



Professor Bernie Bindon

Chief Executive Officer - Cooperative Research Centre for Cattle & Beef Quality

Bernard Bindon is the Chief Executive Officer of the Cooperative Research Centre for Cattle and Beef Quality, a \$146 million project established in 1993 and funded to June 2006. He is well known locally and internationally for research in reproductive biology and genetics of cattle and sheep and began his career in beef cattle research in CSIRO, Brisbane in 1963.

Since 1990, Bernie Bindon has made a significant contribution to the Australian beef industry by putting in place Australia's largest integrated beef research program, designed to understand the genetic and environmental factors influencing beef quality. The Cattle and Beef CRC, conceived in 1990, recognised the need to integrate genetics, nutrition and meat science in studies of pedigree cattle from Australian seedstock herds. This led to the establishment of a large progeny test for meat quality traits, based on seven purebreds and a terminal crossbreeding project based on 1,000 Brahman females and nine sire breeds. At the same time, the CRC initiated world-class research in molecular biology, designed to identify gene markers and candidate genes for carcase and meat quality attributes.

INNOVATIVE APPROACH TO BEEF INDUSTRY RESEARCH

SUMMARY

Australia's beef industry in the year to June 2003 was worth \$9.6 billion, with more than \$6 billion in export earnings. With only 2.5% of world cattle numbers, Australia is the world's largest beef trader (23%). Hereford cattle have played an extraordinary part in the history of the Australian beef industry. In 1949 Herefords accounted for 50% of cattle in the southern Australian beef cattle population of 8 million. The breed also represented 40% of the 6 million cattle in northern Australia at that time. By 1965 Herefords accounted for 50% of cattle in Queensland, replacing Shorthorns (24%) as the dominant breed in the tropics. Since then we have witnessed the gradual "*Zebu hybridization*" of the northern herd, with Brahman-infused cattle now estimated to represent 53% of the national herd of 28 million. But this historical perspective attests to the Herefords' adaptive qualities across two hundred years of beef production in Australia's difficult environments.

In the CRC context, Herefords have played a significant role in Beef Quality research. In 1992 the CRC set up a comprehensive progeny test for carcase and meat quality at a cost of around \$32 million, involving Hereford, Angus, Shorthorn, Murray Grey, Brahman, Santa Gertrudis and Belmont Red breeds. This was done to position Australia for the emerging liberalisation of the Japanese and Korean beef markets and to address consumer concerns about beef eating quality in Australia and elsewhere.

The CRC has worked closely with the northern and temperate cattle breeds to identify the main genetic and non-genetic factors affecting tenderness, marbling, retail beef yield, meat colour, the fatness traits and Net Feed Intake. This paper presents results showing favourable opportunities to select for these traits to improve the value of the carcase and its eating quality. It also draws attention to the genetic associations between traits which may be antagonistic. These genetic correlations are essential knowledge to implement breeding programs designed to change more than one trait. The CRC has delivered new knowledge about gene marker technologies which open up new possibilities for genetic improvement of beef quality traits using commercial DNA tests for marbling and tenderness. We need to understand how to incorporate these technologies into practical beef improvement programs. At the World Hereford Congress this paper will focus on results from CRC research that relate to:

- The scope for genetic improvement of tenderness by direct selection and by using favourable genetic correlations with temperament (flight time), meat colour and marbling.
- The scope for genetic improvement of Retail beef Yield and marbling.
- The genetic correlation between marbling and MSA eating quality.
- The size of effect and frequency of candidate genes affecting tenderness.
- The performance of northern and temperate cattle for these traits in grain- and grass-finishing environments and in northern versus southern regions of Australia.
- The genetic improvement of Net Feed Intake.

Collectively these results provide a blueprint for genetic improvement of beef quality and efficiency in Australian beef herds.

The paper will also announce plans for a new CRC to capture opportunities for the Australian beef industry arising from the explosion in knowledge of molecular genetics and gene expression (the Human and Bovine Genome projects) and the so-called livestock Revolution which promises significant growth in demand for meat and milk by the developing world through to 2020.

INTRODUCTION

The CRC portfolio began in 1993 to concentrate on the genetic and non-genetic factors influencing beef quality (Figure 1). This followed many years of emphasis on the genetic improvement of cattle growth and adaptation to stressful northern environments. It was timely to combine our expertise in genetics, meat science and growth and nutrition to address the beef issues of the 1990s. A parallel development in molecular genetics in 1992 provided the opportunity to pursue gene markers and candidate genes for beef quality traits. A third area of endeavour chosen by the CRC was to expand Australian research on the efficiency of feed utilization, in the hope of providing long-term improvement in the economy of beef production in pasture- and grain-fed environments. The Hereford Society of Australia and the Australian Poll Hereford Society members provided cattle resources and cash to make these investigations possible.

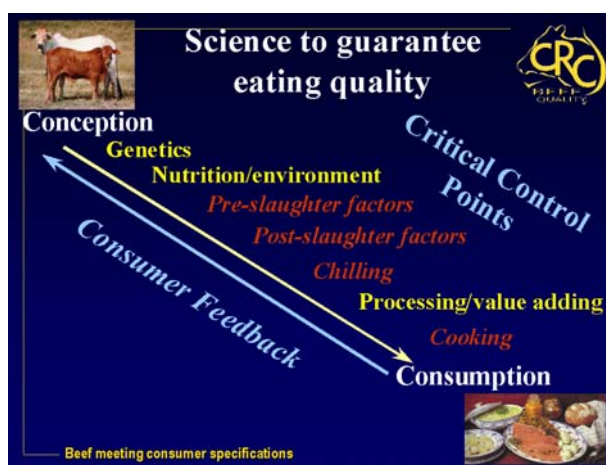


Figure 1. Critical control points for beef eating quality.

SCOPE OF CRC BREEDING/FEEDING/SLAUGHTER PROJECTS

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

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

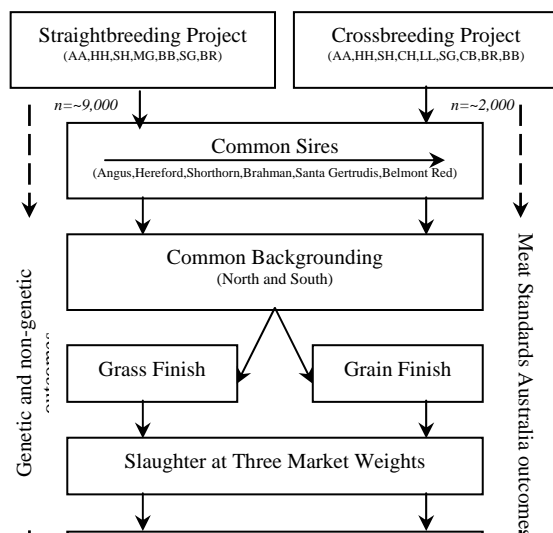


Figure 2. Design of CRC progeny tests for meat quality traits.

