Industry outcomes of the CRC for Cattle and Beef Quality

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Abstract

Since 1992 the CRC has worked closely with the northern and temperate cattle breeds to identify the main genetic and non-genetic factors affecting tenderness, marbling, retail beef yield, meat colour, the fatness traits and Net Feed Intake. These results represent favourable opportunities to select for these traits to improve the value of the carcase beef eating quality and costs of production. The results also draw attention to the genetic associations between traits which may be antagonistic. These genetic correlations are essential knowledge to implement breeding programs designed to change more than one trait. The CRC has delivered new knowledge about gene marker technologies which open up new possibilities for genetic improvement of beef quality traits. There are already promising DNA tests for traits such as marbling and tenderness. We need to understand how to incorporate these technologies into practical beef improvement programs.

Non-genetic effects on meat quality arise from CRC investigations of grain (feedlot) and grass finishing and from our studies of genotype x environmental interaction between cattle bred in northern Australia but finished in southern (temperate) regions of Australia. The next phase of this research is described in this paper.

Introduction

The CRC portfolio concentrated on the genetic and non-genetic factors influencing beef quality (Figure 1). This followed many years of emphasis on the genetic improvement of cattle growth and adaptation to stressful northern environments. It was now time to combine our expertise in genetics, meat science and growth and nutrition to address the beef issues of the 1990s. A parallel development in molecular genetics in 1992 provided the opportunity to pursue gene markers and candidate genes for beef quality traits. A third area of endeavour chosen by the CRC was to expand Australian research on the efficiency of feed utilization, in the hope of providing long-term improvement in the economy of beef production in pasture- and grain-fed environments. This included special projects to develop vaccines against Bovine Respiratory Disease.

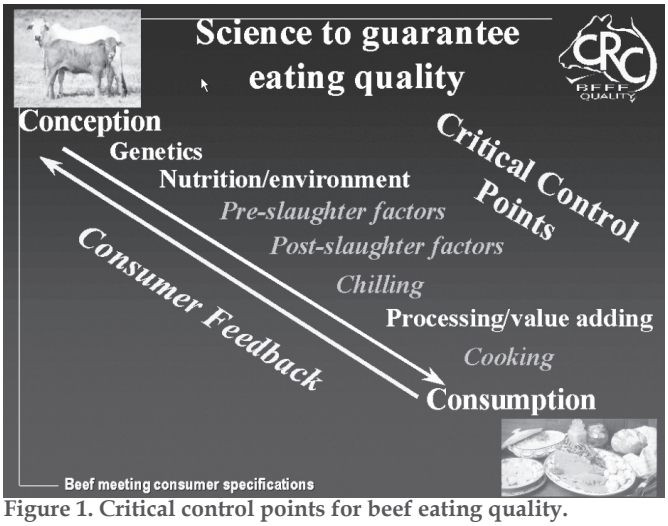


Figure 1. Critical control points for beef eating quality.

Scope of CRC Breeding/Feeding/Slaughter Projects

The CRC has carried out the world's largest progeny-test program for carcase and beef quality traits and their other genetically related traits such as growth. The straightbreeding project is a within-breed progeny test involving seven breeds from 49 cooperating seedstock herds. The northern cross-breeding project is a progeny test based on 1,000 Brahman females (donated by industry) and nine terminal sire breeds. These are illustrated in Figure 2. Progeny testing is an expensive business because it involves:

- generation of pedigreed progeny;
- purchase of progeny by CRC;
- transport to grow-out properties;
- management and agistment costs during grow out;
- grain versus grass finishing;
- transport to abattoirs;
- slaughter costs and retrieval of carcase sub-samples;
- laboratory measurement and taste panel assessment of meat samples;
- collation, analysis and reporting results.

