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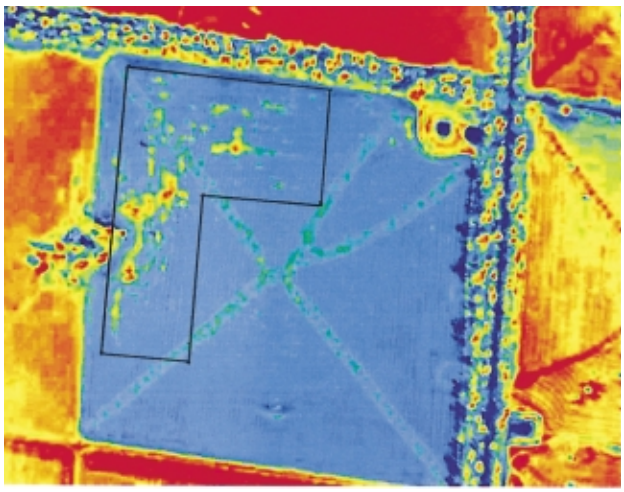

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CRC breeding program design, measurements and database: methods that underpin CRC research results

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Abstract. The Cooperative Research Centre (CRC) for the Cattle and Beef Industry (Meat Quality) developed an integrated research program to address the major production and processing factors affecting beef quality. Underpinning the integrated program were 2 large-scale progeny testing programs that were used to develop genetic, nutritional, management and beef processing technologies to overcome deficiencies in beef quality. This paper describes the experimental design, generation of experimental cattle and the collection and storage of data derived from these straightbreeding and crossbreeding progeny testing programs.

Additional keywords: data storage, experimental design, measurement protocols.

Introduction

As outlined by Bindon (2001), the Cooperative Research Centre (CRC) for the Cattle and Beef Industry (Meat Quality) developed an integrated research program to address the major production and processing factors affecting beef quality. Underpinning this program were 2 large-scale progeny testing programs that were used to develop quantitative and molecular genetic technologies to breed cattle better suited to new and existing markets and to design novel feeding, management and meat processing strategies to ensure eating quality of beef.

The aim of this paper is to describe the experimental design, generation of experimental cattle and the collection and storage of data derived from the progeny testing programs. Results from the progeny testing programs are described in research papers elsewhere in this special edition.

Straightbreeding program

The CRC's straightbreeding program involved 7 breeds in which pedigreed calves were generated in 34 commercial herds throughout eastern Australia. The calves were purchased by the CRC at weaning, and were managed through a complex research protocol that enabled scientists from multi-disciplinary teams to work together to identify genetic, nutritional, management and meat processing factors that affect beef quality.

Participation in the straightbreeding program was by invitation to managers of seedstock herds that had greater than 80 females recorded on GROUP BREEDPLAN and by canvassing through the relevant breed societies. A minimum of 3 herds within a breed that could produce a minimum of 15 progeny per sire (not necessarily all in the same year), from a minimum of 3 sires per year was essential for a breed to be represented in the straightbreeding program.

Breeds included in the program were from biologically diverse types of cattle and from environmentally diverse properties of origin. *Bos taurus* breeds were 4 British breeds (Angus, Hereford, Murray Grey and Shorthorn) and the Sanga-derived Belmont Red breed. Sanga cattle are derived from southern Africa and are classified as *Bos taurus sudafricanus* (Frisch *et al.* 1997). Large European *Bos taurus* breeds were not included because cow herds of sufficient size to generate the required numbers of progeny could not be located. The Brahman breed represented *Bos indicus* breeds. The Santa Gertrudis breed represented the *Bos indicus* × British stabilised breeds. Belmont Red, Brahman and Santa Gertrudis breeds are all tropically adapted breeds. With the single exception of 1 Hereford herd in southern Queensland, British breed cattle for the program were bred only in temperate areas and tropically adapted cattle were bred only in tropical and subtropical areas of Australia (see Fig. 1).

All sires represented in the program were performance recorded through GROUP BREEDPLAN to allow evaluation of sires relative to industry standards. Breed average and average estimated breeding values (EBVs) for growth, fertility and carcass attributes for all sires used in the CRC straight-breeding program are summarised within breeds in Table 1. Individual collaborating breeders and the breed societies selected sires for the program. The CRC was not involved in the selection of sires. In some cases, sires were joined to BREEDPLAN-recorded females, but most

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females used in the program were non-pedigreed commercial cows of the same breed as the sires. Genetic linkages were generated between herds of the same breed by use of common ('link') sires in all herds. Breeding occurred by a combination of natural mating in either single or multiple sire natural mating groups, or by artificial insemination (AI), depending on the herd of joining.

In southern Australia, breeding to generate experimental straight-bred calves occurred in either spring (August–November) or autumn (March–May), beginning in spring 1992 and was repeated each year over the next 5 years. Breeding to generate tropically adapted calves occurred over the summer wet season, between November and March for most properties in most years, but between February and April for 1 property in the Northern Territory and another property in the Gulf region of Queensland in 1 year. Initial joinings in northern Australia began in December 1992 and were repeated for 4 years in Brahman herds and for 5 years in Belmont Red and Santa Gertrudis herds.

