value of meat sample calculated as the mean of 4 measurements using a probe-type combined electrode (normal values 5.5 to 5.7) |
| phenotype | The appearance, structure or biochemical characteristics of an organism, contrasted against genotype, which refers to sequences within the DNA. In the context of discovery of DNA markers, it means the accurately measured record of an animal for a particular trait of interest. |
| polymorphic | Having many forms. In this context, the term refers to multiple forms of a gene that lead to slight but measurable variation in phenotype. Also relates to the various forms in which fat crystallizes |
| polymorphism | The situation where more than one allele or variant of a gene is found in a population |
| quantitative real time PCR (qRT-PCR) | A technique that allows quantification of extremely low amounts of nucleic acid: both RNA and DNA |
| QTL | Quantitative Trait Loci – stretches of DNA that are closely linked to the genes that underlie an economically important trait (see DNA marker) |
| RBY% | Retail beef yield percentage – is generally referred to when carcasses are boned out to commercial standards and trim. RBY% - saleable meat divided by cold carcass weight multiplied by 100. |
| RNA | Ribonucleic acid, the string of nucleotides (usually single-stranded) that is "transcribed" from DNA |
| Sanga | Adapted Bos taurus breeds that evolved in Southern Africa independent of the European Bos taurus. They retain the productive attributes of the European Bos taurus but have resistance closer to that of the Bos indicus |
| sequencing | DNA, RNA, protein or oligosaccharide structure determination |
| shear force | An objective measure of meat toughness, measured as the force required to sever the muscle fibres of a meat sample (measured in kgs, with the higher the value, the tougher the meat) |
| SNP | Single nucleotide polymorphism. A polymorphism at a specific base or nucleotide in the DNA sequence. For instance, at a point in the DNA sequence where one allele contains an 'A', another allele contains a 'T' |
| supply chain | Enterprises acting in concert to improve the economies of specific activities. The relationship may include alliances to vertically or horizontally integrated individuals in (a) sector(s) of the beef industry |
| trait | Attribute or characteristic of animals that can be improved genetically (for example, growth rate, fertility, carcase or meat quality etc.) |
| UNE | University of New England |
| USDA | United States Department of Agriculture |
| validation | Validation of DNA markers occurs after the discovery and confirmation phases, when prediction equations from those phases are tested independently in another set of cattle that have been measured for the trait. Where possible, Beef CRC plans to use at least 5,000 animals to validate the prediction equations to provide an unbiased estimate of the correlation between prediction and breeding value or phenotype. |

# Education and Training

## Education and Training


*Emily Piper (right) at the Early Career Scientist Award presentation with Bernie Hobbs, ABC Science*

# Education and Training

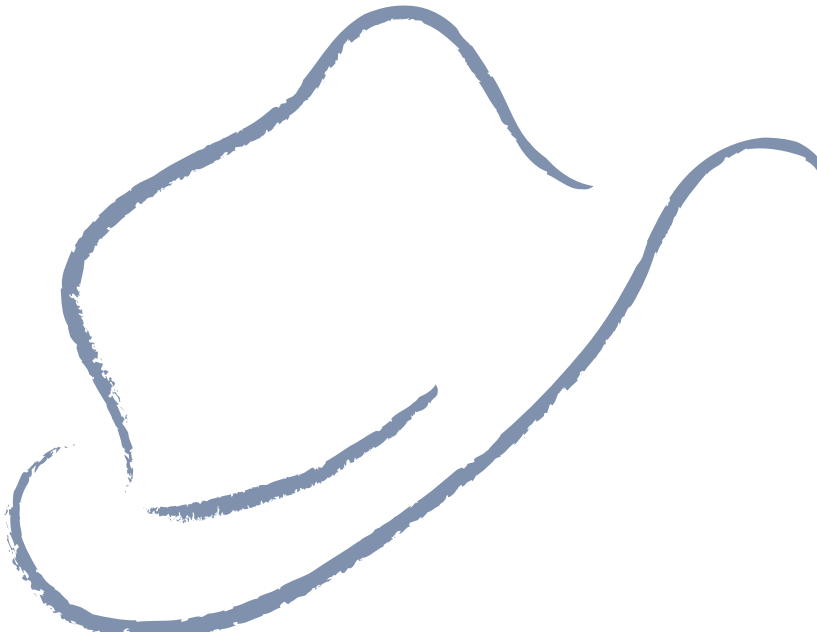
The purpose of the education and training program is to produce a skilled beef industry workforce as a consequence of postgraduate, undergraduate and vocational training in the sciences underpinning beef genetic improvement and effective innovation, commercialisation and adoption of outputs to meet beef industry outcomes.

There are currently 36 students enrolled in the Beef CRC's postgraduate project with one student having completed his PhD and another having withdrawn (Table 1). This is in excess of whole-of-CRC projections. The high level of student enrolments (while maintaining the budget within its projected limits) has been achieved largely through a high success rate of students securing University Postgraduate and Australian Postgraduate Awards. All students applying for CRC scholarships are encouraged to apply for these awards, with Beef CRC then providing a top-up scholarship to increase their overall stipend. This approach has paid a handsome dividend through greater than expected student numbers.

A postgraduate conference run in conjunction with the Sheep CRC was held at the QDPI conference centre on Bribie Island (Brisbane) in October 2007. All students presented either 15 minute seminars (2nd and 3rd year students) or posters (1st year category only). Beef CRC students were successful, with Emily Piper coming second in the overall category for best presentation and abstract and Brendon O'Rourke coming 3rd. Following the conference, Russell Barnett presented a workshop on adoption science and the approach to restructuring research to enhance adoption. This workshop was well received by all students.

Subsequently, Emily Piper and Brendon O'Rourke were invited to participate as Beef CRC representatives in the CRC Association postgraduate student competition. Emily was selected to present a three-minute talk without visual aids at the national CRC Association Conference, where she was awarded a prestigious Early Career Scientist award.

All milestones for the 2007/08 financial year have been completed and exceeded with a total of 36 students currently enrolled, all doing PhD's except 3 students enrolled in Masters degrees. A projected round of scholarship offers, scheduled for June 2008, is no longer necessary to meet our student intake quota. However a final round of scholarship offers will occur in December 2008 to ensure outstanding postgraduate students are given a further opportunity to study through Beef CRC.



| Name | Uni of enrolment | Course | Completion Status | Short thesis description | Principal Supervisor | Other Supervisors | Stipend Funding Source | Graduate Employment Destination |
|---|---|---|---|---|---|---|---|---|
| Ainu Husna M S Suhaimi | University of Queensland | PhD | In progress | Post-partum anoestrus in cows: gene expression profiling of the preoptic area and hypothalamus | Dr Sigrid Lehnert | Prof. Michael D'Occhio | 50% Malaysia(MARDI ) Scholarship | MARDI, Malaysia |
| Alastair Rayner | University of Queensland | Masters | In progress | An investigation into methods of achieving accelerated adoption of emerging technologies within beef supply chains | Dr Don Cameron | Mr Bill McKiernan | Beef-n-omics (CRC & NSW DPI) | NSW DPI |
| Andrew Doljanin | University of New England | Masters in Economics | In progress | Estimation of economic weights for carcase traits | Prof. John Thompson | Dr Garry Griffith | 100% Beef CRC | Polkinghornes / Oxhill Past Co |
| Andrew Egarr | University of Adelaide | PhD | In Progress | The molecular genetics of fat deposition in cattle | Prof. Cindy Bottema | A/Prof. Wayne Pitchford | University and CRC top up | |
| Andrew Slacksmith | University of New England | Masters | In progress | Production and processing validation to optimise beef supply chain yield and quality and optimising supply chain economic efficiency. | Dr Garry Griffith | Prof. John Thompson | 100% Beef CRC | |
| Baldwin Nengovhela | University of Queensland | PhD | In Progress | Improving the wellbeing of people dependent on the low income beef industry of South Africa | Prof. Bob Beaton | | ACIAR & ARC-South Africa | ARC-South Africa |
| Brendon O'Rourke | University of Melbourne | PhD | In Progress | Muscling in beef cattle: a molecular investigation | Prof. Mike Goddard | Dr Paul Arthur, A/Prof. Paul Greenwood | $25,000 MLA, $3000 Beef CRC | NSW DPI |
| Bron Bevan | University of Queensland | PhD | In Progress | Investigation of fat distribution in cattle | Dr Yonghong Wang | Dr Simon Quigley, A/Prof. Dennis Poppi, Prof. David Pethick | UQPRS with Beef CRC top up | |
| Chantal Coles | University of Melbourne | PhD | In progress | The role of intra and extracellular metalloproteases involved in muscle development and marbling in beef | Dr Matthew McDonagh | Dr Jason White | 100% Beef CRC | |
| Dannielle Hulett | University of Melbourne | PhD | In Progress | Identification of DNA markers associated with beef cattle feed efficiency. | Prof. Mike Goddard | Prof Brian Leury, Dr Helen McPartlan, Dr Ben Hayes, Dr Brendan Tatham | Melbourne Uni and Beef CRC | |
| David Lines | University of Adelaide | PhD | In Progress | Protein turnover in beef cattle | A/Prof Wayne Pitchford | Prof. Cynthia Bottema | Beef CRC | |

| Name | Uni of enrolment | Course | Completion Status | Short thesis description | Principal Supervisor | Other Supervisors | Stipend Funding Source | Graduate Employment Destination |
|---|---|---|---|---|---|---|---|---|
| Emily Piper | University of Queensland | PhD | In Progress | Changes in immune responses and gene expression of tick resistant versus susceptible cattle. | A/Prof Nicholas Jonnson | Dr Louise Jackson | 100% Beef CRC | |
| Hayley Moreland | University of Queensland | PhD | In Progress | Facilitating uptake of productivity-enhancing technologies within beef supply chains - an action research approach | Dr Don Cameron | Prof. Paul Hyland | 100% Beef CRC | |
| Heidi Rodgers | University of New England | PhD | In Progress | The economics of quality differentials in beef | Dr Garry Griffith | Prof. Euan Fleming | 100% Beef CRC | |
| Jessica Mayes | University of Queensland | PhD | In Progress | Early-life predictors of the fertility of tropically adapted beef bulls | Prof. Michael McGowan | Dr. Richard Holroyd | 100% MLA | |
| Kirsty Moore | University of New England | PhD | In Progress | Using DNA technologies in Australian beef cattle breeding | Dr David Johnston | Prof. John Gibson | 100% MLA | |
| Klara Verbyla | University of Melbourne | PhD | In Progress | Genomic selection: development and implementation in beef cattle | Prof. Mike Goddard | | Beef CRC | |
| Linda Cafe | University of New England | PhD | In Progress | Cattle temperament and stress-responsiveness in relation to productivity, efficiency and beef quality | Prof. Paul Greenwood | Dr Drewe Ferguson | Beef CRC & NSW DPI | |
| Maree Storer | University of Queensland | PhD | In Progress | The impact of genetic technology on innovation in pharmaceutical and nutraceutical supply chains | Prof. Andrew Griffiths | Prof. Paul Hyland | Beef CRC | |
| Matt Wolcott | University of New England | PhD (part time) | In Progress | Genetic parameters of female fertility and marbling in bos indicus cattle. | Dr David Johnston | | AGBU employee | |
| Michael Laurence | Murdoch University | PhD | In Progress | Maternal productivity investigation in beef cattle. | Prof. Anne Barnes | Prof. Dave Pethick, Dr Jeisane Accioly | 100% Beef CRC | |
| Nadia de Jager | University of Queensland | PhD | In Progress | Meat tenderness studies in beef | Dr Yonghong Wang | A/Prof. Ross Barnard | Beef CRC | |
| Peter McGilchrist | Murdoch University | PhD | In Progress | Physiological responses of beef cattle to gene markers and Estimated Breeding Values for muscling and marbling | Dr Graham Gardner | Dr Paul Greenwood, Prof. David Pethick, Dr David Millar | Murdoch CPA, Beef CRC top-up | |

