SmartGene for Beef: A Summary of the Results
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The "SmartGene for Beef" project is providing valuable information to further develop genetic evaluation in the Australian beef industry, provide new EBVs and increase the accuracy of some existing BREEDPLAN EBVs.

By integrating DNA marker information with BREEDPLAN phenotypic data and pedigree information to calculate marker-assisted Estimated Breeding Values "SmartGene for Beef" aims to help producers select more efficiently for economically important traits.

Major Project Outcome

Tenderness was the key trait targeted by "SmartGene for Beef" because no EBV is available yet, and the trait cannot be directly measured on live animals.

Tenderness is the most significant characteristic in consumer taste panel tests. Research has shown that it is a major limitation particularly for tropical adapted beef breeds consistently meeting eating quality standards.

The SmartGene results for tenderness are very consistent. Of the four GeneSTAR tenderness markers examined, T1 and T2 consistently showed significant effects in British breeds and T1, T2 and T3 showed effects in tropically-adapted breeds of cattle. These markers will be the major components of BREEDPLAN trial Tenderness EBVs to be released in October 2008.

Marker-assisted EBVs will allow producers to identify animals that are genetically pre-disposed to producing more tender meat. This will not only provide significant benefits to the Queensland (and the Australian) beef industry but also to our global customers.

The project was undertaken in three distinct stages:

Stage 1 - Genotyping was performed by Catapult Genetics using ~12,000 DNA samples from Beef CRCI and II animals plus two industry projects. All animals were tested for the 12 commercially available GeneSTAR DNA tests (4 markers each for tenderness, marbling and feed efficiency). Results from the testing were transferred to the Beef CRC's database.

Stage 2 - The Animal Genetics and Breeding Unit (AGBU) then undertook analyses. DNA test results and performance measures (phenotypic measures of tenderness, intramuscular fat or IMF, marbling and feed efficiency in fully pedigreed animals) were analysed to estimate the full range of parameters required to calculate marker-assisted EBVs. Specifically this research estimated gene frequencies and evaluated the effects of each marker individually as well as sets of markers (T1-T4, M1-M4 and FE1-FE4) on each trait. The amount of variation accounted for by each DNA marker in each cattle population was estimated using these gene frequencies and gene effects.

Stage 3 – Software development is now being done by AGBU (funded by MLA) to calculate trial BREEDPLAN marker-assisted EBVs. They will combine the DNA test results from Stage 1, the DNA test results from seedstock animals already reported with BREEDPLAN, the genetic parameters from Stage 2 and the phenotypic records collected in CRC-I and II to deliver the marker-assisted EBV methodology to BREEDPLAN.

Animals tested in "SmartGene for Beef" project came from two Beef CRC projects conducted over the past 15 years and two field experiments conducted by breed associations. These projects are summarised below.

BEEF CRCI	These data comprise seven purebred breeds, 4 temperate breeds (Angus, Hereford, Murray Grey and Shorthorn) (n=3,229) and 3 tropically adapted breeds (Brahman, Santa Gertrudis and Belmont Red) (n=3,615)
BEEF CRCII	These data are from the CRCII northern breeding project focussed on tropically adapted cattle-including purebred Brahman (n=2,039) as one breed and Tropical Composites (from various pastoral companies) as another (n=2,400).
Angus Progeny Test	Angus Australia progeny test program conducted using the NSW DPI Trangie Angus herd as dams (n=415).
Durham Progeny Test	The Shorthorn Beef progeny test program conducted in Durham herd (n=347), Orange, NSW.

GeneSTAR DNA test results

Catapult Genetics supplied the DNA tests. Results were reported as 0, 1 or 2 'stars' for each marker. A result of 0, 1 or 2 'stars' means the animal carries zero, one or two copies (alleles) of the 'favourable' form of each gene or marker.

Comparing the allele frequencies of different experiments for the same breed showed only small differences. Where extreme frequencies exist (i.e. where fewer than 5% of animals have two copies of a particular allele or where >95% of animals have the same combination of genes for the marker of interest), a larger number of tested animals with phenotypes are required to establish the marker effects with confidence. Even when the effects can be established, they may have little utility as the markers with extreme frequency explain only a small amount of the genetic variation in that population, particularly if the favourable marker is at very high frequency.

Statistical analyses

Extensive analyses were done within each trait (tenderness, marbling and NFI). The performance measures (phenotype) and DNA test results were analysed extensively to determine the effects of each individual marker, as well as collectively as the total effect of all of the markers applicable to the trait. Each trait had a panel of 4 markers with the total number of favourable "stars" for each trait potentially ranging from 0 to 8 "stars". A brief outline of the key results are presented here. More detailed results will be available from the websites of the SmartGene partners.

Tenderness Results

Figure 1 shows the average effect of increasing numbers of "stars" on beef tenderness when measured as *longissimus dorsi* (LD; loin muscle) shear force.

Shear force is a mechanical measure that can be likened to how much force a person needs to chew a piece of steak. **The lower the shear force value, the more tender the beef.**

The effect of increasing numbers of "stars" was statistically significant ($P<0.05$) in each of the populations tested. Key points in the tenderness results include:

- Of the four GeneSTAR tenderness markers examined, T1 and T2 consistently showed significant effects in British breeds and T1, T2 and T3 showed effects in tropically-adapted breeds of cattle. These markers will contribute significantly to BREEDPLAN trial Tenderness EBVs by October 2008.