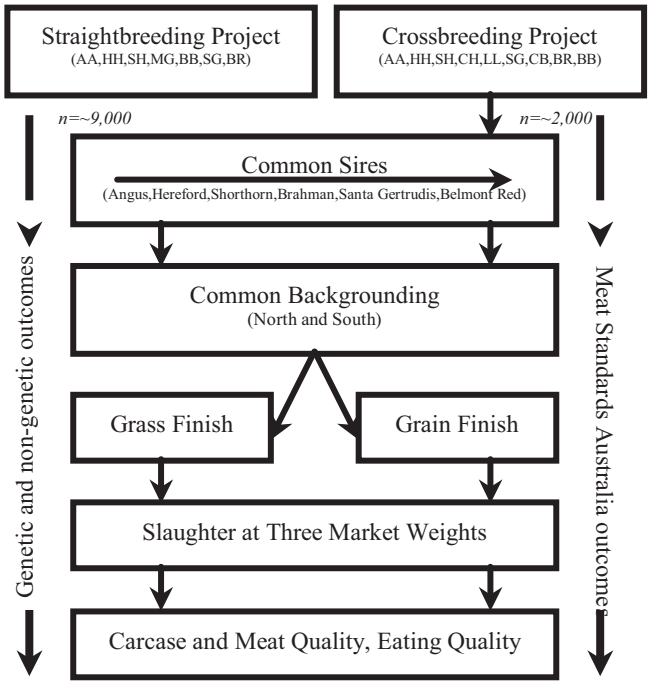


Figure 2. Design of CRC progeny tests for meat quality traits.

It is estimated that the CRC has spent nearly $32 million on this process. Thirty-two million dollars seems like a lot of money, but to keep this in perspective it must be appreciated that the Australian beef industry is worth some $6 billion annually. If this research guarantees the quality and competitiveness of this important export industry, then it is money well spent.

Industry Outcomes From the CRC - 1993-2001

The following is an abbreviated list of outcomes considered useful for the Australian beef industry. There are many more outputs, such as scientific publications (about 800), patents (4), commercial products (vaccines; equipment) and research reports:

- A compendium of genetic parameters (heritabilities and genetic correlations) to define the boundaries of genetic improvement of beef cattle.
- Definitive carcase and meat quality measurements, based on 13,000 progeny test results, for incorporation into BREEDPLAN.
- A blueprint for straightbreeding and crossbreeding strategies to improve retail beef yield, intramuscular fat percentage, tenderness and eating quality of Australian beef cattle.
- Identification of outstanding sires, in seven Australian beef breeds, to enable beef breeders to rapidly improve carcase and meat quality traits.
- The world's first EBVs for net feed efficiency of sires based on steers finished on a standard feedlot diet.
- The world's first evidence to confirm a strong correlation between cattle finished on grass versus grain diets. (We need only ONE genetic improvement scheme, not TWO.)
- Identification of the relative contribution of genetics, growth path, meat processing and beef ageing to beef eating quality.
- Identification of sire breed effects on beef eating quality in outcrossing programs in Queensland, based on Brahman females.
- Quantification of ossification score and correlated Meat Standards Australia MQ4 score of Brahman cross cattle finished on grain or grass in Queensland and northern NSW.
- Discovery of gene markers and candidate genes for retail beef yield, marbling and tenderness in temperate and tropically adapted cattle.
- World's first direct Gene Marker for tenderness in beef cattle.
- Development of electronic equipment to measure individual feed intake of groups of feedlot cattle.
- Definitive test of "Flight Time" as an indirect selection criterion to improve tenderness of tropical cattle.
- New knowledge of the relative contribution of genetics and nutritional manipulation to the achievement of Japanese B3 marbling scores in seven beef breeds.
- An understanding of pre- and post-weaning growth checks on ultimate fatness and eating quality of beef.
- A vaccine against a rumen micro-organism to prevent acidosis in grain-fed cattle.
- A new steroid growth promotant technique to achieve prolonged growth increases in Bos indicus-derived cattle.
- Two new killed vaccines against Pasteurella and pestivirus which cause bovine respiratory disease (BRD). Firsts for Australia.
- A patented procedure to create a mutant version of Pasteurella hemolytica, essential for development of a novel live, sub-unit vaccine with worldwide sales potential.
- New knowledge to ensure responsible recycling of feedlot waste to achieve a sustainable feedlot sector.
- Definitive results to show the effects of hormone growth promotants on beef eating quality.
- Education and training courses to create a more skilled beef industry workforce.
- Pre-boosting techniques to enhance performance of feedlot cattle.
- An explanation of the influence of marbling on eating quality of beef.
- A knowledge of the biochemical basis of why high Bos indicus content cattle do not undergo effective post-slaughter tenderisation.
- A confirmed plan, including MNRF to use novel internet based technologies to streamline technology transfer to beef sector.