It is estimated that the CRC has spent nearly \$32 million on this process. But the project has provided invaluable information for four areas of beef technology. These are:

1. Provision of Estimated Breeding Values (EBVs) for carcass and beef quality traits.
2. Genetic parameters (heritabilities, h^2) and genetic correlations (rg) for balanced breeding programs.
3. A compendium of information to underpin Australia's novel "Meat Standards Australia (MSA)" grading scheme based on beef eating quality.
4. A database of performance measurements (phenotypes) and matching DNA of Australian cattle as a platform for gene marker discovery.

The CRC's breeding projects (progeny tests) have made progress towards achieving the largest-ever bank of knowledge about carcass and meat quality of Australian beef cattle. In the CRC database there are now records of 10,000 carcasses, comprising British breeds, tropically adapted breeds and crossbred animals (Figure 3).

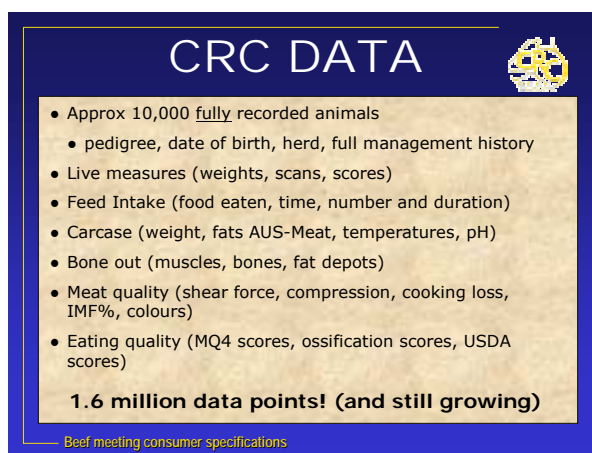


Figure 3. CRC data to achieve meat quality improvement.

Heritability estimates of Beef Quality Traits

Estimates of heritability (h^2) of (objectively measured) tenderness are low in British breeds (Angus, Hereford, Shorthorn, Murray Grey) for different muscles and are moderate in tropically adapted breeds (Brahman, Belmont Red, Santa Gertrudis). Direct selection to improve these traits may not be successful in British cattle. Non-genetic approaches, by controlling growth path and pre- and post-slaughter practices may be a more reliable method of guaranteeing beef tenderness (Figure 4).

Heritability estimates (38%) for marbling, as measured by chemical intramuscular fat percentage are more promising.

By contrast, retail beef yield percentage (RBY%) is an important new trait studied by the CRC (achieved by bone-out of one side of most CRC carcasses). The trait is moderately heritable (>40%; Figure 4) in all breeds studied so far, and is of great potential economic value to the Australian beef industry. VIAscan® may provide indirect prediction of the trait.

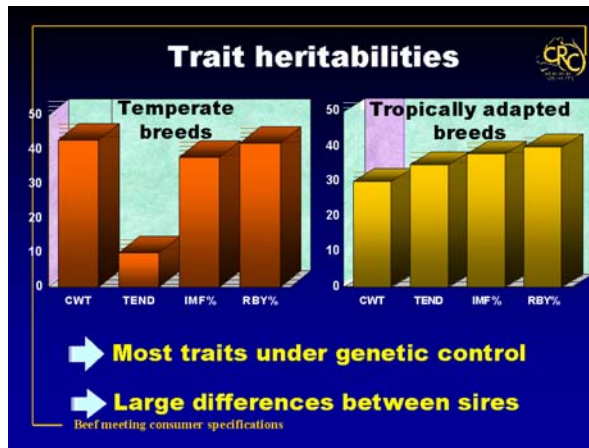


Figure 4. Heritability estimates (%) for carcass weight, tenderness of the strip loin, intramuscular fat % (marbling) and retail beef yield %.

Currently, most of this economic benefit would flow to beef processors, but with progress in value-based marketing, cattle producers should be rewarded for using sires whose progeny have higher retail beef yield. Note that these genetic differences are not the result of heavier carcasses: they result from genuine differences in body composition.

In Figure 5 the heritability values for the two measures of tenderness (shear force and instron compression), cooking loss, post-slaughter pH and meat colour (measured colorimetrically) are presented. The results confirm that there is no genetic influence on pH, but the others are all under some degree of genetic control.

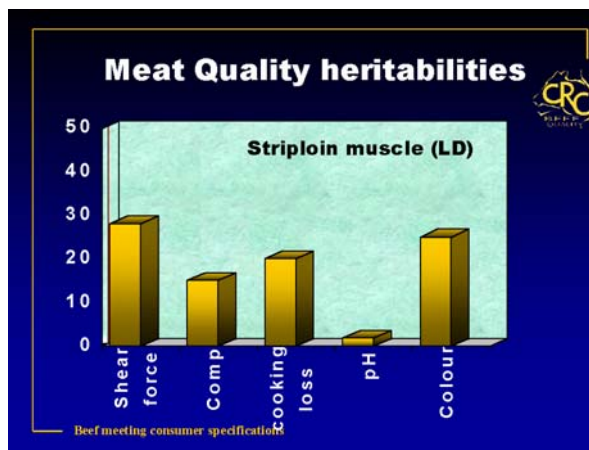


Figure 5. Heritability estimates of shear force, compression, cooking loss, post-slaughter pH and meat colour. (Legend: Shear force = objective measure of myofibrillar component of tenderness; Comp = Instron compression test of the collagen component of tenderness; Cooking loss = Percentage weight loss of a pre- and post-cooked sample of muscle; pH = Digital pH meter glass electrode measurement of pH of muscle; Colour = objective measurement (Minolta Chrome Meter) of colour of muscle.

Meat colour's heritability is an important new development as we shall see later it is genetically correlated with tenderness and may provide an opportunity for indirect selection.

Genetic association (correlations) between meat quality traits

It is important to understand the genetic association between different traits. (If you select for tenderness what happens to marbling in a sire's progeny? If you select for growth, what happens to fatness?) The CRC now has results for many different traits.

These are presented in Table 1 for 16 different traits in the tropically adapted breeds Brahman, Santa Gertrudis and Belmont Red.

Table 1. Heritabilities (h^2 diagonal) and genetic correlations (rg) for 16 traits from Tropically adapted breeds: Brahman, Santa Gertrudis and Belmont Red. (Key to Traits: 1 = condition score; 2 = flight speed [measure of temperament] assessed by electronic measurement as the animal emerges from a crush; 3 = liveweight; 4 = p8 fat measured by Real Time Ultra South [RTUS]; 5 = RTUS scan measure of eye muscle area; 6 = average daily gain during the finishing phase of growth on grass or grain; 7 = carcass weight; 8 = retail beef yield from carcass bone-out and fat trimmed to 3mm; 9 = AusMeat p8 fat direct measurement; 10 = direct measurement of eye muscle area; 11 = AusMeat meat colour score; 12 = AusMeat marble score; 13 =

chemically extracted fat % in the striploin; 14 = objective measurement [Minolta Chroma Meter] of colour of the striploin; 15 = shear force objective measurement of myofibrillar component of tenderness of the striploin; 16 = shear force measurement of tenderness of the eye-round.)

