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MEAT & LIVESTOCK AUSTRALIA

finalreport

Links between the genetics of beef quality and components of herd profitability in northern Australia

CRC BEEF

Abstract

This project targeted a pivotal issue in Australia's beef genetic improvement dilemma: *Can we change carcass and beef quality attributes of beef cattle without unduly compromising key fitness traits like reproductive performance and adaptation to harsh environmental stressors?* Industry outcomes targeted multiple traits and multi-faceted strategies including carcass and beef quality, feed efficiency, female fertility and tropical adaptation using a range of tools such as EBVs, DNA tests, ultrasound scanning and meat processing and cattle management strategies planned to impact on most sectors of the beef industry. Project results are globally unique. In the short to medium term, they will allow beef producers in tropical and sub-tropical environments to precisely target the specifications of premium beef markets, whilst simultaneously maintaining or improving female reproductive performance, without compromising adaptation to harsh environmental conditions. Within five years, it is realistic to expect the project will have achieved major economic impacts in northern Australian beef herds, with significant spin-off benefits for feedlotters, beef processors and southern Australian beef producers. Flow on benefits will also have accrued to cattle breeders worldwide.

Executive Summary

Results from the CRC for the Cattle and Beef Industry (Meat Quality) indicated that traits such as retail beef yield percentage (RBY%), intramuscular fat percentage (IMF%) and net feed intake (NFI) were heritable and would respond to selection. However, moderate to strong antagonistic genetic relationships existed between RBY% and NFI on the one hand and IMF% and fat thickness on the other. Higher yielding, more efficient sires produced progeny that were leaner and marbled less than progeny of lower yielding, less efficient sires. Hence, selection to improve RBY% or NFI is likely to reduce fat deposition throughout the body. Studies from humans, rats and cattle suggest a minimum fat cover may be necessary for puberty and conception. Selection of beef cattle for increased RBY% or improved NFI that results in reduced fat cover in breeding females may therefore reduce female fertility. Such relationships may be stronger in harsh environments and in *Bos indicus* breeds that suffer from lactational anoestrus. Hence a specifically designed breeding program was implemented to generate experimental progeny to investigate the hypothesised relationships.

The project targeted a pivotal issue in Australia's beef genetic improvement dilemma: *Can we change carcass and beef quality attributes of beef cattle without unduly compromising key fitness traits like reproductive performance and adaptation to harsh environmental stressors?* Industry outcomes from the project targeted multiple traits and multi-faceted strategies including carcass and beef quality, feed efficiency, female fertility and tropical adaptation using a range of tools such as Estimated Breeding Values (EBVs), genetic markers, ultrasound scanning and meat processing and cattle management strategies planned to impact on most sectors of the Australian beef industry.

Three separate but inter-related components of the project targeted the following objectives, to:
1.   Identify and communicate to cattle breeders the impact of selecting for carcass and beef quality attributes, efficiency of feed utilisation, adaptability to stressors of tropical environments and female reproductive attributes in order to maximise herd profitability in northern Australian environments.
2.   Demonstrate to producers the role and value of genetic markers for selecting commercial cattle for carcass and beef quality and adaptability.
3.   Extend the Australian and South African beef genetic evaluation schemes for Belmont Red and Bonsmara breeds to estimate breeding values for traits of economic importance across both countries with the aim of improving the productivity of beef herds in northern Australia.

To address objectives 1 and 2, 4,445 "generation 1" animals, representing 105 sires from Brahman and Tropical Composite breeds, were bred by AI and natural mating in co-operating herds owned by the Northern Pastoral Group of companies, individual seedstock breeders and CSIRO Livestock Industries. Generation 1 steers were grown on Queensland research stations and finished at the CRC's "Tullimba" feedlot. Generation 1 heifers were grown on 4 Queensland research stations and joined the breeding herd at ~2 years of age, where they were mated to produce "generation 2" progeny. For each Generation 1 and 2 animal produced, records included birth date, sex, birth weight (some properties), dam id and age, sire id (by DNA), breed composition (Composites), DNA sample id, generation and cohort, plus a very wide range of repeated measures of steer and heifer growth, individual feed intake and full carcase and beef quality attributes (steers only), scanned carcase attributes and adaptive measures (resistance to parasites and heat stress, dry season weight loss/gain and flight time as a measure of temperament (steers and heifers), scanned measures of female reproductive performance and full records of breeding herd performance in Generation1 females joined in multiple sire groups.

Genetics of beef quality and components of herd profitability in northern Australia

Objective 1: The impacts of selecting for carcass and beef quality attributes, feed efficiency, adaptation to tropical environments and female reproduction were determined and reported as estimates of genetic parameters for all traits. Results were delivered directly to co-operating breeders and key CRC stakeholders, particularly those based in northern Australia. However, widespread communication of the results to the cattle industry in general will not occur until the full extent of trade-offs from selection (arising from the direction and magnitude of relationships between the various groups of traits) is understood. That research is still ongoing, with the aim of publishing the complete results in a Special Issue of the new *Australian Journal of Animal and Food Science* in late 2007. Full economic analyses of all project traits (additional to project milestones) have now commenced, to enable practical recommendations to be made about how beef producers in northern Australia can utilise the full complement of project results to maximise herd profitability in their environments. An accurate and validated understanding of appropriate selection emphasis on carcass and beef quality, feed efficiency, female fertility and adaptability will only be available with knowledge of relationships amongst the entire range of traits and an examination of GxE interactions, genetic antagonisms and of differences between breeds in those parameter estimates, GxE interactions and genetic antagonisms. Those results will be presented in the Special Issue of the *Australian Journal of Animal and Food Science* in late 2007 and to beef industry end-users more widely as part of the Beef CRC's industry delivery activities.

Objective 2: Due to very rapid advances in genomics technology and some technical problems in the project, planned approaches to achieving Objective 2 changed substantially. *Preliminary* project results indicate that DNA markers described statistically significant additive variance in tenderness in Brahmans and Tropical Composites, but the percentage of additive variance that each of the markers explained individually and collectively was very small. At this point in time, the use of genetic markers for tenderness selection in young animals with no phenotype records for the trait is impractical. Development and validation of more markers associated with beef tenderness and other traits may mean DNA markers can be used for genetic improvement of those traits in future. DNA from project animals is now being used with the project's phenotypic database in other CRC projects to discover and validate DNA tests for many traits. Based on current progress, it is likely that multiple DNA tests for feed efficiency, parasite resistance and female reproductive performance will become available over the next 1-2 years. Hence in the short-medium term, these associated objectives will be significantly exceeded. In conjunction with the current 'Smartgene for Beef' project, the effect of commercially available DNA markers on economically important traits will provide extremely valuable information on the utility of commercially available markers in Brahmans and Tropical Composites and all production systems in this study. The results will also assist greatly in progressing the development of marker assisted EBVs and marker assisted selection.

Objective 3: The objective as described was not achieved due to a third-party dispute outside Beef CRC's control and project objectives were therefore modified. The modified objectives were significantly exceeded, with the project delivering substantial impacts on the commercialisation and profitability of the project's emerging farmers in South Africa. Project results also demonstrated considerable opportunities for beef producers in northern Australia to enhance herd productivity through replacement of a component of their high-grade Brahman herds using indigenous breeds and lines of cattle from southern Africa, to improve beef quality and female reproductive performance without compromising adaptation to tropical environments.

Project results are globally unique, providing Beef CRC, MLA and project scientists with world leadership in these areas. In the near future they will allow beef producers in tropical and sub-tropical environments to precisely target the specifications of premium beef markets whilst simultaneously maintaining or improving female reproductive performance, without compromising adaptation to harsh environmental conditions. Within five years, it is realistic to expect the project will have achieved major economic impacts in northern Australian beef herds, with significant spin-off benefits for feedlotters, beef processors and southern Australian beef producers. Flow on benefits will also have accrued to cattle breeders worldwide.

Contents

1 Background

Results from the Cooperative Research Centre (CRC) for the Cattle and Beef Industry (Meat Quality - CRCI) indicated that traits such as retail beef yield percentage (RBY%), intramuscular fat percentage (IMF%) and net feed intake (NFI) were heritable and would respond to selection (Reverter *et al.*, 2003a; Robinson and Oddy, 2004). However, moderate to strong antagonistic genetic relationships existed between RBY% and NFI on the one hand and IMF% and fat thickness on the other. Higher yielding, more efficient (low NFI) animals produce progeny that are leaner and marble less than progeny of lower yielding, less efficient animals (Reverter *et al.*, 2003b; Robinson and Oddy, 2004). Hence, selection to improve RBY% or NFI is likely to reduce fat deposition throughout the body. Studies from humans and rats (Frisch, 1984) and tropical breeds of cattle (O'Kelly *et al.*, 1988) suggest a minimum fat cover may be necessary for puberty and conception. Selection of beef cattle for increased RBY% or improved NFI that results in reduced fat cover in breeding females may therefore reduce female fertility. Such relationships may be stronger in harsh environments and in *Bos indicus* breeds that suffer from lactational anoestrus (Frisch *et al.*, 1987). A specifically designed breeding program was implemented to generate experimental progeny to quantify the hypothesised relationships.

The project targeted the pivotal issue in Australia's beef genetic improvement dilemma: *Can we change carcass and beef quality attributes of beef cattle without unduly compromising key fitness traits like reproductive performance and adaptation to harsh environmental stressors?* Industry outcomes from the project targeted multiple traits and multi-faceted strategies including carcass and beef quality, feed efficiency, female fertility and adaptation to tropical environments using a range of tools such as Estimated Breeding Values (EBVs), genetic markers, ultrasound scanning and meat processing and cattle management strategies that will impact on most sectors of the Australian beef industry. The major winners of the project are cattle breeders in the tropics and subtropics of Australia, although the results also have flow on benefits for cattle breeders worldwide. Outcomes from the project are aimed at:

➢ encouraging better designed breeding programs, specifically targeting tropical and sub-tropical beef production systems;
➢ providing informed decisions on the economic viability of changed management practices to improve carcass and beef quality attributes or female fertility;
➢ incorporating gene marker profiles into genetic evaluation schemes like BREEDPLAN to increase genetic progress;
➢ through the South African component of the project, identifying genetically superior animals to promote the international exchange of superior germplasm to enhance productivity of beef herds in northern Australia.

2 Project Objectives

1. By June 2006, to identify and communicate to cattle breeders the impact of selecting for carcass and beef quality attributes, efficiency of feed utilisation, adaptability to stressors of tropical environments and female reproductive attributes in order to maximise herd profitability in northern Australian environments.

2. By June 2005, to demonstrate to producers the role and value of genetic markers for selecting commercial cattle for carcass and beef quality and adaptability.

By December 2005, the following objectives will be achieved:

3. The Australian and South African beef genetic evaluation schemes for Belmont Red and Bonsmara breeds will be extended to estimate breeding values for traits of economic importance across both countries, in order to improve the productivity of beef herds in northern Australia.

4. An accurate and validated understanding of appropriate selection emphasis on carcass and beef quality, feed efficiency, female fertility and adaptability.

5. New techniques based on ultrasound scanning to identify minimum fatness levels that are compatible with high fertility.

6. An accurate and validated understanding of specific genetic markers for selecting commercial cattle for carcass and beef quality and adaptability.

7. Knowledge of genetic parameters between all traits and marker assisted selection.

8. Identification of breeds and lines of cattle with outstanding genetic merit for carcass and beef quality, adaptation to tropical environments and female fertility.

3 Methodology

A total of 4,445 "generation 1" animals, representing 105 sires from two genotypes, were bred from the mating of industry and CRC-nominated sires to base cows ("Generation 0") in co-operating herds belonging to the Northern Pastoral Group of companies, individual seedstock breeders and CSIRO Livestock Industries at Belmont Research Station, which is owned by AgForce Queensland (see Burrow *et al.* 2003 and Burrow and Bindon, 2005 for complete details). Female progeny produced by the project were grown out at 4 locations and mated each year to produce "generation 2" progeny. Key features of the design were:

- Use of two tropically adapted genotypes (Brahman and Tropical Composites), representing large differences amongst tropically adapted breeds for carcass and beef quality, adaptation and male and female fertility traits.
- Approximately 2,200 progeny (original target of 2,400) per breed were generated from about 50 sires (i.e. 20-30 progeny per sire and sex). These numbers were required to enable accurate estimates of the genetic relationships between traits, particularly between lowly heritable female fertility traits.
- Sires used included a mix of those nominated by the collaborating breeders and sires nominated by the CRC, the latter mainly used through AI. Most sires nominated by the collaborators were young, unproven bulls. CRC-nominated sires were selected primarily on the availability of moderate to high accuracy BREEDPLAN EBVs for retail beef yield percent (RBY%) and intramuscular fat percent (IMF%). Sires representing high and low EBVs for the two traits were used. Additional selection criteria included known heterozygosity for gene markers identified in CRCI, or the ability of a sire to genetically link to other genetics projects (e.g. CRCI straightbreeding and crossbreeding projects) and to industry data (e.g. Brahman BREEDPLAN herds). Sires with BREEDPLAN EBVs derived outside the project data also allow examination of the ability of EBVs to predict progeny differences in a range of different production systems.
- A proportion of each breeding herd was mated by AI followed by natural service joining in large multiple sire groups to generate genetic linkages across co-operator breeding herds and years.
- A DNA sample was collected on all animals (generations 1 and 2), all sires, and many base dams (generation 0). This allowed sire parentage assignment for all animals. Used in conjunction with the phenotypic measures, the DNA forms an extremely value resource for gene marker mapping and validation studies.
- Calves were generated by 8 co-operators. At weaning, all calves were delivered to the control of the CRC and ownership remained with the co-operators.
- Generation 1 calves were produced across 4 years.
- Steers and heifers were allocated to post-weaning groups on the basis of property of origin and sire. The allocation was carefully done to ensure genetic linkage was maintained across post-weaning cohorts.
- Heifers were relocated post-weaning to one of 4 Queensland research stations (QDPI and CSIRO) where they entered the breeding herd at 2 years of age. Generation 2 male progeny are being retained for a third-term CRC genetics of male fertility experiment. The heifers are sold or returned to their owners at weaning. All generation 2 calves are parentage identified using DNA fingerprinting.
- Steers were backgrounded at one of 5 growout properties and when the average liveweight of the group was 400-440 kg they were transferred to the Tullimba feedlot for grain finishing and slaughter to achieve carcass weights of around 320 kg.
- Environments for measuring heifer/cow performance traits were chosen to represent the range encountered by each breed, also recognising that the expected range for performance includes harsher (e.g. greater tick and worm prevalence) environments for Brahmans than for the Tropical Composites.

Measurements

1) Animal details

For each animal produced by the project (generation 1 and 2) records included property of origin, date of birth, sex, birth weight (not all properties or locations), dam id, dam age (days or year), sire id (by DNA), breed composition (for Tropical Composites), DNA sample id, Breed Society registration number, generation number (1 or 2), and post weaning cohort. Current BREEDPLAN EBVs are also available for animals recorded with Brahmans or Belmont Red Society databases.

2) Pre-weaning and post-weaning measures

Numerous traits (growth, adaptability, composition) were recorded on both sexes and many of the traits were repeatedly measured. The date of measurement and the location of the animal (including paddock) were recorded for each record. Traits included: weaning weight, post-weaning weight (usually monthly), hip height, ultrasound scans (EMA, P8, rib and IMF fat), condition score, feet scores, teat and udder scores, IGF-1, flight time, faecal egg counts, tick scores and counts, buffalo fly lesion scores, rectal temperature, coat colour, coat score, sheath and navel scores. For steers the 3 distinct stages of post-weaning, feedlot entry and feedlot exit were identified. For heifers the periods of out of 1st post-weaning wet season and end of 2nd post-weaning dry season (i.e. into mating) were identified as 2 stages of interest for defining heifer development.