| Name | Uni of enrolment | Course | Completion Status | Short thesis description | Principal Supervisor | Other Supervisors | Stipend Funding Source | Graduate Employment Destination |
|---|---|---|---|---|---|---|---|---|
| Sebastian Kurscheid | Murdoch University | PhD | In Progress | Identification of novel tick therapeutic targets | Prof. Matthew Bellgard | Dr Ala Lew-Tabor | 100% Beef CRC | |
| Seung Hwan Lee | University of New England | PhD | In progress | Functional genomics study for discovering genes to regulate marbling in cattle. | Prof. John Gibson | Profs. Julius van der Werf and John Thompson | 100% Beef CRC | |
| Sophia Butler | University of Queensland | PhD | In Progress | Expression of genes associated with postpartum re-conception in tropically adapted parity one cows | Prof. Michael McGowan | Prof. Michael D'Occhio | Beef CRC | |
| Tricia Finch | University of Queensland | PhD | Withdrawn | Developing assays for acaricide resistance in Boophilus Microplus | A/ Prof. Nicholas Jonnson | Dr Shelly Hope | 100% Beef CRC | |
| Emilio Morales | University of New England | PhD | In Progress | Promoting innovation in the Australian beef marketing system | Prof. Euan Fleming | Dr. Garry Griffith and Dr. Vic Wright | Beef CRC | |
| Percy Madzivandila | University of New England | PhD | In Progress | Designing an effective evaluation model for the South African Department of Agriculture | Dr. Garry Griffith | Prof. Euan Fleming | ACIAR & ARC-South Africa | ARC-South Africa |
| Madan Naik | University of Adelaide | PhD | Completed | Identification and characterization of genetic markers and metabolic pathways controlling net feed efficiency in beef cattle | Prof. Cindy Bottema | A/Prof Wayne Pitchford | University & Beef CRC | |
| Irida Novianti | University of Adelaide | Masters | In Progress | Molecular genetics of cattle body conformation | Prof. Cindy Bottema | A/Prof. Wayne Pitchford | University & Beef CRC | |
| Nadia Zulkifi | University of Adelaide | PhD | In Progress | Molecular genetics of net feed efficiency and mitochondrial function in cattle | Prof. Cindy Bottema | A/Prof Wayne Pitchford | Aus-Aid and Beef CRC | |
| LeiYao Chang | University of Adelaide | PhD | In Progress | Localisation and characterisation of genes affecting beef tenderness | Prof. Cindy Bottema | A/Prof. Wayne Pitchford | University & Beef CRC | |
| Stephanie Sinclair | University of Queensland | PhD | In Progress | The behavioural and physiological responses of horned, dehorned and polled Bos indicus cattle | Dr Kishore Prayaga | Dr Carol Petherick; Prof. Michael McGowan; Prof. Clive Phillips | 100% Beef CRC | |
| Stephen Lee | University of Adelaide | PhD | In Progress | Maternal productivity in beef cattle: An interdisciplinary approach | A/Prof. Wayne Pitchford | Dr Ian Nuberg | Beef CRC | |

| Name | Uni of enrolment | Course | Completion Status | Short thesis description | Principal Supervisor | Other Supervisors | Stipend Funding Source | Graduate Employment Destination |
|---|---|---|---|---|---|---|---|---|
| Sarah Truran | University of Adelaide | PhD | In Progress | Genetic by environmental interactions in body composition and maternal productivity in beef cattle | A/Prof. Wayne Pitchford | Prof. Ari Verbyla, Dr Michelle Hebart | Beef CRC | |
| Laercio Porto-Neto | University of Queensland | PhD | In Progress | Identification of a functional mutation associated with tick burden in cattle | Prof Michael D'Occhio | A/Prof Nick Jonsson, Dr Bill Barendse | UQ(IPRS) & Beef CRC | |
| Daowei Sun | University of Queensland | PhD | In Progress | Systems approaches towards enhancing continuous improvement and innovation in the beef industry | Prof. Kambiz Maani | Prof. Ockie Bosch and Prof. Paul Hyland | 100% Beef CRC | |

# Technology Transfer



Relationships between Beef CRC's separate, but well integrated, projects aimed at providing vocational education and training and awareness, communication and accelerated adoption are shown diagrammatically below.

### "AWARENESS"

The overall aim of the "Awareness" project is to distil and deliver research outputs and/or innovations to increase awareness and understanding of Beef CRC products by beef businesses. The Awareness Project gained significant momentum during 2007/08. Milestones and budget for this project are on track. The Awareness team has been increasingly integrated with all aspects of Beef CRC and is involved in the preparation of the awareness components for the "Path to Adoption" product areas, including documentation and implementation of a product development process. Many CRC staff involved in "Awareness" activities are also involved in Project 5.4's "Beef Profit Partnership" (BPP) network, ensuring consistent delivery as well as distilling key messages from research outputs that are ready for adoption by the BPP network and other end-users.

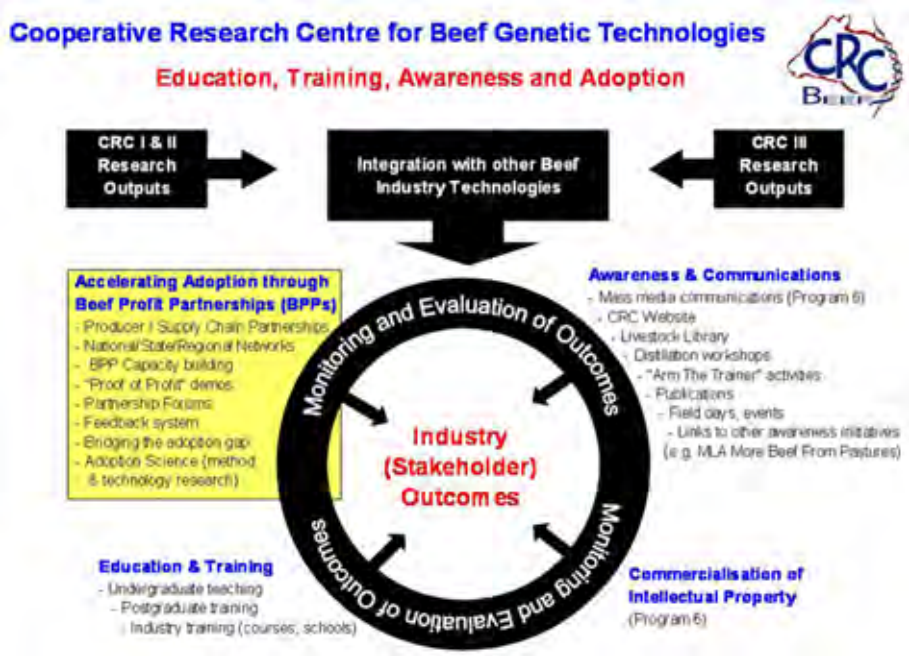
Key achievements during 2007/08 include:

### Beef CRC Website

The web is an important communication tool for Beef CRC's internal and external stakeholders. There were 84 changes, additions and uploads to the Beef CRC website over Year 3. The Beef CRC website underwent modifications and upgrades of software this year, with the addition of a new file management tool for "re:fract", an auditing search engine to collect more accurate statistics on website usage and software to enable a decrease in page loading times. The CRC website is updated with information including beef industry events, media releases, fact sheets, publications and research results. It is also being used as a tool to expand the CRC's contacts database. Visitors have the opportunity to register their details to receive regular Beef CRC updates. From 1 July 2008, management of the website will be transferred to the Communications Project 6.4 and a major upgrade will occur under its auspices. Plans are underway to re-launch the website with a new look and more interactive feel to increase the CRC's exposure in Australia and around the world.

### Livestock Library

There is a large volume of livestock production research and extension published in recent decades. While this information is still highly relevant to today's livestock industries and is generally held in the public domain, the material is often difficult to access. On-line access to this information will assist producers, technology transfer specialists, students or researchers to gain additional skills and knowledge and to make more informed decisions. There has been a concerted effort over the past 12 months to make the Livestock Library accessible to even more people. A federated search function was incorporated in November 2007 to allow users to search a range of selected livestock production websites. The addition of the federated search function has increased the number of documents that can be accessed through the Livestock Library from 22,000 to over 60,000. Users gain simultaneous access to



each state Department of Agriculture, Meat and Livestock Australia, Australian Wool Innovation (AWI) and the Beef and Sheep CRC websites. More than 2,000 industry publications and records have been added to the Livestock Library in the period from 1 July 2007 to 30 June 2008. Discussions have been held with Australian Agriculture and Natural Resources Online (AANRO) to pursue options for them assuming responsibility for the Livestock Library in future.

**Distillation**

A key achievement has been the distillation of information from the "Regional Combinations" and "Growth Paths" CRCII projects. PowerPoint presentations and supporting material were developed and piloted by extension staff and this material has been made available to extension officers and industry via the Beef CRC website, training and a CD of the material. Distillation activities involved representatives from MLA, the BPP network and the Beef CRC Board as well as key extension and research staff from WA, NSW, Vic and SA. Involvement of a broad cross-section of industry and extension personnel means the benefits of integrating new information and products into beef businesses can be confidently articulated.

**Training**

A "Train the Trainer" workshop was held in Wagga Wagga, NSW on 27-28 May 2008. Approximately 55 private and public sector participants and CRC researchers from across Australia and New Zealand attended. The workshop provided in-depth training on CRCII's "Growth Paths" and "Regional Combinations" outputs. An online survey has been developed and will be conducted each quarter to track the use of material from the training workshop by participants.

**Delivery**

Publications - Development of material from Beef CRC is occurring at an accelerating rate. Numerous documents and visual aids were developed this year including 37 written articles, 21 PowerPoint presentations, 20 fact sheets and the booklet "Science for Quality Beef", which has had 6000 hard copies printed and distributed and has been uploaded to the Beef CRC Website to enable electronic access.

CRC Awareness workshops and events - There were 68 Beef CRC field days and workshops conducted across Australia and New Zealand during 2007/08. These were supplemented by presentations at industry meetings, conferences and with other programs (e.g. Meat and Livestock Australia's More Beef from Pastures (MBfP)). Direct participant feedback and surveys independently conducted for MLA clearly demonstrate delivery of information in this format is an effective method to increase the understanding and awareness of Beef CRC outputs. Participants who attended CRC events during 2007/08 were surveyed to gauge the effectiveness and enable continuous improvement of these events.

Sponsorship of Events - The Awareness Project provided funds for two events to assist the groups to organise and run specialised workshops and/or courses. In 2007/08 funds were provided for the Feeder Steer School and the Ebor Beef Group Stakeholders' Forum. Approximately 200-250 people attended these sponsored events.

**"ACCELERATED ADOPTION"**

The Beef CRC's "Accelerated Adoption" project 5.4 has established a network of "Beef Profit Partnerships" (BPPs) among beef businesses across Australia and New Zealand designed to achieve and accelerate improvements and innovations for sustainable impact on business profit and industry growth. The initial focus is to demonstrate achievement of an additional 5% average improvement in annual profitability of BPP participants. Three target outcomes contribute to achieving this focus: (i) rapid and measurable improvements among partners in productivity, profit and growth; (ii) a supportive network of rewarding partnerships, contributing to accelerated industry growth; and (iii) partners equipped to achieve sustainable improvement and innovation. The key difference in the adoption strategy being implemented by this project is an emphasis on the use of industry partnerships focused on achieving continuous innovation, instead of simply relying on broad communication and awareness activities. The Continuous Improvement and Innovation (CI&I) process used in the project involves rapid cycles of focus, design, action, measurement, evaluation and re-focus (Figure 5.4.1).

The CI&I process has been implemented successfully in other sectors of the economy, especially in manufacturing. However, the approach has not been widely applied in the agricultural sector, especially in developed economies. It is anticipated the development

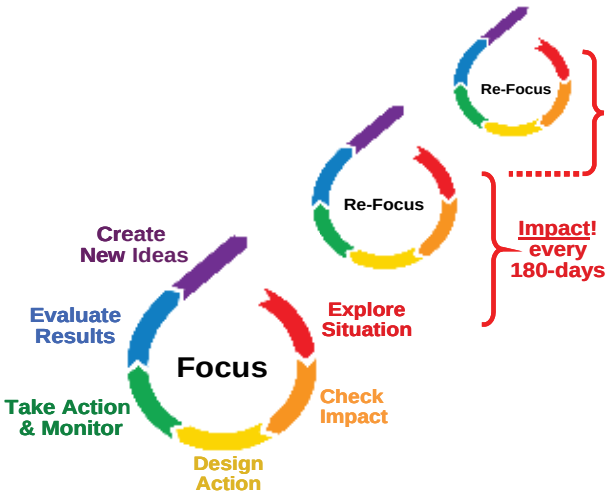



*Figure 5.4.1. The Continuous Improvement and Innovation (CI&I) process, designed to achieve measurable impacts every 180-days.*

of a supportive culture for innovation across the BPP network will contribute to the development of an industry environment that will accelerate the transformation and integration of Beef CRC-derived technology into beef businesses, as well as enhancing the adoption of other relevant technologies and business tools. An important objective of the project is to build the necessary capacity for the partnership network to become self-sustaining and to continue to contribute to industry innovation and improvement beyond the life of the Beef CRC.

In June, 2008 there were 33 effective BPPs, involving 349 businesses across Australia and New Zealand. In addition, new partnerships are under development, including large beef businesses from the corporate sector and some private sector sponsored BPPs. Several unsuccessful BPPs established during the early stages of the project have been discontinued. They were based on previous groups with different roles and they had difficulty measuring, monitoring and reporting in line with expectations of BPPs, a major difficulty experienced by many agricultural enterprises throughout Australia, regardless of sector. Figure 5.4.2 shows the extent of the BPP network as at June 2008.

Many BPP partners have already implemented practice changes as part of their improvement and innovation focus. However, data are not yet available from the BPP network to enable an evaluation against the project's target outcomes or to enable an analysis of aggregated project outcomes. This has been at least partially due to the need to achieve a paradigm shift amongst many facilitators and partners in accepting the role of measurement, monitoring and evaluation as a critical component of CI&I. This is being addressed by providing further capacity-building opportunities and support in implementing CI&I in individual businesses and partnerships. Initial results indicate success in establishing a supportive partnership network involving beef businesses in Australia and NZ. Work is still underway to evaluate the effectiveness of this strategy to accelerate the process of innovation and to achieve improved profitability in the beef industry.