Quantitative Genetics Results

These include:

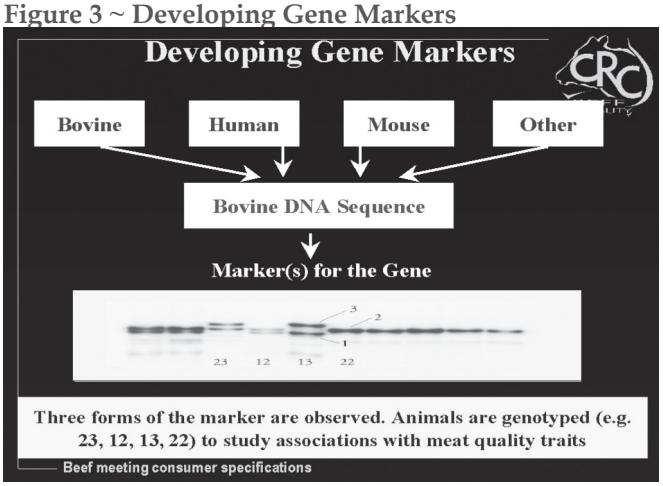
- Estimates of heritabilities for the following traits in temperate and tropically adapted cattle:
- Tenderness
- IMF%
- Retail Beef Yield
- Carcase weight
- Meat colour
- Fat colour
- Eye Muscle Area
- Fat depth
- Carcase pH
- Flight time (temperament)
- Net Feed Intake
- Genetic correlations between the above traits in each breed and finishing environment.
- Genetic correlations (for the above traits) between:
- Feedlot versus pasture finishing
- Domestic versus Export markets
- North versus South finishing environments (for tropically adapted cattle only)
- Genetics of marbling, with particular reference to:
- Method of measurement (including scanning, IMF%, marble score)
- Grain versus grass finish
- Domestic versus Export cattle
- EBVs for many sires, many traits.

Collectively, the results above provide a blueprint for genetic improvement of beef quality and efficiency traits in Australian beef cattle.

Gene Markers For Carcase and Beef Quality

Genetic evaluation for carcase and beef quality attributes in breeding cattle is generally difficult and expensive. Use of real-time ultrasound scanning for eye muscle area, IMF% and fat thickness, is a widely used and effective tool for genetic evaluation of these traits and RBY%. The only other tool currently available to genetically evaluate carcase and beef quality attributes is by obtaining abattoir data from designed progeny tests, a long-term and expensive option. The development of Marker Assisted Selection could potentially allow direct evaluation of breeding animals for these traits and significantly reduce the time needed for evaluation. Preliminary data from genome-wide screening of DNA markers through the CRC's program have revealed a number of putative Quantitative Trait Loci (QTL) associated with carcase and beef quality attributes (Figure 3; Table 1).

Figure 3 ~ Developing Gene Markers



Linked Markers

Hetzel et al (1997) and Hetzel and Davis (1999) reported outcomes from three large half-sib families of about 200 progeny/sire that were bred from F1 Charolais x Brahman bulls mated to unrelated tropically adapted composite breed dams. The progeny were finished on pasture in central Queensland and slaughtered at about three years of age. Details of design, measurements and genotyping are reported by Hetzel et al (1997). More than 100 QTL associated with variation in growth, carcase and beef quality were detected (Hetzel and Davis, 1999). Table 1 shows the size of effects of some of the QTL detected for carcase and beef quality attributes.

Main Outcomes of the Project Include:

- Growth: An average of 4.1 QTL per growth trait were detected. Quantitative trait loci were located on eight different chromosomes, with a concentration on five chromosomes (5, 6, 14, 19 and 21). Sizes of effect ranged from 0.5 to 1.6 s.d., with a relatively high frequency of large QTL in excess of 1 s.d. The QTL will allow selection for combinations of early and late growth.
- Retail yield: On average, three QTL per beef yield trait were detected. The effects were smaller than for growth, being in the range of 0.5 to 0.7 s.d. and accounting for <30% of phenotypic variance within sires. A large QTL of almost 1 s.d. was found for carcase value.

Table 1. Quantitative Trait Loci (QTL) for meat quality traits.

