

Implications of Beef CRC genetic outcomes for feedlot profitability

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Introduction

Since its commencement in 1993 the Beef CRC has contributed a considerable amount of knowledge to clarify our understanding of the underlying genetic basis of the differences between animals in feedlot performance, feed intake, carcass yield, marbling and meat quality. Importantly, much of this new knowledge has been rapidly adopted by the beef industry through its incorporation into the BREEDPLAN genetic evaluation system. This has provided the potential for seedstock and commercial cattle producers to make better breeding decisions for the benefit of the entire beef supply chain. In addition, the Beef CRC has established a platform of knowledge about potential candidate gene markers for future use in accelerating the rate of genetic improvement for a range of economic traits of relevance to the industry.

This paper summarises several important Beef CRC genetic outcomes of importance to the feedlot sector. In addition, the paper discusses some important requirements for the beef industry to fully exploit the potential benefits of this knowledge. In particular, it is argued that a more effective flow of performance information and market signals across the beef supply chain is required for the industry to fully capture the benefits of our advances in genetic technology. The feedlot sector can play a pivotal role in helping to achieve this objective.

The Beef CRC Progeny test

Prior to the commencement of the Beef CRC in 1993 the beef industry had insufficient knowledge to enable the implementation of effective genetic improvement programs for important carcass and meat quality traits. There was a lack of information about the genetic relationships among measures of carcass yield, meat quality and other important economic traits. In particular, considerable uncertainty existed about the robustness of these relationships when expressed across varying market weight end-points and different production environments (eg grain versus pasture finishing systems).

For example, it was not possible to confidently predict whether superior genotypes for say, domestic pasture finished yearling product, would also be superior for long-fed export production.

Also, little information existed to verify the genetic relationships between live-animal assessments of body composition in seedstock herds (eg via ultrasound) and abattoir measures of carcass yield, marbling and meat quality among slaughtered progeny.

In order to answer these questions the Beef CRC conducted a large structured progeny test program involving the generation of several thousand straightbred and crossbred progeny representing a range of temperate and tropically adapted breeds.

The straightbred component of the Beef CRC progeny test program included the production of sire-identified progeny representing 7 breeds (Angus, Hereford, Shorthorn, Murray Grey, Brahman, Belmont Red and Santa Gertrudis) from 36 co-operator herds throughout Eastern Australia. These herds provided an average of 25 sire-identified progeny born from 1993 to 1998 from each of four home bred sires per year. In addition, each herd produced an average of about 12 progeny per year from each of two "link" sires used via artificial insemination. This ensured that adequate genetic links existed between the herds, thereby providing an appropriate data structure for subsequent genetic analysis.

The crossbreeding component of the Beef CRC progeny test program was based on a 1,000 female Brahman herd (donated by industry) located in central Queensland. These cows were joined to nine terminal sire breeds (Angus, Belmont Red, Brahman, Charolais, Hereford, Limousin, Santa Gertrudis, Shorthorn and Charbray) to produce progeny representing a range of crossbred genotypes.

Following weaning, all progeny were purchased from the cooperators by the Beef CRC and backgrounded prior to being assigned to a particular finishing treatment group. The various finishing treatment groups were designed to represent different target carcass weight endpoints (ie Domestic, 220 kg; Korean, 280kg; or Japanese, 340kg), finishing regimes (ie Pasture or Feedlot) and different finishing regions for the tropically adapted breeds (ie Sub-Tropical North or Temperate, South). In total, over 8,000 progeny from almost 400 industry sires were recorded for a range of live



animal, carcass and meat quality traits. The design of the CRC progeny test program is illustrated in Figure 1. Further details of the design were presented by Robinson (1995), and a comprehensive description of the measurements taken in each finishing treatment were presented by Upton *et al.* (2001).

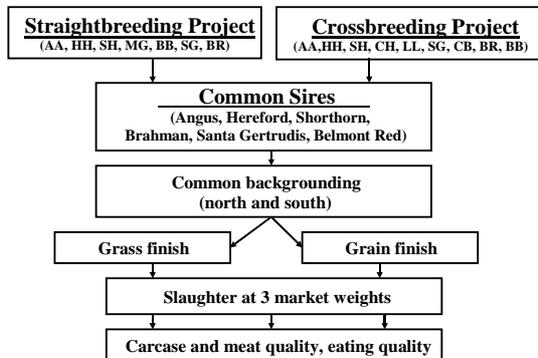


Figure 1. Design of Beef CRC progeny test program (from Bindon, 2001)

All animals involved in the CRC progeny test were measured for a comprehensive range of live animal, carcass and meat quality traits. Samples from approximately 3000 carcasses were submitted for Meat Standards Australia (MSA) consumer taste panel assessments of meat quality. In addition, a sample of the progeny was measured for differences in feed intake. This data was linked to the feed efficiency studies conducted at the Agricultural Research Centre, Trangie to provide unique new knowledge on the genetic basis for differences in feed intake and efficiency, and the genetic relationships of these traits with other production and body composition traits.

Genetic parameter estimates for BREEDPLAN

The unique design and comprehensive nature of the CRC progeny test program provided a large amount of suitable data for the estimation of the genetic parameters required for the incorporation of carcass traits into the BREEDPLAN genetic evaluation system. These parameters included new estimates of the degree of heritability and amount of genetic variation existing within and between breeds for various live animal, abattoir carcass and meat quality measures. In addition, the data was used to produce estimates of the genetic relationships (genetic correlations) between these traits.