A "Bridging the Innovation Gaps" Workshop was conducted in March 2008 to identify priority actions in relation to innovation and adoption of new technologies, and their role in industry development; to explore issues and gaps in relation to innovation and adoption of new technologies, and why they exist; and to identify high impact opportunities and mechanisms to bridge the priority gaps. Key factors and high impact opportunities identified at the workshop to accelerate innovation in the beef industry included:

- Better understanding and quantifiable measurement of the key components of innovation systems;
- Addressing culture, leadership and people;
- Identifying and assessing technologies and potential innovations against specific market needs, to identify gaps and opportunities and then use this to increase the adoption of existing innovations / technologies;
- Establishing "Value-Networks" in the beef industry;
- Developing an "Innovation Framework" for the beef industry;
- Focusing on innovation skills development; and,
- Opening up sources of innovation from outside the industry.

Beef CRC is currently addressing most of these factors through its BPP processes.




*Figure 5.4.2. Extent of Beef Profit Partnerships (BPP) network, June 2008.*

*Bill Hoffman, Technical Specialist, Beef Breeding, NSW DPI explains the latest CRC research to a group of Beef Profit Partnership participants*

# Publications

# Publications



## JOURNAL PAPERS AND BOOK CHAPTERS

Attwood, G.T. and McSweeney, C.S. (2008). Methanogen genomics to discover targets for methane mitigation technologies and options for alternative H2 utilisation in the rumen. Australian Journal of Experimental Agriculture. 48: 28-37.

Barendse, W., Bunch, R.J., Kijas, J.W. and Thomas, M.B. (2007) The effect of genetic variation of the retinoic acid receptor-related orphan receptor C gene on fatness in cattle. Genetics 175, 843-853.

Barendse, W., Harrison, B.E., Hawken, R.J., Ferguson, D.M., Thompson, J.M., Thomas, M.B., Bunch, R.J. (2007) Epistasis between calpain 1 and its inhibitor calpastatin within breeds of cattle. Genetics, 176:2601-2610.

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## PATENT

Barendse, W. Meat quality markers. PTC Provisional Patent 769490 (2005 – current)

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# Financial Report

# Financial Report


## Cooperative Research Centre for Beef Genetic Technologies

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The Directors of the Company declare that:

1. The Cooperative Research Centre Program grant monies received by the Company have been expended solely upon the activities of the CRC and in accordance with the Commonwealth Agreement.

2. The information contained in the attached financial tables:
   (a) gives a true and fair view of the sources and applications of funding of the CRC for the year ended 30 June 2008; and
   (b) gives a true and fair view of the financial position as at 30 June 2008; and
   (c) has been prepared in accordance with the requirements of the Commonwealth Agreement.

This declaration is made in accordance with a resolution of the Board of Directors and is signed for and on behalf of the Board by:

Dr Guy Fitzhardinge
**Chairman**

Dr Heather Burrow
**Chief Executive Officer**

## NOTES TO TABLES

### Table 1a – Staff in-kind contributions from Participants and Supporting Participants

- The "in-kind" contributions from the Participants and Supporting Participants are calculated as the "Full Time Equivalent" (FTE) based on the percentage of time staff worked on CRC projects.
- The Animal Genetics and Breeding Unit (AGBU), based at the University of New England, is funded jointly by the NSW Department of Primary Industries and the University of New England. The "in-kind" contributions from AGBU have been split between NSW Department of Primary Industries and the University of New England on a 50:50 basis.
- Due to changes in experimental procedures SASTEK Pty Ltd will not become a Supporting Participant or contributor to the CRC. The budgeted in-kind contribution of SASTEK Pty Ltd has been made up by the other Participants.
- Catapult Genetics Pty Ltd (formerly Genetic Solutions Pty Ltd) will not become a Supporting Participant of the CRC. However, the budgeted in-kind staff contributions have been made up by the other participants.
- The projected in-kind contributions reflect the fact that Participants are expected to contribute staff to the CRC in line with the Commonwealth agreement over the next five years.

### Table 1b – Non-staff in-kind contributions from Participants and Supporting Participants

- The non-staff in-kind contributions include overheads associated with Participant and Supporting Participant staff contributions to the CRC and the estimated cost of facilities utilised by the CRC. The amounts disclosed are estimated and reported to the CRC by Participants and Supporting Participants in accordance with the terms of their Participants Agreements.
- Northern Pastoral Group non-staff in-kinds are now being contributed as cash contributions to the CRC on a reimbursement of expenditure basis associated with their experimental cattle maintained on Participant research stations.
- Catapult Genetics Pty Ltd (formerly Genetic Solutions Pty Ltd) will not become a Supporting Participant of the CRC. However, the budgeted non-staff in-kind contribution of Catapult Genetics Pty Ltd has been made up by the other Participants.
- Projected non-staff in-kind contributions are expected to be in line with the Commonwealth Agreement with the exception of the Northern Pastoral Group contribution.

### Table 2 – Participant Cash Contributions, Other Firm Cash and CRC Programme Funding

- The Participant Cash Contributions, Other Firm Cash and CRC Programme Funding table has been prepared on a cash basis and represents the funds received by the company from all sources.
- Due to the take over of Sygen International by Genus Ltd, Sygen will no longer become a Supporting Participant of the Beef CRC. Genus Ltd has a significantly reduced focus on research and development and it has been agreed that areas of mutual co-investment in Research and Development are not available. The budgeted cash contribution of Sygen International has been made up by other Participants.
- The "Other Cash Resources" of $1.4 million comprised: GST received of $1.0 million, ACIAR grant of $0.1 million, Queensland State Development Grant of $0.1 million, interest income of $0.1 million and other income of $0.1 million. In order to balance Participants' Cash Contributions, Other Firm Cash and CRC Programme to the total receipts in the quarterly cash flow reports submitted to DIISR, other Cash Resources includes GST received.
- The Meat and Livestock Australia and Australian Lot Feeders' Association cash contributions are gross contributions and include contributions funded from industry levies and matching Government funds. In the Commonwealth Agreement the Meat and Livestock Australia and Australian Lot Feeders' Association matching Government funds of $500k and $60k respectively are shown as "Other Cash Resources".
- Projected cash contributions are expected to be in line with the Commonwealth Agreement with the exception of Sygen International.

### Table 3 – Expenses

- The Expenses table has been prepared on an accruals basis.
- The Tullimba Cattle Research (Feedlot) Facility income and expenditure have been netted off within the financial tables to be consistent with the treatment of the facility in the Commonwealth Agreement where income earned by the facility is viewed as a reduction in the project cost for using the facility.
- The 2008-09 projected expenses are based on the year four operational plan which was approved by the Board in the June 2008 Board meeting. The 2009 to 2012 projections are expected to be in line with the Commonwealth Agreement.

### Table 4 – Capital Items

- The Capital Items table has been prepared on a cash basis.
- There were no Capital Assets greater than $20,000 acquired during the year.
- Due to the rapid technological developments in the genomics area, the Company has elected to outsource whole genome scans in Years 1, 2 and 3 in lieu of capital purchases that could become redundant quickly. The Company may need to reconsider its capital expenditure in future years and purchase the capital equipment then. The projected capital expenditure reflects this outsourcing approach.

### Table 5 – Allocation of Resources

- The Allocation of Resources table has been prepared on an accruals basis and the Tullimba Cattle Research (Feedlot) Facility income and expenditure have been netted off within the table.
- The projections are in line with the projections in tables 1a, 1b and 3.

ROBERTS & MORROW
CHARTERED ACCOUNTANTS

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**AUDITORS REPORT TO THE CO-OPERATIVE RESEARCH CENTRES PROGRAM DEPARTMENT OF INNOVATION, INDUSTRY, SCIENCE AND RESEARCH**

**REPRESENTING THE COMMONWEALTH IN RESPECT OF THE CRC FOR BEEF GENETIC TECHNOLOGIES**

**FINANCIAL INFORMATION FOR YEAR ENDED 30 JUNE 2008**

## SCOPE

***Report on the Financial Report***

The Financial Report and Director's Responsibilities
We have audited the financial report being a special purpose report of the CRC for Beef Genetic Technologies comprising Tables 1(a) - Number of Staff (FTE); 1(b) - Total Non Staff In-Kind; 2 - Participants' Cash Contributions, Other Firm Cash, CRC Programme Funding; 3 – Expenditure; 4 - Capital Items and notes to the tables for the year ended 30 June 2008.

***The Responsibility of Director's***

The Directors' of Beef CRC Limited are responsible for the preparation and fair presentation of the financial report and have determined that the accounting policies are appropriate to meet the financial reporting requirements of the Department of Innovation, Industry, Science and Research. The Directors' responsibility also includes designing, implementing and maintaining internal controls relevant to the preparation and fair presentation of the financial report that is free from material misstatement, whether due to fraud or error; selecting and applying appropriate accounting policies; and making accounting estimates that are reasonable in the circumstances.

***Auditor's Responsibility***

Our responsibility is to express an opinion on the financial report based on our audit. No opinion is expressed as to whether the accounting policies used are appropriate to meet the needs of the members. We conducted our audit in accordance with Australian Auditing Standards. These Auditing Standards require that we comply with relevant ethical requirements relating to audit engagements and to plan and perform the audit to obtain reasonable assurance as to whether the financial report is free from material misstatement.

An audit involves performing procedures to obtain audit evidence about the amounts and disclosures in the financial report. The procedures selected depend on the auditor's judgement, including the assessment of the risks of material misstatement of the financial report, whether due to fraud or error. In making those risk assessments, the auditor considers internal controls relevant to the entity's preparation and fair presentation of the financial report in order to design audit procedures that are appropriate in the circumstances, but not for the purpose of expressing an opinion on the effectiveness of the entity's internal controls. An audit also includes evaluating the appropriateness of accounting policies used and the reasonableness of accounting estimates made by the Directors, as well as evaluating the overall presentation of the financial report.

The financial report has been prepared for the Co-operative Research Centres Program, Department of Innovation, Industry, Science and Research, representing the Commonwealth of Australia for the purpose of fulfilling the Beef CRC Limited's reporting obligations under clause 14.3(vii) of the Commonwealth Agreement. We disclaim any responsibility for any reliance on this report or on the financial information to which it relates to any person other than those mentioned above or for any purpose other than for which it was prepared.

We believe that the audit evidence we have obtained is sufficient and appropriate to provide a basis for our audit opinion.





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***Independence***

In conducting our audit, we have complied with the independence requirements of the Australian professional accounting bodies.

**AUDIT OPINION**

In our opinion, the financial information presented in Tables 1(a) - Number of Staff (FTE); 1(b) - Total Non Staff In-Kind; 2 - Participants' Cash Contributions, Other Firm Cash, CRC Programme Funding; 3 – Expenditure; and 4 - Capital Items presents fairly the sources of funding, the application of funding, and the financial position of the CRC for Beef Genetic Technologies for the year ended 30 June 2008 in accordance with Australian Accounting Standards and the requirements of the Commonwealth Agreement in terms of Clauses 5 (Contributions), 6(1), 6(2) (a) (b) (c) (d)& (e), (Application of Grant and Contributions), and 8 (Accounting for Commonwealth Funding and Contributions). Specifically;

1. Each Researcher's Contribution for the year under report has been provided, on a cumulative basis, at least to the value for the year committed in the Budget as specified in Schedule 3 to the Agreement, with the exceptions on the following page.
2. The Researchers have used the Commonwealth Grant and the Participants' and Supporting Participants' contributions for the activities of the Centre as set out in Schedule 3 to the Commonwealth Agreement and in my professional opinion there appear to be no material reporting irregularities.
3. No capital items as defined by Clause 6.2 (d) of the Commonwealth Agreement were purchased during the current financial year.
4. The CRC has exercised proper accounting standards and controls. The income and expenditure in relation to the Activities are recorded separately from the other transactions of the Company. The cash contributions have been paid into and expended from the CRC's account in accordance with Clause 8 to the Commonwealth Agreement. Tables 1, 2, 3 & 4 have been completed in accordance with the basis of preparation as outlined in the Notes to the Tables.
5. After having regard to the internal controls it is concluded that the Commonwealth Funding and the contributions from Participants and supporting participants have been expended solely for the activities in accordance with Schedule 3 of the Commonwealth Agreement. All CRC transactions have been conducted through the account and the all interest on the balance of the account has been credited to the account.
6. In accordance with Clause 13.4 of the Participants' Agreement each participant is responsible for keeping separate documentation that records each non-cash Contribution. In relation to the audit of Table 1(b) Total Non- Staff In-Kind the scope of our audit testing has been limited to the information supplied by each participant to the Company in accordance with Clause 13.4 of the Participants' Agreement. The Company has reported the information in this table based upon the information supplied to it by each Participant.
7. Table 5, Allocation of Resources, allocates Expenses, Non-Staff In-Kind. In-Kind-Staff (FTE) across each of the programmes. We have ensured that this table reconciles with the information as supplied in Tables 1 to 4 and is mechanically accurate but do not provide an opinion on the allocation of resources to the various programmes as this is considered by ourselves and the Board of Directors to be outside the scope of this audit.