3) Steer traits

Before embarking on extensive research into feed efficiency in tropically adapted cattle, an assessment of the relative economic importance of feed intake traits to northern cattle breeders was undertaken (Barwick, 2002; Barwick and Johnston, 2003). The study also considered whether Net Feed Intake (NFI) was a useful trait for breeders of tropical cattle. This followed from earlier studies suggesting that measures of feed efficiency in the tropics should be based on restricted, low quality diets rather than the unrestricted, high quality diets used in NFI tests (Frisch and Vercoe, 1984). Findings from Barwick and Johnston (2003) include:

- The importance of the NFI measure of feed efficiency is similar in steers in the tropics to that in temperate (domestic market) systems, but may be of quite low importance in cows in the tropics due to lower costs of feed.
- Feed efficiency measures for northern Australia will need to be inexpensive and will likely best involve indirect measures in combination with some amount of NFI testing (Archer et al., 2003).

Based on these results, it was decided to finish all steers in the project on high energy diets at the CRC's "Tullimba" cattle research facility near Armidale NSW, where individual feed intakes of a standard finisher ration offered ad-libitum were recorded using automatic feed intake recorders (see Bindon, 2001)

Steers were backgrounded at one of 5 growout properties and when the average liveweight of the group was 400-440 kg they were transferred to the Tullimba feedlot. A subset of the steers were individually feed intake tested for 70 days using the automatic feeders with approximately 12 animals per pen. All steers were feedlot finishing for approximately 120 days and slaughtered when the average liveweight of the cohort was 550 kg (320 kg carcass). In total there were 26 slaughter groups. For each body the left side was conventionally hung (i.e. Achilles tendon) and the right side was Tenderstretched. A meat sample was removed from both sides and frozen for subsequent meat quality assessment (see Perry et al., 2001 for full details of these analyses).

4) Traits measured specifically on steers included those associated with feedlot finishing, carcass and meat quality.

i) Feedlot traits: individual feed intake (time, duration, amount) for a 70 d test, weights and gains, net feed intake, ultrasound scans, flight time, feet score and IGF-1 (at entry and exit).

ii) Carcass traits: hot carcass weight, hot P8 fat depth, dentition, Ausmeat, MSA and VIA chiller assessments and yield % (either whole side bone out or VIA whole body scan).

iii) Meat quality: shear force, compression, cooking loss, Minolta colour measures, all for each of 2 carcass side hanging methods, and intramuscular fat%.

5) Female traits

Additional traits measured on the heifers and cows included ovarian scanning, full breeding and calving history, calf performance and disposal information. At each location all heifers from the same year of birth were managed as a single group (defined as a cohort). Ultrasound scanning was used to measure fatness attributes and ovarian activity in all heifers to determine factors affecting cyclicity. Subjective reproductive tract scores were also recorded to determine their value as an on-farm tool to assess cyclicity. As heifers achieved weights of 200 kg, they were scanned and scored each 4-6 weeks until the first *corpus luteum* (CL) was detected, when they were deemed to have reached puberty. Liveweight and measures of body composition (scan P8 fat depth and body condition score) were also recorded at this time. The occurrence of a CL prior to, and on the day of, the commencement of their first (i.e. maiden) mating was also derived.

At each location, the heifers joined the breeding herd at an average age of 2 years, where they were joined for 12 weeks in multiple-sire joining paddocks with industry-sourced bulls of the same breed at a bull: female ratio of 3%. The average age at the commencement of joining (JAGE) was approximately 25 months (i.e. to first calve as 3 year olds). Commencement date for mating differed slightly across locations within a year reflecting regional preferences for calving times. Any female failing to wean a calf in 2 consecutive years was culled. Reproductive data were recorded in CRCII on all females until they had the opportunity to rear at least 2 calves to weaning (reproductive performance continues to be recorded in the CRCIII program, to determine relationships between early-life reproductive performance and lifetime fertility).

Ultrasound scanning continued through joining to determine: i) timing of first CL for heifers that had not reached puberty at start of joining; ii) early pregnancies and possibly embryonic losses and iii) return to cyclicity of lactating females. Regular scanning of such large numbers of females has generated significant improvements in our understanding of the basic biology of female fertility.

Traits measured included:
i) Ovarian scanning traits (left and right ovary): primary follicle size, secondary follicle size, ovarian activity score, ovary shape score, ovary size, CL presence, CL size, uterine tract size and tone scores, pregnancy status and foetal age.

ii) Mating details: bull-in / bull-out dates, mating paddock, bull syndicate and IGF-1 into-mating.

iii) Calving details: date of birth, sex, birth weight, weaning records (weight, IGF-1, flight time, coat score and colour, scrotal size) and sire (by DNA).

6) Adaptive traits and other key relationships and analyses

The project also targeted adaptive traits (resistance to parasites and heat stress, flight time as a measure of an animal's adaptation to handling stress etc) and other key relationships that are potentially very important for genetic improvement programs and evaluation of management options, but which required new or additional data to quantify or confirm them. They included:

- Phenotypic and genetic relationships of flight time (a measure of temperament) and feed efficiency with carcass and beef quality attributes and female fertility traits;
- Genetic relationships between plasma insulin-like growth factor (IGF1) concentration measured at different stages of an animal's life and feed efficiency, carcass attributes and female fertility traits;
- A comparison of the effect of method of hanging carcasses (Tenderstretch *vs.* Achilles-hung) on carcass and beef quality and especially on genetic parameters for beef tenderness;
- Complete economic analyses to examine the economic impact of changed genetics and/or management practices on herd profitability.

4   Results and Discussion

Project objectives as originally described (see Section 2 of this report) are inter-related and can readily be re-grouped into 3 broad objectives. Results are presented and discussed within these 3 broad objectives in the following section.

Quantitative Genetic Objectives

- ***Identify and communicate to cattle breeders the impact of selecting for carcass and beef quality attributes, efficiency of feed utilisation, adaptability to stressors of tropical environments and female reproductive attributes in order to maximise herd profitability in northern Australian environments.***

- ***Derive an accurate and validated understanding of appropriate selection emphasis on carcass and beef quality, feed efficiency, female fertility and adaptability.***

- ***Develop new techniques based on ultrasound scanning to identify minimum fatness levels that are compatible with high fertility.***

- ***Identify breeds and lines of cattle with outstanding genetic merit for carcass and beef quality, adaptation to tropical environments and female fertility.***

A very large number of genetic analyses relating to the above objectives have been completed and the results are now being written up and discussed in a series of 3-5 scientific publications to be published as part of a special issue of a new *Australian Journal of Animal and Food Science* (CSIRO Publishing) in late 2007. Analyses were conducted on a trait-by-trait basis both within and pooled across the two genotypes. For each trait, the analyses involved first determining the appropriate fixed effects model and then using these effects in a univariate REML analysis for the estimation of variance components. Genetic and phenotypic correlations within and across the trait complexes were then computed for all pair-wise trait combinations.

Analyses of the female mating and re-breeding data are ongoing within the third-term Beef CRC, as each year generates further data on individual cow reproductive performance. Numerous non-genetic analyses (e.g. follicular development, heifer growth curves, carcass tenderstretch and economic impacts of all results) not considered part of the above objectives are also underway to provide practical recommendations to the Australian beef industry on management practices to improve female reproductive performance.

Figure 1 summarises the genetic analyses that have been undertaken. Squares on the diagonal indicate the groups of traits being targeted by the project, including:

- Steers: repeated measures of growth, net feed intake, ultrasound scans for carcass attributes and scores for a full range of structural and temperament traits
- Heifers: repeated measures of growth, ultrasound scans for carcass attributes and scores for a full range of structural and temperament traits
- Heifers: age, weight and fatness at puberty + repeated measures of ovarian activity between 200kg and time the heifer joined the breeding herd
- Steers and Heifers: repeated measures of resistance to ticks, worms, buffalo flies, heat stress and dry season nutrition (when the stressors were present)
- Steers: a full range of carcass and beef quality attributes including retail beef yield, intramuscular fat percentage and beef tenderness;
- Breeding females: repeated ultrasound scans for reproductive function + complete measures of joining, calving and re-breeding).

Each group of traits has been analysed separately to estimate the variances and heritabilities for every trait. Of greater interest to most beef producers though are the genetic (future herd and achieved by use of breeding strategies shown on the upper quadrant of the matrix pictured in Figure 1) and phenotypic (current herd and achieved by management / non-genetic approaches that logically slot into the lower quadrant of the matrix in Figure 1) relationships between these groups of traits as well as the supplementary economic analyses.

Figure 1. Groups of traits targeted by this project (shown on diagonal) and genetic relationships (r_g) between the groups of traits that identify the magnitude and direction of the trade-offs occurring as a result of selection for traits shown on the diagonal. Phenotypic relationships (r_p) can be inferred in the lower quadrant of the matrix.
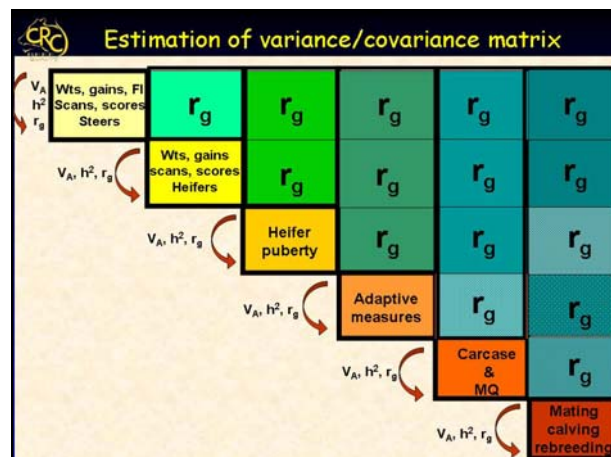
The project has generated an amazing amount of new knowledge on the underlying quantitative genetic mechanisms controlling a wide range of adaptive and productive traits important for beef production in tropical and sub-tropical environments and relationships between all of these traits. This report presents a summary (means and heritabilities) of the traits analysed. However none of the vast number of generalised correlation matrices (across groups of traits) has been included as they continue to be carefully examined to determine their importance in for issues such as Genotype x Environment (GxE) interactions, early-life indicator traits, genetic antagonisms, breed differences and economic impact in breeding herds in the tropics and subtropics. Those matrices and some of the non-genetic results will be published as scientific papers in the Special Issue of the *Australian Journal of Animal and Food Science* in late 2007.

Table 1 shows a list of definitions and abbreviations for each of the traits included in this report.

Table 1. Abbreviations and definition of traits reported in this study

Abbreviation	Definition
Age (days)	Age in days at the time of measurement
LWT (kg)	Liveweight at time of measurement
IGF-1 (ng/mL)	Blood IGF-1 level
CS (score)	Condition score
HH (cm)	Hip height
FT (s*100)	Flight time - electronically recorded time taken for animal to cover a fixed distance after leaving the weighing crush at ~300 days of age
ADG (kg/day)	Average daily gain
SP8 (mm)	Scanned P8 fat depth
SP8G (mm/day)	Change in P8 fat depth since previous scan
SRIB (mm)	Scanned rib fat depth
SEMA (cm^2)	Scanned eye muscle area
SIMF (%)	Scanned intramuscular fat percentage
Age, mid-test (days)	Age of steers at mid-point of feed intake measurement period
FI (kg/day)	Daily feed intake
MWT (kg)	Weight of steers at mid-point of feed intake measurement period
TADG (kg/day)	Average daily gain over feed intake test measurement period
NFI (kg/day)	Net Feed Intake
Slaughter age (days)	Age in days at time of slaughter
Ossification (score)	MSA USDA Ossification
CWT (kg)	Carcass weight
CP8 (mm)	Cold P8 fat depth
HP8 (mm)	Hot P8 fat depth
CRib (mm)	Cold rib fat depth
Hump Ht (mm)	Hump height
CEMA (cm^2)	Chiller AUSMEAT Eye Muscle Area (sq cm)
Marbling (score)	Chiller AUSMEAT assessed Marbling score (new chips 0-6)
CIMF (%)	Chiller intramuscular fat percentage
RBY (%)	Retail beef yield percentage
AT_shear force (kg)	Achilles-hung *m. longissimus dorsi* Shear Force (kg), a mechanical measure of beef tenderness (lower values indicate more tender beef)
TS_ shear force (kg)	Tenderstretch *m. longissimus dorsi* Shear Force (kg)
AT_ compression (kg)	Achilles-hung *m. longissimus dorsi* Instron Compression (kg), a mechanical measure of beef tenderness (lower values indicate more tender beef)
TS_compression (kg)	Tenderstretch *m. longissimus dorsi* Instron Compression (kg)
AT_ cooking loss (%)	Achilles-hung *m. longissimus dorsi* cooking loss

TS_ cooking loss (%)	Tenderstretch *m. longissimus dorsi* cooking loss
Abbreviation	Definition
AGECL (days)	Age at first detection of *corpus luteum*
WTCL (kg)	Weight at first detection of *corpus luteum*
FATCL (mm)	P8 fat depth at first detection of *corpus luteum*
CSCL (score)	Condition score at first detection of *corpus luteum*
TSCORE (mm)	Uterine tract score size
PRIORCL (%)	Whether or not first *corpus luteum* or post-partum return to oestrus had been achieved by start of mating
MDAYCL (%)	Whether or not first *corpus luteum* or post-partum return to oestrus had been achieved mid-way through mating
DC1 (days)	Days to calving (bull in to calving date) for first calf
CS1 (%)	Calving success for first calf
DC2 (days)	Days to calving (bull in to calving date) for second calf
CS2 (%)	Calving success for second calf
TICK	Tick scores recorded on a 0 to 5 scale based on number of engorging ticks of >4.5 mm long on one side of the animal following field infestations. Only tick scores recorded on mature cows at Belmont (May 2004) and Swans Lagoon (October 2003) were included due to lack of tick challenge
EPG	Number of worm eggs per gram of faeces recorded post weaning at around 260 days of age
FLY	Fly lesion scores recorded on a 1 to 5 scale during March / April 2005 each year when flies were endemic (Range from 1 - no visible lesions to 5 - multiple bleeding lesions)
TEMP	Rectal temperatures of animals recorded at around 400 days of age during summer months when the ambient temperatures were > 30^0C.
COAT	Subjective oat scores of animals recorded during post weaning summer months (range from 1 - extremely short and sleek coat, to 7 - very woolly coat)

1) Steer early growth and feedlot performance traits

Table 2. Unadjusted means and standard deviations for steer traits at weaning (WEAN), post-weaning (POSTW), feedlot entry (ENTRY), end of feed test (FEEDTEST) and feedlot exit (EXIT; see Table 1 for a description of traits).