Tropical Breeds
Heritabilities (h^2) & Genetic Correlations (r_g) (if > 0.20)

	Trait Number															
	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16
1. CondSco (1)	33			24	44						25	25	-43		22	
2. FlightSp (1)		30			28			22							-43	
3. LiveWt (2)			31	-46	28	34	82	-34	-25				-25			
4. ScanP8 (2)				27	-27		-36	81							43	
5. ScanEMA (2)					15		35		69				-58			
6. FinishADG						27	73								-21	-27
7. CarcaseWt							37	-27	-29	-55			35	-26	-26	
8. RBV%							48	-28	25	-25	-58		-56	-27		
9. P8								32					22	30		
10. EM LxW									27		-23					
11. Meat Colour										11	-22		-29	-63	44	
12. MarblingSco											25		66	41		
13. IMF%													39	35	-29	
14. LD L Colour													17	-48	-34	
15. LD PF														28	46	
16. ST PF																42

Some important conclusions are:

- Retail beef yield (RBV%) is negatively (-0.56) genetically correlated with marbling (IMF%).
- Flight time (temperament measure) is genetically correlated with tenderness (-0.43). Sires with poor temperament produce progeny with tougher meat.
- Meat colour (AusMeat score or colorimetric measurement) is genetically linked to tenderness (+.30 to +0.43). Sires with light, bright meat produce more tender progeny.

These results on genetic associations are a reminder that if you want to make progress in traits that are antagonistic measure all the traits and select sires using Estimated Breeding Values (EBVs).

Genetic Correlations between Markets, Regions and Grass versus Grain Finishing

The CRC has now worked out the answer to long standing industry questions. Are the same genes (i.e. sires) suitable to produce progeny for domestic versus export markets (i.e. for all production traits)? Are the same genes (sires) suitable to produce progeny for finishing in northern versus southern environments? Are the genes for feedlot and pasture finish the same? These questions have a bearing on Australia's genetic improvement schemes. For example if the Genetic Associations (Correlations) between grain and grass finishing are high (e.g. >0.80) then we can confidently base BREEDPLAN procedures on grass fed performance, in the knowledge that sires whose progeny perform well on grass will also perform well on grain. Conversely, if the genetic correlations between grass and grain are low (e.g. <0.5) it means we need two seedstock systems: one based on grass fed performance and another based on grain fed performance.

The results in Figure 6 present some of the key genetic correlations. These need careful consideration because of their overall industry significance for the future. A few general conclusions are:

- For growth (carcase weight), marbling (IMF%) and tenderness (LDPF) there is little re-ranking of sires across feedlot versus pasture, domestic versus export and north versus south finish. This is good news – for example, current breeding strategies for selecting sires for marbling on pasture has the assurance that their progeny will perform accordingly on feedlot diets.
- For traits like RBV% and P8 fat and meat colour the genetic correlations are generally lower meaning that some re-ranking of sires will occur when you move from pasture to feedlot, domestic to export or north versus south finish,
- For traits under low genetic control (e.g. pH) the correlations are variable and probably meaningless.

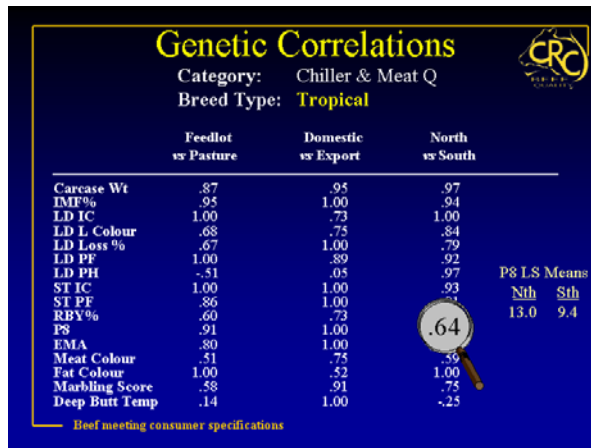


Figure 6. Genetic correlations for major traits for Feedlot versus Pasture, Domestic versus Export and North versus South finish. (For trait definition, see Table 1.)

Temperament, Flight Time and Tenderness

The work of Dr Heather Burrow, CSIRO Rockhampton on the genetics of temperament and Flight Time (i.e. the time taken for an animal to traverse a distance of 1-2 metres after emerging from a cattle crush) has led to an unexpected breakthrough in the search for an easily-measured live animal attribute as a genetic predictor of beef tenderness. This comes about from recent analyses of Flight Time in tropically adapted cattle and its genetic association (i.e. Genetic Correlation) with beef tenderness (measured by Shear Force (SF)) in the CRC database.

The results in Figure 7 confirm that measured Flight Time is indeed moderately heritable (32%). This means the trait is under partial genetic control. Note however that a visual estimate of Flight Speed or a subjective crush score measure of temperament had lower heritability than Flight Time.

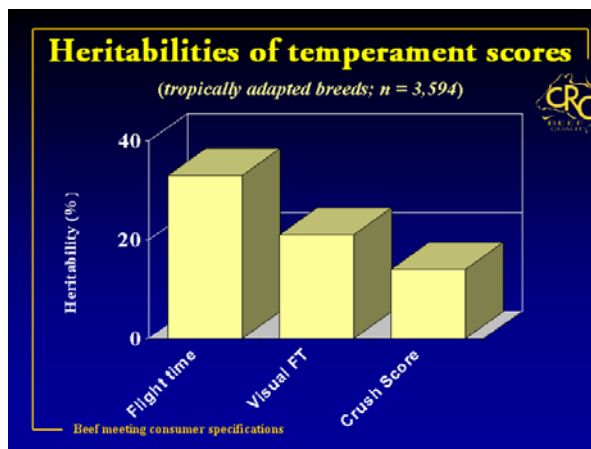


Figure 7. Heritability estimates of Flight Time, Visual FT and Crush Score.

Figure 8 confirms that Flight Time is significantly (-0.53) genetically correlated with shear force Tenderness of the striploin. This means sires with slow Flight Time have progeny with lower Shear Force (i.e. more Tender!) striploins. Note that the Flight Time is also linked to meat colour.