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| | Cumulative Basis 2006 to 2008 Financial Years | | | | | |
|---|---|---|---|---|---|---|
| **Participant** | **Amount Committed Cash & Non -Staff In-Kind** | **Amount Contributed Cash & Non- Staff In-Kind** | **Variance To Amount Committed** | **Amount Committed Staff In-Kind** | **Amount Contributed Staff In-Kind** | **Variance To Amount Committed** |
| | **$'000** | **$'000** | **$'000** | **FTE** | **FTE** | FTE |
| Department of Primary Industries and Resources South Australia | 1,418 | 927 | (491) | 8.1 | 5.7 | (2.4) |
| Department of Primary Industries Victoria | 774 | 464 | (310) | - | - | - |
| Meat and Wool New Zealand | - | - | - | 1.2 | 0.8 | (0.4) |
| The University of Queensland | 2,076 | 1,416 | (660) | 9.3 | 4.3 | (5.0) |
| University of Adelaide | - | - | - | 6.0 | 4.3 | (1.7) |
| University of New England | 2,247 | 2,237 | (10) | 15.9 | 11.2 | (4.7) |
| Dept of Agriculture and Food WA | - | - | - | 14.4 | 8.8 | (5.6) |
| Catapult Genetics Pty Ltd (Formerly Genetic Solutions) | 225 | - | (225) | 2.4 | 0.0 | (2.4) |
| Murdoch University | - | - | - | 9.9 | 4.3 | (5.6) |
| National Livestock Research Institute, Korea | - | - | - | 6.6 | 2.7 | (3.9) |
| SASTEK Pty Ltd | - | - | - | 0.6 | 0.0 | (0.6) |
| Sygen International | 112 | - | (112) | - | - | - |
| The Ohio State University, USA | - | - | - | 6.0 | 2.1 | (3.9) |

It should be noted that the above table shows the exceptions only against the Commonwealth Agreement on a cumulative basis for the 2006 to 2008 financial years.

ROBERTS & MORROW
**Chartered Accountants**

Michelle A Paull
Partner
23rd September 2008
137 Beardy Street
ARMIDALE NSW 2350

*Table 1a: Financial Information / Number of Staff (FTE; 0.0)*

| | Actual | | | | | | | | | Projected | | | | | | | | Totals to 2007-08 | | | Totals for 7 years | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | 2005-06 | | | 2006-07 | | | 2007-08 | | | 2008-09 | | 2009-10 | | 2010-11 | | 2011-12 | | | | | | | |
| | Actual | Agr'mt | Diff | Actual | Agr'mt | Diff | Actual | Agr'mt | Diff | Projected | Agr'mt | Projected | Agr'mt | Projected | Agr'mt | Projected | Agr'mt | Actual | Agr'mt | Diff | ctual/Pr | Agr'mt | Diff |
| **CORE PARTICIPANTS** | | | | | | | | | | | | | | | | | | | | | | | |
| **Department of Primary Industries and Resources SA** | | | | | | | | | | | | | | | | | | | | | | | |
| Programme Leader/Senior Manager | 0.1 | - | 0.1 | - | - | - | 0.1 | 0.0 | 0.1 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.2 | 0.0 | 0.2 | 0.2 | 0.0 | 0.2 |
| Key Researcher/Manager | - | 0.1 | - 0.1 | - | 0.1 | - 0.1 | 0.0 | 0.1 | -0.1 | 0.1 | 0.1 | 0.1 | 0.1 | 0.1 | 0.1 | 0.1 | 0.1 | 0.0 | 0.3 | -0.3 | 0.4 | 0.7 | -0.3 |
| Researcher/Professional | 1.2 | 1.6 | - 0.4 | 1.1 | 1.6 | - 0.5 | 2.6 | 1.6 | 1.0 | 1.6 | 1.6 | 1.6 | 1.6 | 1.6 | 1.6 | 1.6 | 1.6 | 4.9 | 4.8 | 0.1 | 11.3 | 11.2 | 0.1 |
| Support Staff | - | 1.0 | - 1.0 | 0.1 | 1.0 | - 0.9 | 0.5 | 1.0 | -0.5 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 0.6 | 3.0 | -2.4 | 4.6 | 7.0 | -2.4 |
| **TOTAL** | 1.3 | 2.7 | - 1.4 | 1.2 | 2.7 | - 1.5 | 3.2 | 2.7 | 0.5 | 2.7 | 2.7 | 2.7 | 2.7 | 2.7 | 2.7 | 2.7 | 2.7 | 5.7 | 8.1 | -2.4 | 16.5 | 18.9 | -2.4 |
| **Department of Primary Industries Victoria** | | | | | | | | | | | | | | | | | | | | | | | |
| Programme Leader/Senior Manager | 0.3 | 0.9 | - 0.6 | 0.3 | 0.9 | - 0.6 | 0.1 | 0.9 | -0.8 | 0.9 | 0.9 | 0.9 | 0.9 | 0.9 | 0.9 | 0.9 | 0.9 | 0.7 | 2.7 | -2.0 | 4.3 | 6.3 | -2.0 |
| Key Researcher/Manager | - | 1.6 | - 1.6 | 0.2 | 1.6 | - 1.4 | 0.4 | 1.6 | -1.2 | 1.6 | 1.6 | 1.6 | 1.6 | 1.6 | 1.6 | 1.6 | 1.6 | 0.6 | 4.8 | -4.2 | 7.0 | 11.2 | -4.2 |
| Researcher/Professional | 2.6 | 0.7 | 1.9 | 2.6 | 0.7 | 1.9 | 3.1 | 0.7 | 2.4 | 0.7 | 0.7 | 0.7 | 0.6 | 0.7 | 0.6 | 0.7 | 0.6 | 8.3 | 2.1 | 6.2 | 11.1 | 4.6 | 6.5 |
| Support Staff | 0.6 | - | 0.6 | 0.5 | - | 0.5 | 0.5 | 0.0 | 0.5 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 1.6 | 0.0 | 1.6 | 1.6 | 0.0 | 1.6 |
| **TOTAL** | 3.5 | 3.2 | 0.3 | 3.6 | 3.2 | 0.4 | 4.1 | 3.2 | 0.9 | 3.2 | 3.2 | 3.2 | 3.1 | 3.2 | 3.1 | 3.2 | 3.1 | 11.2 | 9.6 | 1.6 | 24.0 | 22.1 | 1.8 |
| **Dept of Primary Industries and Fisheries (QLD)** | | | | | | | | | | | | | | | | | | | | | | | |
| Programme Leader/Senior Manager | 0.6 | 0.3 | 0.3 | 0.3 | 0.3 | - | 0.0 | 0.3 | -0.3 | 0.3 | 0.3 | 0.3 | 0.3 | 0.3 | 0.3 | 0.3 | 0.3 | 0.9 | 0.9 | 0.0 | 2.1 | 2.1 | 0.0 |
| Key Researcher/Manager | 2.5 | 1.9 | 0.6 | 1.8 | 1.9 | - 0.1 | 2.6 | 1.9 | 0.7 | 1.9 | 1.9 | 1.9 | 1.9 | 1.9 | 1.9 | 1.9 | 1.9 | 6.9 | 5.7 | 1.2 | 14.5 | 13.3 | 1.2 |
| Researcher/Professional | 11.2 | 3.3 | 7.9 | 7.5 | 3.3 | 4.2 | 6.7 | 3.3 | 3.4 | 3.3 | 3.3 | 3.3 | 3.2 | 3.3 | 3.2 | 3.3 | 3.2 | 25.4 | 9.9 | 15.5 | 38.6 | 22.8 | 15.8 |
| Support Staff | 3.2 | - | 3.2 | 4.1 | - | 4.1 | 6.1 | 0.0 | 6.1 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 13.4 | 0.0 | 13.4 | 13.4 | 0.0 | 13.4 |
| **TOTAL** | 17.5 | 5.5 | 12.0 | 13.7 | 5.5 | 8.2 | 15.4 | 5.5 | 9.9 | 5.5 | 5.5 | 5.5 | 5.4 | 5.5 | 5.4 | 5.5 | 5.4 | 46.6 | 16.5 | 30.1 | 68.6 | 38.2 | 30.4 |
| **Meat & Livestock Australia Limited** | | | | | | | | | | | | | | | | | | | | | | | |
| Programme Leader/Senior Manager | - | - | - | - | - | - | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| Key Researcher/Manager | - | - | - | - | - | - | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| Researcher/Professional | - | - | - | - | - | - | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| Support Staff | - | - | - | - | - | - | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| **TOTAL** | - | - | - | - | - | - | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| **Meat and Wool New Zealand** | | | | | | | | | | | | | | | | | | | | | | | |
| Programme Leader/Senior Manager | 0.1 | - | 0.1 | - | - | - | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.1 | 0.0 | 0.1 | 0.1 | 0.0 | 0.1 |
| Key Researcher/Manager | 0.3 | - | 0.3 | 0.2 | - | 0.2 | 0.2 | 0.0 | 0.2 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.7 | 0.0 | 0.7 | 0.7 | 0.0 | 0.7 |
| Researcher/Professional | - | 0.4 | - 0.4 | - | 0.4 | - 0.4 | 0.0 | 0.4 | -0.4 | 0.4 | 0.4 | 0.4 | 0.4 | 0.4 | 0.4 | 0.4 | 0.4 | 0.0 | 1.2 | -1.2 | 1.6 | 2.8 | -1.2 |
| Support Staff | - | - | - | - | - | - | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| **TOTAL** | 0.4 | 0.4 | - | 0.2 | 0.4 | - 0.2 | 0.2 | 0.4 | -0.2 | 0.4 | 0.4 | 0.4 | 0.4 | 0.4 | 0.4 | 0.4 | 0.4 | 0.8 | 1.2 | -0.4 | 2.4 | 2.8 | -0.4 |
| **NSW Department of Primary Industries** | | | | | | | | | | | | | | | | | | | | | | | |
| Programme Leader/Senior Manager | 0.1 | 0.4 | - 0.3 | 0.1 | 0.4 | - 0.3 | 0.1 | 0.4 | -0.3 | 0.4 | 0.4 | 0.4 | 0.4 | 0.4 | 0.4 | 0.4 | 0.4 | 0.3 | 1.2 | -0.9 | 1.9 | 2.8 | -0.9 |
| Key Researcher/Manager | 1.5 | 2.1 | - 0.6 | 2.0 | 2.1 | - 0.1 | 3.9 | 2.1 | 1.8 | 2.1 | 2.1 | 2.1 | 2.1 | 2.1 | 2.1 | 2.1 | 2.1 | 7.4 | 6.3 | 1.1 | 15.8 | 14.7 | 1.1 |
| Researcher/Professional | 8.1 | 3.5 | 4.6 | 7.5 | 3.5 | 4.0 | 4.0 | 3.5 | 0.5 | 3.5 | 3.5 | 3.5 | 3.5 | 3.5 | 3.5 | 3.5 | 3.5 | 19.6 | 10.5 | 9.1 | 33.6 | 24.5 | 9.1 |
| Support Staff | 3.0 | 0.2 | 2.8 | 5.8 | 0.2 | 5.6 | 5.6 | 0.2 | 5.4 | 0.2 | 0.2 | 0.2 | 0.2 | 0.2 | 0.2 | 0.2 | 0.2 | 14.4 | 0.6 | 13.8 | 15.2 | 1.4 | 13.8 |
| **TOTAL** | 12.7 | 6.2 | 6.5 | 15.4 | 6.2 | 9.2 | 13.6 | 6.2 | 7.4 | 6.2 | 6.2 | 6.2 | 6.2 | 6.2 | 6.2 | 6.2 | 6.2 | 41.7 | 18.6 | 23.1 | 66.5 | 43.4 | 23.1 |
| **The University of Adelaide** | | | | | | | | | | | | | | | | | | | | | | | |
| Programme Leader/Senior Manager | 0.6 | - | 0.6 | 0.6 | - | 0.6 | 0.5 | 0.0 | 0.5 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 1.7 | 0.0 | 1.7 | 1.7 | 0.0 | 1.7 |
| Key Researcher/Manager | - | 1.1 | - 1.1 | - | 1.1 | - 1.1 | 0.5 | 1.1 | -0.6 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 0.5 | 3.3 | -2.8 | 4.9 | 7.7 | -2.8 |
| Researcher/Professional | 1.3 | 0.9 | 0.4 | 0.5 | 0.9 | - 0.4 | 0.0 | 0.9 | -0.9 | 0.9 | 0.9 | 0.9 | 0.9 | 0.9 | 0.9 | 0.9 | 0.9 | 1.8 | 2.7 | -0.9 | 5.4 | 6.3 | -0.9 |
| Support Staff | 0.1 | - | 0.1 | 0.1 | - | 0.1 | 0.1 | 0.0 | 0.1 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.3 | 0.0 | 0.3 | 0.3 | 0.0 | 0.3 |
| **TOTAL** | 2.0 | 2.0 | - | 1.2 | 2.0 | - 0.8 | 1.1 | 2.0 | -0.9 | 2.0 | 2.0 | 2.0 | 2.0 | 2.0 | 2.0 | 2.0 | 2.0 | 4.3 | 6.0 | -1.7 | 12.3 | 14.0 | -1.7 |