	Brahman			Tropical Composite		
Trait	N	Mean	s.d.	N	Mean	s.d.
		WEAN				
Age (days)	1007	197.1	45.8	1210	194.5	30.6
LWT (kg)	1007	180.5	43.6	1209	198.9	34.1
IGF-1 (ng/mL)	252	312.6	150.3	249	241.7	135.0
		POSTW				
Age (days)	1000	284.2	51.9	1197	313.4	59.0
LWT (kg)	1000	193.3	41.5	1192	217.0	35.4
SEMA (cm^2)	591	33.4	7.4	850	35.0	7.2
CS (score)	698	5.5	1.6	723	6.2	0.9
HH (cm)	715	117.4	6.5	774	116.7	5.6
FT (s*100)	695	105.5	52.1	722	116.1	46.9
IGF-1 (ng/mL)	612	223.3	116.8	735	233.8	140.3
		ENTRY				
Age (days)	991	662.2	124.2	1194	662.5	129.3
LWT (kg)	987	393.3	48.0	1194	405.8	49.5
ADG (kg/day)	981	0.53	0.16	1190	0.56	0.21
SP8 (mm)	986	4.9	2.1	1192	4.4	2.4
SRIB (mm)	988	2.8	1.2	1193	2.8	1.5
SEMA (cm^2)	987	57.9	6.9	1191	58.5	7.7
SIMF (%)	981	2.78	0.61	1190	2.73	0.73
CS (score)	702	7.2	1.2	1007	7.2	1.4
HH (cm)	735	134.8	5.4	895	131.4	4.8
IGF-1 (ng/mL)	953	510.3	183.4	1105	504.5	174.7
		FEEDTEST				
Age, mid-test		732.8	119.6		736.8	125.2
FI (kg/day)	700	11.24	1.94	787	13.10	1.95
MWT (kg)	700	93.6	7.4	787	98.0	7.7
TADG (kg/day)	681	1.128	0.360	783	1.467	0.357
NFI (kg/day)	680	-4.06	1.06	783	-3.73	1.17
		EXIT				
Age (days)		768.9	115.0		772.9	125.3
LWT (kg)	979	539.2	60.7	1192	591.6	64.9
ADG (kg/day)	974	1.21	0.35	1191	1.57	0.35
SP8 (mm)	922	11.8	3.4	1191	12.2	4.0
SRIB (mm)	922	7.4	2.4	1190	8.1	2.8
SEMA (cm^2)	921	72.6	7.5	1190	77.7	8.1
SIMF (%)	809	4.13	0.77	1104	4.62	0.83
CS (score)	568	9.1	1.3	960	9.8	1.3
HH (cm)	831	141.2	5.1	1142	137.8	5.4
IGF-1 (ng/mL)	738	583.8	131.8	1129	602.4	154.2

Table 3. Phenotypic (σ^2_P) and additive genetic (σ^2_A) variances as a percentage of the observed variance (P%) and % heritabilities (h^2) for traits of Brahman and Tropical Composite steers at 5 measurement times (approximate standard errors in parentheses; see Table 1 for a description of traits; WEAN - weaning; POSTW - post-weaning; ENTRY - feedlot entry; FEEDTEST - feed intake test; EXIT - feedlot exit)

Trait	Brahman				Tropical Composite			
	σ^2_P	P%	σ^2_A	h^2	σ^2_P	P%	σ^2_A	h^2
				WEAN				
LWT [B]	367.0	19	62.4	17 (8)	594.6	51	325.8	55 (16)
				POSTW				
LWT [B]	398.9	23	97.7	24 (10)	575.6	46	198.8	35 (13)
SEMA	21.3	39	1.23	6 (9)	23.2	45	12.97	56 (13)
CS	0.668	26	0.048	7 (7)	0.669	83	0.123	18 (9)
HH	15.7	37	6.43	41 (14)	16.8	54	9.39	56 (16)
FT (*100*)	2084.2	77	235.2	11 (9)	2133.6	97	440.8	21 (11)
IGF-1	6325.2	46	3162.8	50 (17)	7378.4	37	699.1	9 (10)
				ENTRY				
LWT	926.5	40	216.9	23 (10)	1145.4	47	478.8	42 (11)
ADG (*100*) [B]	23.94	9	4.20	18 (9)	36.46	8	10.80	30 (9)
SP8 [A]	3.03	69	0.98	32 (10)	2.63	46	0.85	32 (10)
SRIB	1.13	78	0.49	43 (11)	1.21	54	0.27	23 (8)
SEMA	33.3	70	7.44	22 (9)	41.9	71	20.11	48 (11)
SIMF	0.312	84	0.042	13 (7)	0.410	77	0.200	49 (11)
CS [B]	0.550	38	0.040	7 (8)	0.794	41	0.024	3 (5)
HH	19.6	67	10.02	51(1.4)	17.5	76	8.18	47 (14)
IGF-1	12928	38	3963	31 (11)	13267	43	1769.4	13 (7)
				FEEDTEST				
FI	2.86	76	1.39	49 (15)	3.35	88	1.72	51 (14)
MWT [B]	33.7	62	15.7	47 (16)	43.6	74	17.2	39 (13)
TADG (*100*)	1030.9	80	350.9	34 (11)	1114.6	87	224.7	20 (9)
NFI	0.80	71	0.19	24 (11)	1.09	80	0.41	38 (12)
				EXIT				
LWT [B]	2527.0	69	1198.1	47 (14)	3235.6	77	1911.6	59 (14)
ADG (*100*)	886.4	72	366.7	41 (11)	943.4	77	467.2	50 (12)
SP8	9.54	83	3.78	40 (12)	14.28	89	7.58	53 (12)
SRIB [B]	4.48	78	1.97	44 (11)	6.86	88	2.16	31 (10)
SEMA	46.5	83	4.59	10 (8)	57.5	88	23.15	40 (10)
SIMF	0.44	74	0.08	17 (10)	0.65	94	0.29	45 (10)
CS	1.28	76	0.33	26 (13)	1.33	79	0.54	41 (13)
HH	22.5	87	11.85	53 (13)	23.5	81	7.04	30 (10)
IGF-1	12345	71	4136	34 (14)	17037	72	3929	23 (9)

[A,B]*Traits of Brahmans (A) and Tropical Composites (B) where the model included a significant maternal environmental effect*

Genetic correlations for steer feed intake and NFI with growth traits and fatness were estimated separately for Brahmans and Tropical Composites. Heritability of NFI was 0.24 and 0.38 for Brahmans and Tropical Composites respectively (Table 3). Genetic correlations between NFI and growth, hip height and P8 fat depth at feedlot entry (r_g = -0.68, -0.41, -0.56 respectively; Table 4) indicated these traits could be exploited to indirectly improve NFI in Brahmans, but were of little use for the Tropical Composites. IGF-I, sampled at feedlot entry and feedlot exit, had a negative correlation with NFI for these cattle treated with hormonal growth promotants.

Table 4. Genetic correlations (and SE) between feed intake (FI) and net feed intake (NFI), growth and fatness traits and plasma insulin-like growth factor-I concentration (IGF-I) for Brahmans and Tropical Composites measured at feedlot entry and feedlot exit (adapted from Wolcott *et al.*, 2006; see Table 1 for description of traits).

	Brahmans		Tropical Composites		Both Breeds	
	FI	NFI	FI	NFI	FI	NFI
Feedlot entry						
Liveweight	0.67 (0.18)	-0.19 (0.32)	0.69 (0.12)	-0.07 (0.23)	0.68 (0.11)	-0.04 (0.18)
Daily gain	0.25 (0.27)	-0.68 (0.30)	0.75 (0.14)	0.17 (0.24)	0.53 (0.14)	-0.01 (0.20)
P8 fat depth	-0.60 (0.19)	-0.41 (0.26)	-0.14 (0.22)	0.01 (0.24)	-0.38 (0.15)	-0.11 (0.18)
Hip height	0.23 (0.22)	-0.56 (0.26)	0.55 (0.16)	0.05 (0.24)	0.39 (0.14)	-0.17 (0.19)
IGF-I	-0.16 (0.25)	0.03 (0.30)	-0.41 (0.26)	-0.51 (0.29)	-0.33 (0.18)	-0.28 (0.20)
Feedlot Exit						
Liveweight	0.92 (0.05)	0.67 (0.29)	0.92 (0.04)	0.18 (0.21)	0.89 (0.04)	0.11 (0.17)
Daily gain	0.97 (0.04)	0.67 (0.27)	0.90 (0.05)	0.26 (0.22)	0.91 (0.03)	0.20 (0.17)
P8 fat depth	0.29 (0.22)	0.67 (0.28)	0.48 (0.17)	0.38 (0.20)	0.41 (0.13)	0.33 (0.16)
Hip height	0.28 (0.22)	0.67 (0.23)	0.50 (0.20)	-0.12 (0.25)	0.35 (0.15)	-0.32 (0.17)
IGF-I	-0.16 (0.25)	0.67 (0.30)	-0.41 (0.26)	-0.51 (0.29)	-0.33 (0.17)	-0.56 (0.18)

Genetic correlations for corresponding measures of steer and heifer growth and live body composition were examined for Brahman and Tropical Composite cattle to examine the extent of genotype x environment and sex interactions when production systems differ markedly for the sexes (Barwick *et al.* 2006). Steer measures were at feedlot entry and feedlot exit. Heifer measures were at the end of the first "wet" and second "dry" season experienced post-weaning. A number of correlations differed from unity (Table 5). For certain growth and scanned body composition measures, genetic evaluation and selection in these genotypes may need to distinguish heifer wet and dry seasons and steer growth and feedlot environments as separate traits, especially for Brahman heifers and Tropical Composite steers.

Summary results indicate that:
- Feedlot feed efficiency (as NFI) was moderately heritable in both genotypes.
- Genetic correlations between NFI and growth rate prior to feedlot entry, P8 fat depth, and hip height measured at feed entry indicated these traits could be exploited through selection to indirectly improve NFI in Brahmans, but appear to be of limited use for Tropical Composites.
- Selection for improved NFI will on average result in taller leaner cattle.
- Results are consistent with Brahmans being more adapted to harsh, tropical heifer environments and Tropical Composites being better able to exploit feedlot conditions.
- For certain growth and scanned body composition measures, genetic evaluation and selection of Brahman and Tropical Composite cattle for these environments may need to distinguish heifer season and steer growth environments as separate traits, especially for Brahman heifers and Tropical Composite steers.
- The new parameter estimates and data on many traits and genetic linkages from this project will greatly strengthen BREEDPLAN for tropical breeds.

Table 5. Genetic correlations (and SE) between repeat measurements of liveweight, average daily gain, scanned P8 fat depth and scanned eye-muscle area in Brahman and Tropical Composite steers and heifers.

Trait	Sex / Measurement time / Genotype	
	Steer Feedlot Entry vs. Steer Feedlot Exit	
	Brahmans	Tropical Composites
Liveweight	0.79 (0.11)	0.90 (0.04)
Average daily gain	0.10 (0.27)	0.64 (0.15)
P8 fat depth	0.82 (0.10)	0.66 (0.12)
Eye muscle area	1.00 (0.19)	0.74 (0.10)
	Heifer Wet I vs. Heifer Dry II	
	Brahmans	Tropical Composites
Liveweight	0.99 (0.01)	0.99 (0.01)
Average daily gain	0.12 (0.30)	0.49 (0.23)
P8 fat depth	0.95 (0.04)	0.97 (0.03)
Eye muscle area	0.94 (0.07)	0.98 (0.03)
	Heifer Dry II vs. Steer Feedlot Exit	
	Brahmans	Tropical Composites
Liveweight	0.37 (0.21)	0.84 (0.09)
Average daily gain	-0.01 (0.27)	0.50 (0.21)
P8 fat depth	0.67 (0.17)	0.63 (0.12)
Eye muscle area	0.43 (0.34)	0.86 (0.11)

Insulin-like Growth Factor-I (IGF-I) blood test

The inconvenience and cost of testing seedstock cattle for NFI lead the CRC to look for gene markers and physiological tests to increase the accuracy of the NFI EBV and/or to reduce cost of finding superior stock. The first of these, a blood test for the protein IGF-I, was introduced to BREEDPLAN in 2004. It followed from research using feed intake, NFI, and IGF-I records for cattle in the Trangie Angus feed efficiency herd and CRCI straight breeding project. Results showed that IGF-I concentration in plasma taken post-weaning were heritable and genetically correlated with growth and feed efficiency. This provided an opportunity to use an early-life measure as a selection criterion for the genetic improvement of feed efficiency and carcass traits. However further research to investigate the optimal age to measure IGF-I was needed (Johnston *et al.* 2002).

The blood test is performed by the Australian company Primegro Ltd, which has the exclusive right to commercialise this Australian Intellectual Property. Being an indirect indicator for NFI, a NFI EBV computed from an IGF-I record has lower accuracy than a NFI EBV generated from a NFI record. For example, a sire NFI EBV with 50% accuracy can be obtained by feed intake testing 3 progeny or testing 27 progeny for IGF-I. High accuracy NFI EBV will still require some animals to be measured for individual feed intake.

For the tropical breeds examined in this project, IGF-I sampled at post-weaning, feedlot entry and feedlot exit had a negative genetic correlation with NFI for both genotypes (Table 4, opposite to the findings for temperate breeds; Wolcott *et al.* 2006). Both the timing of IGF-I sampling and the use of hormonal growth promotants may have influenced these results, which are outside the current guidelines for use of this test for British breeds in southern Australia.

Research has provided good evidence for genetic variation in feed efficiency in Australian beef cattle breeds. NFI is moderately heritable, responds to selection and presents an opportunity to improve the feed efficiency and profitability of beef production in tropical Australia.

2) Carcass and Meat Quality traits (steers only)

Table 6. Unadjusted trait means, standard deviations and ranged for Brahman and Tropical Composite steer carcass traits (see Table 1 for definition of traits)

Trait	N	Mean	s.d.	Min.	Max.
		Brahman			
Slaughter age (days)	986	791	128	559	1051
Ossification (score)	981	247	75	120	500
CWT (kg)	986	299.7	34.8	192	415
CP8 (mm)	909	12.5	4.0	2	30
HP8 (mm)	986	13.7	4.1	4	30
CRib (mm)	913	7.9	3.3	0	20
Hump Ht (mm)	913	166	34.6	70	250
CEMA (cm^2)	981	72.7	8.3	51	107
Marbling (score)	981	0.61	0.40	0.10	2.40
CIMF (%)	840	2.20	0.80	0.31	6.72
RBY (%)	274	67.9	2.6	56.2	74.4
AT_shear force (kg)	955	5.38	1.16	2.55	9.00
TS_ shear force (kg)	880	4.43	0.58	2.89	6.49
AT_ compression (kg)	977	1.93	0.29	1.09	2.85
TS_compressions (kg)	881	1.82	0.27	1.12	2.77
AT_ cooking loss (%)	972	23.2	4.27	13.8	38.4
TS_ cooking loss (%)	889	20.7	2.63	13.3	29.1
		Tropical Composites			
Slaughter age (days)	1193	787	131	575	1061
Ossification (score)	1192	235	66	90	480
CWT (kg)	1195	324.8	37.1	174.5	428.8
CP8 (mm)	1176	13.5	4.4	2	30
HP8 (mm)	1194	15.2	4.8	5	35
CRib (mm)	1192	10.0	4.1	0	25
Hump Ht (mm)	1192	120.6	24.7	50	230
CEMA (cm^2)	1191	77.5	8.8	46	121
Marbling (score)	1192	0.83	0.55	0.10	3.40
CIMF (%)	1182	2.90	1.10	1.04	8.89
RBY (%)	289	67.0	3.0	57.3	73.1
AT_shear force (kg)	1174	4.73	1.21	1.57	8.85
TS_ shear force (kg)	1046	3.91	0.54	2.41	6.00
AT_ compression (kg)	1183	1.83	0.30	1.02	2.90
TS_compressions (kg)	1041	1.68	0.25	0.84	2.38
AT_ cooking loss (%)	1117	22.5	3.17	14.6	32.6
TS_ cooking loss (%)	1047	20.5	2.41	13.3	30.6

Table 7. Phenotypic (V_p) and additive genetic (V_a) variances and heritabilities (h^2) for carcass and meat quality traits presented separately for Brahman and Tropical Composite steers (approximate standard errors in parentheses)

Trait	Brahman			Tropical Composite		
	V_a	V_p	h^2	V_a	V_p	h^2
Ossification	2369.9	4482.1	0.53 (0.13)	1144.2	2084.4	0.35 (0.10)
CWT (kg)	427.6	865.5	0.49 (0.13)	639.1	1001.0	0.64 (0.12)
CP8 (mm)	4.5	13.1	0.35 (0.10)	6.7	16.5	0.41 (0.12)
HP8 [B] (mm)	4.8	15.0	0.32 (0.10)	5.31	21.9	0.24 (0.09)
CRib [B] (mm)	1.9	8.5	0.22 (0.09)	1.7	12.4	0.14 (0.07)
Hump Ht (mm)	246.6	904.8	0.27 (0.10)	60.8	414.1	0.15 (0.08)
CEMA [A] (cm^2)	10.9	51.7	0.21 (0.09)	22.7	66.4	0.34 (0.11)
Marbling [B] (sc)	0.023	0.129	0.18 (0.08)	0.101	0.240	0.42 (0.13)
CIMF (%)	0.12	0.50	0.24 (0.09)	0.57	0.95	0.60 (0.15)
RBY [A] (%)	2.44	6.00	0.41 (0.32)	3.66	6.74	0.54 (0.23)
AT_shear force (kg)	0.37	1.12	0.33 (0.10)	0.35	1.09	0.32 (0.10)
TS_ shear force (kg)	0.083	0.273	0.30 (0.11)	0.069	0.235	0.30 (0.11)
AT_ compression (kg)	0.013	0.067	0.19 (0.08)	0.012	0.058	0.20 (0.08)
TS_compression (kg)	0.008	0.054	0.15 (0.08)	0.011	0.043	0.26 (0.11)
AT_ cooking loss (%)	0.47	5.36	0.09 (0.07)	1.04	4.76	0.22 (0.08)
TS_ cooking loss (%)	0.24	3.63	0.07 (0.06)	0.73	3.41	0.21 (0.09)

[A] *maternal environmental effect significant for BRAH*
[B] *maternal environmental effect significant for TCOMP*

Meat tenderness can be affected by cold shortening under conditions of rapid chilling relative to the rate of decline in muscle pH post-slaughter (Harris and Shorthose 1988). Application of processing techniques such as electrical stimulation, tenderstretching and correct aging of meat can be used to overcome the effects of cold shortening, but it was not known whether beef tenderness measured with or without correct application of processing techniques to overcome cold shortening was actually measurement for different attributes (and therefore whether selection to improve tenderness based on measurements of carcasses that have been processed using/not using best practice would be effective). Johnston *et al.* (2001) reported that method of electrical stimulation had a large effect on the mean and variance of shear force values, particularly in the striploin in carcasses that had been hung by the Achilles tendon. Non-stimulated slaughter groups were more variable than slaughter groups electrically stimulated with high voltage, which were in turn more variable than slaughter groups stimulated with extra low voltage. It was therefore possible that alternative methods of hanging of carcasses such as tenderstretch (Bouton *et al.* 1973) may reduce the amount of variation in shear force values even further. Hence, one aspect of this project was to examine genetic parameters in carcasses from tropically adapted steers where one side of the carcass was hung by the achilles tendon and the other side was tenderstretched.