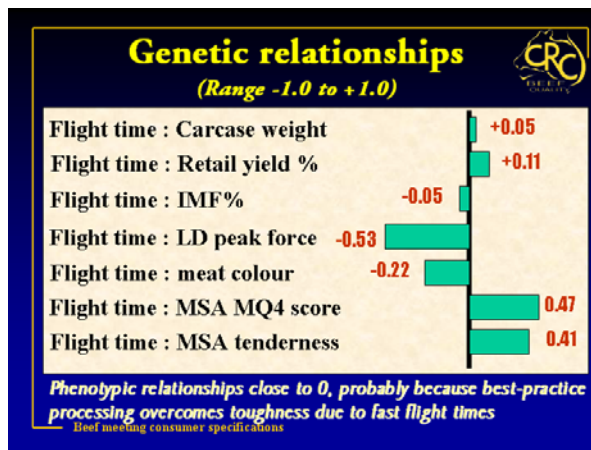


Figure 8. Genetic correlations of Flight Time and Meat Quality.

There is now a great opportunity to measure Flight Time (at weaning or later) on farm, say in young bulls with a view to improving tenderness of their progeny. Cattle breeding experts will advise producers about the correct way to collect records.

Genetics of marbling

The CRC has a strong commitment to marbling research. The objective is to understand how intramuscular fat can be regulated by genetic and non-genetic techniques. This would create opportunities to either increase or decrease marbling, depending on the market specifications for the trait. CRC studies of marbling cover:

- progeny testing sires for intramuscular fat percentage (IMF%);
- measurement of marbling by real-time ultrasound (RTUS) in bulls, steers and heifers to arrive at correlations with IMF%;
- analysis of the possible antagonism between marbling and RBV%;
- comparison of sire progeny on grain *versus* grass finishing to arrive at the genetic correlation between the two nutritional environments (are the “genes” for grain and grass performance the same?);
- development of gene markers and candidate genes for marbling;
- the relationships between marbling, tenderness and eating quality;
- investigation of apparently lower marbling levels in cattle finished in northern *versus* southern feedlots.

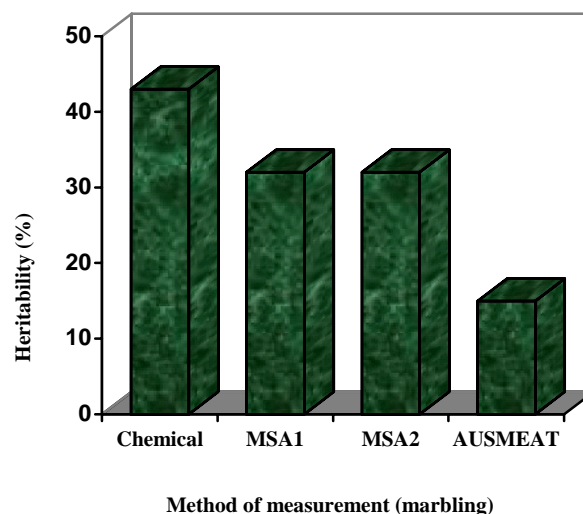


Figure 9. Estimates of heritability of marbling in the same cattle when measured as IMF%, or as marble score using AusMeat or Meat Standards Australia (MSA) graders (n=4,000) (Johnston *et al* 1997)

Measurement of marbling

Intramuscular fat percentage is moderately to highly heritable (Figure 9). AusMeat marble score is less heritable, meaning that this measure may be influenced by environmental factors such as chiller conditions or inconsistencies between assessors. Heritability of marbling assessed by MSA graders, however, is closer to the heritability of intramuscular fat percentage. These results highlight a significant industry issue: we need to find a more reliable way to measure intramuscular fat percentage, perhaps “on-line” in the abattoir. It must be closely calibrated to marble score while ever this measure is the “accepted” trait on which carcass payment is based.

Genetic correlations between marbling and other traits

Recent CRC results (Reverter *et al*, 2003) have highlighted the genetic associations (correlations; rg) between marbling measured as IMF% and other important traits (see Table 2). A most important result is that IMF% is now genetically linked to tenderness and beef eating quality. The genetic correlations are higher in temperate than tropical cattle (Table 2) but still important for the Brahman breed (ie a genetic correlation of +0.37 between IMF% and MSA-MQ4 [eating quality] score).

Table 2. Genetic correlations between IMF and other traits for temperate and tropically adapted breeds (Johnston, 2001).

Trait Group	Trait	Temperate breeds	Tropically adapted breeds
Live animal measures ^a	scan p8 fat	0.39	0.22
	scan eye muscle area	-0.17	-0.59
	live weight	0.09	-0.22
	daily feed intake	0.19 ^b	
	net feed intake	0.21 ^b	
Abattoir carcass	carcass weight	-0.12	-0.03
	retail beef yield %	-0.38	-0.43
	P8 fat depth	0.34	0.22
	12/13 th rib fat depth	0.21	0.20
	AusMeat marble score	0.96	0.89
Meat Quality	meat colour (L-value)	-0.16	0.39
	cooking loss %	-0.14	-0.17
	shear force - strip loin	-0.34	-0.10
	shear force - eye round	-0.33	-0.32
Eating quality ^c	MSA - flavour score	0.75	0.43
	MSA - juiciness score	0.69	0.54
	MSA - tenderness score	0.73	0.29
	MSA - MQ4 score	0.70	0.37
	MSA - marble score	1.0	0.94

^a taken at start of finishing

^b estimates from an analysis pooled across the temperate and tropically adapted breeds

^c only a sub-set of animals had MSA scores: N = 1,152 for temperate breeds and N = 1,585 for tropically adapted breeds

CRC Progeny test results for marbling

Pooled results for marbling (measured as IMF%) for Tropical breeds (Brahman, Belmont Red, Santa Gertrudis) and temperate breeds (Hereford, Angus, Shorthorn, Murray Grey) from the CRC's progeny test are shown in Figures 10 and 11.

Tropically Adapted Breeds (Brahman, Belmont Red, Santa)

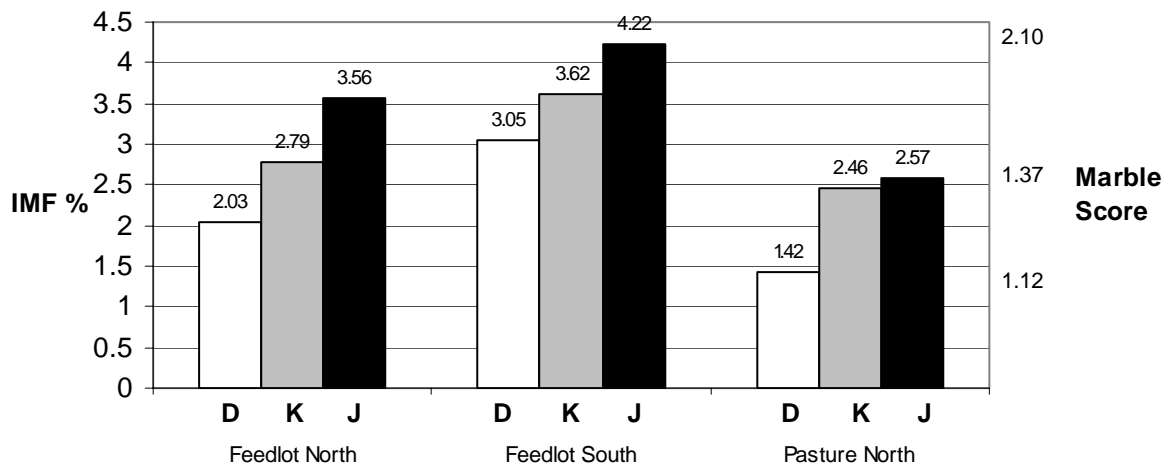


Figure 10. Tropically adapted breeds (IMF%) (D, K, J = Domestic, Korean and Japanese weight carcasses)