Dates of calving were recorded at birth, and sires of calves identified by matching cows and calves with natural mating or AI records, or by DNA fingerprinting in the case of multiple-sire joinings or where sires of calves were equivocal. No selection occurred in male calves, all of which were castrated either at branding on the property of birth or immediately after delivery to the CRC. Collaborating breeders were provided with an opportunity to select within the heifer calves, retaining up to 50% of heifer calves in their own herds. Some breeders supplied very few heifers. Where

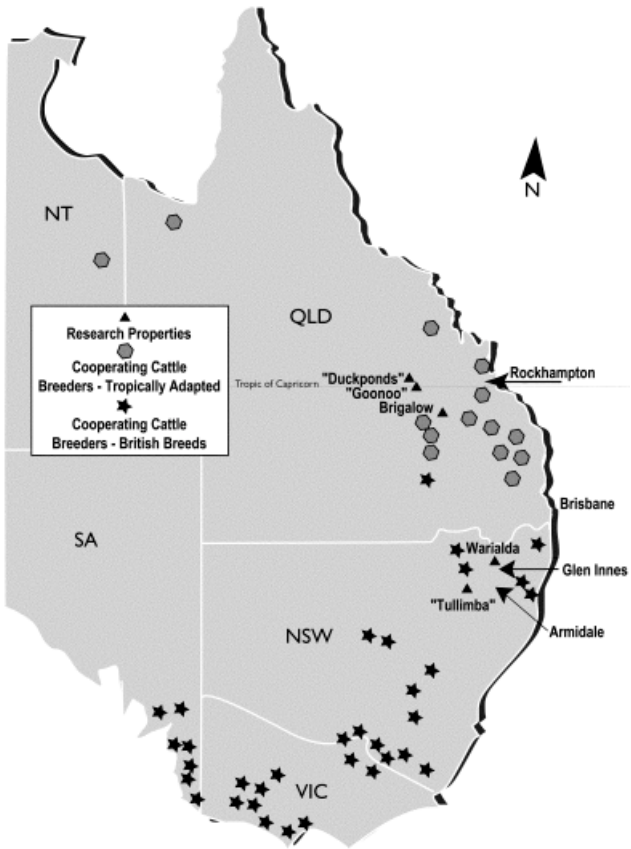

Figure 1. Location of CRC-collaborating straightbred herds and research stations throughout eastern Australia.

Table 1. Average estimated breeding values (EBVs) for growth, fertility and carcass attributes for all sires used in the CRC straightbreeding program, summarised within breed

Breed average EBVs for animals born in 1997 for each of the traits are shown in parentheses
EMA, eye muscle area; IMF, intramuscular fat percentage; RBY, retail beef yield percentage

Breed	Birth weight (kg)	200-day milk (kg)	200-day weight (kg)	400-day weight (kg)	600-day weight (kg)	Mature weight (kg)	P8 fat depth (mm)	EMA (cm^2)	IMF (%)	RBY (%)	Scrotal size (cm)	Days to calving	Calving ease (d) (units)[A]	Calving ease (m) (units)[A]
British breeds														
Angus	3.7	6.7	24	47	62	60	0	1.2	0	0.2	0.9	–0.8	–0.3	–0.2
	(3.8)	(7.0)	(25)	(46)	(61)	(61)	(–0.1)	(0.6)	(0.0)	(0.1)	(0.7)	(–0.6)	(–0.3)	(0.1)
Hereford	4.6	8.8	24	38	57	60	0.1	0.8	–0.1	0.2	1.2	–0.6	–0.9	0.3
	(3.6)	(5.8)	(18)	(28)	(42)	(43)	(0.0)	(0.3)	(–0.1)	(0.1)	(0.7)	(–0.7)	(–0.8)	(–0.1)
Murray Grey	1.3	5.4	12	17	27	32	0.4	0.1	0.1	0.1	–0.1	0.61	0.9	–0.5
	(1.7)	(3.0)	(9)	(15)	(22)	(23)	(0.0)	(0.5)	(0.0)	(0.1)	(–0.1)	(0.0)	(–0.1)	(–0.6)
Shorthorn	1.3	3.5	12	14	21		–0.2	1.2	0.0	0.1	0.6			
	(1.9)	(3.0)	(12)	(17)	(24)		(–0.5)	(1.6)	(0.0)	(0.2)	(0.5)			
Tropically adapted breeds														
Belmont Red	2.3	0.4	8	10	16		0.3	1	0.1	–0.1	0.3			
	(1.6)	(1.0)	(7)	(9)	(14)		(0.0)	(1.5)	(0.1)	(0.1)	(0.2)			
Brahman		–0.3	12	16	22	24	0.1	1.5	0.1	0.2	0.4	0.5		
		(–1.0)	(10)	(14)	(18)	(18)	(0.1)	(1.6)	(0.1)	(0.2)	(0.4)	(0.2)		
Santa Gertrudis		–0.6	4	6	5		0.1	0.6	0.1	0.1	0.1			
		(0.0)	(2)	(2)	(2)		(0.0)	(0.6)	(0.0)	(0.2)	(0.0)			

[A] 'd' indicates direct; 'm' indicates maternal.

Table 2. Number of herds, sires and link sires used to generate straightbred steers and heifers for the CRC's straightbreeding program

Breed	Number of herds	Number of sires[A]	Number of link sires	Total no. of heifers purchased	Total no. of steers purchased	Total no. of progeny purchased
			British breeds			
Angus	11	117	13	233	1616	1849
Hereford	6	57	6	134	1004	1138
Murray Grey	3	23	2	73	385	458
Shorthorn	3	35	3	—	513	513
			Tropically adapted breeds			
Belmont Red	3	64	8	575	1013	1588
Brahman	4	44	2	438	455	893
Santa Gertrudis	4	48	5	594	748	1342
Total	34	388	39	2047	5734	7781

[A]Link sires included.

breeders opted to select within their heifer groups, selection appeared to be primarily on age and weight, with older or heavier calves being preferentially retained in the breeders' herds. Steers were purchased by the CRC in preference to heifers in the Santa Gertrudis and Belmont Red breeds from the 4th calf crop and only steers were purchased from the 5th calf crop in 5 breeds, Angus, Hereford, Shorthorn, Belmont Red and Santa Gertrudis. In the 4th crop of tropically adapted calves, random selection of heifers by the CRC occurred.