Johnston *et al.* (2002a,b); and Reverter *et al.* (2002a,b) have produced a series of comprehensive reports describing the results of the analyses of live animal, carcass and meat quality data from the Beef CRC progeny test. A summary of the main results of particular interest to the feedlot industry are reported in this paper.

Figure 2 shows the estimates of heritability for a range of live animal, carcass and meat quality traits obtained from the analysis of the Beef CRC progeny test data. The heritability of a trait refers to the extent to which the measured variation among animals is due to their genetic differences. Traits with a high heritability are expected to be more responsive to genetic selection (ie a greater portion of the measured variation is passed on to the next generation).

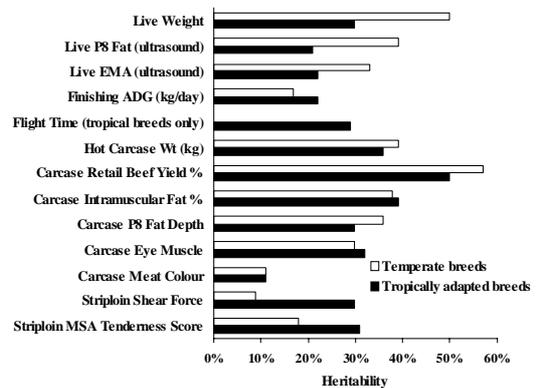


Figure 2. Heritability estimates for a range of live animal measurements (taken at commencement of finishing period), abattoir carcass measurements and meat quality traits for temperate and tropically adapted breeds.

For most live animal and carcass traits both the amount of variation in performance expressed among animals and the heritability of the measured traits was higher in temperate breeds. This indicates that non-genetic factors have a greater relative importance in tropically adapted breeds for these traits.

Interestingly, the amount of genetic variation and the heritability of both objectively measured and MSA consumer assessed meat tenderness indicators were higher for tropically adapted breeds compared to temperate breeds. This indicates a greater scope for genetic improvement in tenderness for the tropically adapted breeds. In temperate breeds, non-genetic approaches such as controlling growth path and pre- and post-slaughter practices (e.g. ensuring effective electrical stimulation) are likely to be more effective for achieving improvements in beef tenderness.

Some differences were found in both the amount of genetic variation and in the heritability estimates obtained for tenderness indicators across different muscle types. This indicates that the underlying genetic mechanisms may vary for these different muscle types.

For all live animal and carcass traits the variation in performance expressed among animals tended to increase at heavier carcass weights. Feedlot finishing decreased the age of slaughter and increased the degree of carcass fatness and muscling compared to pasture finished animals. However, the amount of underlying genetic

variation among animals for the various live animal and carcass traits was similar for both the feedlot and the pasture finished groups.

Included among the live animal measures recorded among progeny of the tropically adapted breeds was a relatively new trait called Flight Time. This is a temperament measure based on the time that an animal takes to move a specified distance after exit from a crush (Burrow *et al.*, 1988). Flight Time was a repeatable and moderately heritable indicator of temperament.

Figure 3 illustrates a sample of the genetic correlations estimated from the Beef CRC data.

Genetic correlations provide a measure of genetic association between various measures and traits. Traits with a high positive genetic correlation (i.e. close to unity) are likely to be influenced by similar genes. In this case, animals with higher than average expression in one trait will have progeny that also tend to have higher than average expression for the correlated trait. Where a negative genetic correlation exists between two traits then higher than average expression in one trait is normally associated with lower than average expression among progeny for the associated trait.