*Table 1a: Financial Information / Number of Staff (FTE; 0.0) continued ...*

| | Actual | | | | | | | | | Projected | | | | | | | | Totals to 2007-08 | | | Totals for 7 years | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | 2005-06 | | | 2006-07 | | | 2007-08 | | | 2008-09 | | 2009-10 | | 2010-11 | | 2011-12 | | | | | | | |
| | Actual | Agr'mt | Diff | Actual | Agr'mt | Diff | Actual | Agr'mt | Diff | Projected | Agr'mt | Projected | Agr'mt | Projected | Agr'mt | Projected | Agr'mt | Actual | Agr'mt | Diff | ctual/Pr | Agr'mt | Diff |
| **The University of New England** | | | | | | | | | | | | | | | | | | | | | | | |
| Programme Leader/Senior Manager | 1.0 | 0.8 | 0.2 | 1.4 | 0.8 | 0.6 | 1.1 | 0.8 | 0.3 | 0.8 | 0.8 | 0.8 | 0.8 | 0.8 | 0.8 | 0.8 | 0.8 | 3.5 | 2.4 | 1.1 | 6.7 | 5.6 | 1.1 |
| Key Researcher/Manager | 0.6 | 1.4 | -0.8 | 0.7 | 1.4 | -0.7 | 0.6 | 1.4 | -0.8 | 1.4 | 1.4 | 1.4 | 1.4 | 1.4 | 1.4 | 1.4 | 1.4 | 1.9 | 4.2 | -2.3 | 7.5 | 9.8 | -2.3 |
| Researcher/Professional | 1.3 | 2.3 | -1.0 | 1.1 | 2.3 | -1.2 | 0.6 | 2.3 | -1.7 | 2.3 | 2.3 | 2.3 | 2.3 | 2.3 | 2.3 | 2.3 | 2.3 | 3.0 | 6.9 | -3.9 | 12.2 | 16.1 | -3.9 |
| Support Staff | 0.5 | 0.8 | -0.3 | 0.7 | 0.8 | -0.1 | 1.6 | 0.8 | 0.8 | 0.8 | 0.8 | 0.8 | 0.8 | 0.8 | 0.8 | 0.8 | 0.8 | 2.8 | 2.4 | 0.4 | 6.0 | 5.6 | 0.4 |
| **TOTAL** | 3.4 | 5.3 | -1.9 | 3.9 | 5.3 | -1.4 | 3.9 | 5.3 | -1.4 | 5.3 | 5.3 | 5.3 | 5.3 | 5.3 | 5.3 | 5.3 | 5.3 | 11.2 | 15.9 | -4.7 | 32.4 | 37.1 | -4.7 |
| **The University of Queensland** | | | | | | | | | | | | | | | | | | | | | | | |
| Programme Leader/Senior Manager | - | 0.1 | -0.1 | - | 0.1 | -0.1 | 0.0 | 0.1 | -0.1 | 0.1 | 0.1 | 0.1 | 0.1 | 0.1 | 0.1 | 0.1 | 0.1 | 0.0 | 0.3 | -0.3 | 0.4 | 0.7 | -0.3 |
| Key Researcher/Manager | 0.4 | 1.5 | -1.1 | 0.4 | 1.5 | -1.1 | 0.2 | 1.5 | -1.3 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.0 | 4.5 | -3.5 | 7.0 | 10.5 | -3.5 |
| Researcher/Professional | 0.5 | 1.5 | -1.0 | 0.8 | 1.5 | -0.7 | 1.8 | 1.5 | 0.3 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 3.1 | 4.5 | -1.4 | 9.1 | 10.5 | -1.4 |
| Support Staff | - | - | - | - | - | - | 0.2 | 0.0 | 0.2 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.2 | 0.0 | 0.2 | 0.2 | 0.0 | 0.2 |
| **TOTAL** | 0.9 | 3.1 | -2.2 | 1.2 | 3.1 | -1.9 | 2.2 | 3.1 | -1.0 | 3.1 | 3.1 | 3.1 | 3.1 | 3.1 | 3.1 | 3.1 | 3.1 | 4.3 | 9.3 | -5.1 | 16.7 | 21.7 | -5.1 |
| **CORE PARTICIPANTS TOTAL STAFF (FTE)** | | | | | | | | | | | | | | | | | | | | | | | |
| Programme Leader/Senior Manager | 2.8 | 2.5 | 0.3 | 2.7 | 2.5 | 0.2 | 2.0 | 2.5 | -0.5 | 2.5 | 2.5 | 2.5 | 2.5 | 2.5 | 2.5 | 2.5 | 2.5 | 7.5 | 7.5 | 0.0 | 17.5 | 17.5 | 0.0 |
| Key Researcher/Manager | 5.3 | 9.7 | -4.4 | 5.3 | 9.7 | -4.4 | 8.4 | 9.7 | -1.3 | 9.7 | 9.7 | 9.7 | 9.7 | 9.7 | 9.7 | 9.7 | 9.7 | 19.0 | 29.1 | -10.1 | 57.8 | 67.9 | -10.1 |
| Researcher/Professional | 26.2 | 14.2 | 12.0 | 21.1 | 14.2 | 6.9 | 18.8 | 14.2 | 4.6 | 14.2 | 14.2 | 14.2 | 14.0 | 14.2 | 14.0 | 14.2 | 14.0 | 66.1 | 42.6 | 23.5 | 122.9 | 98.8 | 24.1 |
| Support Staff | 7.4 | 2.0 | 5.4 | 11.3 | 2.0 | 9.3 | 14.5 | 2.0 | 12.5 | 2.0 | 2.0 | 2.0 | 2.0 | 2.0 | 2.0 | 2.0 | 2.0 | 33.2 | 6.0 | 27.2 | 41.2 | 14.0 | 27.2 |
| **TOTAL** | 41.7 | 28.4 | 13.3 | 40.4 | 28.4 | 12.0 | 43.7 | 28.4 | 15.3 | 28.4 | 28.4 | 28.4 | 28.2 | 28.4 | 28.2 | 28.4 | 28.2 | 125.8 | 85.2 | 40.6 | 239.4 | 198.2 | 41.2 |
| **SUPPORTING PARTICIPANTS** | | | | | | | | | | | | | | | | | | | | | | | |
| **Australian Lot Feeders Association** | | | | | | | | | | | | | | | | | | | | | | | |
| Programme Leader/Senior Manager | - | - | - | - | - | - | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| Key Researcher/Manager | - | - | - | - | - | - | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| Researcher/Professional | - | - | - | - | - | - | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| Support Staff | - | - | - | - | - | - | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| **TOTAL** | - | - | - | - | - | - | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| **Catapult Genetics Pty Limited (formerly Genetic Solutions Pty Ltd)** | | | | | | | | | | | | | | | | | | | | | | | |
| Programme Leader/Senior Manager | - | - | - | - | - | - | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| Key Researcher/Manager | - | 0.4 | -0.4 | - | 0.4 | -0.4 | 0.0 | 0.4 | -0.4 | 0.0 | 0.4 | 0.0 | 0.4 | 0.0 | 0.4 | 0.0 | 0.4 | 0.0 | 1.2 | -1.2 | 0.0 | 2.8 | -2.8 |
| Researcher/Professional | - | 0.4 | -0.4 | - | 0.4 | -0.4 | 0.0 | 0.4 | -0.4 | 0.0 | 0.4 | 0.0 | 0.4 | 0.0 | 0.4 | 0.0 | 0.4 | 0.0 | 1.2 | -1.2 | 0.0 | 2.8 | -2.8 |
| Support Staff | - | - | - | - | - | - | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| **TOTAL** | - | 0.8 | -0.8 | - | 0.8 | -0.8 | 0.0 | 0.8 | -0.8 | 0.0 | 0.8 | 0.0 | 0.8 | 0.0 | 0.8 | 0.0 | 0.8 | 0.0 | 2.4 | -2.4 | 0.0 | 5.6 | -5.6 |
| **CSIRO Livestock Industries** | | | | | | | | | | | | | | | | | | | | | | | |
| Programme Leader/Senior Manager | 0.6 | 1.1 | -0.5 | 0.7 | 1.1 | -0.4 | 1.0 | 1.1 | -0.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 2.3 | 3.3 | -1.0 | 6.7 | 7.7 | -1.0 |
| Key Researcher/Manager | 1.4 | 0.8 | 0.6 | 1.5 | 0.8 | 0.7 | 2.6 | 0.8 | 1.8 | 0.8 | 0.8 | 0.8 | 0.8 | 0.8 | 0.8 | 0.8 | 0.8 | 5.5 | 2.4 | 3.1 | 8.7 | 5.6 | 3.1 |
| Researcher/Professional | 1.5 | 1.9 | -0.4 | 2.8 | 1.9 | 0.9 | 0.9 | 1.9 | -1.0 | 1.9 | 1.9 | 1.9 | 1.9 | 1.9 | 1.9 | 1.9 | 1.9 | 5.2 | 5.7 | -0.5 | 12.8 | 13.3 | -0.5 |
| Support Staff | 1.8 | 1.0 | 0.8 | 1.9 | 1.0 | 0.9 | 2.5 | 1.0 | 1.5 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 6.2 | 3.0 | 3.2 | 10.2 | 7.0 | 3.2 |
| **TOTAL** | 5.3 | 4.8 | 0.5 | 6.9 | 4.8 | 2.1 | 7.0 | 4.8 | 2.2 | 4.8 | 4.8 | 4.8 | 4.8 | 4.8 | 4.8 | 4.8 | 4.8 | 19.2 | 14.4 | 4.8 | 38.4 | 33.6 | 4.8 |
| **Department of Agriculture and Food (formerlyWA Department of Agriculture)** | | | | | | | | | | | | | | | | | | | | | | | |
| Programme Leader/Senior Manager | - | - | - | - | - | - | 0.1 | 0.0 | 0.1 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.1 | 0.0 | 0.1 | 0.1 | 0.0 | 0.1 |
| Key Researcher/Manager | 1.2 | 1.7 | -0.5 | 0.8 | 1.7 | -0.9 | 0.6 | 1.7 | -1.1 | 1.7 | 1.7 | 1.7 | 1.7 | 1.7 | 1.7 | 1.7 | 1.7 | 2.6 | 5.1 | -2.5 | 9.4 | 11.9 | -2.5 |
| Researcher/Professional | 1.1 | 1.1 | - | 1.9 | 1.1 | 0.8 | 3.1 | 1.1 | 2.0 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 6.1 | 3.3 | 2.8 | 10.5 | 7.7 | 2.8 |
| Support Staff | - | 2.0 | -2.0 | - | 2.0 | -2.0 | 0.0 | 2.0 | -2.0 | 2.0 | 2.0 | 2.0 | 2.0 | 2.0 | 2.0 | 2.0 | 2.0 | 0.0 | 6.0 | -6.0 | 8.0 | 14.0 | -6.0 |
| **TOTAL** | 2.3 | 4.8 | -2.5 | 2.7 | 4.8 | -2.1 | 3.8 | 4.8 | -1.0 | 4.8 | 4.8 | 4.8 | 4.8 | 4.8 | 4.8 | 4.8 | 4.8 | 8.8 | 14.4 | -5.6 | 28.0 | 33.6 | -5.6 |
| **Murdoch University** | | | | | | | | | | | | | | | | | | | | | | | |
| Programme Leader/Senior Manager | 0.4 | 0.7 | -0.3 | 0.3 | 0.7 | -0.4 | 0.3 | 0.7 | -0.4 | 0.7 | 0.7 | 0.7 | 0.7 | 0.7 | 0.7 | 0.7 | 0.7 | 1.0 | 2.1 | -1.1 | 3.8 | 4.9 | -1.1 |
| Key Researcher/Manager | 0.5 | 0.5 | - | 0.5 | 0.5 | - | 0.7 | 0.5 | 0.2 | 0.5 | 0.5 | 0.5 | 0.5 | 0.5 | 0.5 | 0.5 | 0.5 | 1.7 | 1.5 | 0.2 | 3.7 | 3.5 | 0.2 |
| Researcher/Professional | 0.2 | 1.8 | -1.6 | 0.5 | 1.8 | -1.3 | 0.3 | 1.8 | -1.5 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.8 | 1.0 | 5.4 | -4.4 | 8.2 | 12.6 | -4.4 |
| Support Staff | 0.1 | 0.3 | -0.2 | 0.2 | 0.3 | -0.1 | 0.3 | 0.3 | 0.0 | 0.3 | 0.3 | 0.3 | 0.3 | 0.3 | 0.3 | 0.3 | 0.3 | 0.6 | 0.9 | -0.3 | 1.8 | 2.1 | -0.3 |
| **TOTAL** | 1.2 | 3.3 | -2.1 | 1.5 | 3.3 | -1.8 | 1.6 | 3.3 | -1.7 | 3.3 | 3.3 | 3.3 | 3.3 | 3.3 | 3.3 | 3.3 | 3.3 | 4.3 | 9.9 | -5.6 | 17.5 | 23.1 | -5.6 |