British breed calves were weaned at an average age of 9 months, at weaning weights of about 250–280 kg. Calves from the tropically adapted breeds were weaned at about 6 months of age. After weaning, calves were transferred to properties under the CRC's control (see Bindon 2001 for a full description of these facilities) for growing and finishing to experimental specifications according to the CRC experimental protocol (see description of this protocol in the following sections). Calves were subsequently managed together within contemporary management or cohort groups. Cohort group definition also included season of birth (autumn and spring joinings) in southern Australia. In northern Australia animals were allocated to different cohort groups according to the average weaning age and weight by property of origin. Calves from properties in northern Australia located in the harshest environments were up to 100 kg lighter and were up to 8 weeks younger at weaning than calves from more benign environments (in extreme years and extreme environments, weaning weights ranged from 120 kg for Brahman weaners bred in the Gulf Region of Queensland to 260 kg for Santa Gertrudis weaners bred in the South Burnett Region of Queensland), and hence they were managed as a separate group to the heavier and/or older calves. Steers grown out at Glen Innes Research Station grazed different sets of pastures according to their allocated nutrition treatments (see Ayres *et al.* 2001; Dicker *et al.* 2001). Management procedures across the different nutrition groups were as similar as possible, but there were some minor differences in dates of measurement if it was not possible to measure all animals in all treatment groups on a single day. Table 2 shows the number of herds, sires and link sires used to produce straightbred steers and heifers for the CRC's straightbreeding program. Table 3 lists the total number of progeny purchased by breed for the straightbreeding program each year. Table 4 outlines average number of progeny purchased per sire and average number of progeny purchased per herd in a year, by breed.

Crossbreeding program

The CRC's northern crossbred cattle were generated in 2 Brahman herds that were under direct control of the CRC, in contrast to the contracted arrangement with cooperating breeders in the straightbreeding program. This approach allowed greater control of the more complicated mating program required to generate the contemporary crossbred calves.

Northern Australian pastoral companies, individual beef producers and the Queensland Department of Primary

Table 3. Number of progeny purchased by breed for the straightbred program each year

Breed	1994	1995	1996	1997	1998	Total
			British breeds			
Angus	266	472	494	460	157	1849
Hereford		257	281	409	191	1138
Murray Grey		188	121	149		458
Shorthorn	49	143	116	129	76	513
			Tropically adapted breeds			
Belmont Red	194	341	373	500	180	1588
Brahman	168	189	248	288		893
Santa Gertrudis	380	250	301	343	68	1342
Total	1057	1840	1934	2278	672	7781

Table 4. Mean number of progeny per sire and average number of progeny purchased from cooperating breeders (range in parentheses)

Breed	No. of progeny/sire	No. of progeny purchased (progeny/herd.year)
	British breeds	
Angus	16	52 (16–99)
Hereford	20	59 (19–113)
Murray Grey	20	69 (40–88)
Shorthorn	15	41 (20–70)
	Tropically adapted breeds	
Belmont Red	25	110 (48–221)
Brahman	20	92 (15–168)
Santa Gertrudis	28	83 (30–149)
All breeds	21	72 (15–221)

Industries donated about 1000 Brahman females, specifically to initiate the crossbreeding program. Seven hundred cows were joined at the CRC's leased property, 'Duckponds' and 300 cows were joined at Brigalow Research Station in Central Queensland (see Bindon 2001) over 3 years to produce comparable purebred Brahman and Brahman-crossbred calves. Crossbred calves were weaned in 1996, 1997 and 1998 at an average age of 6 months. Sire breeds used in the crossbreeding program were selected to represent different biological types and included *Bos indicus* (Brahman–purebred control), *Bos taurus*–British (Angus, Hereford and Shorthorn), *Bos taurus*–European (Charolais and Limousin), Brahman × British-derived (Santa Gertrudis), Brahman × European-derived (Charbray) and Sanga-derived (Belmont Red). All sires except Charbray were performance recorded in their breed society's GROUP BREEDPLAN analysis. Table 5 shows breed average and average EBVs for growth, fertility and carcass attributes for all sires used in the CRC crossbreeding program for all breeds except Charbray. Charbray sires were F_1 Charolais × Brahman, whose own sires had been recorded in the Charolais GROUP BREEDPLAN analysis and whose dams were recorded in the Brahman GROUP BREEDPLAN analysis. Calves in the 1996-calf crop were by 8 sire breeds (Angus, Belmont Red, Brahman, Charolais, Hereford, Limousin, Santa Gertrudis and Shorthorn), while calves in the 1997 and 1998 calf crops also included Charbray sires.

To strengthen the experimental design, genetic linkages were generated between the CRC's crossbreeding and straightbreeding projects by use of common sires across projects. For breeds common to both programs (Angus, Belmont Red, Brahman, Hereford, Santa Gertrudis and Shorthorn), only sires that had been used in the straightbreeding program were used in the crossbreeding program. Most joinings within the crossbreeding program were by AI, followed by natural mating to 'back-up' sires of a different breed. A small number of sires were naturally mated at the same time as the AI programs to ensure calves by natural mating and AI sires were born at the same time. The aim of the program was to generate about 20 steer and

Table 5. Average estimated breeding values (EBVs) for growth, fertility and carcass attributes for all sires used in the CRC crossbreeding program

Breed average EBVs for animals born in 1997 for each of the traits are shown in parentheses
EMA, eye muscle area; IMF, intramuscular fat percentage; RBY, retail beef yield percentage