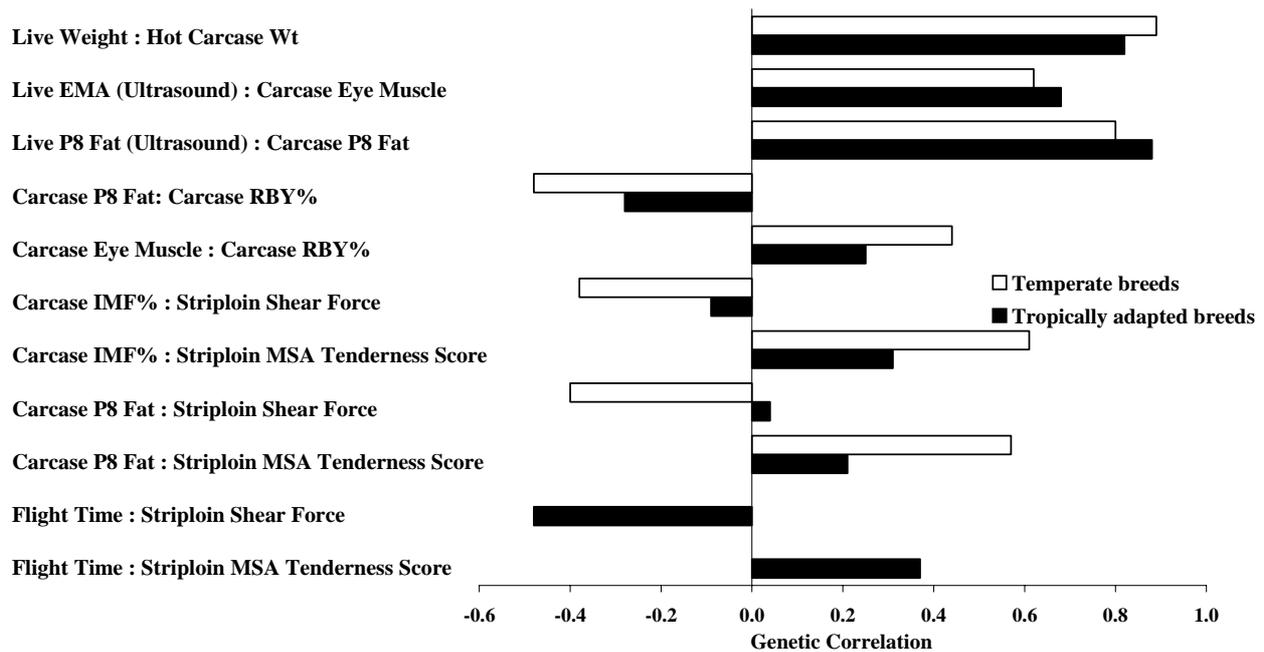


Figure 3. Genetic correlation estimates between a sample of live animal measurements (taken at commencement of finishing period), carcass measurements and meat quality traits for temperate and tropically adapted breeds.

The genetic correlation estimates show that live animal measures taken at the start of the finishing period (e.g. via real-time ultrasound) have a high genetic relationship with abattoir carcass measurements following slaughter in both temperate and tropically adapted breeds. Positive genetic correlations were also observed between Eye Muscle Area (EMA) and Retail Beef Yield (RBY%); and, between both Intramuscular Fat Percentage (IMF%) and P8 Fat Depth with MSA assessed Tenderness Score. Negative genetic associations were found between both IMF% and P8 Fat Depth with objective Shear Force measurement of beef tenderness (NB. lower shear force equates to more tender meat). Again, some differences between the magnitude of these genetic correlations were found between temperate and tropically adapted breeds, and between different muscle types.

An important finding from the analysis of genetic relationships among traits was the relatively strong correlations found between Flight Time with both objectively measured and consumer scored assessments of tenderness in tropically adapted genotypes. These correlations showed that animals with slower flight time (i.e. slower to exit the crush, with more docile temperament) have a genetic tendency towards more tender meat. As a result of these findings northern seedstock herds are being encouraged to record Flight Time on their weaners and to submit the data to BREEDPLAN for future EBV analysis. Equipment for measurement of Flight Time is commercially available through Ruddweigh International Scale Company, Guyra, NSW. The Beef CRC is conducting further trials to assess the use of Flight Time as an objective measure of temperament in temperate breeds.

Combining sources of genetic information in BREEDPLAN

The heritability and genetic correlation estimates for various live animal and abattoir carcass traits obtained from the Beef CRC have been incorporated into BREEDPLAN to enable the development of improved Estimated Breeding Values (EBVs). These improved EBVs are available for commercial bull buyers to assist them make better breeding decisions for particular production environments and market targets. Further details of the developments associated with the incorporation of carcass traits into BREEDPLAN were presented by Johnston *et al.* (1999).

Figure 4 depicts the various sources of information that are used in BREEDPLAN for the calculation of carcass EBVs. The procedure relies on having good estimates of the heritabilities of the various traits and knowledge of the genetic correlations between these traits. For example, in the calculation of EBVs for carcass IMF% use is made of the genetic correlations with live animal ultrasound measures of IMF% in the animal and/or its relatives (e.g. siblings, progeny), plus any information that is available on other correlated traits (e.g. rib and rump fat depth) or actual IMF%.

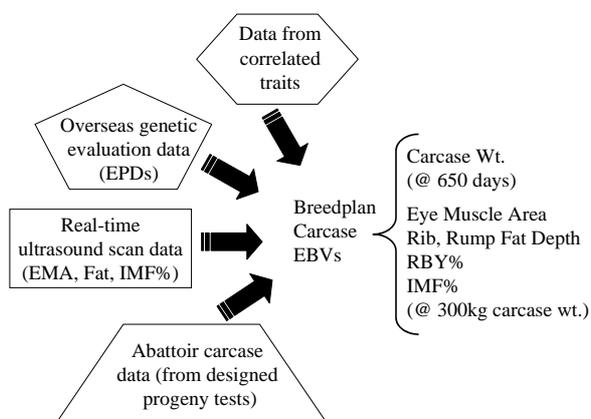


Figure 4. Sources of information contributing to the calculation of Estimated Breeding Values (EBVs) for carcass traits in BREEDPLAN (Sundstrom, 2001).

In addition to providing a compendium of genetic parameter estimates for direct use in BREEDPLAN, the Beef CRC progeny test also provided a large amount of abattoir carcass data to underpin the calculation of the initial carcass EBVs for over 400 contemporary sires across the participating breeds. This abattoir carcass data was incorporated with available live animal ultrasound data in the calculation of EBVs for individual sires involved in the CRC program. In some cases commercial progeny test data and overseas genetic evaluation information also contributed to the EBV calculations. Due to the high cost and practical difficulties in obtaining sire-identified carcass data from commercial slaughter

programs there has been very little additional abattoir carcass data submitted for use by BREEDPLAN. A solution to this problem remains one of the key challenges for the industry to achieve even greater accuracy in selection for carcass traits. At least two breed associations (Angus, Shorthorn) are conducting structured progeny test programs in an attempt to obtain further good quality carcass data for use in genetic evaluation.