Temperate Breeds (Angus, Shorthorn, Murray Grey, Hereford)

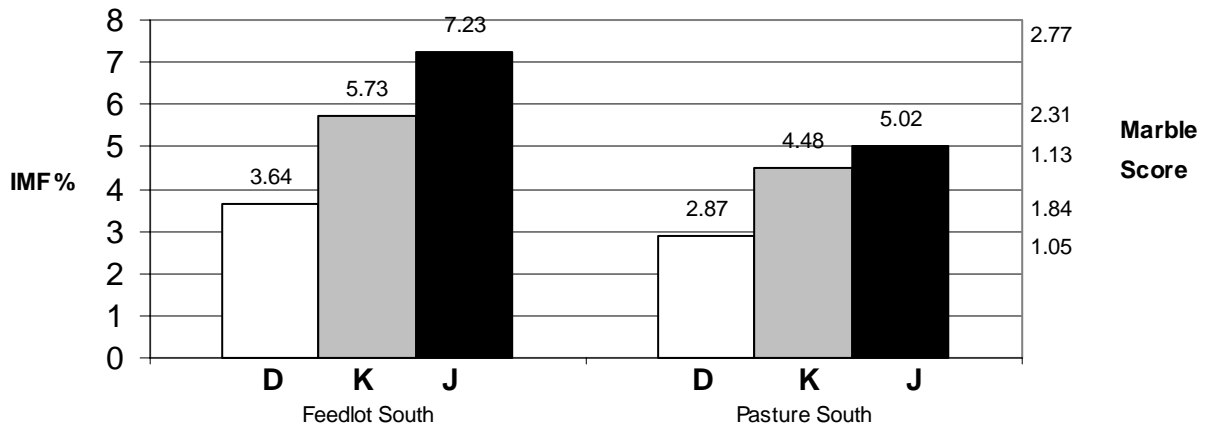


Figure 11. Temperate breeds (IMF%) (D, K, J = Domestic, Korean and Japanese weight carcasses)

There are clear differences in IMF% between grass and grain-finished cattle in both tropical and temperate breed types. An interesting feature of marble score and its relation to IMF% is shown in Table 3, which shows IMF% for different breeds and matched up with AusMeat marble score. There is the expected relationship of increased IMF% with increasing marble score. Yet for each marble score the tropically adapted breeds have lower IMF% than the temperate (i.e. British) breeds. This says that the tropically adapted breeds are achieving higher marble scores than their IMF% would suggest. Is the fat more visible in these breeds? Is this a fat melting point issue? Or, are the differences attributed to operator (grader) variation in northern and southern abattoirs?

Table 3. Least square means for Intramuscular fat (IMF%) according to breed and marble score. Data from CRC straightbreeding project.

Marble Score	Temperate Breeds				Tropically Adapted Breeds		
	1	2	3	4	1	2	3
1	3.95	3.20	4.30	4.09	2.13	2.58	2.26
2	4.51	3.70	5.14	4.58	2.69	3.36	2.91
3	5.64	4.55	5.76	5.08	3.95	4.06	3.80
4	6.88	6.24	7.88	6.11	-	5.18	4.71

The individual breeds (including Hereford) in this study are not named because it is not a strict genetic breed comparison (i.e. the results are confounded by herd-of-origin effects).

Estimated breeding values (EBVs) for marbling and other traits

The CRC has now released EBV tables for carcass and meat quality information, including IMF%, for some 370 sires across 7 breeds. The top 4 sires for IMF% EBV are presented in Table 4. (Note that comparisons across breeds are not valid.)

For completeness, in Table 4, the EBVs for the other carcass traits (carcass weight, eye muscle area, rib fat, P8 fat, Retail Beef Yield %) are listed for each of the 4 sires. There are some outstanding marbling sires in each breed. Across all breeds the top marbling sires were generally below average for RBV%, as expected from the negative correlation between marbling and yield.

Table 4. Estimated breeding values (EBVs) for the 4 highest ranked sires for IMF% in the CRC Sire Progeny Test. EBVs for other carcass traits also listed. (Note: EBVs cannot be contrasted across different breeds.)

Breed	Total Sires in CRC	Sire identification	EBVs for top 4 marbling sires					IMF%
			Carcass weight	EMA	RIB Fat	P8 Fat	RBY%	
Santa Gertrudis	47	1. Gylanda Qantas 75 FM	-1	-1.4	-0.3	-0.8	-1.4	0.8
		2. Kelly Wallah Claudius RW 245	9	-1.0	-1.3	-1.7	-0.8	0.6
		3. Goonoo M129	5	-1.6	-1.5	-2.0	-1.0	0.6
		4. Gyrand Untouchable 1M	1	2.1	1.0	1.1	-0.1	0.7
		Santa Gertrudis Breed Average	1	0.6	0.1	0.1	0.1	0
Brahman	32	1. Burnside Cargo 85.413	-7	5.0	3.3	3.7	1.0	0.9
		2. Waverley Linesman de Manso 3330	16	1.8	0.1	0	0	0.7
		3. Waverley Knight de Manso 3178M	0	2.1	0.9	1.0	0.2	0.6
		4. Waverley 7000	17	-0.3	0.8	1.1	-0.8	0.7
		Brahman Breed Average	12	1.6	0	0.1	0.3	0.1
Belmont Red	62	1. Mt Eugene 93-249	-3	-2.9	2.1	2.6	-2.2	2.0
		2. Montpellier 94257	7	0.8	1.8	1.9	-0.8	1.2
		3. Belmont 87-458	8	-3.7	0.2	0.3	-2.6	1.3
		4. Belmont 86-378	-15	-2.7	1.1	1.2	-1.7	1.2
		Belmont Red Breed average	110	1.4	0.1	0.2	0	0.2
Angus	115	1. Te mania Knight K206	28	1.5	2.4	2.8	-1.5	1.7
		2. Beartooth N01	27	-0.8	0.4	0.7	-1.8	1.5
		3. Te Mania Norman N48	48	4.3	0.1	0.1	-0.4	1.7
		4. Te Mania Platinum P94	51	4.5	-0.1	0	-0.2	1.2
		Angus Breed Average	29	0.7	-0.2	-0.1	0	0.1
Hereford	57	1. Coora Birragurra P145	31	2.5	-0.4	-0.3	-0.4	1.0
		2. Coora Albacutya N058	30	0.3	-1.2	-1.0	0.1	0.6
		3. Glentrevor Prospector 39	28	2.0	0.7	0.8	-0.7	0.7
		4. Gorian Lancelot L0119	19	-0.4	0.7	1.2	-0.7	0.6
		Hereford Breed Average	23	1.7	0	0	0.1	0
Murray Grey	21	1. Glengarret Pilgrim P34	26	0.9	1.2	1.2	-0.3	1.8
		2. Glengarret Muskateer 92M15	25	0.4	0.4	0.5	-0.4	1.2
		3. Glengarret Norseman N46	23	0.1	0.9	1.0	-0.8	1.1
		4. Glengarret Magnate 92M18	2	-0.6	1.3	1.6	-0.2	0.7
		Murray Grey Breed Average	14	0.7	0	0	0.2	0
Shorthorn	34	1. Adair Branny M8	5	1.1	0.4	0.4	0.2	1.3
		2. Broome Waco L82	17	4.2	-0.8	-0.6	0.6	1.1
		3. Adair Discretion P030	7	0.9	1.1	0.9	-0.4	0.9
		4. The Grove Tenth Avenue	-1	-0.2	0.1	0	-0.1	0.8
		Shorthorn Breed average	13	1.6	-0.7	-0.8	0.4	0.4