Breed	Birth weight (kg)	200-day milk (kg)	200-day weight (kg)	400-day weight (kg)	600-day weight (kg)	Mature weight (kg)	P8 fat depth (mm)	Rib fat depth (mm)	EMA (cm^2)	IMF (%)	RBY (%)	Scrotal size (cm)	Days to calving (days)	Calving ease (d) (units)[A]	Calving ease (m) (units)[A]
Angus	3.4	7.2	28	57	74	78	0	0	1.8	0.3	0.2	0.9	–1.6	1.1	1.9
	(3.8)a	(7.0)a	(25)a	(46)a	(61)	(61)	(–0.1)	(–0.1)	(0.6)	(0.0)	(0.1)	(0.7)	(–0.6)	(–0.3)	(0.1)
Belmont Red	2.9	0.1	10	13	19		0.2	0	0.8	0.1	0	0.6			
	(1.6)	(1.0)	(7)	(9)	(14)		(0.0)	(0.0)	(1.5)	(0.1)	(0.1)	(0.2)			
Brahman		0	12	16	23		–0.4	–0.4	1.5	0.1	0.3	1.4			
		(–1.0)	(10)	(14)	(18)		(0.1)	(0.1)	(1.6)	(0.1)	(0.2)	(0.4)			
Charolais	0.8	2.7	10	17	28		–0.1	–0.1	0.1		–0.3	0.6		–0.2	
	(0.7)	(2.0)	(6)	(11)	(14)		(0.0)	(0.0)	(0.9)		(0.0)	(0.2)		(–0.3)	
Hereford	6.1	8.9	27	46	68	73	–0.2	–0.3	1	–0.3	0.4	1.4	–1.1	–4.7	0.1
	(3.6)	(5.8)	(18)	(28)	(42)	(43)	(0.0)	(0.0)	(0.3)	(–0.1)	(0.1)	(0.7)	(–0.7)	(–0.8)	(–0.1)
Limousin	1.7	0.9	9	16	24	25	–0.1	–0.1	0.9	0	0.2	0.3	0.3	–2.3	–0.5
	(1.2)	(1.0)	(10)	(16)	(22)	(21)	(0.0)	(0.0)	(0.5)	(0.0)	(0.0)	(0.2)	(0.0)	(–1.1)	(0.0)
Santa Gertrudis		–1.8	6	9	8	7	–0.1	0.1	0.5	0.1	0.1	0.3			
		(0.0)	(2)	(2)	(2)	(2)	(0.0)	(0.0)	(0.6)	(0.0)	(0.2)	(0.0)			
Shorthorn	1.8	3.9	12	14	19		–0.5	–0.4	0.2	0	0.1	0.5			
	(1.9)	(3.0)	(12)	(17)	(24)		(–0.5)	(–0.5)	(1.6)	(0.0)	(0.2)	(0.5)			

[A]'d' indicates direct; 'm' indicates maternal.

heifer progeny (10 of each sex) per sire for each of the sires used in the crossbreeding program.

Table 6 shows the number of calves weaned within sire breed and sex and the total number of sires represented in each sire breed over the 3 calf crops in the crossbreeding program.

Within 24 h of birth, calves born at Duckponds and their dams were identified and calf birth weights recorded. Calves born at Brigalow Research Station were not weighed at birth, but cows and calves were identified on a daily basis throughout the calving period. Sire identification was determined by AI program and mating records, augmented by gestation length, visual appraisal (for breed of sire), and where necessary, by DNA fingerprinting. A full description of the AI programs and parentage determination in the crossbreeding program is given by Corbet *et al.* (1997, 1999).

Male calves at both properties were castrated at about 4 months of age and all calves were weaned at about 6 months of age. Calves born at Brigalow Research Station were transferred to 'Duckponds' shortly after weaning.

Table 6. Number of calves weaned within sire breed and sex and total number of sires represented in each breed over three calf crops

Sire breed	Number of sires	Calf sex	Calf crop 1996	1997	1998	Total
Angus	10	M	27	33	27	
		F	24	20	26	157
Belmont Red	14	M	93	78	53	
		F	78	58	33	393
Brahman	14	M	93	26	44	
		F	95	30	42	330
Charbray	4	M	0	28	12	
		F	0	30	19	89
Charolais	16	M	19	40	54	
		F	24	28	66	231
Hereford	8	M	21	31	15	
		F	26	24	21	138
Limousin	14	M	43	66	45	
		F	40	60	40	294
Santa Gertrudis	8	M	39	16	11	
		F	50	16	10	142
Shorthorn	8	M	18	21	19	
		F	18	22	22	120
Total		M	353	339	280	972
		F	355	288	279	922
Overall	96	Both	708	627	559	1894

Experimental design

Both the CRC's experimental breeding programs were designed to answer questions relating to the genetics of carcass and beef quality, including genetic and phenotypic relationships between performance of animals finished on a grain-based diet in a feedlot or at pasture to different market endpoints and reared in temperate versus subtropical environments. Theoretical calculations and simulations were carried out to determine the optimal number of sires, calves per sire and arrangement of link sires between herds (Robinson 1995). As a general rule, for traits measured on different animals (e.g. fatness of animals finished in a feedlot or at pasture), estimated genetic correlations have maximum accuracy if equal numbers of offspring of each sire are allocated to each treatment or environment.

Southern herds were required to produce 15–20 calves per sire per year while northern herds were required to produce 25 calves per sire to cater for the extra treatment of relocating to NSW for growing and finishing (see Fig. 2). Where possible, sires were mated a second year to increase these numbers and to generate additional genetic linkages within herds, across years.