Genetic relationships between performance under different finishing regimes and different target market weights

An important objective of the Beef CRC was to validate the assumed relationships between genetic performance across different finishing regimes (ie pasture versus feedlot) and different market targets. Prior to the analysis of the CRC data there was little information available to indicate whether producers targeting feedlot finishing systems would require a different set of EBV tools to those used by producers targeting pasture finished production systems. Also, there was uncertainty about the validity of EBV measures of genetic merit for carcass traits when these traits are expressed across a wide range of carcass weight end-points.

Figure 5 shows the estimated genetic relationships (correlations) for various measures of performance expressed at either domestic or export market end points. In almost all cases the correlations were close to unity, indicating that similar genes were influencing performance to different carcass weight targets. The exception to this was the lower genetic correlation found between measures of Retail Beef Yield % at the different carcass weight end-points for the tropically adapted breeds. This suggests that for these breeds the genes affecting Retail Beef Yield % at some market endpoints are not exactly the same as those influencing the trait at other end-points.

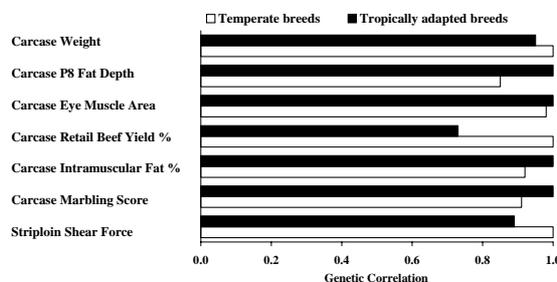


Figure 5. Estimates of genetic correlations between traits expressed at either domestic or export market weight end-points.

Figure 6 shows the estimated genetic relationships for various measures of performance when progeny were finished in either feedlot or

pasture environments. For the temperate breeds these correlations were all close to unity, indicating that similar genes were influencing performance of these traits in both finishing environments. In the tropically adapted breeds the correlations were substantially less than unity for Retail Beef Yield % and Marbling Score. This suggests possible differences in the genes responsible for superior performance in feedlot finishing compared to pasture finishing environments for these traits.

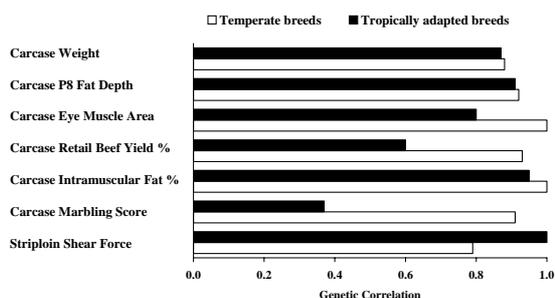


Figure 6. Estimates of genetic correlations between traits expressed following either pasture or feedlot finishing regimes.

The estimated genetic relationships for various measures of performance in tropically adapted breeds when finished in either a northern (sub-tropical) feedlot environment or a southern (temperate) feedlot environment are shown in Figure 7. These results indicate that the relative genetic performance was similar in both environments for most traits, with the exception of P8 Fat Depth and Marbling Score. For these two traits there was some evidence that different genes could be influencing performance in the northern sub-tropical environment compared to the southern temperate environment.

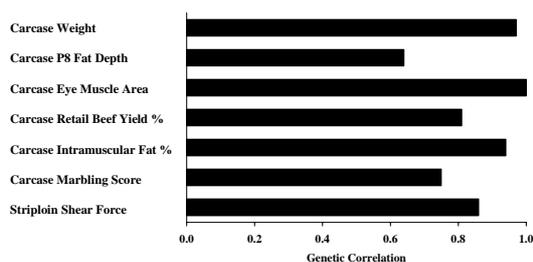


Figure 7. Estimates of genetic correlations between traits expressed in tropically adapted breeds feedlot finished in either a northern (sub-tropical) environment or a southern (temperate) environment.

In general, the genetic correlations between live animal, carcass and meat quality traits across different carcass weight end-points and different finishing environments were sufficiently high to provide confidence that the existing set of EBV tools are reliable for achieving genetic improvement for a wide range of production systems and market targets. In practice, this

means that the relative ranking of the carcass EBVs for sires would be largely unchanged across different environments and market end-points. Further research is required to further investigate the importance of the small number of exceptions to this finding for particular traits among tropically adapted genotypes.

Importantly, from the perspective of the feedlot sector, the Beef CRC results have provided strong evidence that growth and carcass EBVs based on measurements taken in seedstock herds can be confidently used to predict genetic differences among progeny in performance under feedlot finishing regimes across a wide range of carcass weight end-points.

An example of the use of EBVs to achieve genetic improvement in marbling performance

Over the last 5 years there has been widespread adoption of the use of real-time ultrasound measurement of IMF% in seedstock herds for several breeds (particularly Angus, Murray Grey, Shorthorn, Hereford, Poll Hereford). Details of the development and application of ultrasound technology for measurement of IMF% in Australia were provided by Graser *et al.* (1998).