Genetics of feed efficiency

The CRC has invested substantial resources to measure individual feed intake of groups of cattle fed a standard feedlot diet.

Net feed efficiency (NFI) refers to actual feed intake adjusted for an animal's weight and growth rate. The idea is to identify cattle that eat less feed for the same gain. The CRC now has data on some 2,000 British and tropically adapted steers, shown in Figure 12. Net feed efficiency in these data has low heritability (~18%), lower than that for feed intake. Figure 12 also presents the genetic correlations between net feed efficiency (NFI) and daily feed intake (DFI) and the post-slaughter traits, carcass weight, retail beef yield, IMF%, P8 fat, eye muscle area (EMA) and striploin tenderness. The genetic correlation of NFI with RBY% is favourable (efficient steers have higher RBY). NFI and marbling (and P8 fat) are unfavourably correlated (more efficient steers are leaner and have lower marbling).

So far we have identified significant between-sire differences in net feed efficiency within each of the Hereford, Angus, Murray Grey, Shorthorn, Belmont Red, Brahman and Santa Gertrudis breeds.

The present difficulty with this technology is to work out how to test enough sires for net feed efficiency to ensure that enough steer progeny by high net feed efficiency sires are available for feedlot use. We must also ensure that such progeny have acceptable merit for other traits such as growth, marbling and beef quality.

Feed Intake Genetics				
Genetic Parameters: h^2 (diagonal), r_g (above), r_p (below)				
	DFI	Wt ^{0.73}	ADG	NFI
DFI	24	76	86	41
Wt ^{0.73}	71	41	78	-22
ADG	73	57	20	04
RFI	57	-01	-01	18
r_g with abattoir traits:				
59	Carcass Wt	-30		
-38	RBY %	-77		
19	IMF %	21		
22	P8 Fat	48		
02	EMA	-28		
-08	LD Peak Force	-17		

Beef meeting consumer specifications

Figure 12. Genetics of Feed Intake. CRC data 2000 steers, feedlot diet. Heritabilities (h^2) and Genetic Correlations with Carcass traits. (Legend: DFI = daily food intake; Wt^{0.73} = liveweight adjusted by the factor 0.73; ADG = average daily gain; NFI = net feed intake; r_g = genetic correlation; r_p = phenotypic correlation [RBY%, IMF%, p8 fat, EMA, LDPF = see Table 1].)

The CRC, in partnership with AGBU, NSW Agriculture and PrimeGRO Ltd has recently completed studies to show that a blood hormone, Insulin like Growth Factor (IGF-I) measured at weaning age is genetically linked to Net Feed Intake. This patented test owned by PrimeGRO Ltd was launched for Australian use in August 2003. It may provide a cheap method to screen young cattle for feed efficiency prior to measuring food intake in a smaller group of animals.

CRC RESEARCH ON GENETIC MARKERS FOR PRODUCTION, EFFICIENCY, CARCASS AND MEAT QUALITY TRAITS

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

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

- Gene Marker "Families" set up (1990)
- Measure many traits
- Markers linked to traits by Quantitative Trait Loci (QTL) (i.e. Carcass value, Retail Beef yield (RBY), Eye Muscle Area (EMA), Fat Colour, Marbling, Tenderness, Feed Efficiency, Tick and Worm Resistance)
- Fine scale mapping of chromosome "regions"
- Evaluation in CRC database

- “Positional” candidate genes chosen
- Identify (and patent) Gene Polymorphism
- Commercial testing of gene effect (validation)
- Commercial release of DNAtest.

The CRC emphasises the difficulty of achieving success in identifying commercially useful gene marker tests. However we are encouraged by the successful commercialisation of a DNA test for marbling by CSIRO and MLA in 2000. (The test is marketed as “GeneStar Marbling”.) A second gene marker for tenderness was launched in December 2002 (GeneSTAR Tenderness). The commercial partner is Genetic Solutions Pty Ltd.

CRC/MLA/CSIRO Strategy

The objective of this project is to map, identify and commercialise genes for tenderness, marbling, meat yield, resistance to ticks and worms and feed conversion efficiency. To do this we have established a pipeline that starts with statistical analyses that suggest the presence of genes of large effect and ends with a commercial DNA test. In between these two ends of the pipeline we start with mapping genes to broad chromosomal regions, and proceed to fine scale mapping to narrow chromosomal regions and tests of specific genes. The pipeline is shown in Figure 13.

Where are we at?

Potential gene markers for *tick and worm resistance* in tropically adapted cattle have been linked to broad chromosomal regions and are now to the “fine scale mapping” phase (see Gene Marker Pipeline diagram).

Gene markers for *Net Feed Intake* (NFI) are based on chromosome regions affecting feed intake in MLA/University of Adelaide experiments. These regions are being tested in NSW Agriculture’s Angus cattle lines selected for high and low NFI. Potential new markers for *Retail Beef Yield* (RBY) and *marbling* arose from CSIRO’s Gene Marker families and have been evaluated in the CRC’s pedigree cattle population. These have progressed from the fine scale mapping phase to the choice of positional candidate genes responsible for the effects.

Gene markers for *Beef Tenderness* have progressed beyond the DNA test and patent protection phase. One marker (Tend 1) has entered the commercial market. A different gene affecting tenderness (Tend 2) is one step further back in the pipeline. The CRC’s commercial partner is evaluating a gene marker for tenderness developed by a 3rd party.