*Table 1a: Financial Information / Number of Staff (FTE; 0.0) continued ...*

| | Actual | | | | | | | | | Projected | | | | | | | | Totals to 2007-08 | | | Totals for 7 years | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | 2005-06 | | | 2006-07 | | | 2007-08 | | | 2008-09 | | 2009-10 | | 2010-11 | | 2011-12 | | | | | | | |
| | Actual | Agr'mt | Diff | Actual | Agr'mt | Diff | Actual | Agr'mt | Diff | Projected | Agr'mt | Projected | Agr'mt | Projected | Agr'mt | Projected | Agr'mt | Actual | Agr'mt | Diff | ctual/Pr | Agr'mt | Diff |
| **National Livestock Research Institute, Korea** | | | | | | | | | | | | | | | | | | | | | | | |
| Programme Leader/Senior Manager | - | 0.2 | - 0.2 | - | 0.2 | - 0.2 | 0.0 | 0.2 | -0.2 | 0.2 | 0.2 | 0.2 | 0.2 | 0.2 | 0.2 | 0.2 | 0.2 | 0.0 | 0.6 | -0.6 | 0.8 | 1.4 | -0.6 |
| Key Researcher/Manager | - | 0.2 | - 0.2 | - | 0.2 | - 0.2 | 0.0 | 0.2 | -0.2 | 0.2 | 0.2 | 0.2 | 0.2 | 0.2 | 0.2 | 0.2 | 0.2 | 0.0 | 0.6 | -0.6 | 0.8 | 1.4 | -0.6 |
| Researcher/Professional | 0.3 | 1.6 | - 1.3 | 0.6 | 1.6 | - 1.0 | 0.8 | 1.6 | -0.8 | 1.6 | 1.6 | 1.6 | 1.6 | 1.6 | 1.6 | 1.6 | 1.6 | 1.7 | 4.8 | -3.1 | 8.1 | 11.2 | -3.1 |
| Support Staff | 1.0 | 0.2 | 0.8 | - | 0.2 | - 0.2 | 0.0 | 0.2 | -0.2 | 0.2 | 0.2 | 0.2 | 0.2 | 0.2 | 0.2 | 0.2 | 0.2 | 1.0 | 0.6 | 0.4 | 1.8 | 1.4 | 0.4 |
| **TOTAL** | 1.3 | 2.2 | - 0.9 | 0.6 | 2.2 | - 1.6 | 0.8 | 2.2 | -1.4 | 2.2 | 2.2 | 2.2 | 2.2 | 2.2 | 2.2 | 2.2 | 2.2 | 2.7 | 6.6 | -3.9 | 11.5 | 15.4 | -3.9 |
| **Northern Pastoral Group of Companies** | | | | | | | | | | | | | | | | | | | | | | | |
| Programme Leader/Senior Manager | - | - | - | - | - | - | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| Key Researcher/Manager | - | - | - | - | - | - | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| Researcher/Professional | - | - | - | - | - | - | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| Support Staff | - | - | - | - | - | - | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| **TOTAL** | - | - | - | - | - | - | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| **SASTEK Pty Ltd** | | | | | | | | | | | | | | | | | | | | | | | |
| Programme Leader/Senior Manager | - | - | - | - | - | - | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| Key Researcher/Manager | - | - | - | - | - | - | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| Researcher/Professional | - | 0.1 | - 0.1 | - | 0.1 | - 0.1 | 0.0 | 0.1 | -0.1 | 0.0 | 0.1 | 0.0 | 0.1 | 0.0 | 0.1 | 0.0 | 0.1 | 0.0 | 0.3 | -0.3 | 0.0 | 0.7 | -0.7 |
| Support Staff | - | 0.1 | - 0.1 | - | 0.1 | - 0.1 | 0.0 | 0.1 | -0.1 | 0.0 | 0.2 | 0.0 | 0.2 | 0.0 | 0.2 | 0.0 | 0.2 | 0.0 | 0.3 | -0.3 | 0.0 | 1.1 | -1.1 |
| **TOTAL** | - | 0.2 | - 0.2 | - | 0.2 | - 0.2 | 0.0 | 0.2 | -0.2 | 0.0 | 0.3 | 0.0 | 0.3 | 0.0 | 0.3 | 0.0 | 0.3 | 0.0 | 0.6 | -0.6 | 0.0 | 1.8 | -1.8 |
| **Sygen International** | | | | | | | | | | | | | | | | | | | | | | | |
| Programme Leader/Senior Manager | - | - | - | - | - | - | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| Key Researcher/Manager | - | - | - | - | - | - | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| Researcher/Professional | - | - | - | - | - | - | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| Support Staff | - | - | - | - | - | - | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| **TOTAL** | - | - | - | - | - | - | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| **The Ohio State University, USA** | | | | | | | | | | | | | | | | | | | | | | | |
| Programme Leader/Senior Manager | - | 0.7 | - 0.7 | - | 0.7 | - 0.7 | 0.0 | 0.7 | -0.7 | 0.7 | 0.7 | 0.7 | 0.7 | 0.7 | 0.7 | 0.7 | 0.7 | 0.0 | 2.1 | -2.1 | 2.8 | 4.9 | -2.1 |
| Key Researcher/Manager | 0.6 | 0.2 | 0.4 | 0.4 | 0.2 | 0.2 | 0.1 | 0.2 | -0.1 | 0.2 | 0.2 | 0.2 | 0.2 | 0.2 | 0.2 | 0.2 | 0.2 | 1.1 | 0.6 | 0.5 | 1.9 | 1.4 | 0.5 |
| Researcher/Professional | - | 0.1 | - 0.1 | - | 0.1 | - 0.1 | 0.1 | 0.1 | 0.0 | 0.1 | 0.1 | 0.1 | 0.1 | 0.1 | 0.1 | 0.1 | 0.1 | 0.1 | 0.3 | -0.2 | 0.5 | 0.7 | -0.2 |
| Support Staff | 0.6 | 1.0 | - 0.4 | 0.2 | 1.0 | - 0.8 | 0.1 | 1.0 | -0.9 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 0.9 | 3.0 | -2.1 | 4.9 | 7.0 | -2.1 |
| **TOTAL** | 1.2 | 2.0 | - 0.8 | 0.6 | 2.0 | - 1.4 | 0.3 | 2.0 | -1.7 | 2.0 | 2.0 | 2.0 | 2.0 | 2.0 | 2.0 | 2.0 | 2.0 | 2.1 | 6.0 | -3.9 | 10.1 | 14.0 | -3.9 |
| **SUPPORTING PARTICIPANTS TOTAL STAFF (FTE)** | | | | | | | | | | | | | | | | | | | | | | | |
| Programme Leader/Senior Manager | 1.0 | 2.7 | - 1.7 | 1.0 | 2.7 | - 1.7 | 1.4 | 2.7 | -1.3 | 2.7 | 2.7 | 2.7 | 2.7 | 2.7 | 2.7 | 2.7 | 2.7 | 3.4 | 8.1 | -4.7 | 14.2 | 18.9 | -4.7 |
| Key Researcher/Manager | 3.7 | 3.8 | - 0.1 | 3.2 | 3.8 | - 0.6 | 4.0 | 3.8 | 0.2 | 3.4 | 3.8 | 3.4 | 3.8 | 3.4 | 3.8 | 3.4 | 3.8 | 10.9 | 11.4 | -0.5 | 24.5 | 26.6 | -2.1 |
| Researcher/Professional | 3.1 | 7.0 | - 3.9 | 5.8 | 7.0 | - 1.2 | 5.2 | 7.0 | -1.8 | 6.5 | 7.0 | 6.5 | 7.0 | 6.5 | 7.0 | 6.5 | 7.0 | 14.1 | 21.0 | -6.9 | 40.1 | 49.0 | -8.9 |
| Support Staff | 3.5 | 4.6 | - 1.1 | 2.3 | 4.6 | - 2.3 | 2.9 | 4.6 | -1.7 | 4.5 | 4.7 | 4.5 | 4.7 | 4.5 | 4.7 | 4.5 | 4.7 | 8.7 | 13.8 | -5.1 | 26.7 | 32.6 | -5.9 |
| **TOTAL** | 11.3 | 18.1 | - 6.8 | 12.3 | 18.1 | - 5.8 | 13.5 | 18.1 | -4.6 | 17.1 | 18.2 | 17.1 | 18.2 | 17.1 | 18.2 | 17.1 | 18.2 | 37.1 | 54.3 | -17.2 | 105.5 | 127.1 | -21.6 |
| **OTHER IN-KIND RESOURCES** | | | | | | | | | | | | | | | | | | | | | | | |
| Programme Leader/Senior Manager | - | - | - | - | - | - | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| Key Researcher/Manager | - | - | - | - | - | - | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| Researcher/Professional | - | - | - | - | - | - | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| Support Staff | - | - | - | - | - | - | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| **TOTAL** | - | - | - | - | - | - | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| **TOTAL STAFF IN-KIND (FTE)** | | | | | | | | | | | | | | | | | | | | | | | |
| Programme Leader/Senior Manager | 3.8 | 5.2 | - 1.4 | 3.7 | 5.2 | - 1.5 | 3.4 | 5.2 | -1.8 | 5.2 | 5.2 | 5.2 | 5.2 | 5.2 | 5.2 | 5.2 | 5.2 | 10.9 | 15.6 | -4.7 | 31.7 | 36.4 | -4.7 |
| Key Researcher/Manager | 9.0 | 13.5 | - 4.5 | 8.5 | 13.5 | - 5.0 | 12.4 | 13.5 | -1.1 | 13.1 | 13.5 | 13.1 | 13.5 | 13.1 | 13.5 | 13.1 | 13.5 | 29.9 | 40.5 | -10.6 | 82.3 | 94.5 | -12.2 |
| Researcher/Professional | 29.3 | 21.2 | 8.1 | 26.9 | 21.2 | 5.7 | 24.0 | 21.2 | 2.8 | 20.7 | 21.2 | 20.7 | 21.0 | 20.7 | 21.0 | 20.7 | 21.0 | 80.2 | 63.6 | 16.6 | 163.0 | 147.8 | 15.2 |
| Support Staff | 10.9 | 6.6 | 4.3 | 13.6 | 6.6 | 7.0 | 17.4 | 6.6 | 10.8 | 6.5 | 6.7 | 6.5 | 6.7 | 6.5 | 6.7 | 6.5 | 6.7 | 41.9 | 19.8 | 22.1 | 67.9 | 46.6 | 21.3 |
| **GRAND TOTAL** | 53.0 | 46.5 | 6.5 | 52.7 | 46.5 | 6.2 | 57.2 | 46.5 | 10.7 | 45.5 | 46.6 | 45.5 | 46.4 | 45.5 | 46.4 | 45.5 | 46.4 | 162.9 | 139.5 | 23.4 | 344.9 | 325.3 | 19.6 |

*Table 1b: Financial Information / Total Non-Staff In-Kind ($'000s) (per participant)*

| | Actual | | | | | | | | | Projected | | | | | | | | Totals to 2007-08 | | | Totals for 7 years | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | 2005-06 | | | 2006-07 | | | 2007-08 | | | 2008-09 | | 2009-10 | | 2010-11 | | 2011-12 | | | | | | | |
| | Actual | Agr'mt | Diff | Actual | Agr'mt | Diff | Actual | Agr'mt | Diff | Projected | Agr'mt | Projected | Agr'mt | Projected | Agr'mt | Projected | Agr'mt | Actual | Agr'mt | Diff | ctual/Pr | Agr'mt | Diff |
| **CORE PARTICIPANTS** | | | | | | | | | | | | | | | | | | | | | | | |
| Department of Primary Industries and Resource | 273 | 422 | -149 | 252 | 423 | -171 | 252 | 423 | -171 | 422 | 422 | 423 | 423 | 423 | 422 | 423 | 423 | 777 | 1,268 | -491 | 2,468 | 2,958 | -490 |
| Department of Primary Industries Victoria | 63 | 258 | -195 | 186 | 258 | -72 | 215 | 258 | -43 | 258 | 258 | 258 | 258 | 258 | 258 | 258 | 258 | 464 | 774 | -310 | 1,496 | 1,806 | -310 |
| Dept of Primary Industries and Fisheries (QLD) | 916 | 859 | 57 | 916 | 859 | 57 | 1,030 | 859 | 171 | 859 | 859 | 859 | 859 | 859 | 859 | 859 | 859 | 2,862 | 2,577 | 285 | 6,298 | 6,013 | 285 |
| Meat & Livestock Australia Limited | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Meat and Wool New Zealand | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| NSW Department of Primary Industries | 927 | 669 | 258 | 1,629 | 669 | 960 | 1,262 | 669 | 593 | 669 | 669 | 669 | 669 | 669 | 669 | 669 | 669 | 3,818 | 2,007 | 1,811 | 6,494 | 4,683 | 1,811 |
| The University of Adelaide | 627 | 543 | 84 | 466 | 543 | -77 | 670 | 543 | 127 | 542 | 542 | 543 | 542 | 543 | 542 | 543 | 542 | 1,763 | 1,629 | 134 | 3,934 | 3,797 | 137 |
| The University of New England | 706 | 737 | -31 | 718 | 736 | -18 | 775 | 736 | 39 | 737 | 737 | 736 | 736 | 736 | 737 | 736 | 736 | 2,199 | 2,209 | -10 | 5,144 | 5,155 | -11 |
| The University of Queensland | 685 | 685 | 0 | 355 | 685 | -330 | 355 | 685 | -330 | 686 | 686 | 685 | 685 | 685 | 685 | 685 | 685 | 1,395 | 2,055 | -660 | 4,136 | 4,796 | -660 |
| **TOTAL CORE PARTICIPANTS** | 4,197 | 4,173 | 24 | 4,522 | 4,173 | 349 | 4,559 | 4,173 | 386 | 4,173 | 4,173 | 4,173 | 4,172 | 4,173 | 4,172 | 4,173 | 4,172 | **13,278** | **12,519** | **759** | **29,970** | **29,208** | **762** |
| **SUPPORTING PARTICIPANTS** | | | | | | | | | | | | | | | | | | | | | | | |
| Australian Lot Feeders Association | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Catapult Genetics Pty Limited (formerly Genetic | 0 | 75 | -75 | 0 | 75 | -75 | 0 | 75 | -75 | 0 | 75 | 0 | 75 | 0 | 75 | 0 | 75 | 0 | 225 | -225 | 0 | 525 | -525 |
| CSIRO Livestock Industries | 1,113 | 828 | 285 | 1,427 | 828 | 599 | 1,668 | 828 | 840 | 828 | 828 | 828 | 828 | 828 | 828 | 828 | 828 | 4,208 | 2,484 | 1,724 | 7,520 | 5,796 | 1,724 |
| Department of Agriculture and Food (formerlyV | 120 | 120 | 0 | 220 | 120 | 100 | 203 | 120 | 83 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 543 | 360 | 183 | 1,023 | 840 | 183 |
| Murdoch University | 500 | 490 | 10 | 500 | 490 | 10 | 500 | 490 | 10 | 490 | 490 | 490 | 491 | 490 | 491 | 490 | 491 | 1,500 | 1,470 | 30 | 3,460 | 3,433 | 27 |
| National Livestock Research Institute, Korea | 286 | 286 | 0 | 286 | 286 | 0 | 286 | 286 | 0 | 286 | 286 | 286 | 286 | 286 | 286 | 286 | 286 | 858 | 858 | 0 | 2,002 | 2,002 | 0 |
| Northern Pastoral Group of Companies | 0 | 214 | -214 | 0 | 214 | -214 | 0 | 214 | -214 | 0 | 214 | 0 | 214 | 0 | 214 | 0 | 215 | 0 | 642 | -642 | 0 | 1,499 | -1,499 |
| SASTEK Pty Ltd | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Sygen International | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| The Ohio State University, USA | 346 | 286 | 60 | 360 | 286 | 74 | 373 | 286 | 87 | 286 | 286 | 286 | 286 | 286 | 286 | 286 | 286 | 1,079 | 858 | 221 | 2,223 | 2,002 | 221 |
| **TOTAL SUPPORTING PARTICIPANTS** | 2,365 | 2,299 | 66 | 2,793 | 2,299 | 494 | 3,030 | 2,299 | 731 | 2,010 | 2,299 | 2,010 | 2,300 | 2,010 | 2,300 | 2,010 | 2,301 | **8,188** | **6,897** | **1,291** | **16,228** | **16,097** | **131** |
| **OTHER NON-STAFF IN-KIND RESOURCES** | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| **GRAND TOTAL** | 6,562 | 6,472 | 90 | 7,315 | 6,472 | 843 | 7,589 | 6,472 | 1,117 | 6,183 | 6,472 | 6,183 | 6,472 | 6,183 | 6,472 | 6,183 | 6,473 | 21,466 | 19,416 | 2,050 | 46,198 | 45,305 | 893 |