Straightbred and crossbred animals were allocated to finish at pasture or in a feedlot, to different target carcass weights [about equal to domestic (220 kg), Korean (280 kg) and Japanese (340 kg) market weights] and, for tropically adapted breeds, to grow-out at pasture in either Central Queensland ('Duckponds') or north-eastern NSW (Glen Innes Research Station or the CRC's property, 'Tullimba', near Armidale; see Fig. 1 and Bindon 2001) using the optimisation procedures outlined by Robinson (1999).

Figure 2 shows the cattle flow chart for all experimental animals produced in the straightbreeding and crossbreeding programs. All British breed cattle were grown in north-eastern NSW. One half of British breed progeny were finished at pasture and one half finished in the CRC's feedlot at 'Tullimba'. About one third of the tropically adapted calves were transferred to northern NSW shortly after weaning. Cattle that remained at 'Duckponds' were finished either at pasture at 'Duckponds' or on a grain-based diet in a commercial feedlot, 'Goonoo', located about 40 km from 'Duckponds'. Some minor variations occurred to grow-out locations, dictated by seasonal conditions or other experimental design requirements. For example, about two thirds of the CRC's tropically adapted straightbred progeny from the first calf crop were transferred to Glen Innes Research Station as part of the backgrounding experiment described by Dicker *et al.* (2001) and one third remained at 'Duckponds'.

Cattle finished on a grain-based diet to domestic target weights entered the feedlot at an average liveweight of 300 kg, while those finished to export (Korean and Japanese) target weights entered the feedlot at an average liveweight of 400 kg. Cattle targeted for domestic market weights remained in the feedlot for at least 60 days, while those targeted for export market weights remained in the feedlot for a minimum of 90 days. As far as possible, protein, energy and digestibility levels of the diets at 'Tullimba' and 'Goonoo' were similar and remained constant for the duration of the experimental period. However, grains used as the basis of

diets differed between the feedlots, and commercial considerations impacted more on the diets at 'Goonoo' than at 'Tullimba', with the result that the ingredients in the diets changed over the experimental period at 'Goonoo'.

In some cases, as cattle targeted for finishing on a grain-based diet moved to the feedlot, their contemporaries destined for pasture finishing at the same market weight moved to finishing pastures. Most steers grown at Glen Innes Research Station were relocated at this time to Warialda (see Bindon 2001) for finishing, although a small proportion of groups were retained at Glen Innes for finishing due to poor seasonal conditions at Warialda. Most pasture-finished heifers grown at Glen Innes were finished at 'Tullimba'. The quality of pasture at 'Tullimba' improved over the experimental period, with the addition of fertiliser and improved management practices over time. In Queensland, growing and finishing at pasture occurred on predominantly buffel grass (*Cenchrus ciliaris*) pasture at 'Duckponds'.

Animals were slaughtered when the average weight of the cohort was predicted to achieve target carcass weights of 220 kg (domestic market), 280 kg (Korean market) or 340 kg (Japanese market).

As indicated by Robinson (1995), it was desirable to evaluate sires at all target carcass weights and for several grow-out nutritional and finishing regimes. A designed approach using all target weights and finishing regimes each year was therefore preferable to evaluating each target carcass weight or finishing regime in turn, thereby confounding these effects with years and sires. This approach also allowed investigation of variability over years and provided a more realistic estimate of sire and treatment effects over the range of years encountered.

As part of the experimental design process for the CRC's straightbreeding and crossbreeding programs, a suite of computer programs was developed to allocate animals to treatments (Robinson 1995). The first of these programs generates designs that are as balanced as possible with respect to (i) main effect of treatments, (ii) 2-way interactions between treatment factors, and (iii) higher order interactions for offspring of each sire, as well as for all animals in each herd and for all animals in the management group. By way of example, Table 7 illustrates the balance achieved within herds, and overall, for one of the 2-way interactions, nutrition during growout × finishing regime.