Due largely to the availability of the comprehensive set of genetic parameters obtained from the Beef CRC progeny test this ultrasound IMF% data can now be effectively analysed through BREEDPLAN to produce EBVs for carcass IMF% for a large number of sires across these breeds. Importantly, the Beef CRC data has validated the usefulness of ultrasound scan data measured on seedstock animals (normally reared on pasture) for the calculation of EBVs that are relevant for predicting differences in the marbling performance of steer progeny managed under either feedlot or pasture finishing regimes.

In order to demonstrate the affect of selection for $EBV_{IMF\%}$ on marbling performance it is necessary to make some simplifying assumptions about the relationship between the traits and their underlying patterns of variation. In the following example, it is assumed that Marbling Score 1 is equivalent to about 3.0% IMF and that each additional Marbling Score is equivalent to a further 1.5% IMF. In reality, the relationship between IMF% and Marbling Score tends to vary across different groups of animals. Nevertheless, the example still serves as a useful guide to the potential magnitude of benefits obtained from selection for increased IMF%.

Suppose, for example, that the average IMF% of the progeny of particular sire (Bull A) with an $EBV_{IMF\%}$ of -0.2, under a particular feeding and management regime, was 6.0%. Given the above

assumptions, we would expect that approximately 50% of the progeny would achieve Marbling Score 3 or better when slaughtered. From the same female herd, and under the same feeding and management regime, we would expect that the progeny of a sire (Bull B) with an $EBV_{IMF\%}$ of +0.8 to achieve an average IMF% of 6.5% (i.e. 0.5% higher than progeny of Bull A). Using the same assumptions, we would expect that over 70% of the progeny of Bull B would achieve Marbling Score 3 or better.

Figure 8 illustrates the expected distributions of IMF% and Marbling Score performance among progeny of Bull A and Bull B in the above example. Similar analyses can be conducted to estimate the expected differences in progeny performance for other traits based on EBV differences between sires.

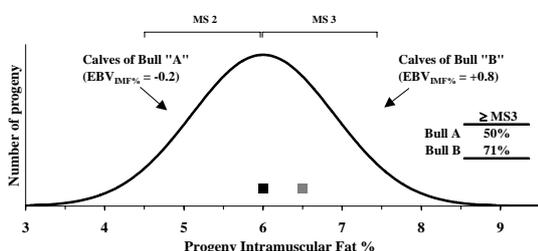


Figure 8. Example distributions of Intramuscular Fat % (IMF%) and Marbling Score among progeny of bulls with different Estimated Breeding Values for IMF% ($EBV_{IMF\%}$).

The use of selection indices to assist with multi-trait selection decisions

In any practical breeding program there will be numerous traits under genetic influence that can be potential targets for genetic improvement. One of the dilemmas facing beef producers when making breeding decisions is to decide the appropriate emphasis to place on these different traits. The optimal solution to this dilemma will obviously vary between individual circumstances, depending on the production environment, primary market target(s) and the current performance level of the herd.

Barwick *et al.* (1994) described a formal process of defining an appropriate economic breeding objective for specific situations. They showed how to combine an animal's EBVs for various traits into a single aggregate \$Index Value designed to optimise progress towards a particular breeding objective. This procedure, implemented via a software program called "BreedObject", requires reliable estimates of the heritability of traits included in breeding objective and knowledge of the genetic relationships between these traits and various EBV measures.

Coinciding with the use of Beef CRC results in the development of new carcass EBVs for BREEDPLAN was the derivation of parameters required for the incorporation of these traits into

BreedObject. The Beef CRC data has provided essential information used in BreedObject for linking the various EBV and breeding objective traits related to growth performance, retail beef yield and marbling performance.

Over the past three years BreedObject has been rapidly adopted by the Australian beef industry. It is now used by most of the major breed associations to provide \$Index Values for a range of case study examples via their website animal listing services. Feedback from several breed associations indicates that differences in \$Index Values is now one of the primary factors explaining variation in bull sale (and semen) prices across the seedstock sector.

Trends in the average \$Index Values over time provide an indication of the effectiveness of the seedstock industry in achieving genetic progress in overall profitability. For example, Figure 9 illustrates the average \$Index Values among progeny in the recorded Angus seedstock sector for a selection index targeting the Japanese B3 market. The trend over time shows that the estimated annual rate of genetic improvement in profitability over the past five years (ie for progeny born between 1995 and 2000) is more than double the rate of improvement achieved during the first 5 years of BREEDPLAN (1986-1990). Increases in genetic trend for profitability (\$Index Value) have also been recorded for other breeds with different market targets. At least part of the reason for the increased rate of genetic improvement over recent years is likely to be due to the implementation of improved carcass EBVs resulting from the Beef CRC work.

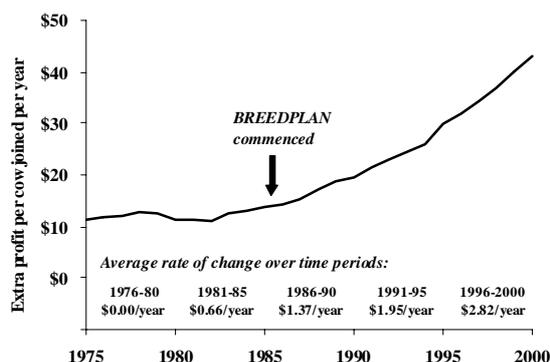


Figure 9. Trends in \$Index Value in the recorded Australian Angus seedstock population for the "Japanese B3 selection index" (Source: The Angus Society of Australia).