QTL detected for carcase and meat quality traits in the CBX herd

Trait	Unit	Effect
Carcase value	$	43.5
Carcase weight	kg	10.9
Saleable meat yield	kg	7
Dressing percentage	%	1.3
Eye muscle area	cm2	4.6
Fat colour b (LD)	units	1.44
Marbling score (MRL)	score	0.4
Instron compression (LD)	kg	0.27
Peak force (LD)	kg	1.7
Tenderness index	units	1.46

Beef meeting consumer specifications

- Fatness traits: These were analysed for sexes separately and combined, due to differences in means and variances. Using this approach, an additional QTL was detected in females for rib fat and for marbling in males. Some QTL had effects of >1.5 s.d. Because the distribution of marbling scores was binary rather than normal, estimated sizes were likely to be biased upwards (Figure 4). Different QTL were observed in each sex for both rib and rump fat. Similarly, QTL detected for marbling and IMF% were on different chromosomes. By contrast, the IMF% and moisture loss QTL were in the same reigon.

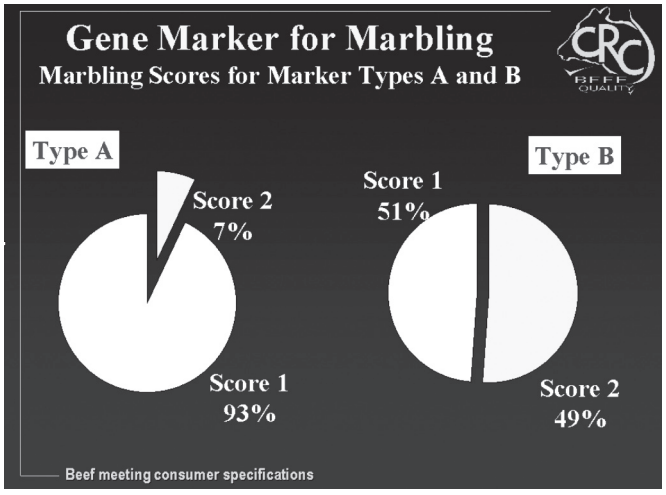


Figure 4. A linked (or indirect) gene marker for marbling

- Beef tenderness: An average of 2.2 QTL were detected per tenderness trait. Sizes of the effect ranged from 0.5 to 0.8 s.d., accounting for up to 25% of phenotypic variance. QTL for beef tenderness attributes in either the longissimus dorsi or semitendinosus muscles were often in the same chromosomal region. However, there was little commonality in QTL location between the two muscles.

- Meat and fat colour: The number of QTL detected for meat and fat colour traits averaged only 1.2. There were no QTL regions in common between fat and meat colour.

- Quantitative trait loci for carcase and beef quality traits: These were distributed throughout the genome, with a concentration on chromosomes 5, 6 and 14.

Evidence to date shows that genetic markers can be used to identify specific chromosomal regions where genes constituting QTL are located. However, it is likely that the linkage phases identified from one particular set of families may not apply to other populations. This means that QTL detected using linkage analysis will be difficult to exploit beyond the research population where they were discovered. Before commercial use, markers must be validated in independent populations and ideally, the genes themselves identified and cloned to provide direct tests for the genes of interest. Fine scale mapping in CRCII is attempting to achieve this.

Summary of Gene Marker Technology

Two marker types:

(i) Linked Markers (QTL)

- Anonymous bits of DNA close to genes affecting beef attributes.
- Use in breeding programs in cattle of known pedigree.
- Some progeny testing required
- Combine with EBVs in Breedplan.

(ii) Direct markers (see below).

Direct Markers

Direct Gene Markers arise from research where a candidate gene of known effect (e.g. from bovine, human, mouse studies or from our knowledge of biochemistry and physiology) is shown to influence a certain meat quality attribute. If such a gene controls a significant amount of genetic variation for the trait, then it is potentially useful for genetic improvement. CSIRO and Meat and Livestock Australia have recently patented such a candidate gene affecting marbling (intramuscular fat %) in Australian beef cattle. The particular allele (form of the gene) is known as TG5 (thyroglobulin) on chromosome 14 commercialised by GeneStar.

Figure 5 shows three different form of the TG5 allele inheritance, showing DNA profiles for cattle that have 0, 1 or 2 "copies" of the allele.