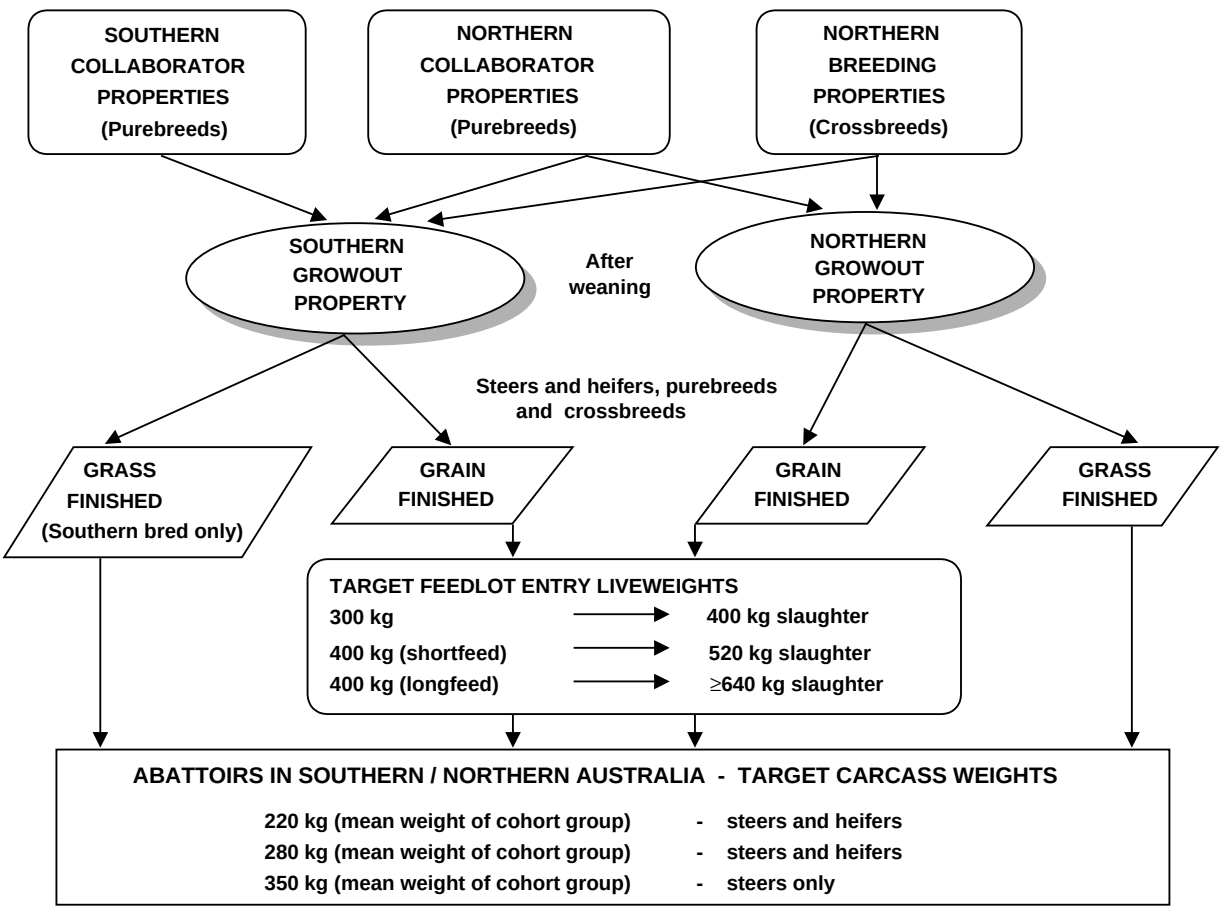

Figure 2. Cattle breeding flowchart for crossbred and straightbred progeny in the CRC programs.

Table 7. Example of allocation of numbers of animals to nutrition treatments during the grow-out period (pasture, pasture + concentrates, pasture + forage) and finishing regime (pasture or feedlot finishing) for one contemporary management group of calves from one breed (from Robinson 1995)

	Pasture only		Pasture + concentrates		Pasture + forage	
	Pasture	Feedlot	Pasture	Feedlot	Pasture	Feedlot
Herd 1	11	10	10	11	10	10
Herd 2	7	6	6	7	6	6
Herd 3	8	8	8	8	9	8
Herd 4	5	6	6	5	5	6
Herd 5	4	4	4	4	5	4
All herds	35	34	34	35	35	34

The software was written to cope with a large range of factors resulting from the CRC treatments. The algorithms attempted to achieve balance over all main effects and interactions, with an option to ignore any that were not relevant. For example, heifers were not finished for the Japanese market, so it was not useful to consider balance over sex × market. Instead, balance was sought over steer × market and heifer × market combinations. When necessary, the software was also used to superimpose additional treatment factors such as a comparison of barley and oats grains in addition to nutrition, herd, breed and other factors for a group of Japanese market steers finished at 'Tullimba'.

Balance was used as the primary screening criterion for the designs. The statistical theory of dual designs (John 1987) indicates that, for a design involving 2 factors, A and B, the best designs to estimate A are those in which the levels of A and B are as balanced, or orthogonal, as possible. So a good design to estimate A (assuming B is a nuisance factor and of no interest) is also a good design to estimate B, when A is of no interest, and, therefore, a good design to get the best information about both A and B.

Potential designs generated by the computer programs were assessed according to an efficiency criterion known as A-optimality that identifies designs with the lowest possible average variance of estimated differences between all pairs of treatments and all pairs of sires (Robinson 1995). Comparisons were made for all sires and treatments in the year of allocation, and for all sires and treatments in the current and all previous years.

Table 8. Definition of measurements recorded at each phase during the life of CRC straightbred and crossbred animals

Measurement	Description
Liveweight (kg)	Recorded at 1–6 weekly intervals, depending on location of animals (weights recorded most frequently at 'Tullimba' and least frequently at 'Duckponds').
Body structural measurements	
Body condition score	Visual assessment of amount of fat coverage on the body, scored on a 1–5 scale, from very poor to overfat (Lowman *et al.* 1976).
Muscle score	Visual assessment for muscle based on thickness and convexity of shape relative to frame size, after allowing for fatness. Scored on an A–E scale, from heavily muscled to poorly muscled with each alpha category having '+' and '–' subcategories (Perry *et al.* 1993). The A^+ to E^- scores were converted to numeric scores in the database.
Temperament	
Flight speed score (s)	Electronically recorded time taken for an animal to cover a fixed distance after leaving a weighing crush (Burrow *et al.* 1988).
Crush score	Subjective score assessed on a scale of 1–5, from very good to very bad. Animals were confined for up to 10 s in a crush but were not restrained in a head bail. An overall temperament score was subjectively recorded but the behaviour primarily assessed was the amount of movement exhibited by the animal, from calm to struggling wildly.
Scanning for carcass attributes	All animals were scanned using accredited technicians for rump and rib fat (mm) and eye muscle area (cm^2) using an Aloka 500 (Upton *et al.* 1999) at repeated intervals of less than 6 months between weaning and 5 days before slaughter. As well, since 1997, animals finished in north-eastern NSW were scanned for intramuscular fat percentage (IMF%) using the same Aloka 500 scanner and IMF% was calculated using software developed by Iowa State University (Wilson *et al.* 1998).
Feed intake	The majority of animals finished in the feedlot at 'Tullimba' had feed intakes recorded using automatic 'Tullimba' feeders, described by Bindon (2001). Data were automatically captured and stored electronically for the following measurements:
No. of feeding sessions per day	the number of times an animal entered the automatic feeder in a day.
Time spent in the feeder	the total amount of time (in minutes) that an animal spent in the feeder during a day.
Total feed eaten per day (kg)	the total amount of feed consumed in all feeding sessions in a day.