The appropriate emphasis of different traits in a breeding objective derived by BreedObject varies depending on the perspective of the decision-maker. For example, from the perspective of the feedlot sector, final turn-off weight, feed intake and traits related to carcass yield and carcass value are the major determinants of an animal's profitability. In contrast, from the perspective of a commercial breeding sector additional traits such

as female fertility (turn-off rate), calving ease, maternal performance and early growth performance will also contribute to overall profitability.

Barwick and Henzell (1999) calculated BreedObject selection indexes for a range of case study examples representing different market targets and enterprise perspectives. Figure 10 shows the relative emphasis on selected breeding objective traits included in two of the example indexes from the perspective of a “Feedlot Only” enterprise and from the perspective of an integrated “Breeding plus Feedlot” enterprise, both targeting production for the Japanese B3

market. It can be seen from this example that while traits of importance to the feedlot sector should also be considered by the commercial breeding sector these traits only form part of the overall breeding objective. In situations where the commercial breeding sector is not integrated with the finishing sector, or where price signals for feeder cattle fail to reflect differences in subsequent performance, then there may be little or no incentive for the breeding sector to include traits of importance to the feedlot sector in their breeding objectives.

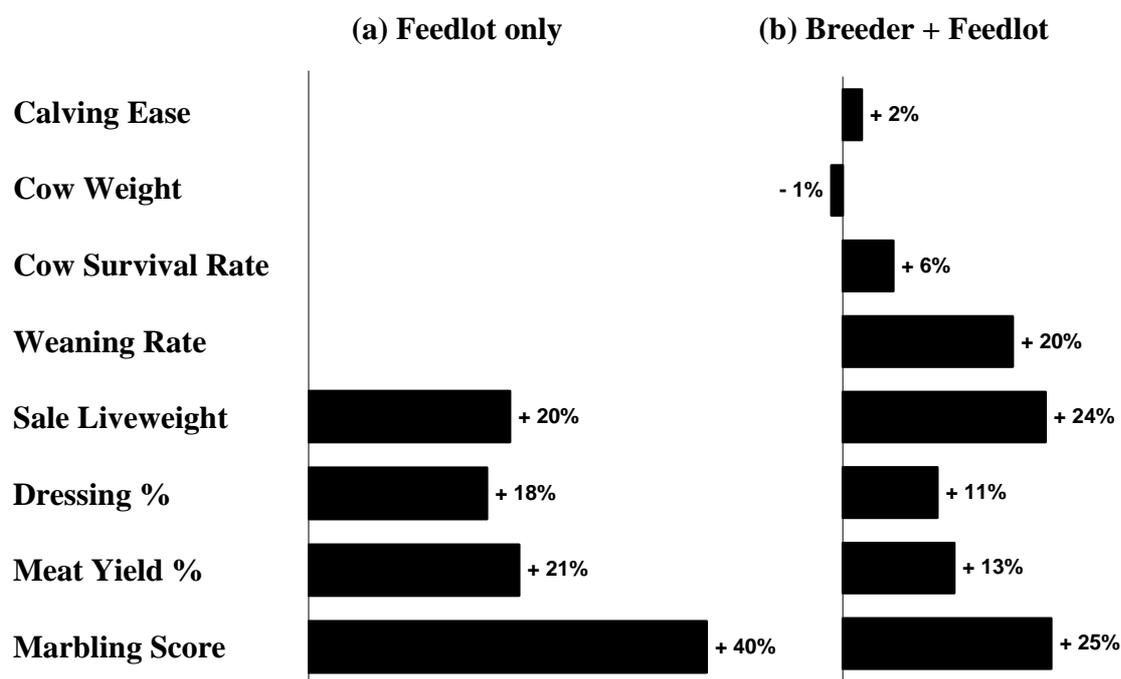


Figure 10. Relative emphasis on major traits in the breeding objectives derived for example beef enterprises comprising (a) feedlot only sector, and (b) breeding plus feedlot sector, both targeting the grainfed Japanese B3 market (after Barwick and Henzell, 1999).

Understanding the genetics of feed intake and efficiency

In addition to the large amount of data obtained for carcass and meat quality traits from the Beef CRC research there has also been a considerable amount of new knowledge developed to assist in our understanding of the genetic basis for differences among animals in feed intake and efficiency. This knowledge has complemented the results of the extensive studies on feed conversion efficiency conducted by NSW Agriculture at the Trangie Agricultural Research Centre (described by Exton, 2002).

Among the progeny generated in the Beef CRC progeny test program, approximately 1,600 straightbred steers and heifers were evaluated for individual feed intake at the CRC’s research

feedlot at Tullimba. These tests were conducted over a 50 day period (on average) during the finishing phase, using a typical feedlot ration delivered via automated feeding units. The resulting data was used to calculate estimates of heritabilities and genetic associations (correlations) for various efficiency measures, including Net Feed Intake (NFI). This trait refers to the variation in feed intake among animals beyond that related to differences in growth rate and body weight. Exton (2002) has described the advantages of NFI over other measures of efficiency as a criterion for genetic selection.