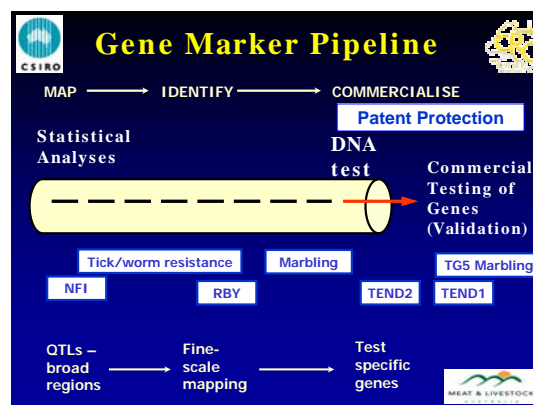


Figure 13. Gene Marker Pipeline in CRC for Cattle and Beef Quality

Take home messages for cattle breeders

- Gene marker technology for production traits is in its infancy in the cattle business. The practical success of GeneStar marbling and GeneSTAR Tenderness proves that it works.
- Gene marker research in Australia looks promising for other important traits.
- Australian geneticists are working on the best strategies to incorporate gene marker tests into breeding programs and for predicting which cattle in your herd to subject to DNA testing.
- Gene marker research is expensive and internationally very competitive. Australian cattle producers must decide what level of resources to devote to this challenge.

- For the present gene markers will be used for identifying seedstock for breeding purposes. In future if individual or groups of gene markers can account for enough of the variation in certain traits they could be used for “drafting” cattle for production purposes.

NORTHERN CROSSBREEDING PROJECT

The CRC's northern crossbreeding project was based on ~1,000 Brahman females, joined over three breeding periods between 1995/96 and 1997/98. Sire breeds used in the project were selected to represent different biological types and included *Bos indicus* (Brahman – purebred control); *Bos Taurus* – British (Angus, Hereford, Shorthorn); *Bos Taurus* – European (Charolais, Limousin); Brahman x British-derived (Santa Gertrudis); Brahman x European-derived (Charbray); and Sanga-derived (Belmont Red) (Figure 14).

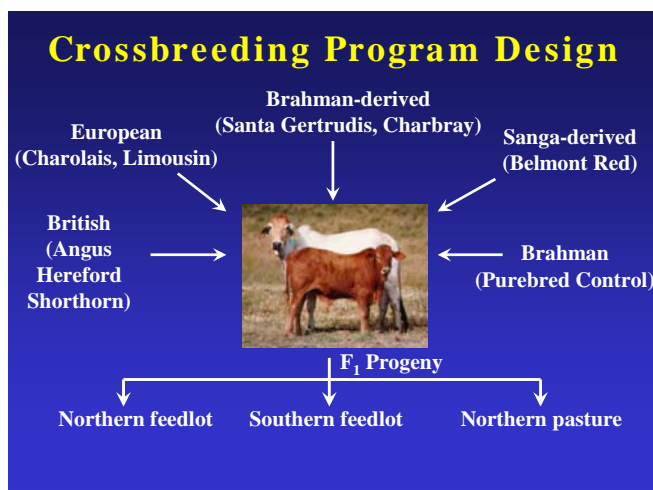


Figure 14. Design of CRC's northern crossbreeding progeny test.

Experimental progeny were finished to one of three target carcass weights (domestic market ~220kg; Korean market ~280kg; or Japanese market ~340kg) either on grain or at pasture in central Queensland or in the CRC's experimental feedlot near Armidale in NSW.

Measurements recorded on all animals included growth from weaning to slaughter, repeated ultrasound scans for carcass attributes recorded at least at six-monthly intervals between weaning and slaughter and complete carcass and meat quality measurements. As well, since July 1998, samples of striploin of every carcass generated in the project have been evaluated by consumer taste panel as part of Meat and Livestock Australia's Meat Standards Australia (MSA) scheme.

Sire breed effects on carcass traits

Table 5 shows significant differences in least squares means between sire breeds for AGE at slaughter ($P < 0.0001$), hot carcass weight (HCWT) ($P < 0.0001$), hot P8 fat depth (HOTP8) ($P < 0.0001$), retail beef yield % (RBY) ($P < 0.0001$), kilograms of retail primal cuts (RTPM) ($P < 0.0001$) and intramuscular fat % (IMF) ($P < 0.0001$). As expected, there were significant differences in HCWT between breeds. However, some of this variation can be attributed to British crossbreds being significantly older than the European and tropically adapted crossbreds at slaughter. Brahman progeny produced the lightest carcasses while Charolais progeny had the heaviest carcasses. Differences between breeds of more than 10kg were considered significant. There were significant differences in HCWT between all three tropically adapted breeds, while the British and European crossbred progeny were significantly heavier than the topically adapted crossbreds.

Table 5. Least-squares mean (\pm s.e.) effect of sire breed on age at slaughter and carcass quality attributes in steers and heifers. Trait means adjusted to a common HCWT.

Sire breed	No.	AGE* (days)	HCWT* (kg)	RBY \emptyset (%)	RTPM \emptyset (kg)	HOT P8 \emptyset (mm)	IMF* (%)
Angus	151	726 \pm 2	292 \pm 2	65.9 \pm 0.3	62.1 \pm 0.3	13.7 \pm 0.6	3.25 \pm 0.08
Belmont Red	379	715 \pm 2	255 \pm 1	66.4 \pm 0.2	63.0 \pm 0.2	12.9 \pm 0.3	3.02 \pm 0.05
Brahman	320	713 \pm 2	242 \pm 2	66.3 \pm 0.2	62.9 \pm 0.2	12.6 \pm 0.3	2.35 \pm 0.06
Charolais	225	711 \pm 2	296 \pm 2	67.2 \pm 0.4	64.3 \pm 0.4	10.2 \pm 0.7	2.53 \pm 0.07
Hereford	134	724 \pm 3	292 \pm 2	66.0 \pm 0.3	62.8 \pm 0.3	12.7 \pm 0.6	2.85 \pm 0.09
Limousin	291	713 \pm 2	286 \pm 2	68.4 \pm 0.3	65.0 \pm 0.3	9.7 \pm 0.5	2.47 \pm 0.06

Santa Gertrudis	142	722 ± 3	272 ± 2	66.1 ± 0.3	62.6 ± 0.3	13.4 ± 0.4	2.28 ± 0.08
Shorthorn	115	730 ± 3	289 ± 3	65.9 ± 0.4	62.3 ± 0.4	11.9 ± 0.8	3.05 ± 0.09
	1757	P<0.0001	P<0.0001	P<0.0001	P<0.0001	P<0.0001	P<0.0001

AGE = slaughter age, HCWT = hot carcass weight, HOTP8 = hot p8 fat depth, RBY = adjusted retail beef yield, RTPM = retail primals, IMF = intramuscular fat percentage.