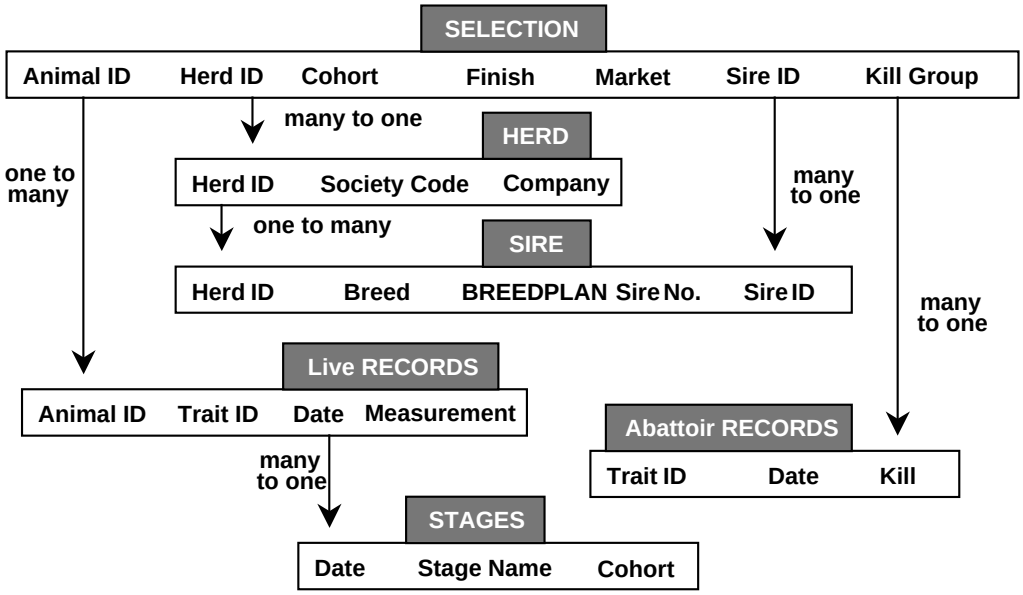

Figure 3. Example of the relational nature of the CRC's database ('one to many' and 'many to one' refers to the number of categories; ID, identification; Society Code, Breed Society Code associated with the particular seedstock herd; Stage Name, name of stage within the growth of experimental animals, e.g. transfer to growout, induction into feedlot, transfer to finishing property, etc.).

Once the best design was identified, a third program allocated the offspring of the designated sires to treatment combinations, attempting to balance over the actual age and weaning weight of the animals. The result was a design allowing efficient estimation of genetic parameters for all target carcass weights and treatments of interest (Robinson 1995). In addition, because sires and all other factors were as balanced as possible, adjustment of treatment means for sire, age and other factors was minimised. This made the data more robust and easier to interpret, and reduced the uncertainty that may have arisen from partial confounding of effects. Subsequent evaluation of the actual designs used indicated that achieving the same accuracy of estimation of treatment and sire effects without this level of sophisticated design would have required 5–10% more animals, at a cost of $150 000–300 000 for purchase, transport and feeding of animals (Robinson 1999). If all additional costs of experimentation (sample collection, carcass downgrading, measurement, data analysis and reporting) were included, the total savings by use of an efficient design were estimated at between $0.5 and $1 million.

Measurements

On arrival at CRC-controlled properties, all experimental animals were weighed, cross-branded and blood samples collected by venipuncture for subsequent DNA extraction. When necessary, animals were also re-tagged and tattooed to ensure permanent identification, castrated, dehorned, vaccinated against clostridial diseases and treated to control internal and external parasites.

The following 4 data collection stages were defined as critical:

(i) Growout: representing the time between arrival of all animals in a cohort group to the CRC properties and when the average weight of the entire cohort was 300 kg for animals allocated to domestic market weights or 400 kg for animals allocated to Korean or Japanese market weights.

(ii) Finishing: representing the period between end of growout until the average liveweight of the entire cohort was predicted to achieve target carcass weights of 220 kg (domestic), 280 kg (Korean) or 340 kg (Japanese) depending on the allocated target market.

(iii) Pre-slaughter: representing the 5–7-day period immediately before slaughter, and including the pre-slaughter transport period.

(iv) Slaughter: representing the day of slaughter of all experimental animals in a cohort.

In general all animals within a cohort were managed as a single group during growout, finishing, pre-slaughter and slaughter. Animals were separated into appropriate finishing treatment groups within the cohort at the appropriate times, for example domestic market animals left the cohort at 300 kg for finishing while the Korean and Japanese market steers continued in growout. During growout, *Bos taurus* steers in all but one straightbred calf crop were allocated to nutritional treatments within the cohort group (see Dicker