*Table 2: Financial Information / Participants Cash Contributions, Other Firm Cash and CRC Programme Funding ($'000s) continued ...*

| | Actual | | | | | | | | | Projected | | | | | | | | Totals to 2007-08 | | | Totals for 7 years | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | 2005-06 | | | 2006-07 | | | 2007-08 | | | 2008-09 | | 2009-10 | | 2010-11 | | 2011-12 | | | | | | | |
| | Actual | Agr'mt | Diff | Actual | Agr'mt | Diff | Actual | Agr'mt | Diff | Projected | Agr'mt | Projected | Agr'mt | Projected | Agr'mt | Projected | Agr'mt | Actual | Agr'mt | Diff | ctual/Pr | Agr'mt | Diff |
| **CORE PARTICIPANTS** | | | | | | | | | | | | | | | | | | | | | | | |
| Department of Primary Industries and Resources S | 50 | 50 | 0 | 50 | 50 | 0 | 50 | 50 | 0 | 50 | 50 | 50 | 50 | 50 | 50 | 50 | 50 | 150 | 150 | 0 | 350 | 350 | 0 |
| Department of Primary Industries Victoria | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Dept of Primary Industries and Fisheries (QLD) | 38 | 13 | 25 | 0 | 12 | -12 | 200 | 13 | 187 | 600 | 0 | 400 | 0 | 194 | 0 | 0 | 0 | 238 | 38 | 200 | 1,432 | 38 | 1,394 |
| Meat & Livestock Australia Limited | 1,034 | 500 | 534 | 469 | 500 | -31 | 2,485 | 500 | 1,985 | 1,135 | 500 | 1,225 | 500 | 1,495 | 500 | 180 | 500 | 3,988 | 1,500 | 2,488 | 8,023 | 3,500 | 4,523 |
| Meat and Wool New Zealand | 293 | 293 | 0 | 293 | 293 | 0 | 293 | 293 | 0 | 293 | 293 | 293 | 293 | 293 | 293 | 293 | 293 | 879 | 879 | 0 | 2,051 | 2,051 | 0 |
| NSW Department of Primary Industries | 38 | 13 | 25 | 0 | 12 | -12 | 32 | 13 | 19 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 70 | 38 | 32 | 70 | 38 | 32 |
| The University of Adelaide | 100 | 100 | 0 | 100 | 100 | 0 | 100 | 100 | 0 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 300 | 300 | 0 | 700 | 700 | 0 |
| The University of New England | 38 | 13 | 25 | 0 | 13 | -13 | 0 | 12 | -12 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 38 | 38 | 0 | 38 | 38 | 0 |
| The University of Queensland | 0 | 7 | -7 | 14 | 7 | 7 | 7 | 7 | 0 | 7 | 7 | 7 | 7 | 7 | 7 | 8 | 8 | 21 | 21 | 0 | 50 | 50 | 0 |
| **TOTAL CORE PARTICIPANTS' CASH** | 1,591 | 989 | 602 | 926 | 987 | -61 | 3,167 | 988 | 2,179 | 2,185 | 950 | 2,075 | 950 | 2,139 | 950 | 631 | 951 | 5,684 | 2,964 | 2,720 | 12,714 | 6,765 | 5,949 |
| **SUPPORTING PARTICIPANTS** | | | | | | | | | | | | | | | | | | | | | | | |
| Australian Lot Feeders Association | 120 | 60 | 60 | 120 | 60 | 60 | 120 | 60 | 60 | 120 | 60 | 120 | 60 | 120 | 60 | 120 | 60 | 360 | 180 | 180 | 840 | 420 | 420 |
| Catapult Genetics Pty Limited | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| CSIRO Livestock Industries | 38 | 13 | 25 | 0 | 13 | -13 | 0 | 12 | -12 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 38 | 38 | 0 | 38 | 38 | 0 |
| Department of Agriculture and Food WA | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Murdoch University | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| National Livestock Research Institute, Korea | 0 | 14 | -14 | 4 | 14 | -10 | 50 | 14 | 36 | 13 | 13 | 14 | 14 | 14 | 13 | 0 | 13 | 54 | 42 | 12 | 95 | 95 | 0 |
| Northern Pastoral Group of Companies | 242 | 0 | 242 | 525 | 0 | 525 | 347 | 0 | 347 | 300 | 0 | 300 | 0 | 0 | 0 | 0 | 0 | 1,114 | 0 | 1,114 | 1,714 | 0 | 1,714 |
| SASTEK Pty Ltd | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Sygen International | 0 | 37 | -37 | 0 | 38 | -38 | 0 | 37 | -37 | 0 | 38 | 0 | 38 | 0 | 38 | 0 | 38 | 0 | 112 | -112 | 0 | 264 | -264 |
| The Ohio State University, USA | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| **TOTAL SUPPORTING PARTICIPANTS' CASH** | 400 | 124 | 276 | 649 | 125 | 524 | 517 | 123 | 394 | 433 | 111 | 434 | 112 | 134 | 111 | 120 | 111 | 1,566 | 372 | 1,194 | 2,687 | 817 | 1,870 |
| **OTHER CASH** | | | | | | | | | | | | | | | | | | | | | | | |
| Other Cash Resources | 2,436 | 688 | 1,748 | 1,197 | 884 | 313 | 1,412 | 845 | 567 | 100 | 666 | 100 | 549 | 100 | 392 | 0 | 196 | 5,045 | 2,417 | 2,628 | 5,345 | 4,220 | 1,125 |
| CRC Program Funding | 4,500 | 4,500 | 0 | 6,000 | 6,000 | 0 | 5,700 | 5,700 | 0 | 5,100 | 5,100 | 4,200 | 4,200 | 3,000 | 3,000 | 1,500 | 1,500 | 16,200 | 16,200 | 0 | 30,000 | 30,000 | 0 |
| **TOTAL OTHER CASH** | 6,936 | 5,188 | 1,748 | 7,197 | 6,884 | 313 | 7,112 | 6,545 | 567 | 5,200 | 5,766 | 4,300 | 4,749 | 3,100 | 3,392 | 1,500 | 1,696 | 21,245 | 18,617 | 2,628 | 35,345 | 34,220 | 1,125 |
| **TOTAL CASH** | 8,927 | 6,301 | 2,626 | 8,772 | 7,996 | 776 | 10,796 | 7,656 | 3,140 | 7,818 | 6,827 | 6,809 | 5,811 | 5,373 | 4,453 | 2,251 | 2,758 | **28,495** | **21,953** | **6,542** | **50,746** | **41,802** | **8,944** |

*Table 3: Financial Information / Expenses (Accrual) ($'000s)*

| | Actual | | | | | | | | | Projected | | | | | | | | Totals to 2007-08 | | | Totals for 7 years | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | 2005-06 | | | 2006-07 | | | 2007-08 | | | 2008-09 | | 2009-10 | | 2010-11 | | 2011-12 | | | | | | | |
| | Actual | Agr'mt | Diff | Actual | Agr'mt | Diff | Actual | Agr'mt | Diff | Projected | Agr'mt | Projected | Agr'mt | Projected | Agr'mt | Projected | Agr'mt | Actual | Agr'mt | Diff | ctual/Prc | Agr'mt | Diff |
| Employee Expenses | 2,031 | 1,929 | 102 | 2,655 | 2,574 | 81 | 3,325 | 2,444 | 881 | 3,606 | 2,186 | 1,800 | 1,800 | 1,286 | 1,286 | 643 | 643 | 8,011 | 6,947 | 1,064 | 15,346 | 12,862 | 2,484 |
| Supplier Expenses | 4,165 | 2,243 | 1,922 | 4,848 | 3,224 | 1,624 | 5,845 | 3,180 | 2,665 | 4,666 | 2,874 | 4,120 | 2,365 | 2,909 | 1,698 | 1,437 | 849 | 14,858 | 8,647 | 6,211 | 27,990 | 16,433 | 11,557 |
| Other Expenses | 77 | 1,748 | -1,671 | 37 | 2,456 | -2,419 | 9 | 2,442 | -2,433 | 55 | 2,143 | 55 | 1,810 | 55 | 1,266 | 55 | 643 | 123 | 6,646 | -6,523 | 343 | 12,508 | -12,165 |
| **TOTAL EXPENSES** | 6,273 | 5,920 | 353 | 7,540 | 8,254 | -714 | 9,179 | 8,066 | 1,113 | 8,327 | 7,203 | 5,975 | 5,975 | 4,250 | 4,250 | 2,135 | 2,135 | **22,992** | **22,240** | **752** | **43,679** | **41,803** | **1,876** |

*Table 4: Financial Information / Capital Items ($'000s)*

| | Actual | | | | | | | | | Projected | | | | | | | | Totals to 2007-08 | | | Totals for 7 years | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | 2005-06 | | | 2006-07 | | | 2007-08 | | | 2008-09 | | 2009-10 | | 2010-11 | | 2011-12 | | | | | | | |
| | Actual | Agr'mt | Diff | Actual | Agr'mt | Diff | Actual | Agr'mt | Diff | Projected | Agr'mt | Projected | Agr'mt | Projected | Agr'mt | Projected | Agr'mt | Actual | Agr'mt | Diff | ctual/Pro | Agr'mt | Diff |
| **TOTAL EXPENDITURE** | 224 | 500 | -276 | 0 | 285 | -285 | 0 | 75 | -75 | 20 | 20 | 20 | 20 | 0 | 0 | 0 | 0 | 224 | 860 | -636 | 264 | 900 | -636 |