* Data for animals born 1996, 1997, 1998

☉ Data for 1996 only

European crossbreds were significantly leaner than the progeny of other sire breeds. Angus sired progeny had the highest amount of subcutaneous fat cover with 13.7mm at the HOTP8 site. Limousin progeny were the leanest with 9.7mm. Progeny of Angus, Belmont Red and Shorthorn had highest marbling as measured by IMF%.

Limousin crossbreds produced the highest RBY (68.4 ± 0.3%) and kilograms of RTPM (65.0 ± 0.3kg), and the lowest subcutaneous fat cover. Angus progeny had the lowest RTPM of 62.1 ± 0.3kg. Results were consistent with the negative correlation between fatness traits and yield traits. British breeds produced high fat cover and low RBY and RTPM, while European breeds had leaner, higher yielding carcasses. The tropically adapted breeds ranked intermediately for RBY and RTPM.

Sire breed effects on meat quality traits

Table 6 shows significant differences between sire breeds for tenderness (PFLD) (P<0.0001), marbling (IMF%) (P<0.0001) and beef eating quality (MQ4) (P<0.0001). Brahman progeny had the highest scores for PFLD ie least tender, the second lowest IMF and the lowest MQ4 score of 38.1 ± 1.1. All crossbred progeny groups were significantly more tender (PFLD) and had higher MSA Eating Quality scores than pure Brahmans.

Table 6. Least-squares mean (± s.e.) effect of sire breed on meat quality attributes in steers and heifers. Trait means adjusted to a common HCWT.

Sire breed	No. Progeny	Striploin tenderness (PFLD) (kg)	IMF (%)	MQ4 (Score)
		1425	1428	688
Angus	129	4.73 ± 0.08	3.36 ± 0.08	51.7 ± 1.5
Belmont Red	299	4.91 ± 0.05	3.12 ± 0.06	49.4 ± 0.9
Brahman	245	5.42 ± 0.06	2.41 ± 0.07	38.1 ± 1.1
Charolais	193	4.95 ± 0.07	2.62 ± 0.08	48.4 ± 1.5
Hereford	110	4.82 ± 0.08	2.90 ± 0.09	49.5 ± 1.5
Limousin	241	4.78 ± 0.06	2.55 ± 0.07	49.8 ± 1.1
Santa Gertrudis	116	4.92 ± 0.08	2.36 ± 0.09	46.5 ± 1.3
Shorthorn	95	5.05 ± 0.09	3.13 ± 0.10	48.2 ± 1.6

PFLD = longissimus dorsi peak force, MQ4 = meat quality 4 score, IMF = intramuscular fat percentage.

These are a summary only of a very complex data set. The presentation at the World Hereford Congress will examine steers vs heifers, pasture vs grain finish and Domestic vs Korean vs Japanese market weights.

DISCUSSION

The results in this paper provide the heritability and genetic correlations for meat quality traits in 7 Australian breeds. The paper also identifies standout sires for the important traits of Growth (carcass weight), fatness, Retail Beef Yield, Marbling and Tenderness.

Gene Marker Technology is new and promising. Direct markers (DNA tests) are now confirmed for marbling and beef tenderness. For the present we do not know exactly how to combine gene marker information with

traditional measures of genetic merit for beef traits (i.e. Estimated Breeding Values - EBVs). In Australia the gene markers are being used for selection of seedstock. If the predictive value of these markers is sufficiently high (i.e. the marker accounts for a significant proportion of the observed variation in the trait), then the tests could be used for drafting cattle, such as steers for feedlot finishing.

The new gene polymorphisms associated with tenderness open a new phase in genetic improvement. Urgent research is in progress to accurately describe the size of effect of these candidate genes. Producers can then decide if it is economically worthwhile to pay for DNA tests for these genes. Coupled with progress in Gene Expression, Australia should be better prepared to guarantee cattle with the right genetics for each production environment and market.

Flight Time, a measure of temperament is genetically linked to beef tenderness and is available as a simple strategy to improve this trait. Insulin like Growth Factor (IGF-I) is also favourably linked (genetic correlation) to Net Feed Intake and should simplify the genetic improvement of this important trait.

CRC studies provide an expanded knowledge of the genetics of marbling and a better understanding of its genetic associations with other traits. The fact that marbling (IFM%) is genetically linked to tenderness and MSA eating quality scores is an important reality for beef breeding programs where both traits are economically important.

Future Directions

The Beef CRC has worked with the beef industry to develop a new CRC proposal for the period 2005-2012. Under the title of “**CRC for Beef Genetic Technologies**”, the theme is Gene Discovery and Expression. The purpose is to capture for the Australian beef industry, opportunities from the Genomics (Human/Bovine Genome Projects) and Livestock (beef demand by developing countries to increase steeply by 2020) Revolutions. Novel structural and functional genomics, proteomics and bioinformatics research will value-add the existing CRC's Knowledge Base, providing world leadership in precision cattle breeding, achieving quality, efficiency and profit. Australia's position as No. 1 World Beef Trader depends on this investment.

Accelerated outcomes for Australian beef will be:

- Achievement of quality specifications global markets.
- Reduced production costs, methane emissions from cattle and chemical/antibiotic residues.
- Internationally credible cattle welfare measures.
- Enhanced beef yield and herd reproductive efficiency.

CRC research programs and projects feature 3 common approaches:

1. *Gene Discovery* ~ identifying the genes and gene networks affecting economically important traits of beef cattle and developing and commercialising DNA-based tests to help cattle breeders and producers identify those cattle carrying favourable genes for breeding and/or management purposes (i.e. for use in seedstock and commercial herds).
2. *Gene Expression* ~ understanding the function of these genes and identifying the non-genetic “triggers” that promote expression of favourable genes or down-regulation of unfavourable genes to develop non-genetic treatments or management systems to ensure compliance of Australian beef with exacting global market specifications.
3. *Accelerated Adoption of Beef Industry Technologies* ~ reducing the “Research to Adoption Cycle” in the beef sector from 3 years to 18 months. Accelerated Adoption will be achieved through the use and R&D of participative and partnership processes that set world-class targets for *Innovation*, *Effectiveness* (Outcomes for Inputs) and *Efficiency* (Outputs for Inputs). Innovation processes will be enhanced by customising delivery of *Intelligent Business Solutions* to targeted segments of the Beef Supply Chain.

Potential partners named in the Expression of Interest include:

- CSIRO Livestock Industries
- DPI Queensland
- DPI Victoria
- Meat and Livestock Australia
- NSW Agriculture
- University of Adelaide

- University of New England
- AgResearch New Zealand
- Agriculture WA
- Cargill Beef Australia
- European Union "Framework 6" collaborative project Meat Quality and Food Safety
- Meat New Zealand
- Murdoch University
- National Food Research Centre, Ireland
- National Livestock Research Institute, Korea
- Northern Pastoral Group of Companies
- SARDI
- The Ohio State University, USA
- University of Queensland

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