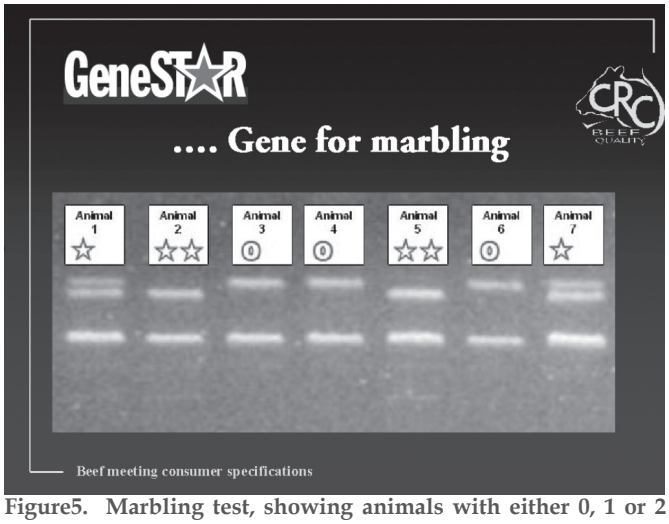


Figure5. Marbling test, showing animals with either 0, 1 or 2 copies of the TG5 (thyroglobulin) gene.

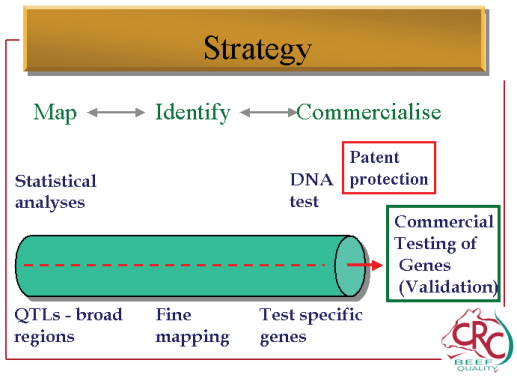
Commercial Angus and Shorthorn cattle (of unknown pedigree) being grain fed for the Japanese B3 market were measured for marble score, then "genotyped" (DNA tested) for the "GeneStar Marbling" allele. Since September 2000 some 3000 commercial tests have been marketed by our commercial partner Genetic Solutions Pty Ltd.

Search for Other Gene Markers

The CRC for Cattle and Beef Quality has formed a consortium with CSIRO and MLA to study gene markers. The idea is to develop DNA tests to identify cattle which have specific genes for traits of significance in Australia's beef business.

This is a complex process that began in 1990 and is likely to be a permanent part of the R&D landscape for many years into the future.

The objective of this project is to map, identify and commercialise genes for tenderness, marbling, meat yield, resistance to ticks and worms and feed conversion efficiency. To do this we have established a pipeline that starts with statistical analyses that suggest the presence of genes of large effect and ends with a commercial DNA test. In between these two ends of the pipeline we start with mapping genes to broad chromosomal regions, and proceed to fine scale mapping to narrow chromosomal regions and tests of specific genes. The pipeline looks like this:



Gene markers for Beef Tenderness have progressed beyond the DNA test and patent protection phase. One marker (Tend 1) has entered the commercial testing phase to identify the size of effect of different forms of the gene (i.e. "polymorphism") in the seven breeds of cattle contained in the CRC's database. If that is successful commercial release of the test would follow. A different gene affecting tenderness ('Tend 2') is one step further back in the pipeline.

Non Genetic Effects on Beef Quality

Feedlot Finishing

In the CRC's progeny test program half of each sire group has been grain-finished and half pasture-finished. This was done to identify the influence of finishing environment.

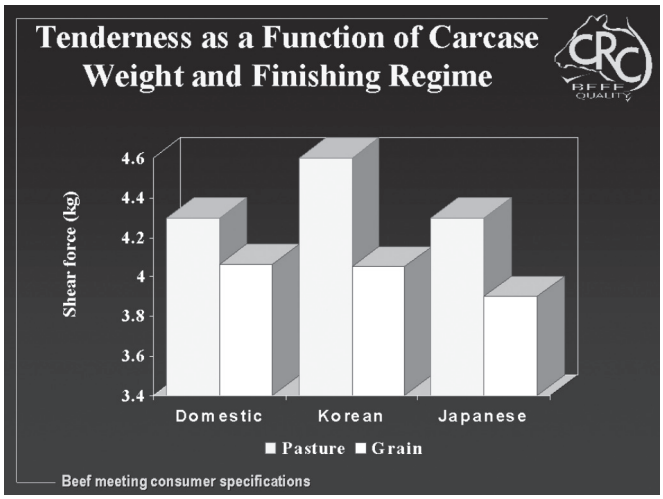


Figure 8. Tenderness (shear force) of grain- and pasture- finished cattle in the CRC progeny test

Tenderness. Figure 8 shows the objective ('Shear Force') measurement of tenderness of the striploin from 8000 carcases finished for the domestic (220 kg cw), Korean (270 kg cw), and Japanese (320 kg cw) markets. (Note that the lower the shear force, the more tender the beef.) It is clear that for all three markets, feedlot finished animals produced more tender beef.