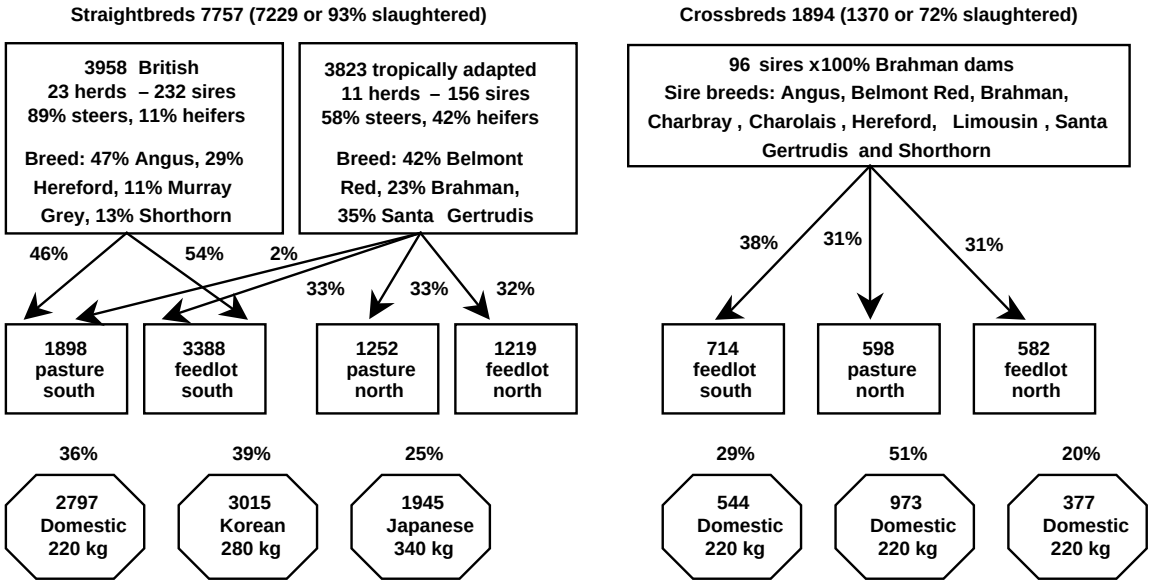

Figure 4. Numbers of records in the CRC's straightbreeding and crossbreeding databases.

et al. 2001). In those cases, animals within a cohort group were managed within treatment groups during the growout period but returned to the original cohort group for finishing, pre-slaughter and slaughter.

Measurements recorded during the growout, finishing and pre-slaughter phases were the same for animals being grown in northern NSW and Central Queensland and for animals finished at pasture and in a feedlot, although the frequency of measurements varied between the different sites. Measurements recorded during all phases were determined by an annual workplan agreed to at the commencement of the CRC protocol by the multidisciplinary team of scientists using the animals. These measurements are described in Table 8. Measurements recorded at time of slaughter, and carcass and meat quality measurements for all animals are described by Perry *et al.* (2001).

Storage of data from the straightbreeding and crossbreeding programs

Data from the CRC's straightbreeding and crossbreeding programs are stored on a central database using PROGRESS software, which is interactive with other programming languages. It is a relational database specifically designed for the CRC's cattle breeding programs. Figure 3 demonstrates the relational nature of the CRC database.

The CRC database is a multi-user system. At the time of writing there were 21 regular users, with an average of 5 users per day. These users were from all organisations and locations throughout the CRC network.

The basic structure and number of records from the straightbreeding and crossbreeding programs are shown in Figure 4. Each record is checked for integrity and biological

Table 9. An example of some of the fields contained within the live animal and abattoir measurement fields of the CRC's database

Values in parentheses adjacent to trait names indicate the number of measurements for each of the traits

Trait	Straightbred animals	Crossbred animals
Number of live animal measurements (at December 1999)		
Crush score (13)	8166	5107
Condition score north	5873	4013
Condition score south	25893	
Flight speed	9752	5097
Visual flight score	6928	3090
Hip height	11452	4521
Maturity score	675	
Muscle score	14072	2269
Sheath score	1998	1183
Scanned fat 12/13th rib	20207	5116
Scanned fat P8 site	20509	5116
Scanned eye muscle area	18960	5036
Liveweight	144937	31853
Number of abattoir measurements (at December 1999)		
Hot carcass (6)	7230	1370
Chiller carcass (8)	7114	1366
Primal cuts (18)		
Retail	3181	498
Untrimmed	3185	498
Intermuscular fat	3180	498
Subcutaneous fat	3180	498
Total fat	3180	498
Wholesale	4583	673
Bones (12)	3179	497
Meat quality (21)	6919	1223
Total bone-outs (13)	3143	489

consistency before being entered onto the database. Over 100 different data fields exist.

Table 9 shows some of the traits measured and the amount of data currently on the database for each trait. Over 200 separate traits exist within the abattoir measurement fields for each animal.

The key field in the database is the animal's unique CRC identification. This allows linkage within the CRC database, but importantly, the unique identifier also allows data on CRC animals to be matched to other key industry databases where CRC data are being stored. For example, a sample of animals is being evaluated through Australia's meat grading scheme, Meat Standards Australia (MSA). The link between CRC and MSA databases allows expedient analysis and quality control of MSA results and provides the CRC with information it might otherwise not have been able to collect. The CRC database also contains a breed society identification that allows electronic transfer of data to participating breed societies. Pedigree information has been transferred to the relevant breed societies and performance data to the Agricultural Business Research Institute (ABRI) in Armidale. ABRI provides the Australian beef industry with BREEDPLAN, the national beef genetic evaluation scheme. As a direct result of the use of CRC data, BREEDPLAN has introduced 3 new carcass traits to the national evaluations. These traits are carcass weight, intramuscular fat percentage and retail beef yield percentage, with all carcass traits adjusted to a 300-kg steer carcass weight (Johnston *et al.* 1999).

DNA and semen banks

DNA was extracted from either blood or semen samples obtained from the majority of sires and experimental progeny in the straightbreeding and crossbreeding programs. The DNA bank now comprises samples from 380 sires and about 12000 offspring. The DNA bank has been utilised for the marker evaluation studies within the CRC and will be invaluable for collaborating breeders to use as a basis for Marker Assisted Selection in the future.

Semen from most sires used in the CRC's breeding programs has also been stored for use in future experimental breeding programs.

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