Estimates of variances and heritabilities from the project steers are presented separately for Brahmans and Tropical Composites in Table 7 for a range of abattoir carcass traits. Table 8 shows estimates of heritabilities pooled across breeds for the same traits including Meat Standards Australia (MSA) and Video Image Analysis (VIA) measures. The number of records varied for the VIA and bone-out yield due to changes in abattoir and the non-recording (or loss of data) from some kill groups. In general, heritability estimates were moderate to high and similar to previous CRC studies. All traits, with the exception of MSA pH, showed significant amounts of genetic variation and large differences between sires for their progeny performance.

Table 8. Estimates of additive variance (σ_A^2), heritability (h^2) and standard errors (SE) for carcass traits pooled across Brahman and Tropical Composite steers.

Trait	Units	n	σ_A^2	h^2	SE
Carcass Weight	kg	2160	547.12	0.59	0.09
Hot Carcass P8 Fat Depth	mm	2162	4.96	0.27	0.07
Cold Carcass P8 Fat Depth	mm	2067	5.34	0.37	0.08
MSA Eye Muscle Area (EMA)	cm^2	2155	15.24	0.26	0.07
MSA Hump Height	mm	2087	148.7	0.23	0.06
MSA Ultimate pH	pH	2155	0.0004	0.06	0.04
MSA 12/13th Rib Fat Depth	mm	2087	2.08	0.20	0.06
MSA Ossification	score	2155	1734.35	0.46	0.08
MSA AUSMEAT Marbling	score	2155	0.063	0.34	0.08
MSA USDA Marbling	score	2154	1524.4	0.35	0.07
Chemically extracted IMF	%	2005	0.391	0.55	0.10
VIA Chiller Assessment (CAS) predicted IMF	score	1234	0.026	0.20	0.09
VIA CAS EMA	cm^2	1234	37.55	0.40	0.10
VIA CAS predicted Carcass Yield	%	1234	0.537	0.43	0.10
VIA Whole Body System Predicted Carcass Yield	%	1580	0.579	0.34	0.09
Bone-out Carcass Wholesale Yield	%	554	2.91	0.48	0.16

Additional results shown in Table 9 clearly indicate significant benefits accrue from use of tenderstretch. The benefits of tenderstretch were larger in poorer quality carcasses and had the greatest effect on shear force (tenderness), with the greatest favourable effects seen in the toughest carcasses. Brahmans and Tropical Composites benefited equally from the use of tenderstretch. Large sire differences for tenderness existed, but these differences were significantly reduced for shear force in carcasses that had been tenderstretched.

Correlations between shear force measures in achilles-hung *vs.* tenderstretched carcasses in Brahman, Tropical Composite and steers pooled across breeds show the genetic correlations are significantly higher than the phenotypic correlations, indicating the relationships are strongest at the genetic level. They also indicate that selection to improve tenderness using measures of tenderness based on either achilles-hung or tenderstretched carcasses will be equally effective, with only minor re-ranking of sires if the processing methods were to be altered.

Table 9. Least squares mean, additive genetic variances (σ^2_A) and heritabilities (h^2) for carcass tenderness traits within Brahman and Tropical Composite steers (AT: achilles tendon; TS: tenderstretch; shear force: objective measure of myofibrillar (muscle) toughness with lower values indicating more tender beef; compression: objective measure of collagen toughness with lower values indicating more tender beef; cooking loss: amount of moisture loss during cooking, with higher values indicating greater propensity for moisture loss during cooking)

Breed / Trait	AT shear force (kg)	TS shear force (kg)	AT compress. (kg)	TS compress. (kg)	AT cook loss (%)	TS cook loss (%)
Brahmans	5.3	4.4	1.9	1.8	23.0	20.9
Composites	4.6	3.9	1.8	1.7	22.4	20.4
Sed	0.1	0.1	0.02	0.03	0.3	0.2
Brahmans						
σ^2_A	0.37	0.08	0.01	0.01	0.48	0.24
h^2	0.33	0.30	0.20	0.15	0.09	0.07
Composites						
σ^2_A	0.35	0.07	0.01	0.01	1.07	0.72
h^2	0.32	0.30	0.20	0.27	0.23	0.21

To improve the consistency of eating quality of beef, multiple genetic and non-genetic strategies are needed, as incorporated through the MSA prediction model. Selection of breeds and animals within breeds using both quantitative and molecular genetic tools, nutritional strategies that optimize growth pathways, animal handling on-farm and pre-slaughter and post-mortem processing technologies all represent potential methods to improve beef eating quality. A value-based marketing system that rewards beef producers, processors and retailers for implementation of such strategies is the economic driver needed to guarantee the quality of Australian beef in future.

5) Heifer growth

Table 10. Unadjusted means, standard deviations and ranges for traits at 2 measurement times for Brahman heifers (see Table 1 for a description of traits; WET1 - end of first 'wet' season post-weaning; DRY2 - end of second 'dry' season post-weaning)

Trait	N	Mean	s.d.	Min.	Max.
		WET1			
Age (days)[A]	1026	518.0	54.8	369.0	636.0
LWT (kg)	1027	287.6	43.8	168.0	414.0
ADG (kg/day)	1022	0.61	0.15	0.02	1.11
SP8 (mm)	1027	3.7	1.9	1.0	12.0
SP8G (mm/day)	710	0.019	0.013	-0.030	0.092
SRIB (mm)	1027	2.0	1.0	0.5	6.0
SEMA (cm^2)	1024	44.1	6.6	26.0	65.0
CS (score)	954	8.3	1.4	4.0	12.0
HH (cm)	623	127.4	4.9	115.0	141.0
IGF-1 (ng/mL)	916	182.6	84.3	42.0	707.0
		DRY2			
Age (days)[A]	1025	713.4	60.4	551.0	860.0
LWT (kg)	1026	320.0	58.7	186.0	486.0
ADG (kg/day)	1022	0.14	0.23	-0.30	0.66
SP8 (mm)	1025	3.1	1.8	0.5	15.0
SRIB (mm)	1025	1.9	1.0	0.5	6.0
SEMA (cm^2)	1023	44.1	8.8	23.0	74.0
CS (score)	1026	7.4	1.4	3.0	12.0
HH (cm)	950	132.4	4.9	119.0	147.0
IGF-1 (ng/mL)	759	215.4	92.3	39.0	846.0

[A]*Average HH and IGF measurement age was 530 and 542 days, respectively, at WET1; and 711 and 728 days, respectively, at DRY2*

Table 11. Unadjusted means, standard deviations, and ranges for traits at 2 measurement times for Tropical Composite heifers (see Table 1 for a description of traits; WET1 - end of first 'wet' season post-weaning; DRY2 - end of second 'dry' season post-weaning)

Trait	N	Mean	s.d.	Min.	Max.
		WET1			
Age (days) [A]	1132	555.0	33.8	455.0	648.0
LWT (kg)	1132	313.6	41.0	174.0	462.0
ADG (kg/day)	1125	0.58	0.14	-0.20	1.27
SP8 (mm)	1132	3.1	1.8	0.5	11.0
SP8G (mm/day)	1089	0.018	0.014	-0.070	0.162
SRIB (mm)	1132	2.0	1.1	0.5	7.0
SEMA (cm^2)	1131	45.8	6.9	21.0	71.0
CS (score)	1132	7.5	0.9	2.0	11.0
HH (cm)	1131	125.0	6.0	105.0	154.0
IGF-1 (ng/mL)	867	224.9	76.2	14.0	511.0
		DRY2			
Age (days) [A]	1127	748.7	33.6	642.0	838.0
LWT (kg)	1127	354.3	38.9	232.0	479.0
ADG (kg/day)	1130	0.26	0.17	-0.24	0.85
SP8 (mm)	1127	2.9	1.7	0.5	11.0
SRIB (mm)	1126	2.0	1.1	0.5	7.0
SEMA (cm^2)	1126	48.9	6.6	29.0	72.0
CS (score)	1127	7.0	1.1	4.0	11.0
HH (cm)	1122	130.2	4.8	110.0	144.0
IGF-1 (ng/mL)	817	239.3	71.7	74.0	586.0

[A] *Average IGF measurement age was 551 days at WET1 and 747 days at DRY2*

Table 12. Phenotypic (V_p) and additive genetic (V_a) variances, V_p as a percentage of the observed variance (P%) and % heritabilities (h^2) for heifer traits of Brahmans and Tropical Composites (approximate standard errors in parentheses; see Table 1 for a description of traits; WET1 - end of first 'wet' season post-weaning; DRY2, end of second 'dry' season post-weaning)

Trait	Brahman				Tropical Composite			
	V_p	V_a	P%	h^2	V_p	V_a	P%	h^2
				WET1				
LWT	587.3	225.8	38		866.6	531.5		61 (15)
ADG (*100*)	75.04	19.06	25 (9)		101.09	39.93		39 (12)
SP8 [A]	2.45	1.02	42 (9)		1.75	0.77		44 (13)
SP8G	1.29	0.44	34		1.31	0.17		13 (7)
SRIB [A,B]	0.76	0.32	42 (9)		0.78	0.26		33 (11)
SEMA	25.0	6.58	26		30.6	14.9		49 (13)
CS [B]	0.590	0.240	41		0.61	0.18		30 (12)
HH	14.4	8.42	59		19.07	11.08		58 (13)
IGF-1	2415.6	1019.3	42		3051.9	998.1		33 (13)
				DRY2				
LWT	664.2	260.9	39		1025.2	759.9		74 (16)
ADG (*100*)	31.74	4.43	14 (6)		45.61	8.37		18 (9)
SP8	1.8	0.71	39 (9)		1.88	1.23		65 (16)
SRIB	0.7	0.37	53		0.90	0.47		52 (13)
SEMA	22.4	9.98	45		27.9	13.1		47 (13)
CS	0.8	0.29	36		0.68	0.26		38 (12)
HH	14.7	7.42	51		20.4	15.63		77 (14)
IGF-1 [A,B]	3839.6	1390.3	36		3381.8	589.4		17 (9)

[A,B]*Traits of Brahmans (A) and Tropical Composites (B) where model included a significant maternal environmental effect*

6) Heifer pubertal traits

Female reproductive performance is an important component of profitable beef production and can be improved by genetic and non-genetic means. Several studies have shown breed differences in fertility exist for tropical genotypes in northern Australia (e.g. Mackinnon *et al.* 1989). Significant within-breed genetic differences also exist for tropical beef cattle for female reproduction and related calf output traits (Davis 1993). However female reproductive traits are expressed relatively late in life, are sex limited and are often difficult to measure and lowly heritable, thus making genetic improvement in these traits difficult. Worldwide there are currently few female fertility traits recorded and analysed in beef genetic evaluation schemes, the exceptions being "days to calving" in Australia (Graser *et al.* 2005) and heifer pregnancy percentage in the US Red Angus.

To achieve higher rates of genetic progress in these traits (and in the profit objective) requires measures that can be recorded earlier, that are heritable and that are correlated to the underlying profit trait. One trait that may influence maiden calving performance is age at puberty. Breed differences have been reported for age and weight at puberty (Martin *et al.* 1992) and Brahmans have been reported to be older at puberty than other breeds (Bolton *et al.* 1987, Hearnshaw *et al.* 1994). Several studies have shown age at puberty is heritable in beef cattle, particularly in *Bos taurus* breeds (e.g. Martin *et al.* 1992, Gregory *et al.* 1995), but limited studies exist for *Bos indicus* genotypes. Vargas *et al.* (1998) reported from a small study, a heritability for age at puberty in Brahmans of 0.42. However relationships between age at puberty and subsequent measures of female fertility were inconclusive. Some studies show a favourable relationship between improved pregnancies and earlier age at puberty (Morris *et al.* 2000). However several others (e.g. Dow *et al.* 1982, Cundiff *et al.* 1986) have observed no relationship.

Summary statistics for pubertal traits for Brahmans and Tropical Composites are shown in Table 13. Mean AGECL was 750.6 and 650.8 days for Brahmans and Tropical Composites respectively. Both breeds showed considerable variation (18% CV). Differences in raw means reflected breed, location, birth month and cohort effects. Trait means for DC1 (d), CS1 (%) and JAGE (d) were 346.4, 0.71 and 748 for BRAH and 318.9, 0.90 and 759 for TCOMP respectively.

Table 13. Unadjusted trait means, standard deviations for pubertal and 1st and 2nd mating performance in Brahman and Tropical Composite heifers (see Table 1 for definition of traits)

Trait	N	Mean	s.d.	Min.	Max.
Brahman					
AGECL (days)	1007	750.6	142.1	394	1211
WTCL (kg)	993	334.4	44.8	196	485
FATCL (mm)	951	4.47	2.19	1.0	15.0
CSCL (score)	951	8.2	1.4	4.0	12.0
TSCORE (mm)	947	13.5	3.8	5.0	25.0
PRIORCL (%)	1008	0.51	0.50	0	1.0
MDAYCL (%)	978	0.43	0.50	0	1.0
DC1 (days)	1020	346.4	49.8	279	423
CS1 (%)	1020	0.71	0.45	0	1
DC2 (days)	851	364			
CS2 (%)	851	56			
Tropical Composite					
AGECL (days)	1108	650.8	119.5	344	945
WTCL (kg)	1094	329.6	45.9	206	474
FATCL (mm)	1083	2.90	1.66	0.5	11.0
CSCL (score)	1108	7.2	1.2	3.0	11.0
TSCORE (mm)	1119	16.3	4.8	5.0	30.0
PRIORCL (%)	1108	0.79	0.41	0	1.0
MDAYCL (%)	1103	0.63	0.48	0	1.0
DC1 (d)	1115	318.9	39.0	275	425
CS1 (%)	1115	0.90	0.31	0	1
DC2 (days)	977	346			
CS2 (%)	977	73			

Genotype effects

Brahmans were not significantly different for WTCL (337 and 331 kg, respectively) but Brahmans were on average 84 days older for AGECL, 1.3 mm fatter and had significantly lower percentage PRIORCL, longer DC1 and lower CS1 compared to Tropical Composites (see Table 13). These results are consistent with several papers reporting increased age of puberty in Brahmans (e.g. Hearnshaw *et al.* 1994; Bolton *et al.* 1987). The reduced percentage of Brahman heifers showing a CL prior to mating clearly influenced the reproductive performance for the first calving (DC1 and CS1). However it is not possible to extrapolate genotype differences outside the range of environments in the experiment. Tropical Composites were purposely not allocated to the Swans Lagoon location because it was perceived they would be too poorly adapted and survival and reproductive performance were likely to have been compromised.