*Table 5: Financial Information / Allocation of Resources*

| | 2005-06 | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | Expenses ($'000s) | | | | Non-Staff In-kind ($'000s) | | | | In-Kind Staff (FTE; 0.0) | | | |
| | Actual | Agr'mt | Diff | %Diff | Actual | Agr'mt | Diff | %Diff | Actual | Agr'mt | Diff | %Diff |
| **PROGRAM** | | | | | | | | | | | | |
| Research Program 1 | 1,352 | 953 | 399 | 42 | 1,891 | 1,393 | 498 | 36 | 12.6 | 8.2 | 4.4 | 53.7 |
| Research Program 2 | 1,078 | 877 | 201 | 23 | 1,818 | 1,292 | 526 | 41 | 9.7 | 8.2 | 1.5 | 18.3 |
| Research Program 3 | 255 | 768 | -513 | -67 | 762 | 1,180 | -418 | -35 | 3.1 | 7.5 | -4.4 | -58.7 |
| Research Program 4 | 1,272 | 989 | 283 | 29 | 1,596 | 1,474 | 122 | 8 | 16.2 | 9.4 | 6.8 | 72.3 |
| Education Program | 202 | 465 | -263 | -57 | 121 | 485 | -364 | -75 | 0.6 | 2.4 | -1.8 | -75.0 |
| Commercialisation | 808 | 1,245 | -437 | -35 | 318 | 324 | -6 | -2 | 10.6 | 9.4 | 1.2 | 12.8 |
| Administration | 1,306 | 623 | 683 | 110 | 56 | 324 | -268 | -83 | 0.2 | 1.4 | -1.2 | -85.7 |
| **TOTAL** | **6,273** | **5,920** | **353** | **6** | **6,562** | **6,472** | **90** | **1** | **53.0** | **46.5** | **6.5** | **14.0** |

| | 2006-07 | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | Expenses ($'000s) | | | | Non-Staff In-kind ($'000s) | | | | In-Kind Staff (FTE; 0.0) | | | |
| | Actual | Agr'mt | Diff | %Diff | Actual | Agr'mt | Diff | %Diff | Actual | Agr'mt | Diff | %Diff |
| **PROGRAM** | | | | | | | | | | | | |
| Research Program 1 | 1,265 | 1,358 | -93 | -7 | 2,043 | 1,393 | 650 | 47 | 13.5 | 8.3 | 5.2 | 62.7 |
| Research Program 2 | 1,488 | 1,255 | 233 | 19 | 2,201 | 1,292 | 909 | 70 | 8.8 | 8.2 | 0.6 | 7.3 |
| Research Program 3 | 1,055 | 1,120 | -65 | -6 | 733 | 1,180 | -447 | -38 | 6.2 | 7.5 | -1.3 | -17.3 |
| Research Program 4 | 1,617 | 1,414 | 203 | 14 | 1,647 | 1,474 | 173 | 12 | 14.3 | 9.3 | 5.0 | 53.8 |
| Education Program | 401 | 620 | -219 | -35 | 122 | 485 | -363 | -75 | 0.9 | 2.3 | -1.4 | -60.9 |
| Commercialisation | 683 | 1,658 | -975 | -59 | 512 | 324 | 188 | 58 | 8.7 | 9.4 | -0.7 | -7.4 |
| Administration | 1,031 | 829 | 202 | 24 | 57 | 324 | -267 | -82 | 0.3 | 1.5 | -1.2 | -80.0 |
| **TOTAL** | **7,540** | **8,254** | **-714** | **-9** | **7,315** | **6,472** | **843** | **13** | **52.7** | **46.5** | **6.2** | **13.3** |

| | 2007-08 | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | Expenses ($'000s) | | | | Non-Staff In-kind ($'000s) | | | | In-Kind Staff (FTE; 0.0) | | | |
| | Actual | Agr'mt | Diff | %Diff | Actual | Agr'mt | Diff | %Diff | Actual | Agr'mt | Diff | %Diff |
| **PROGRAM** | | | | | | | | | | | | |
| Research Program 1 | 1,263 | 1,347 | -84 | -6 | 2,058 | 1,393 | 665 | 48 | 12.4 | 8.3 | 4.1 | 49.4 |
| Research Program 2 | 1,485 | 1,249 | 236 | 19 | 2,148 | 1,292 | 856 | 66 | 11.9 | 8.2 | 3.7 | 45.1 |
| Research Program 3 | 1,815 | 1,119 | 696 | 62 | 816 | 1,180 | -364 | -31 | 6.9 | 7.5 | -0.6 | -8.0 |
| Research Program 4 | 1,682 | 1,400 | 282 | 20 | 1,855 | 1,474 | 381 | 26 | 14.4 | 9.4 | 5.0 | 53.2 |
| Education Program | 679 | 589 | 90 | 15 | 128 | 485 | -357 | -74 | 0.9 | 2.4 | -1.5 | -62.5 |
| Commercialisation | 1,191 | 1,575 | -384 | -24 | 522 | 324 | 198 | 61 | 10.6 | 9.4 | 1.2 | 12.8 |
| Administration | 1,064 | 787 | 277 | 35 | 62 | 324 | -262 | -81 | 0.1 | 1.3 | -1.2 | -92.3 |
| **TOTAL** | **9,179** | **8,066** | **1,113** | **14** | **7,589** | **6,472** | **1,117** | **17** | **57.2** | **46.5** | **10.7** | **23.0** |

*Table 5: Financial Information / Allocation of Resources continued ...*

| | 2008-09 | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | Expenses ($'000s) | | | | Non-Staff In-kind ($'000s) | | | | In-Kind Staff (FTE; 0.0) | | | |
| | Projected | Agr'mt | Diff | % Diff | Projected | Agr'mt | Diff | % Diff | Projected | Agr'mt | Diff | % Diff |
| **PROGRAM** | | | | | | | | | | | | |
| Research Program 1 | 1,138 | 1,211 | | | 1,374 | 1,394 | | | 8.1 | 8.3 | | |
| Research Program 2 | 1,419 | 1,126 | | | 1,273 | 1,292 | | | 8.0 | 8.2 | | |
| Research Program 3 | 1,478 | 1,005 | | | 1,161 | 1,180 | | | 7.3 | 7.5 | | |
| Research Program 4 | 1,057 | 1,256 | | | 1,242 | 1,473 | | | 9.1 | 9.4 | | |
| Education Program | 626 | 519 | | | 485 | 485 | | | 2.3 | 2.4 | | |
| Commercialisation | 1,466 | 1,391 | | | 324 | 324 | | | 9.2 | 9.4 | | |
| Administration | 1,143 | 695 | | | 324 | 324 | | | 1.5 | 1.4 | | |
| **TOTAL** | **8,327** | **7,203** | | | **6,183** | **6,472** | | | **45.5** | **46.6** | | |

| | 2009-10 | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | Expenses ($'000s) | | | | Non-Staff In-kind ($'000s) | | | | In-Kind Staff (FTE; 0.0) | | | |
| | Projected | Agr'mt | Diff | % Diff | Projected | Agr'mt | Diff | % Diff | Projected | Agr'mt | Diff | % Diff |
| **PROGRAM** | | | | | | | | | | | | |
| Research Program 1 | 1,011 | 1,011 | | | 1,374 | 1,394 | | | 8.1 | 8.1 | | |
| Research Program 2 | 939 | 939 | | | 1,273 | 1,292 | | | 8.0 | 8.2 | | |
| Research Program 3 | 837 | 837 | | | 1,161 | 1,180 | | | 7.3 | 7.5 | | |
| Research Program 4 | 1,044 | 1,044 | | | 1,242 | 1,473 | | | 9.1 | 9.4 | | |
| Education Program | 427 | 427 | | | 485 | 485 | | | 2.3 | 2.4 | | |
| Commercialisation | 1,144 | 1,144 | | | 324 | 324 | | | 9.2 | 9.4 | | |
| Administration | 573 | 572 | | | 324 | 324 | | | 1.5 | 1.4 | | |
| **TOTAL** | **5,975** | **5,974** | | | **6,183** | **6,472** | | | **45.5** | **46.4** | | |

| | 2010-11 | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | Expenses ($'000s) | | | | Non-Staff In-kind ($'000s) | | | | In-Kind Staff (FTE; 0.0) | | | |
| | Projected | Agr'mt | Diff | % Diff | Projected | Agr'mt | Diff | % Diff | Projected | Agr'mt | Diff | % Diff |
| **PROGRAM** | | | | | | | | | | | | |
| Research Program 1 | 722 | 722 | | | 1,374 | 1,394 | | | 7.8 | 7.9 | | |
| Research Program 2 | 672 | 672 | | | 1,273 | 1,292 | | | 8.1 | 8.3 | | |
| Research Program 3 | 593 | 593 | | | 1,161 | 1,180 | | | 7.3 | 7.5 | | |
| Research Program 4 | 738 | 738 | | | 1,242 | 1,473 | | | 9.2 | 9.4 | | |
| Education Program | 303 | 303 | | | 485 | 485 | | | 2.4 | 2.4 | | |
| Commercialisation | 814 | 814 | | | 324 | 324 | | | 9.3 | 9.5 | | |
| Administration | 408 | 407 | | | 324 | 324 | | | 1.4 | 1.4 | | |
| **TOTAL** | **4,250** | **4,249** | | | **6,183** | **6,472** | | | **45.5** | **46.4** | | |

*Table 5: Financial Information / Allocation of Resources continued ...*

| | 2011-12 | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | Expenses ($'000s) | | | | Non-Staff In-kind ($'000s) | | | | In-Kind Staff (FTE; 0.0) | | | |
| | Projected | Agr'mt | Diff | % Diff | Projected | Agr'mt | Diff | % Diff | Projected | Agr'mt | Diff | % Diff |
| **PROGRAM** | | | | | | | | | | | | |
| Research Program 1 | 371 | 371 | | | 1,374 | 1,394 | | | 7.0 | 7.0 | | |
| Research Program 2 | 347 | 347 | | | 1,273 | 1,293 | | | 8.2 | 8.4 | | |
| Research Program 3 | 296 | 296 | | | 1,161 | 1,180 | | | 7.5 | 7.7 | | |
| Research Program 4 | 367 | 367 | | | 1,242 | 1,475 | | | 9.4 | 9.6 | | |
| Education Program | 149 | 149 | | | 485 | 488 | | | 2.4 | 2.4 | | |
| Commercialisation | 403 | 403 | | | 324 | 321 | | | 9.5 | 9.7 | | |
| Administration | 202 | 201 | | | 324 | 322 | | | 1.5 | 1.5 | | |
| **TOTAL** | **2,135** | **2,134** | | | **6,183** | **6,473** | | | **45.5** | **46.3** | | |

| | CUMULATIVE TOTAL TO 2007-08 | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | Expenses ($'000s) | | | | Non-Staff In-kind ($'000s) | | | | In-Kind Staff (FTE; 0.0) | | | |
| | Projected | Agr'mt | Diff | % Diff | Projected | Agr'mt | Diff | % Diff | Projected | Agr'mt | Diff | % Diff |
| **PROGRAM** | | | | | | | | | | | | |
| Research Program 1 | 3,880 | 3,658 | 222 | 6 | 5,992 | 4,179 | 1,813 | 43 | 38.5 | 24.8 | 13.7 | 55.2 |
| Research Program 2 | 4,051 | 3,381 | 670 | 20 | 6,167 | 3,876 | 2,291 | 59 | 30.4 | 24.6 | 5.8 | 23.6 |
| Research Program 3 | 3,125 | 3,007 | 118 | 4 | 2,311 | 3,540 | -1,229 | -35 | 16.2 | 22.5 | -6.3 | -28.0 |
| Research Program 4 | 4,571 | 3,803 | 768 | 20 | 5,098 | 4,422 | 676 | 15 | 44.9 | 28.1 | 16.8 | 59.8 |
| Education Program | 1,282 | 1,674 | -392 | -23 | 371 | 1,455 | -1,084 | -75 | 2.4 | 7.1 | -4.7 | -66.2 |
| Commercialisation | 2,682 | 4,478 | -1,796 | -40 | 1,352 | 972 | 380 | 39 | 29.9 | 28.2 | 1.7 | 6.0 |
| Administration | 3,401 | 2,239 | 1,162 | 52 | 175 | 972 | -797 | -82 | 0.6 | 4.2 | -3.6 | -85.7 |
| **TOTAL** | **22,992** | **22,240** | **752** | **3** | **21,466** | **19,416** | **2,050** | **11** | **162.9** | **139.5** | **23.4** | **16.8** |

| | TOTAL FOR 7 YEARS | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | Expenses ($'000s) | | | | Non-Staff In-kind ($'000s) | | | | In-Kind Staff (FTE; 0.0) | | | |
| | Projected | Agr'mt | Diff | % Diff | Projected | Agr'mt | Diff | % Diff | Projected | Agr'mt | Diff | % Diff |
| **PROGRAM** | | | | | | | | | | | | |
| Research Program | 28,656 | 26,384 | 2,272 | 9 | 39,768 | 37,376 | 2,392 | 6 | 259.5 | 232.4 | 27.1 | 11.7 |
| Education Program | 2,787 | 3,072 | -285 | -9 | 2,311 | 3,398 | -1,087 | -32 | 11.8 | 16.7 | -4.9 | -29.3 |
| Commercialisation | 6,509 | 8,230 | -1,721 | -21 | 2,648 | 2,265 | 383 | 17 | 67.1 | 66.2 | 0.9 | 1.4 |
| Administration | 5,727 | 4,114 | 1,613 | 39 | 1,471 | 2,266 | -795 | -35 | 6.5 | 9.9 | -3.4 | -34.3 |
| **GRAND TOTAL** | **43,679** | **41,800** | **1,879** | **5** | **46,198** | **45,305** | **893** | **2** | **344.9** | **325.2** | **19.7** | **6.1** |

## CORE PARTICIPANTS










## SUPPORTING PARTICIPANTS








# World class science, creating first class beef

## About Us

The Beef Cooperative Research Centre (Beef CRC) is Australia's largest integrated beef research program bringing together leading beef researchers from across Australia along with prestigious national and international beef industry partners and biotechnology businesses.

The world class research underway by the Beef CRC aims to increase profits for Australia's cattle industry by at least $179 million per annum from 2012.

To do this, the Beef CRC is focusing on gene discovery and gene expression which will create precision breeding and management strategies to improve profitability for all sectors of the Australian beef industry - breeding, growing, finishing, processing and retailing.

### Beef CRC Major Research Sites


## Contact Us


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