The amount of genetic variation observed for NFI among steer and heifer progeny evaluated by the Beef CRC was similar to that observed at Trangie where tests were conducted on Angus bulls and heifers immediately post-weaning on a medium

energy hay and grain ration. The heritability estimate for NFI obtained from the Beef CRC data was about 20% (ie 20% of the observed differences were estimated to be due to genetic differences among animals). This was lower than the value obtained from the analysis of the Trangie data, possibly due to the shorter feed test interval used in the Beef CRC evaluations and to differences in the age of testing and the rations used in the tests. Nevertheless, the heritability for NFI was still sufficiently high to suggest that genetic selection for reduced NFI would be an effective means of improving the feed conversion efficiency of growing animals.

Positive genetic correlations were estimated between NFI and fatness traits (eg P8 Fat Depth and Intramuscular Fat %). The estimated genetic correlations with Carcase Weight, Eye Muscle Area and Retail Beef Yield % were negative. These results suggest that selection for reduced NFI may result in more efficient animals that will also tend to be genetically leaner, more muscular and heavier at slaughter. Importantly, the correlations between NFI and these traits were only moderate in size. Consequently, through the use of EBVs it should be possible to select for desirable changes in NFI without necessarily suffering adverse genetic changes in these other traits.

The biggest impediment to the routine collection of NFI data for use in industry breeding programs is the high cost and practical difficulties of measuring differences in feed intake among animals. The Beef CRC is pursuing the development of cheaper and simpler indirect indicators of differences in efficiency. The most promising indicator at present is the blood hormone IGF-1 (Insulin-like Growth Factor). This hormone is related to differences in feed efficiency and body composition in pigs. Early results indicate that IGF-1 levels in beef cattle are moderately heritable and are indeed correlated with differences in NFI (Johnston *et al.*, 2001). Further research is currently in progress across a large number of co-operating herds to determine the genetic relationships between IGF-1 with other important production and body composition traits.

Exton (2002) describes recent developments in the industry application of measurement and genetic evaluation of NFI. He also provides further details of the consequences for the feedlot industry of selection for this trait.

Preliminary Northern Crossbreeding results

In Beef CRC Northern Crossbreeding Project, Brahman cows were joined to nine sire breeds representing British (Angus, Hereford, Shorthorn), European (Charolais, Limousin), British x Brahman derived (Santa Gertrudis), British x

European derived (Charbray), Sanga derived (Belmont Red) and Brahman (control) over three years. Steer and heifer progeny were either grain-finished in central Queensland or northern NSW or finished at pasture in central Queensland.

Preliminary analyses have shown that sire breed effects were important for all carcase traits. European crossbreds were tended to be leaner than the tropically adapted crossbreds, which were leaner than the British crossbreds. Generally, breeds that produced the highest amount of subcutaneous fat cover produced the highest amount of marbling. European crossbreds produced significantly higher Retail Beef Yield % than all other breeds, with no significant differences between British crossbreds and tropically adapted crossbreds for this trait.

There was no major re-ranking of sire breeds across market end-points or finishing regimes for any weight or carcase attribute. But, the relative difference in performance between breeds did vary across finishing treatments for some traits, particularly marbling, shear force and MSA tenderness scores. Further examination of these results is necessary before any general conclusions can be drawn.

Additional sire-identified Brahman, Belmont Red and tropically adapted Composite animals have been generated in Beef CRC co-operator herds to further investigate the genetic relationships between component traits affecting profitability in northern Australia. In particular, the study will explore the consequences of selection for Retail Beef Yield % and Intramuscular Fat % on body composition, efficiency of feed utilisation, adaptability to tropical stressors and female reproductive performance.

Gene markers for future genetic improvement

The Beef CRC has made a considerable investment into the investigation of the underlying biological mechanisms associated with differences in carcase attributes, meat quality, feed efficiency and growth performance. One of the primary goals of this work has been to establish a platform of knowledge from which further genetic studies at the individual gene (allele) level can be conducted to identify (map) candidate gene markers to assist in future genetic improvement of these traits.

The Beef CRC gene mapping studies on research populations have identified numerous candidate gene markers linked to important performance and meat quality traits, including Carcase Weight, Retail Beef Yield %, Dressing %, Eye Muscle Area, Marbling Score and Tenderness. These linked markers may be specific to the families of animals included in the studies and need to be validated in commercial populations before they

can be effectively used by the industry. The discovery of these linked markers has demonstrated the potential for the future identification of individual genes (alleles) having a direct influence on important economic traits.

The Beef CRC is currently conducting further fine scale mapping studies in an attempt to identify direct gene markers that have a known influence on the expression of particular traits. Fortunately, there are many similarities between the bovine gene sequence and the genome of other mammals, including humans. As a result, it is expected that the beef cattle mapping studies will also benefit from the massive global investment in mapping the human genome.