Location effects

Location had a large effect on AGECL. In particular, heifers at Swans Lagoon were significantly older, tended to be fatter at first CL, had lower PRIORCL, and subsequently longer DC1 and lower CS1 but similar WTCL compared to the other locations. Hearnshaw *et al.* (1994) reported a large nutrition effect on age at puberty mainly through its effect on weight, where Brahmans could not increase growth under high nutrition relative to other genotypes. Ferrell (1982) showed that slower growth rate delayed age at puberty and subsequently reduced pregnancy compared to heifers that gained weight rapidly post-weaning, suggesting that weight was more important than age in determining puberty. These results suggest that management to achieve minimum live weights (e.g. around 320kg) will decrease age at puberty and improve subsequent calf output (Rudder *et al.* 1985). However Mackinnon *et al.* (1989) hypothesized that once sexual maturity was reached there was little effect of increasing weight on subsequent fertility.

Birth month and season

Birth month, and associated seasonal effects, had a large effect on all traits. Late born heifers (e.g. March) had significantly increased AGECL and DC1, reduced PRIORCL and CS1 but increased FATCL compared to early born heifers (i.e. September). However there was little observed effect on WTCL. AGECL of late-born heifers was likely to be influenced by the effect of the distinct wet and dry seasons experienced by these cattle in northern Australia and its effect on weight gain. Arije and Wiltbank (1971) reported seasonal pasture availability and birth month affected age at puberty in Hereford heifers. Bolton *et al.* (1987) reported large differences between spring and autumn calving season in the percentage of pubertal heifers at time of first joining and attributed the effect to reduced growth rate of autumn-born calves which slowed the rate of sexual development, particularly as Brahman content increased. Results from the current study may also include the effect of photoperiod of sexual development of later-born heifers.

<u>Additive variances and heritabilities</u>

Additive variances and heritabilities for pubertal and first and second mating performance traits are shown separately for Brahmans and Tropical Composites in Table 14. All pubertal traits were moderately heritable with the exception of PRIORCL in Tropical Composites (see Table 14). Heritabilities for AGECL were slightly higher than in the review of Martin *et al.* (1992), where a pooled estimate of 0.40 was reported. In general, additive variances for pubertal traits were larger for Brahmans than Tropical Composites. These results indicate large differences between sires in their daughters' ages at first CL and also weight and fatness at first CL. The differences could be used to alter these traits if that was considered desirable. PRIORCL was heritable for Brahmans (0.33) but less heritable for Tropical Composites (0.13). This result is likely to be related to the differences in the mean of the binary trait, with the Brahman trait average closer to 50%. DC1 and CS1 were more heritable for Brahman than Tropical Composites (0.16, 0.21 versus 0.11 and 0.06 respectively) and with larger additive variances. Heritabilities were higher than reviewed by Davis (1993) and may reflect the sampling of sires and the environments in this study.

Table 14. Additive variances and heritabilities for pubertal and first and second mating performance traits (see Table 1 for definition of traits)

Trait	Brahman			Tropical Composite		
	V_a	V_p	h^2	V_a	V_p	h^2
AGECL (days)	7375	13050	0.57 (0.12)	5670	10980	0.52 (0.12)
WTCL (kg)	981	1755	0.56 (0.12)	789	1701	0.46 (0.11)
FATCL (mm)	2.41	4.37	0.55 (0.13)	0.88	2.29	0.39 (0.11)
CSCL (score)	0.34	5.6	0.22 (0.10)	0.17	1.02	0.16 (0.07)
TSCORE (mm)	0.12	5.05	0.03 (0.06)	1.92	9.48	0.20 (0.09)
PRIORCL [A] (%)	0.052	0.156	0.33 (0.10)	0.022	1.31	0.13 (0.07)
MDAYCL (%)	0.034	0.169	0.20 (0.09)	0.016	0.222	0.07 (0.05)
DC1	321.7	2010	0.16 (0.09)	170.0	1545	0.11 (0.06)
CS1	0.031	0.17	0.18 (0.09)	0.0071	0.09	0.08 (0.05)
DC2	307.4	1921	0.16 (0.09)	219.5	1995	0.11 (0.07)
CS2	0.038	0.18	0.21 (0.10)	0.019	0.17	0.11 (0.07)

[A]*= maternal environmental effect significant for TCOMP*

<u>Genetic correlations among heifer pubertal traits</u>

Moderate to strong positive correlations were estimated between each of the pubertal traits (see Table 15) showing animals that were older at first CL were also genetically heavier and fatter at the time of their first CL. Laster *et al.* (1979) also reported a positive genetic correlation between age at puberty and weight at puberty of 0.52. However the genetic correlations of AGECL with live weight and fat depth on an age constant basis were -0.34 and –0.30 (not shown), indicating animals with younger ages at puberty were genetically heavier and fatter at the same age.

The occurrence of a CL at commencement of mating was highly negatively correlated with younger age at CL and with weight and fatness, indicating those sires' daughters with higher age, weight and/or fatness at puberty are genetically less likely to have shown a CL prior to the commencement of their maiden mating.

Table 15. Correlations[#] (± SE) between pubertal traits combined across genotypes

Trait	AGECL	WTCL	FATCL	PRIORCL
AGECL		0.74 (0.06)	0.53 (0.10)	-0.99 (0.04)
WTCL	0.67		0.44 (0.11)	-0.81 (0.09)
FATCL	0.26	0.38		-0.66 (0.12)
PRIORCL	-0.55	-0.43	-0.23	

[#]*phenotypic (below) and genetic correlations (above)*

Genetic correlations between DC1 and CS1 and with AGECL

For both genotypes, the genetic correlations between first DC and CS were not significantly different from one, indicating they are very similar traits (see Table 16). However, DC1 contains additional information resulting from additive genetic differences in days to calving within the group of cows that calve, particularly for Brahmans. Conversely, for Tropical Composites the additive variance for DC1 was mostly due to the inclusion of penalty records for cows that failed to calve.

AGECL was strongly genetically correlated with DC1 and CS1 in Brahmans, indicating that females that were younger at AGECL had genetically shorter DC1 and increased CS1 when mated for the first time at approximately 25 months of age. Although in the same direction, the correlations for Tropical Composites were smaller in magnitude (and with large SE), indicating AGECL was not as good a genetic predictor of calving performance traits in that genotype when heifers were first mated at 25 months. This is most likely because the average AGECL for Tropical Composite heifers was 108 days before the start of joining compared to Brahmans whose average AGECL was 6 days after the start of joining. As a result, 79% of Tropical Composites had an observed CL prior to commencement of joining compared to 51% for Brahmans. Morris *et al.* (2000) reported genetic correlations for first behavioural oestrus with calving date (same trait as days to calving) and pregnancy rate of 0.57 and -0.36, respectively in Angus cattle. Laster *et al.* (1979) reported a genetic correlation between age at puberty and heifer pregnancy of -0.42. Genotype differences in genetic parameter estimates from this study include the effects of the different production environments used in the study, in particular the effect of the harsher northern coastal location for Brahmans.

Table 16. Genetic and phenotypic correlations[#] for female reproductive performance traits in Brahmans and Tropical Composites

Genotype	Traits	DC1	CS1	AGECL
Brahman	DC1 (days)		-0.93 ± 0.05	0.87 ± 0.19
	CS1 (%)	-0.92 ± 0.01		-0.58 ± 0.19
	AGECL (days)	0.40 ± 0.03	-0.37 ± 0.03	
Tropical Composite	DC1		-1.00 ± 0.09	0.23 ± 0.31
	CS1	-0.90 ± 0.01		-0.24 ± 0.34
	AGECL	0.05 ± 0.03	-0.03 ± 0.03	

[#]*Genetic and phenotypic correlations (±SE.) above and below the diagonals respectively.*

Ultrasound ovarian scanning technology has been used to generate a trait (i.e. age at first CL) that was moderately to highly heritable in both genotypes and which was subsequently shown to be related to two calving performance traits (DC1 and CS1). The technology and scanning protocols employed in this project were able to deliver a very powerful means by which to estimate genetic differences in age at puberty and associated traits and genetic correlations with female reproductive performance traits.

Results showed large genotype, location and birth month effects on age and fatness at first CL but not weight at first CL. Age at presence of the first CL (AGECL) was moderately to highly heritable: 0.57 and 0.52 for Brahmans and Tropical Composites respectively. Other pubertal traits were also moderately heritable. Heritability estimates for DC1 and CS1, were 0.16 and 0.18 for Brahmans and 0.11 and 0.08 for Tropical Composites respectively. DC1 and CS1 were genetically correlated with AGECL, particularly for Brahmans (0.87 and -0.58 respectively).

Selection to improve first parity female reproductive performance is feasible in both genotypes. For Brahmans, AGECL could be used as an indirect selection criterion provided it can be measured cost effectively in industry. Associations with lifetime reproductive performance will be required before final recommendations can be made on recording and selection breeding schemes. These differences could also be used to develop management strategies to improve AGECL. For example calving times (i.e. start of mating and its duration) could be altered to reduce the number of calves born after January to significantly improve subsequent reproductive performance of the herd.

Genetic variation existed for pubertal traits with greater variance observed for Brahmans. The two female reproductive traits examined in this study (DC1 and CS1) had considerable genetic basis under the production environments of this experiment and selection could improve these traits. Age at puberty was also highly heritable in both genotypes and, for Brahmans, was strongly correlated with the reproductive performance traits and could be used as an indirect selection criterion. The challenge is to be able to measure the trait cost effectively in beef herds. For Tropical Composites, there was less genetic variation for the traits measured, though significant sire differences existed. Age at puberty was heritable in Tropical Composites but was not strongly genetically correlated with the calving traits under the current management system (i.e. first joining at 2 years of age). Ongoing research in CRCIII will determine the relationship between AGECL and subsequent calving outcomes and lifetime reproductive performance in both genotypes. As well, possible early-life genetic indicator traits for female fertility will be assessed. The correlated responses to selection for improved reproductive performance on steer profit traits (e.g. carcass weight, fatness, tenderness) will be reported in the Special Issue of the *Australian Journal of Animal and Food Science* to be published in late 2007.

7) Adaptive traits (heifers only)

Tropical adaptation can be defined as an animal's ability to survive, grow and reproduce in the presence of endemic stressors of tropical environments (e.g. parasites, diseases, high temperatures and humidity, poor seasonal nutrition). The economic implications for production systems due to the lack of adaptation include production losses, mortalities, treatment costs (where treatment is feasible) and marketing issues, for example associated with the presence of chemical residues in beef resulting from treatments to control parasites. This project investigated several of these adaptive traits in Brahmans and Tropical Composites in northern Australia.

A focus on the genetics of adaptation in cattle is gaining importance primarily because of the need to produce consistent beef eating quality, which is generally easiest to deliver from *Bos taurus* breeds that are poorly adapted to tropical environments. Tick counts, worm egg counts, rectal temperatures, coat colour and coat scores were studied as indicator traits of tropical adaptation. Summary statistics and heritability estimates of these adaptive traits are shown in Tables 17 and 18 respectively.

Table 17. Least squares means of adaptive traits (heifers only; see Table 1 for definition of traits)

	TICK	EPG	FLY	TEMP	COAT	FLIGHT TIME
Genotype						
Brahman	1.0	165	1.3	39.3	1.9	1.29
Composite	2.0	485	1.6	39.4	2.7	1.09
Overall SED	*0.09*	*34.5*	*0.06*	*0.05*	*0.09*	*0.04*
Location						
Brian Pastures	-	320	1.3	-	2.1	1.14
Toorak	-	276	1.1	39.1	2.7	0.79
Belmont	1.6	321	1.7	40.1	2.2	1.73
Swans Lagoon	0.9	382	1.9	38.2	2.2	0.72
Overall SED	*0.08*	*54*	*0.08*	*0.5*	*0.11*	*0.04*

Table 18. Variance components and heritabilities of adaptive traits (heifers only; see Table 1 for definition of traits; h^2 – heritability; c^2 – permanent environment of animal as a proportion of phenotypic variance; tick and fly lesion scores are log transformed due to right-skewed distribution; faecal egg counts are cube-root transformed and flight times are log transformed to approximate normal distribution)

Traits	N	Phenotypic variance	Additive genetic variance	$h^2 \pm$ s.e.	$c^2 \pm$ s.e.
Individual measures					
TICK	901	0.018	0.0023	0.13±0.08	-
EPG	1753	3.72	1.22	0.33±0.07	-
FLY	1966	0.025	0.003	0.12±0.05	-
TEMP	1065	0.15	0.031	0.21±0.09	-
COAT	1775	4.04	2.49	0.62±0.09	-
FLIGHT	2061	0.018	0.0045	0.25±0.06	-
Repeated measures*					
TICKs	-	-	-	-	-
EPGs	4569	4.28	1.13	0.27±0.05	0.09±0.04
FLYs	4060	0.027	0.004	0.15±0.04	0.34±0.04
TEMPs	1457	0.15	0.016	0.11±0.06	0.06±0.08
COATs	5847	3.77	1.54	0.41±0.02	0.00
FLIGHT TIMEs	5128	0.019	0.0043	0.23±0.05	0.33±0.05

Tables 19 and 20 show genetic and phenotypic correlations (± standard errors) among single and repeated measures respectively of adaptive traits in heifers only, pooled across Brahmans and Tropical Composites.

Table 19. Genetic and phenotypic correlations (± SE) among adaptive traits (heifers only; see Table 1 for definition of traits; genetic correlations above the diagonal; phenotypic correlations below the diagonal; standard errors are given in the parentheses)

	TICK	EPG	FLY	TEMP	COAT	FLIGHT TIME
TICK	-	-0.09	-0.07	0.05	0.34	-0.03
		(0.32)	(0.38)	(0.40)	(0.27)	(0.31)
EPG	0.11	-	0.37	0.22	-0.20	-0.02
	(0.04)		(0.22)	(0.25)	(0.14)	(0.18)
FLY	-0.02	0.05	-	0.03	0.11	0.30
	(0.03)	(0.03)		(0.31)	(0.20)	(0.22)
TEMP	0.01	-0.03	-0.05	-	-0.01	0.01
	(0.04)	(0.04)	(0.03)		(0.23)	(0.23)
COAT	0.08	-0.01	0.02	0.05	-	-0.21
	(0.04)	(0.03)	(0.03)	(0.04)		(0.15)
FLIGHT TIME	0.00	-0.03	0.01	-0.17	0.00	-
	(0.03)	(0.03)	(0.02)	(0.03)	(0.03)	

Table 20. Genetic and phenotypic correlations among repeated measures of adaptive traits (heifers only; see Table 1 for definition of traits; genetic correlations above the diagonal; phenotypic correlations below the diagonal; standard errors are given in the parentheses)

	EPGs	FLYs	TEMPs	COATs	FLIGHTs
EPGs	-	0.18 (0.18)	0.16 (0.27)	0.10 (0.12)	-0.10 (0.15)
FLYs	0.01 (0.02)	-	-0.12 (0.32)	0.01 (0.16)	0.20 (0.19)
TEMPs	-0.02 (0.03)	-0.07 (0.03)	-	0.25 (0.24)	-0.02 (0.25)
COATs	0.01 (0.02)	-0.02 (0.02)	0.06 (0.03)	-	-0.15 (0.13)
FLIGHTs	-0.01 (0.02)	0.04 (0.02)	-0.18 (0.02)	-0.01 (0.02)	-

Consistent with the earlier literature from Belmont Research Station, all adaptive traits were moderately to highly heritable (Table 18). Moderate favourable genetic correlations were also found between various adaptive traits (Tables 19 and 20), indicating that selection to improve performance in any adaptive attribute may have favourable correlated responses that increase performance in other adaptive traits. Genetic relationships between resistance to parasites and growth traits vary. While low and positive (unfavourable) genetic correlations were reported between resistance to ticks and worms and post-weaning growth traits by Prayaga and Henshall (2005), moderate and negative genetic correlations (favourable) were reported by Burrow (2001).