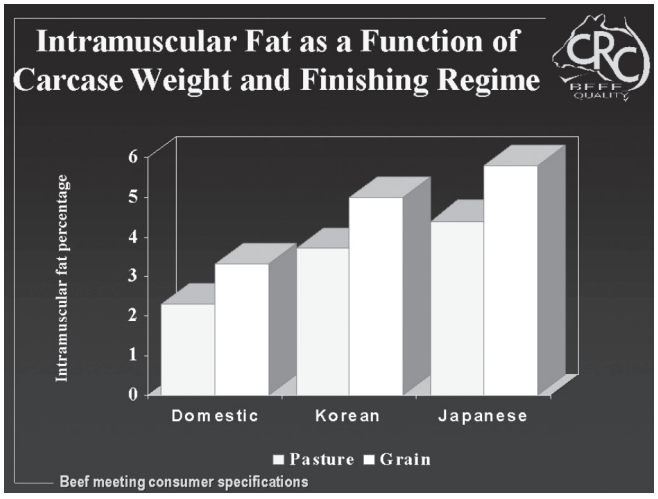


Figure 9. Marbling in grain- and grass-finished carcases from the CRC progeny test.

Grain finishing significantly increased marbling (IMF%) in domestic, Korean and Japanese carcases when compared to pasture finishing (Figure 9). These results (Figures 8 and 9) confirm the importance of grain feeding for both the domestic (where tenderness is the key trait)

and export markets (where tenderness and marbling are important).

CRC Vaccines

There has been a disappointing delay in the commercial release of three vaccine products developed by the CRC. These delays result from the tedious process of registration through the National Registration Authority (NRA) and/or difficulties arising from commercial partner negotiations. Efficacy of the vaccines has long since been proven and the underpinning science was complete at least 3 years ago:

The Northern Industry Project

Background

Research from the CRC for the Cattle and Beef Industry (Meat Quality) identified breeds and sire lines that have the capacity to consistently produce beef of guaranteed eating quality when their progeny are grown in relatively benign environments in Central Queensland. However, if herd productivity is not to be compromised, female progeny from these breeds and sire lines must be able to grow and reproduce well in harsh tropical environments. Results from the Meat Quality CRC indicate that traits such as retail beef yield percentage and marbling will respond well to genetic selection. However, moderate to strong antagonistic genetic relationships exist between retail beef yield percentage, marbling, fat thickness and feed efficiency, with higher yielding animals being more efficient but leaner and marbling less than lower yielding animals. Hence, selection to improve retail beef yield percentage or feed efficiency is likely to reduce fat deposition at all sites throughout the body. Body condition is an important factor in female reproductive performance and a minimum fat cover may be necessary for puberty and conception. Selection of beef cattle for increased beef yield or improved feed efficiency that results in reduced fat cover in breeding females may therefore reduce female fertility. Such relationships may be stronger in harsh environments, and be exacerbated by seasonal conditions and in Bos indicus breeds that suffer more from lactational anoestrus than other breeds.

Project Design

- Two tropically adapted breeds (Brahman and Belmont Red / tropically adapted composite) representing the extreme between-breed differences amongst the tropically adapted breeds for traits such as adaptation to stressors of tropical environments, male and female fertility, and carcase and beef quality were used for the project;
- The number of progeny per sire was largely determined by the minimum number of female progeny required for subsequent joining in the breeding herds. The program was designed to produce 50-60 progeny (25-30 progeny of each sex) per sire;
- A minimum of ~2400 progeny (1200 steers / 1200 heifers) per breed will be generated to estimate the genetic relationships between the traits of interest;
- Specific sires were required to link different groups of cattle (e.g. AI / natural mating groups; across years and across herds within breeds). As well, sires were used to link project 2.3 with other projects (e.g. CRC Mk I core cattle projects and CRC Mk II project 2.1) and with industry (some high profile Brahman sires were used to provide better genetic linkages between this project and non-CRC Brahman herds);
- To maximise value of the project to the supporting partners (Northern Pastoral Group of Companies ~ NPG) two "types" of sires were nominated for the project (i.e. sires nominated by the CRC and those nominated by NPG.) The number of sires nominated by NPG was proportional to the number of cows provided by them for the project. The contributors to the project are shown in Figure 10;
- Sires nominated by the CRC were selected primarily on divergence for EBV for retail beef yield percentage (RBY%) and intramuscular fat percentage (IMF% ~ marbling). Secondary selection criteria included known heterozygosity for gene markers identified as part of the CRC Mk I gene marker project (including sires from Alexandria Station used in the linked START project), EBVs for scrotal size or days to calving and, in Brahman sires, whether they were prominent sires within the Brahman breed that also met some of the other selection criteria.