An example of a direct gene marker of relevance to the feedlot industry is a gene (allele) contributing to the genetic potential for marbling called TG5 (thyroglobulin), discovered by CSIRO. A commercial available test for the TG5 allele, known as the GeneStar Marbling test, is the first of several direct marker tests likely to be available to the industry over the next few years. A key requirement for the beef supply chain to benefit from the expected developments in gene marker technologies for meat quality traits will be the provision of appropriate market signals (i.e. economic incentives) for the breeding sector to invest in the testing and use of markers in their breeding programs.

The need for value based payment for feedlot and carcass performance

The beef supply chain in Australia (and globally) is very segmented and generally suffers from inadequate communication of effective market signals and performance/compliance information across and between sectors. Historically, market signals between sectors of the supply chain have simply tended to reflect the short-term dynamics of “commodity” supply and demand. A key reason for this has been the high degree of fragmentation and open market competition in the supply chain. This is exacerbated by the concentration of market power and influence in the processing and retailing/exporting sectors. In contrast there are a large number of independent participants in the commercial breeding sector, with the vast majority having very little market influence. The feedlot sector sits between the breeding and processing sectors and can play a pivotal role in facilitating the effective flow of market signals and performance information across the industry.

The realisation of the potential benefits to the beef supply chain from the adoption of genetic technology in the commercial breeding sector will depend on the provision of appropriate financial incentives and delivery of adequate feedback information to encourage participants in that

sector to adopt market focused breeding objectives. This is particularly relevant for carcass and meat quality traits which are important determinants of the profitability of the processing and retail/export sectors, but which may have no direct impact on the financial returns of commercial breeders. Similarly, the feedlot sector can only benefit from improved genetic performance via the adoption of relevant selection criteria in the breeding programs of their suppliers.

Figure 11 illustrates the segmented structure of the beef supply chain showing the importance of value based marketing and performance feedback to facilitate the adoption of market focused breeding objectives by the seedstock and commercial breeding sectors.

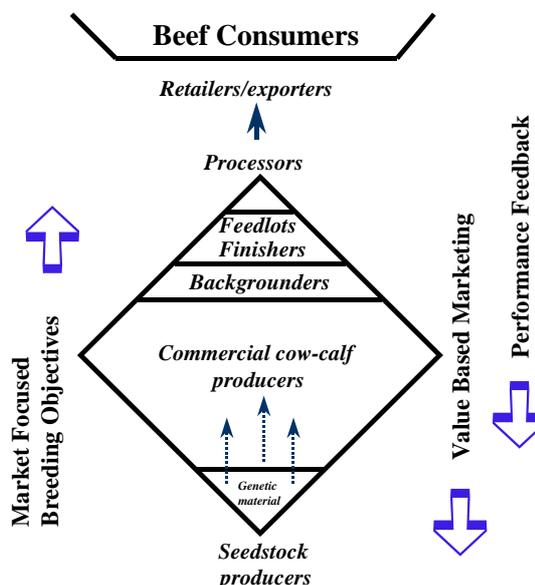


Figure 11. Representation of the segmented structure of the beef supply chain showing the importance of value based marketing and performance feedback to facilitate the adoption of market focused breeding objectives by the seedstock and commercial breeding sectors.

As described in this paper, the Beef CRC and other research programs have established a powerful array of genetic technologies that can potentially be utilised to significantly improve the profitability of the entire beef supply chain. Unfortunately, the impact of these technologies will be far less than optimal unless some major developments are made towards achieving greater co-operation between the different sectors of the supply chain, including the widespread adoption of the principles of value based marketing.

Summary of key messages for lot feeders

The Beef CRC has made a major investment in the development of new knowledge about the genetic basis for differences in performance,

carcase and meat quality traits in beef cattle. This has included the conduct of the world's largest progeny test program and the subsequent evaluation of genetic differences among animals across a range of breeds, production environments and market end-points.

Some of the key outcomes of particular relevance to the feedlot sector include:

- A compendium of genetic parameters (variances, heritabilities, genetic correlations) that have been incorporated in BREEDPLAN to provide more reliable Estimated Breeding Values (EBVs) for a range of performance and carcase traits;
- Validation of the reliability of carcase EBVs for predicting differences in progeny performance under both feedlot and pasture finishing systems, and across a range of carcase weight end-points;
- Validation of the use of real-time ultrasound measurements on seedstock as predictors of carcase merit among slaughtered progeny;
- Provision of direct abattoir carcase data on over 8,000 progeny to underpin the calculation of carcase EBVs for over 400 contemporary industry sires across 7 breeds;
- Provision of the necessary parameter estimates for the derivation of appropriate selection indexes and aggregate \$Index Values (using BreedObject) for individual breeding enterprises, taking into account the requirements commercial breeding, feedlot and processing sectors;
- Important contributions to the necessary knowledge required for the effective implementation of selection programs to improve feed conversion efficiency;
- Establishment of a platform of knowledge for the future identification of direct gene markers for important performance and meat quality traits.

A major requirement for the future realisation of the potential benefits of these genetic outcomes in the feedlot and processing, and retail/export sectors will be the provision of appropriate market signals and feedback information to the seedstock and commercial breeding sectors of the industry.

Acknowledgements

Many scientists, technicians, support staff and co-operating breeders have contributed to the genetic outcomes of the Beef CRC. Meat and Livestock Australia have co-funded much of the research conducted in the Beef CRC, and provide considerable financial assistance for the on-going development of BREEDPLAN.

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