Based on a review of the literature, Davis (1993) also reported variable estimates and suggested this may be due to the different breeds in the various studies. Mackinnon *et al.* (1991) and Burrow (2001) reported positive (unfavourable) genetic correlations between body weights and fly counts leading to suggestions that higher testosterone levels or other metabolic products in heavier animals attract buffalo flies. An alternative explanation could simply be that larger skin surface areas in heavier animals allow an increased number of flies. However, the reported lack of relationship between buffalo flies and growth traits leads us to believe that flies pose a greater animal welfare and hide damage problem, rather than a production problem, at least from a northern Australian perspective.

Genetic correlations between resistance to heat stress and growth traits are generally significantly negative (favourable) across the several studies cited above, emphasising the close relationship between genes controlling growth in the tropics and rectal temperatures. Genetic correlations between growth traits and coat scores were favourable but lower than those between growth and rectal temperatures (Prayaga and Henshall, 2005), indicating the complexity of thermoregulation with components such as sweating, respiratory cooling and lower metabolic heat production contributing to this trait (Turner, 1984). Favourable genetic correlations have been reported between resistance to heat and measures of female fertility (Turner, 1982; Burrow, 2001) but further analyses (now underway) are required to understand female fertility in the tropics in general, and its relationship with adaptation, in particular.

8) Genetic differences between project sires

Large differences were identified between the sires in the project, indicating there are significant economic gains for breeders willing to base joinings on genetics and producers purchasing bulls proven to be genetically superior based on measured performance. Information relating to all sires (good and poor) used in the project were returned directly in the first instance to the co-operating breeders to allow them to maximise the value of the information in their own herds. Estimated Breeding Values (EBVs) of the Generation 0 sires evaluated in the project were calculated for some of the project traits. Table 21 shows the range of BREEDPLAN EBVs between the best and worst Brahman sires for a number of different attributes.

Table 21. Highest and lowest EBVs for project Brahman sires for a range of traits

Trait	Lowest EBV	Highest EBV	Range	Difference in sire progeny group between extreme sires
Carcass Weight	-8	+44	52 kg at 650 days of age	26 kg carcass weight
Retail Beef Yield %	-1.2	+ 3.6	4.8% at 300 kg carcass	2.4% saleable meat yield at a 300 kg carcass = 7.2 kg saleable yield
Days to Calving	+16.6	-12.9	30 days	15 days
Jap Ox $ Index	-23	+54	$77 per cow joined/year	$38.50 per cow joined/year

Using current market prices, results show that basing selection of breeding cattle on measured performance will generate increased economic returns. For example, one sire was able to breed progeny that produced an extra 26 kilograms in carcass weight, equating to about an extra $90 dollars per carcass, achieved simply by careful genetic selection of sires. Similarly significant economic gains were identified for saleable meat yield. The bull with the best EBVs for saleable meat yield trait produced progeny an extra 7.2 kilograms of saleable meat. Multiply this by a conservative $10 per kg and an extra $72 a head is achievable.

Another trait identified having a major impact on productivity in this project is days to calving. One bull in the project was able to reduce the days to calving of his daughters by 15 days, equating to more than a 15% difference in calving rate, with the added benefit of steers that are born early in the calving period and all at the same time of the year. This provides a significant added advantage when preparing and managing sale progeny.

Table 22 shows the range of performance for Generation 1 Brahman heifer progeny for traits associated with reproduction. Whilst the average age at first CL was slightly more than two years of age in the CRC environments (Toorak, Swans Lagoon and Belmont Research Stations near Julia Creek, Ayr and Rockhampton respectively), some Brahman heifers achieved puberty at about 13 months, whilst others did not achieve puberty until more than 39 months.

Weight and fat depth at the time the heifers achieved puberty varied enormously. One aim of the CRC study is to identify those sire lines which reached puberty early and determine whether they are also the same sire lines that have best lifetime fertility. Another aim is to identify indicator traits of lifetime fertility (e.g. growth rate and body composition traits) that could be modified using non-genetic approaches, to determine the economic feasibility of managerial interventions to improve reproductive performance. Age at first CL was strongly genetically correlated with days to calving and calving success following first joining in Brahmans, indicating that females that were younger at puberty had genetically shorter days to calving and increased calving success when mated for the first time at approximately 25 months.

Table 22. Trait means and ranges of performance for Brahman heifer progeny

Trait	Mean	Min.	Max.
Age at puberty* (days)	751	394	1211
Weight at puberty (kg)	334	196	485
P8 Rump fat depth at puberty* (mm)	4.5	1.0	15.0
Heifers achieving puberty* by commencement of first joining at 2 years (%)	0.51	0.0	1.0
Days to calving following first joining (days)	346	279	423
Calving success following first joining (%)	0.71	0.0	1.0

First observed/scanned CL

All data collected from the Beef CRC project goes into BREEDPLAN and EBVs are readily available on the web at http://breedplan.une.edu.au/.

To date this aspect of the project has yielded two significant findings relating to female reproductive traits: the first is that the difference in the age of puberty for the bulls' daughters could vary by as much as six months; and secondly there is an overall difference of 25 percent in the calving rate between the daughters of the project, a trait which is estimated to have a heritability of 18 percent.

In Brahmans, age at first CL could be used as an indirect selection criterion to improve subsequent reproductive performance, provided it can be measured cost effectively in industry and providing the associations with lifetime reproductive performance indicate the approach would be economically important for industry. Full results on the performance of each of the 50 sires and their progeny will be publicly released early in 2007 after the project sponsors have had the opportunity to capitalise on their early access to the information.

9) Use of scanned fat measurements to predict female reproductive performance

Failure of breeding females to rear a calf to weaning is the major component of production inefficiency of the cow herd, particularly in tropical environments. Improvement of female reproduction involves selection of heifers with higher genetic potential to breed early in their first season and then continue to rebreed and calve early, every year, as mature cows. Selection for age at puberty in beef cattle is effective though slow due to low heritabilities for most female reproductive traits. Because of these low heritabilities, it is likely that environmental effects will have the greatest impact on reproduction rate of beef cattle, at least in the short-medium term until, for example, DNA tests associated with female reproductive rate can be identified for commercial use.

Market demands for carcass and meat quality characteristics focus selection on liveweight, retail beef yield, subcutaneous fat cover and intramuscular fat percent. With tightening profit margins, commercial cattle producers are also focusing greater attention on feed efficiency. CRC research shows moderate to strong genetic and phenotypic antagonisms between carcass fatness traits and retail beef yield in *Bos taurus* and *Bos indicus* breeds (Reverter *et al.* 2003*a*) and undesirable genetic correlations between feed efficiency and fatness traits (Robinson and Oddy 2004). There is growing concern that selection for improved retail beef yield or feed efficiency may reduce carcass fatness to a point where reproductive performance of replacement females is compromised. This may be exacerbated under northern Australian beef production environments where seasonal fluctuations in feed quality, parasite loads, high ambient temperatures and humidity, together with high *Bos indicus* content in breeding herds, provide real challenges for reproductive success. This project examined whether scanned measures of subcutaneous fat depth at start of joining could be used to predict pregnancy rates, days to calving and calving success in Brahman and Tropical Composite females of varying age and lactation status bred at Belmont Research Station. The aim was to identify fat depth benchmarks that could allow beef producers to make informed decisions about the economic viability of changing management practices to achieve predetermined pregnancy rates and calving success.

Prediction plots were calculated for 2 year old maiden heifers, primiparous cows (3 year-olds with first calf at foot at start of joining) and 4+ year-old cows. While into-mating weight and scanned rib fat were significant for days to calving (DTC) in heifers, fat depth at the P8 rump site was not important. If the aim is to have heifers conceiving within 1-2 oestrous cycles of start of joining (i.e. calving at 303-324 days post-mating), scanned rib fat in the range of 1.5-11.5 mm and a minimum 310 kg weight into mating would be recommended based on these results (Figure 2).

Figure 2. Prediction plot showing phenotypic relationships between days to calving and i) scanned rib fat depth and ii) into-mating weight in maiden two-year old heifers

(i) Rib fat for heifers (n=516).　　　　　(ii) Into mating weight for heifers (n=516).
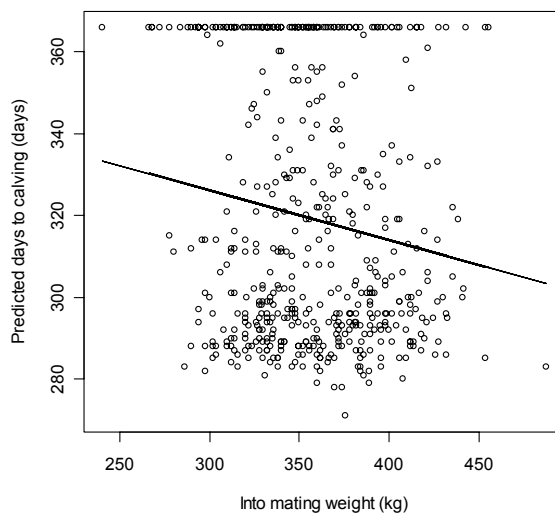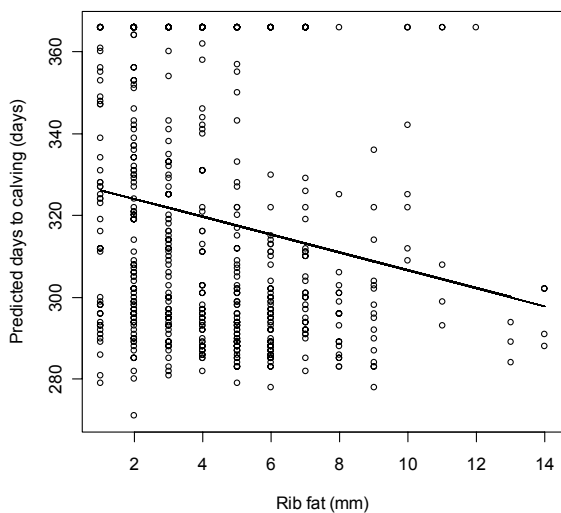
For 3-year old primiparous cows (i.e. with first calf at foot at start of joining), a minimum 6 mm fat at the rib site and into-mating weights of 550 kg would be recommended to achieve conception within 1-2 oestrus cycles (Figure 3).

For lactating 4+ year old cows, a minimum of 5 mm fat at the rib site, 6.5 mm fat at the P8 rump site and 450kg weight at start of joining (Figure 4) would be recommended for conception within 1-2 oestrous cycles of the start of mating.

Figure 3. Prediction plot showing phenotypic relationships between days to calving and i) scanned rib fat depth and ii) into-mating weight in primiparous three-year old cows

(i) Rib fat for 3-yr old cows (n=387).　　　　　(ii) Into mating weight for 3-yr old cows (n=387).
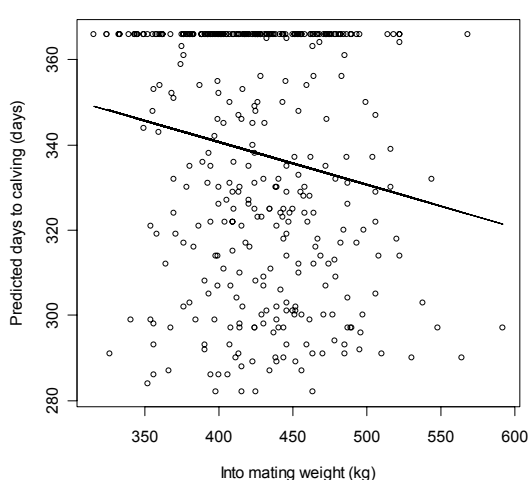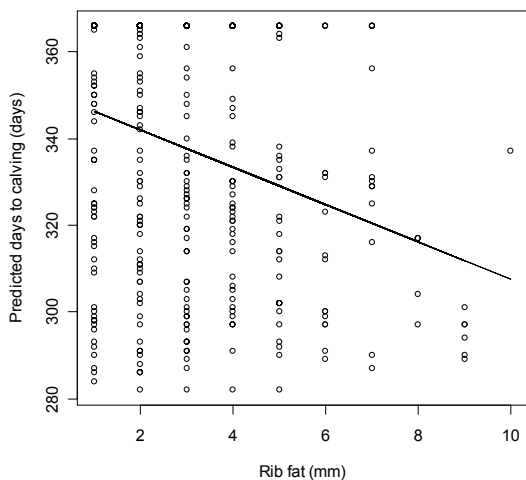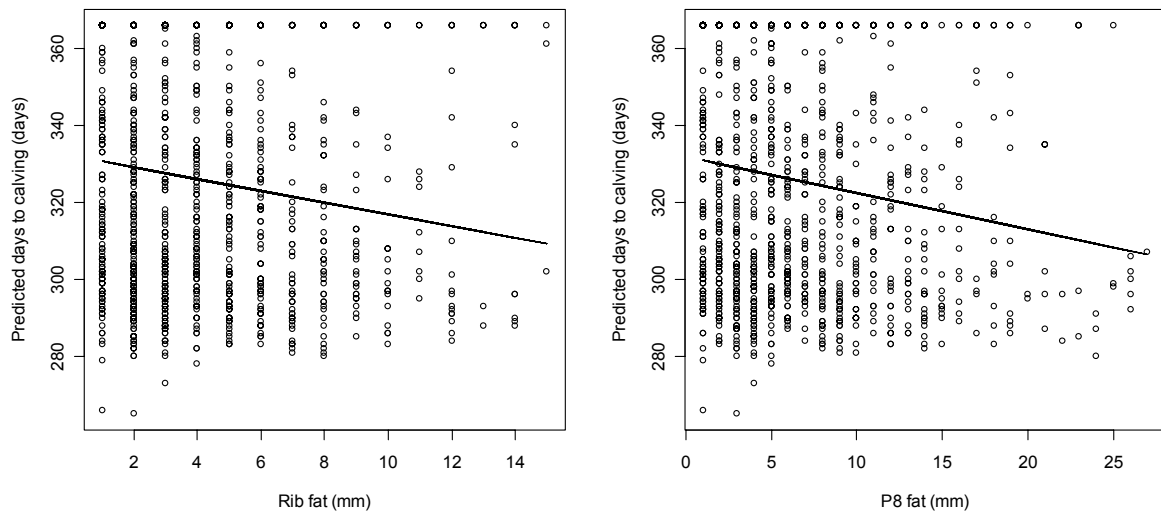
Figure 4. Prediction plot showing phenotypic relationships between days to calving and i) scanned rib fat depth and ii) into-mating weight in 4+ year old cows

(i) Rib fat for 4+ yr old cows (n=1153).   (ii) Into mating weight for 4+ yr old cows (n=1153).

To achieve 80% pregnancy rates and conception within the first two oestrus cycles after start of mating (i.e. to achieve days to calving of 305-326 days), the following recommendations are made:

i)   2-year old maiden heifers require a minimum weight into mating of 330 kg
ii)   3-year old primiparous (first-calf) cows require a minimum rib fat depth of 5 mm and weights at start of joining of 550 kg; and
iii)   4+ year old lactating cows require a minimum rib fat depth of 5 mm, P8 rump fat depth of 6.5 mm and weight at start of joining of 520 kg.

This study confirmed that scanned measures of subcutaneous rib fat depth and into mating liveweight can be used to predict pregnancy rates, days to calving and calving success in both Brahman and Tropical Composite females of different age and lactation status. Fat depth and liveweight benchmarks to achieve predetermined pregnancy rates, days to calving and calving success are possible through use of prediction procedures. Work is now underway to determine the economic feasibility of achieving these benchmarks in vastly variable seasonal conditions. Further development of the prediction methods, including economic models to derive benefit: cost estimates will be of immense benefit to the commercial breeding sector as fat scanning and weighing are relatively inexpensive and easy to measure in practice.

Molecular Genetic Objectives

• *Demonstrate to producers the role and value of genetic markers for selecting commercial cattle for carcass and beef quality and adaptability.*

• *Derive an accurate and validated understanding of specific genetic markers for selecting commercial cattle for carcass and beef quality and adaptability.*

• *Knowledge of genetic parameters between all traits and marker assisted selection.*

Research in CRCI identified a number of linked genetic markers that were potentially useful for improving carcass and beef quality attributes in industry herds. However, those markers had not been evaluated under industry breeding programs. Experimental progeny generated as part of this project were all to be routinely DNA-fingerprinted to determine sire parentage. It was therefore decided to use a suite of known DNA markers to determine parentage, in lieu of the traditional, non-informative DNA markers used by commercial fingerprinting services, to evaluate the role of those known markers in commercial breeding programs.