- In most cases, sires nominated by NPG were young, unproven bulls. Bulls from the North Australia Pastoral Company (NAPCO) were selected on a combination of phenotypic growth performance in the paddock and the feedlot.

Steers bred specifically for the project will be grown out in one of three locations - Brigalow Research Station and a commercial property "Crescendo" in Central Queensland or a sponsor's property in northern NSW. All steers will be finished

Key to Figure 10.
[☆ = Newcastle Waters Station, Brunette Downs Station and Meteor Downs Station]
[★ = Alexandria Station, Kynuna Station, Alcala Station, Mimong Station, Weetalaba Station, "Beresford", "Tartrus", "Cona Creek", "Mt Eugene" and Belmont Research Station]
[◆ = Brigalow Research Station, "Crescendo" and "Tullimba" Feedlot Research Facility
[● = Toorak Research Station, Swans Lagoon Research Station, Brian Pastures Reserach Station and Belmont Research Station]

on grain at the CRC's "Tullimba" Research Feedlot, where individual feed intakes will be recorded on every animal, prior to slaughter at the Grantham abattoir owned by NPG partners. Complete carcase and beef quality evaluations will be conducted on all steers.

Heifer progeny will be grown out and subsequently enter the breeding herds at Belmont, Swan's Lagoon, Toorak or Brian Pastures Research Stations, where they will remain until they have had the opportunity to rear at least two calves to weaning (minimum of 4.5 years of age.)

Funding

This project has received extensive support from the Australian beef industry and the Commonwealth Government, by way of the following cash and in-kind contributions:

- ~$2.96m in cash and in-kind contributions over 7 years from the major Australian pastoral companies;
- ~$1.13m cash from Meat and Livestock Australia over 7 years;
- ~$1.3m cash from the Australian Centre for International Agricultural Research (ACIAR) over 5 years for a linked project in South Africa, with ~$600k to be spent in Australia on a stand-alone component of this project;
- ~$450k from CRC Commonwealth funds over 7 years to develop and maintain the project's quantitative and molecular genetics databases.

Discussion

Results from the CRC's progeny test program provide comprehensive guidelines for the genetic improvement of the major meat quality traits and Net Feed Efficiency. The data hold true for seven breeds of cattle in Australia: Angus, Hereford, Shorthorn, Murray Grey, Santa Gertrudis, Belmont Red and Brahman.

Gene Marker Technology is new and promising. Direct markers (DNA tests) are now confirmed for marbling and beef tenderness. For the present we do not know exactly how to combine gene marker information with traditional measures of genetic merit for beef traits (i.e. Estimated Breeding Values - EBVs). In Australia the gene markers are being used for selection of seedstock purposes. If the predictive value of these markers is sufficiently high (i.e. the marker accounts for a significant proportion of the observed variation in the trait), then the tests could be used for drafting cattle, such as steers for feedlot finishing. In Australia for example, it would save millions if we could select steers that would be guaranteed to achieve marble score 4 for the Japanese market. At the moment many cattle are fed for 200 days and do not meet the marbling specification. The penalty for this is serious loss of money.

The whole idea of identifying cattle genotypes and the production environment to meet market specification is helping the Australian industry. It begins with producers deciding which particular market they are in. The CRC's new breeding projects offer significant additional information to enhance profitability of northern herds.

Acknowledgements

The CRC is most grateful to the Cattle Council of Australia, Australian Lot Feeders' Association and Meat and Livestock Australia for continued support.

The assistance of Nicole Jones is gratefully acknowledged.

A schematic summary of the project is shown opposite.