A panel of 23 DNA RFLP (linked or indirect) markers was selected in 2001 for the dual purposes of 1) assigning sire parentage to all project calves and 2) testing linked DNA markers associated with meat quality and resistance. Problems were subsequently experienced in using the panel of markers to accurately identify the sires of experimental progeny. Hence, parentage verification was undertaken using a commercial DNA fingerprinting service. Attempts were made to compare the sire assignments made by the commercial fingerprinting service to those made using the CRC's panel of markers to determine why the problem occurred with the CRC's markers and to validate the accuracy of those markers for use in QTL segregation analyses. However, several of the linked markers in the CRC's panel of markers were rapidly superseded by commercially available SNP-based DNA tests, which were more accurate as well as more useful from a practical sense. As a result, the comparison was never completed.

An alternative approach was used by a project PhD student, who genotyped all project progeny for two fatness-related SNP (Leptin and RORC). Those genotypes are still being analysed against a range of carcass and beef quality and female fertility phenotypes to determine relationships between these genes and traits. It is planned to publish results from these analyses in the Special Issue of the *Australian Journal of Animal and Food Science* in late 2007.

Currently, and in addition to the planned objectives, all project animals are now being genotyped for the 12 commercially available GeneStar tests (4 tenderness, 4 marbling and 4 feed efficiency tests) as part of the separate CRCIII 'Smartgene for Beef' project aimed at delivering DNA markers through BREEDPLAN, Australia's beef genetic evaluation scheme. Preliminary results from this study were published in a student (honours) thesis submitted for examination through the University of New England in December 2006.

Those *preliminary* results indicate DNA markers were significant in describing additive variance in tenderness between animals within each breed (full analysis of all animals for tenderness, marbling and feed efficiency will not commence until completion of the genotyping in June 2007). In reality though, the percentage of additive variance that each of the markers explained was very small. At this point in time, the use of genetic markers for tenderness selection in young animals with no phenotype records for the trait is impractical. Such selection is likely to be risky and low in accuracy because each of the markers explains only a small amount of variation in tenderness. Development of more markers associated with beef tenderness may mean that genetic markers can be used for early selection of tenderness in beef cattle. Until DNA markers are able to explain a large proportion of variation in tenderness though, the benefit of genetic markers in beef breeding systems is limited.

Although not a specific outcome of this project, the phenotypic and genetic information generated on the project's experimental progeny is now also providing an extremely valuable resource for detection and validation of gene markers for female reproduction, feed efficiency and adaptive traits. Data and DNA from project animals are currently being used to validate potential DNA markers for feed efficiency discovered in other cattle populations (e.g. Trangie Angus and Adelaide University's Limousin x Jersey populations), with the aim of commercialising these markers in coming months, if the validation work confirms the preliminary association.

As well, project data are currently being used to discover new DNA tests for female reproductive performance. Following a whole genome scan of selected project (Brahman) heifers aimed at identifying markers associated with age at puberty, fifty (50) highly significant single nucleotide polymorphisms (SNP) are being further investigated.

Fine mapping of three significant QTL areas is continuing. These areas include genes related to cell cycling, which have a high level of expression in the ovary, testis and brain. Another area relates to one of the major antigenic systems in human red blood cells and has shown expression in the spleen, testis and heart. A third area controls a cytoplasmic peripheral membrane protein that is predominantly expressed in the brain. Though these are human genes, their levels of expression in the brain and reproductive tissues highlight them as potentially interesting candidate genes. SNP are being discovered in and around these genes for associations with components of reproduction rate. A gene of interest to cattle has also been found in sheep fertility studies, with SNP identified in and around this gene to examine an association with cattle fertility phenotypes. A pseudo-gene for this sheep gene has been identified and preliminary analysis has shown it to be present only in Brahman animals. Work is ongoing in this area.

Objectives from the South African component of the project

- ***Extend the Australian and South African beef genetic evaluation schemes for Belmont Red and Bonsmara breeds to estimate breeding values for traits of economic importance across both countries, in order to improve the productivity of beef herds in northern Australia.***

As an extension of an earlier collaborative project between CSIRO and the South African Agricultural Research Council's Animal Improvement Institute, Belmont Red breeders in Australia and Bonsmara breeders in South Africa agreed to exchange genetic material between their herds to strengthen genetic linkages between herds in both countries. From an Australian perspective, the idea was to then use the Bonsmara breed to benchmark Bonsmara and other tropically adapted southern African indigenous breeds to identify superior breeds and lines of cattle potentially for importation to replace a component of Australia's northern high-grade *Bos indicus* herd to improve productivity without reducing tropical adaptation (e.g. through formation of composites based on Brahmans and southern African tropically adapted indigenous breeds).

To that end, Bonsmara embryos were imported to Australia from South Africa and Belmont Red semen, including some from CRCI sires, was exported to South Africa after 1998. Semen from Bonsmara bulls born in Australia was subsequently re-exported to South Africa and simultaneously used in Australia to further increase genetic linkages between the herds.

The research activity written into this project was funded by the Australian Centre for International Agricultural Research (ACIAR) and managed through this project in the Beef CRC. It was designed to capitalise on the breeding programs already in place in both Australia and South Africa, whereby the commercial breeders in both countries paid entirely for the generation of the experimental progeny and the data collection. Primary aims of this objective were to:
i) Provide a capacity-building opportunity for South African scientists from previously disadvantaged backgrounds; and simultaneously
ii) Provide an opportunity for South African and Australian seedstock breeders to identify genetically superior animals from the Belmont Red and Bonsmara breeds to promote the commercial exchange of germplasm to improve productivity of herds in both countries.

Genetics of beef quality and components of herd profitability in northern Australia

Preliminary analyses by two South African scientists (Drs Khatu Nephawe and Norman Maiwashe) examined whether sufficient genetic linkage existed between Belmont Red herds in Australia and Bonsmara herds in South Africa to allow the full genetic evaluation to proceed. However the subsequently planned complete joint genetic evaluation of data from both countries did not proceed due to a commercial dispute between the genetic evaluation schemes in South Africa and Australia (Australia's BREEDPLAN system competes directly with the South African scheme in South Africa; BREEDPLAN was willing to proceed with these analyses, but ARC - which runs the South African scheme - was not). With agreement from ACIAR, the joint genetic evaluation remains incomplete, but with an expectation that it may proceed at some time in future, if the dispute between the genetic evaluation schemes can be resolved. Instead, project funds were used to support travel to Australia of other South African project scientists to present results of their ACIAR-funded activities at an international conference in Australia.

In spite of the commercial dispute though, it was possible for a CRC MSc student to analyse 19 years of comparative Belmont Red and Bonsmara data from the South African performance testing scheme to benchmark the two breeds and estimate genetic parameters for a range of growth and female reproductive traits (see Corbet *et al.*, 2006*a,b*). Results from those analyses indicated very few differences in performance between the two breeds for growth, feed efficiency, frame size, scrotal circumference, female reproductive attributes, resistance to ticks and carcass and beef quality. Bonsmara-sired animals generally scored higher than Belmont Red progeny for "functional efficiency" (a visual scoring system used in South Africa). Belmont Red sired calves were lighter at birth (35.9 *vs.* 37.3 kg) and cows by Belmont Red sires had a shorter average calving interval (440 *vs.* 455 days). Sire breed by region interaction was not important when four very diverse climatic regions in South Africa were examined (high-veld, low-veld, bush-veld and sub-Kalahari). Differences in scored and measured traits generally reflected differences in selection policies adopted by the breed societies. Variation in growth and fertility traits due to sire was greater than variation due to breed and demonstrated the potential for identifying superior individuals. The performance of the sire breeds for the range of traits and environments studied advocated that selected Bonsmara and Belmont Red animals from South African herds would be suitable for inclusion in breeding programs in Australian Belmont Red herds. Genetic parameter estimates from this study provide useful reference values for estimation of breeding values in the proposed combined across-country genetic evaluation program.

In addition, a separate component of the ACIAR-funded project in South Africa benchmarked and developed the role of Southern African indigenous cattle genotypes for profitable production and marketing of beef (i.e. through the South African commercial beef system) relative to commercial Bonsmara cattle, to determine their value in replacing a proportion of the several hundred thousand weaner steers or tens of thousands of tonnes of beef imported each year to satisfy South Africa's domestic demand for beef. As well, because of their perceived productive attributes (fertility, carcase and beef quality) in the presence of stressors of tropical environments (e.g. ticks, gastrointestinal helminths, heat and high humidity and seasonally poor nutrition), it is believed these *Bos taurus* breeds could form the basis of an entirely new export market for South African farmers by potentially replacing a component of Australia's northern high grade *Bos indicus* herd to improve productivity without compromising adaptation. Hence this component of the project evaluated a number of tropically adapted indigenous Southern African breeds (Nguni, Tuli and Drakensberger) relative to the Bonsmara (a Sanga-derived breed) and Brahman.

As part of the project, representative steers were sourced from emerging and communal farmer herds after weaning in 2002 (Phase 1) and 2003 (Phase 2) and transferred to the ARC's Irene campus for comparison with steers sourced from commercial herds. Steers from commercial herds were used as controls to benchmark the suitability of steers from emerging and communal herds to meet specifications of commercial markets. All animals were finished under commercial conditions, where animals were fed a grain-based diet.

Intensive data collection occurred between weaning and slaughter. Measurements included growth rate, feed intake, flight time as a potential indirect indicator of meat tenderness, real-time ultrasound scans for carcase attributes and commercial carcase characteristics and incidence of disease at slaughter. In addition, full carcase and meat quality attributes were measured. Phase 2 steers also underwent enzyme analyses (calpain, calpastatin and collagen parameters) and were taken to three market weights including a heavy export weight, to determine the ability of these breeds to marble, a requirement for premium export markets such as those in north Asia.

Results from both phases show growth rates and feed efficiencies of steers from emerging and communal farmer herds parallel those from commercial herds. They entered the feedlot at a lighter weight than commercial cattle, but during the feedlot period they grew as well and had similar feed conversion ratios, to achieve acceptable, albeit lighter carcase weights. The incidence of disease was low in all experimental steers and was no different between commercial, emerging and communal herds. Meat quality analyses indicated small or no differences between herd types or breeds in carcase and meat quality attributes, though the Brahman steers had significantly tougher meat than the Sanga and Sanga-derived breeds. Based on dentition, cattle from the emerging and communal herds were slightly older at slaughter than cattle from commercial herds. It was concluded that cattle from emerging and communal farmer herds have the ability to meet the specifications of South Africa's commercial beef markets, indicating a genuine opportunity exists for import substitution, whereby the >5 million cattle in emerging and communal herds could be used to overcome the significant shortfall in South Africa's domestic beef market demand. The performance of these breeds relative to the commercial Bonsmara and Brahman breeds indicates they would also be of value in replacing a component of the Brahman herd in northern Australia to improve beef quality without compromising adaptation to harsh environments.

Another component of the project tested widely used South African sires (~300 sires in total) using GeneSTAR™ Marbling and Tenderness tests to provide information about genes associated with those traits. Results show that Southern African breeds have a high frequency of the favourable form of the Calpastatin (tenderness) gene, with 98% of sires tested having at least one copy of the favourable gene. They have a lower frequency of the Calpain gene, with only 38% of sires tested having one or two copies of the favourable form of that gene. The breeds also have a very low frequency of the favourable form of the TG5 Marbling gene, even though some of these breeds were previously tested in Australia and USA as being high marbling breeds. This suggests that genes other than TG5 are involved in expression of high marbling in these breeds, perhaps offering an opportunity to increase marbling through introgression of favourable TG5 genes from the British breeds and other genes associated with marbling (yet to be identified) from the African breeds in environments that are suited to the African breeds of cattle. Sires tested in the project were not from resource-poor herds because sires in those herds were not widely used and characterized. However, the results provide additional evidence and an economic incentive to further genetically develop herds controlled by resource-poor farmers to develop a national and international seedstock market for these breeds.

Delivery of project information to industry

Project scientists have commenced work with the CRC's technology transfer specialists to distil the results into industry applicable messages, ready for very widespread distribution to other technology transfer specialists, consultants, breed societies and professional societies and the media. Economic analyses of project results will provide proof of profit to assist with uptake and adoption of project results through the CRC's "awareness" and "accelerated adoption" strategies.

Results from this project are extremely unique worldwide. However only limited release has occurred to date. Key early results were released directly to the co-operators in October and November, 2006. This was achieved via a series of one-on-one presentations and subsequent distribution of various documents including trial EBVs for several new traits measured in the project for each of the co-operator's bulls.

Knowledge of the genetic effects along with many of the non-genetic outcomes (e.g. location / year effects) on female reproduction in tropical breeds will provide opportunities to improve reproductive rates in northern Australia and will undoubtedly have spin-offs for southern Australia. Key relationships between female reproduction and steer traits, including feed efficiency, will be pivotal in allowing more accurate targeting of breeding objectives, particularly for self-replacing production systems.

In conjunction with the 'Smartgene for Beef' project, the effect of commercially available DNA markers on the primary trait (and also all correlated traits) will provide extremely valuable information on the utility of these markers in the 2 genotypes and production systems used in this study. The results will assist greatly in progressing the development of marker assisted EBVs and marker assisted selection. However, extensive efforts, through both existing and new elements, will be required to ensure adoption of the outputs (and commitment to the further measurement) by seedstock breeders, commercial producers and other sectors of the Australian beef industry.

Acknowledgements

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5 Success in Achieving Objectives

<u>Quantitative Genetic Objectives</u>

- ***Identify and communicate to cattle breeders the impact of selecting for carcass and beef quality attributes, efficiency of feed utilisation, adaptability to stressors of tropical environments and female reproductive attributes in order to maximise herd profitability in northern Australian environments.***

- ***Derive an accurate and validated understanding of appropriate selection emphasis on carcass and beef quality, feed efficiency, female fertility and adaptability.***

    The impacts of selecting for carcass and beef quality attributes, efficiency of feed utilisation, adaptability to stressors of tropical environments and female reproductive attributes have been determined and are reported herein through the estimates of genetic parameters for those traits. The results have been delivered directly to co-operating breeders and to key CRC stakeholders, particularly those based in northern Australia. However, widespread communication of the results to the cattle industry in general will not occur until the full extent of trade-offs from selection (arising from the direction and magnitude of relationships between the various groups of traits) is understood. That research is still ongoing, with the aim of publishing the complete correlation matrices by late 2007. In addition, full economic analyses of all project traits will commence as soon as the project scientists are confident the magnitude and direction of the estimated relationships are accurate. These economic analyses will enable practical recommendations to be made about how breeders in northern Australia can utilise the full complement of project results to maximise herd profitability in their environments.

    An accurate and validated understanding of appropriate selection emphasis on carcass and beef quality, feed efficiency, female fertility and adaptability will only be available with a complete knowledge of relationships amongst the entire range of traits and an examination of GxE interactions, genetic antagonisms and of differences between breeds in those parameter estimates, GxE interactions and genetic antagonisms. It is planned to publish these results in the Special Issue of the *Australian Journal of Animal and Food Science* in late 2007.

- ***Develop new techniques based on ultrasound scanning to identify minimum fatness levels that are compatible with high fertility.***

    Ultrasound scanning for ovarian activity has been used to effectively and accurately measure age at puberty and return to ovarian activity post-partum. The traits are moderately to highly heritable in both Brahmans and Tropical Composites and are related to subsequent calving performance. The technology and scanning protocols were able to deliver a very powerful means by which to estimate genetic differences in age at puberty and associated traits and genetic correlations with female reproductive performance traits. However the extent to which the technology can be used and such measurements could be measured cost-effectively in industry cannot be determined until the extent of associations between early-life and whole-of-life reproductive performance is known.

- *Identify breeds and lines of cattle with outstanding genetic merit for carcass and beef quality, adaptation to tropical environments and female fertility.*

  Breeds and lines of cattle with outstanding (and poor) genetic merit for the full range of project traits have been identified and detailed results provided directly to the co-operating breeders in the first instance, to allow them to maximise the use of the information in their own herds. The results will be made more generally available in 2007.

Molecular Genetic Objectives

- *Demonstrate to producers the role and value of genetic markers for selecting commercial cattle for carcass and beef quality and adaptability.*

- *Derive an accurate and validated understanding of specific genetic markers for selecting commercial cattle for carcass and beef quality and adaptability.*

- *Knowledge of genetic parameters between all traits and marker assisted selection.*

  Due to very rapid advances in molecular genetics technology and some technical problems that arose during the course of project experiments, the planned approaches to achieving the above objectives changed substantially over the life of the project. Within the next 1-2 years, all these objectives will be significantly exceeded. Whilst project data have not yet been useful for demonstrating the role and value of genetic markers for selecting commercial cattle for the full range of project traits, the role of the project's DNA bank and phenotypic database is now proving to be an extremely valuable resource for discovery and validation of DNA markers that will in the short to medium term deliver outcomes of considerable benefit to the entire Australian beef industry, with impacts at the global level.

  In conjunction with the CRCIII 'Smartgene for Beef' project, the effect of commercially available DNA markers on the primary trait (and also all correlated traits) will provide extremely valuable information on the utility of these markers in both project genotypes and all production systems used in this study. The results will assist greatly in progressing the development of marker assisted EBVs and marker assisted selection.

Objectives from the South African component of the project

- *Extend the Australian and South African beef genetic evaluation schemes for Belmont Red and Bonsmara breeds to estimate breeding values for traits of economic importance across both countries, in order to improve the productivity of beef herds in northern Australia.*

  The precise objective as described above was not achieved due to a third-party dispute outside the Beef CRC's control. With approval of ACIAR, which funded this component of the project, the project objectives were slightly modified. The modified objectives were significantly exceeded, with the project delivering substantial impacts on the commercialisation and profitability of the project's emerging farmers in South Africa. Project results also demonstrated considerable opportunities for beef producers in northern Australia to enhance herd productivity through replacement of a component of their high-grade Brahman herds using indigenous breeds and lines of cattle from southern Africa, to improve beef quality and female reproductive performance without compromising adaptation to harsh tropical and sub-tropical environments.

6 Impact on Meat and Livestock Industry – now & in five years time

Full project results will undergo external scientific peer review for publication as a group of linked papers in a "free-to-air" Special Issue of the new *Australian Journal of Animal and Food Science* to be published in late 2007. Until the peer-reviewed results are available though (to ensure their accuracy), only limited release of results is occurring directly to the project's co-operators, by way of trial EBVs for sires contributed to the project by the co-operators and customised reports aimed at uptake of project results in co-operator herds. This means the current impact of the project on the Australian industry is still limited, though the impacts on emerging farmers in South Africa have been very significant, with national recognition of the success of the project in that country.

Project results confirm that beef processors could immediately utilise technologies such as tenderstretch to improve beef eating quality. However it is still premature to recommend other project technologies such as ultrasound scanning for female reproductive performance. Once the full genetic and phenotypic correlation matrices and estimates of GxE interactions have been verified by scientific peer review, the project's economists will immediately commence their research to deliver economic recommendations on a wide range of genetic and non-genetic options aimed at improving productivity and profitability in northern Australian herds. It is expected those recommendations will be delivered very widely to the Australian beef industry by the CRC's "awareness" and "accelerated adoption" projects from late 2007 or during 2008. It is also planned to include relevant project results in formal and vocational educational packages developed by, or in conjunction with, Beef CRC education program staff.

Relevant project data have been transferred to BREEDPLAN to be used to produce EBVs for the sires for existing BREEDPLAN traits and also for several new traits that are likely to arise from this project once the correlation matrices are verified by peer review. However decisions on whether to introduce new reproductive traits to BREEDPLAN will not be made until the relationships between early-life and whole-of-life reproduction become clearer in coming years. The extent, direction and magnitude of those same relationships will also determine the feasibility or otherwise of using ultrasound scanning in commercial herds to genetically improve female reproductive performance.

Based on current progress, it is highly likely that multiple DNA tests for project traits such as feed efficiency, parasite resistance and female reproductive performance will be discovered, validated and commercialised using project DNA and phenotypic database resources in the next 1-2 years.

Results from this project are absolutely unique, providing the Beef CRC, MLA and the project's scientists with world leadership in the project's fields. They will allow beef producers in tropical and sub-tropical environments to precisely target the specifications of premium beef markets whilst simultaneously maintaining or improving female reproductive performance, without compromising adaptation to harsh environmental conditions. Key relationships between female reproductive performance and steer traits, including feed efficiency, will be pivotal in allowing more accurate targeting of breeding objectives, particularly for self replacing production systems. In conjunction with the 'Smartgene for Beef' project, the effect of commercially available gene markers will provide extremely valuable information on the utility of DNA tests in the two tropically adapted genotypes and the beef production systems used in this study. Project results will assist greatly in progressing the development of marker assisted EBVs and marker assisted selection. However, extensive efforts, through both existing and new CRC projects, will be required to ensure adoption of the outputs (and commitment to ongoing measurement) by seedstock breeders, commercial producers and other sectors of the Australian beef industry.

Within five years, it is therefore realistic to expect the project will have achieved major economic impacts in northern Australian beef herds, with significant spin-off benefits for feedlotters, beef processors and southern Australian beef producers. Flow on benefits will also have accrued to cattle breeders worldwide.

The very wide scope and number of the traits measured in the project, the large number of repeated measures for many of the traits and the high degree of accuracy of the measurements mean the project's dataset will continue to have a very significant impact on the development of recommendations for northern Australian beef producers for many years to come.

7 Conclusions and Recommendations

Full conclusions and recommendations from the project will not be available until late 2007. Delivery of project research outputs and industry outcomes over the next 12-18 months is being managed and oversighted through CRCIII Program 4. However conclusions and recommendations already available from the project include:

Steer feed efficiency traits
- Feedlot feed efficiency (as NFI) is moderately heritable in both Brahmans and Tropical Composites, indicating the trait will respond to selection.
- Genetic correlations between NFI and growth rate prior to feedlot entry, P8 fat depth, and hip height measured at feed entry indicate these traits can be exploited through selection to indirectly improve NFI in Brahmans, but may be of limited use for Tropical Composites.
- Selection for improved NFI will on average result in taller leaner cattle.
- Results are consistent with Brahmans being more adapted to harsh, tropical heifer environments and Tropical Composites being better able to exploit feedlot conditions.
- For certain growth and scanned body composition measures, genetic evaluation and selection of Brahmans and Tropical Composites for these environments may need to distinguish heifer season and steer growth environments as separate traits, especially for Brahman heifers and Tropical Composite steers.
- The new parameter estimates and data on many traits and genetic linkages from this project will greatly strengthen BREEDPLAN for tropical breeds.

Carcase and beef quality traits
- All carcase and beef quality traits, except MSA pH, showed significant amounts of genetic variation and large differences between sire for their progeny performance.
- Significant benefits in beef tenderness accrue from the use of tenderstretch.
- The benefits of tenderstretch were larger in poorer quality carcasses and had the greatest effect on shear force (tenderness), with the greatest favourable effects seen in the toughest carcasses.
- Brahmans and Tropical Composites benefited equally from the use of tenderstretch.
- Large sire differences for tenderness exist in both Brahmans and Tropical Composites, but these differences are significantly reduced for shear force in carcasses that are tenderstretched.
- Correlations between shear force measurements in achilles-hung *vs.* tenderstretched carcasses in Brahman, Tropical Composite and steers pooled across breeds show the genetic correlations are significantly higher than the phenotypic correlations, indicating the relationships are strongest at the genetic level.

- These relationships also show that selection to improve tenderness using measures of tenderness based on either achilles-hung or tenderstretched carcasses will be equally effective, with only minor re-ranking of sires if the processing methods were to be altered.
- To improve the consistency of beef eating quality, multiple genetic and non-genetic strategies are needed, as identified by the MSA prediction model.
- Selection of breeds and animals within breeds using both quantitative and molecular genetic tools, nutritional strategies that optimize growth pathways, animal handling on-farm and pre-slaughter and post-mortem processing technologies all represent potential methods to improve beef eating quality.
- A value-based marketing system that genuinely rewards beef producers, processors and retailers for implementation of such strategies is the economic driver needed to underpin the quality of Australian beef in future.

Female reproductive performance
- There were no differences between Brahman and Tropical Composite heifers for weight at first CL (deemed to be achievement of puberty), but Brahmans were on average 84 days older and 1.3 mm fatter at that time.
- Only 51% of Brahmans had achieved an observed CL before the start of first joining at about 25 months of age, compared to 79% of Tropical Composites.
- Brahmans also had a longer days to calving (346 *vs.* 319 days) and lower calving success (71% *vs.* 90%) following first joining than Tropical Composites. Note though – it is not possible to extrapolate genotype differences outside the range of environments in the experiment, as Tropical Composites were purposely not allocated to the Swans Lagoon environment as it was perceived they would not be well enough adapted for that environment.
- Location had a large effect on age at first CL. In particular, heifers at Swans Lagoon were significantly older, tended to be fatter at first CL, had a lower proportion of pubertal heifers at the start of joining and subsequently longer days to calving and lower calving success following first joining.
- Birth month and associated seasonal effects had a large effect on all traits. Late-born heifers (e.g. March) were significantly older and fatter at time of first CL, had a lower proportion of pubertal heifers at start of joining, longer days to calving and reduced calving success relative to early-born (i.e. September) heifers. However there was little observed effect of birth month on weight at first CL.
- All traits associated with puberty in heifers were moderately heritable, except proportion of Tropical Composite heifers that had achieved puberty at start of joining.
- In general, additive variances for pubertal traits were larger for Brahmans than Tropical Composites, indicating large differences between sires in their daughters' ages at first CL and also weight and fatness at first CL. The differences can be use to alter these traits if this is considered desirable.
- Days to Calving and Calving Success were more heritable for Brahmans than Tropical Composites with larger additive variances when heifers were joined for the first time at around 2 years of age.
- Moderate to strong positive correlations were estimated between each of the pubertal traits, showing animals that were older at first CL were also genetically heavier and fatter at the time of their first CL.
- However the genetic correlations between age at first CL and live weight and fat depth on an age-constant basis indicate animals with younger ages at puberty were genetically heavier and fatter at the same age.

- Achievement of puberty by the start of first joining was highly negatively correlated with younger age at first CL and with weight and fatness, indicating those sires' daughters with higher age, weight and/or fatness at puberty were genetically less likely to have shown a CL by the start of their maiden mating.
- For both genotypes, genetic correlations between first days to calving and calving success were not significantly different from one, indicating they are very similar traits.
- The average age at first CL for Tropical Composites was 108 days before the start of first joining, whereas the average age of Brahmans at first CL was 6 days after the start of first joining.
- Genotype differences in genetic parameter estimates in this study include the effects of the different production environments, and in particular, the effects of the harsher Swans Lagoon environment for Brahmans.
- Ultrasound scanning technology has been shown to be a very effective research tool for use in female reproduction studies. However its use in commercial breeding herds as a tool to improve reproductive performance is yet to be proven.
- Non-genetic strategies such as changed calving dates (i.e. through start of mating and duration of joining periods) could be implemented immediately to reduce the number of calves born after January each year, to significantly improve subsequent reproductive performance of the herd.

Heifer adaptive traits
- All adaptive traits studied in this project were at least moderately heritable.
- Moderate favourable genetic correlations were found between different adaptive traits, indicating that selection to improve any resistance trait may have favourable correlated responses that increase performance in other resistance traits.

Genetic differences between project sires
- Large differences were identified between sires in the project, across the full range of project traits, indicating there are significant economic gains to be made for breeders willing to base their matings on genetics and producers purchasing bulls known to be genetically superior based on measured performance.
- Differences between extreme Brahman sires (not affected by differing breed composition as occurs in Tropical Composites) show differences in sire progeny groups of 26 kg of carcass weight and 7.2 kg of saleable beef yield.
- Differences between extreme Brahman sires for age at puberty indicate the bulls' daughters could vary by as much as 6 months.
- There is an overall difference of 25% in the calving rates of extreme Brahman sire progeny groups.
- In Brahmans, age at first CL could be used as an indirect selection criterion to improve subsequent reproductive performance, provided it can be measured cost-effectively in industry and providing the associations with lifetime reproductive performance indicate the approach is economically important for industry.

Use of scanned fat measures to predict female reproductive performance
- To achieve 80% pregnancy rates and conception within the first 2 oestrus cycles after start of mating (i.e. to achieve days to calving of 305-326 days), the following recommendations are made:
  i) 2-year old maiden heifers require a minimum weight into mating of 330 kg
  ii) 3-year old primiparous (first-calf) cows require a minimum rib fat depth of 5 mm and weights at start of joining of 550 kg; and
  iii) 4+ year old lactating cows require a minimum rib fat depth of 5 mm, P8 rump fat depth of 6.5 mm and weight at start of joining of 520 kg.

- If the above recommendations cannot be achieved in northern herds, beef producers will need to make decisions about whether it is economically more valuable to supplementary feed to achieve the recommended weights and fat depths or to accept pregnancy rates of less than 80% and conception at periods more than 2 oestrus cycles after start of joining. Once available, economic analyses of project data that are now underway will help beef producers make these decisions.
- This study confirmed that scanned measures of subcutaneous rib fat depth and start-of-mating liveweight can be used to effectively predict subsequent pregnancy rates, days to calving and calving success in both Brahman and Tropical Composite females of different age and lactation status.
- Management options to achieve minimum live weights and fat depths can be used to decrease age at puberty and improve subsequent calf output, but the economic feasibility of such management options needs to be examined closely.

Use of DNA marker tests
- *Preliminary* results indicate that DNA markers described statistically significant additive variance in tenderness between Brahman and Tropical Composite, but the percentage of additive variance that each of the markers explains individually and collectively is small. At this point in time, the use of genetic markers for tenderness selection in young animals with no phenotype records for the trait is impractical. Such selection is likely to be risky and low in accuracy because each of the markers explains only a small amount of variation in tenderness.
- Development and validation of more markers associated with beef tenderness and other traits may mean that DNA marker tests can be used for early selection of those traits in beef cattle.
- Until DNA markers are able to explain a large proportion of variation in tenderness though, the benefit of genetic markers in beef breeding systems is limited.
- DNA from project animals is currently being used in conjunction with the animals' measured performance to discover and validate DNA tests for a wide range of performance attributes with the aim of commercialising these tests in industry in the next 1-2 years to improve herd productivity and profitability.

Results from South African component of the project
- Comparative performance of Belmont Red and Bonsmara sires across four very diverse environments in South Africa indicates that Bonsmara and Belmont Red animals from South African herds would be suitable for inclusion in breeding programs in Australian Belmont Red (seedstock) herds.
- Genetic parameter estimates derived from 19 years of comparative data provide useful reference values for estimation of breeding values in a joint, across-country genetic evaluation program.
- The performance of Nguni, Tuli and Drakensberger steers relative to commercial Bonsmara and Brahman steers indicates these tropically adapted *Bos taurus* breeds would also be of value in replacing a component of the high-grade Brahman herd in northern Australia (e.g. through the formation of composites based on Brahman and Sanga or Sanga-derived breeds) to improve beef quality and reproductive performance without compromising adaptation to tropical environments.
- Southern African indigenous *Bos taurus* breeds have a high frequency of the favourable form of the Calpastatin (tenderness) gene, with 98% of sires testing having at least one copy of the favourable allele. They have a lower frequency of the favourable Calpain gene, with only 38% of sires tested having one or two copies of the favourable allele.

- These breeds also have a very low frequency of the favourable form of the TG5 Marbling gene, even though some of those breeds were previously tested in Australia and the USA as being breeds with high levels of marbling. This suggests that genes other than TG5 are involved in expression of high marbling in those breeds, providing new opportunities to increase marbling through introgression of other genes associated with marbling.

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