- While the CRCI temperate population contained animals used in marker discovery; the results were also statistically significant in the independent CRCII populations.

- The markers identified variation in both normally-hung and tenderstretched carcases. However, as the tenderstretched carcases were more tender and had less variation for tenderness than normally-hung carcases, the effects of the tenderness markers were reduced under tenderstretch hanging.
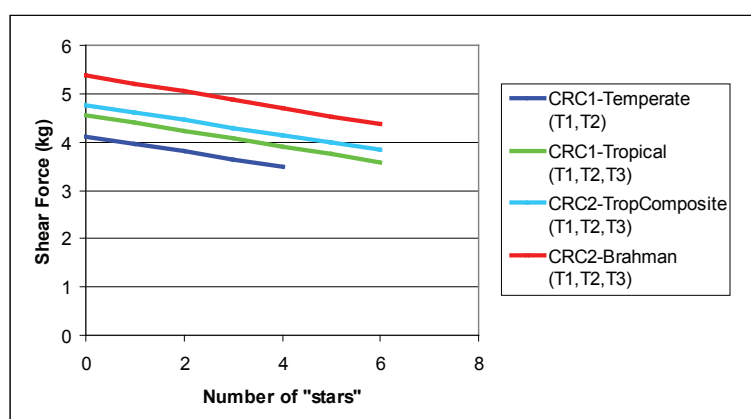
Figure 1. *The average effect of increasing "stars" on LD shear force.*

- Although statistically significant, the total amount of phenotypic variation in tenderness accounted for by the GeneSTAR tenderness markers was only around 4% in temperate breeds and 6% in tropical breeds. While encouraging, it means many more markers are required in both breeds to account for a sizeable percentage of variation.

- For CRCI temperate breeds, results showed estimates were not accurate for Shorthorn due to the extreme gene frequencies and low numbers of animals. For Angus and Murray Grey, the T1 and T2 markers were significant, had modest effects on tenderness and acted additively, but T3 and T4 were not significant. For Herefords, only T1 was significant.

- For tropically adapted breeds, results for T1, T2 and T3 fitted jointly showed significant and additive effects, except for T2 in CRCII Brahmans. However when T4 was added to the model, it had inconsistent effects, ranging from negative in CRC1 Brahman (that includes the discovery animals), to no observed effect in CRCII breeds, to positive in CRCI Santa Gertrudis and Belmont Red.

- T1, T2 and T3 in tropically adapted breeds were significant for tenderness in normally-hung carcases and had consistent effects on Meat Standards Australia (MSA) consumer taste panel scores. The marker effects appear to be additive in their effects on tenderness.

- The effect of T3 was not consistent in British breeds and T4 does not appear to be a useful marker for tenderness in these breeds.

Marbling Results

The marker effect as either individual markers or as increasing 'stars' was neither statistically significant (P>0.05) or consistent for IMF, MSA marble score or AUS-MEAT marble score in any of the populations tested, including the Angus progeny test animals. Points to note with respect to the IMF and marbling results include:

- None of the four marbling markers had a consistent effect either individually or collectively on IMF or marble score.

- The extreme gene frequencies of these markers made it difficult to assess the difference between 0 and 2 star or 1 and 2-star genotypes in most breeds.

- Animals tested for these markers were grain-fed for up to 180 days but there were no very long-fed animals in these datasets.

- IMF and marble scores were relatively low reflecting the days-on-feed; nevertheless, they are representative of Australian grain-finished cattle for most markets.

- To increase the statistical power of estimating significant effects, the information was pooled for CRCI Angus and Murray Grey and the Angus progeny test datasets and was used to examine MSA marbling score in these higher marbling breeds. This combined dataset comprised 1123 animals with MSA marble scores and a mean MSA marble score of 1.55 (± 0.80). In this dataset, none of the markers was individually significant and no statistical trends were observed. Similar results were observed when considering the markers together.

Feed Efficiency Results

Net feed intake (NFI) is a measure of how much an animal eats relative to an expected amount for its weight and growth rate. The lower the NFI value, the less the animal eats for its weight and growth rate and the greater the animal's feed efficiency.

The effect of increasing number of 'stars' was statistically significant for NFI (P<0.05) in the CRC1 temperate breed population, but not statistically significant in any other population. The effects of the markers on other traits associated with feed efficiency (e.g. daily feed intake and feed conversion ratio) were very similar to the effects on NFI.

Because the feed efficiency (FE) markers were discovered from research on some of the CRCI temperate and tropically adapted animals it was expected the effect of the markers would be statistically significant in that population. However, the marker effects were not statistically significant in any other population, showing that when tested in totally independent populations, the estimated marker effects were not consistent or informative. Points to note with respect to the NFI results include:

- The variance explained by the four FE markers in CRCI temperate breeds (i.e. comprising the discovery animals) was about 1.8% of the phenotypic variance for the trait.

- Gene frequencies for FE markers in Brahman were extreme for three of the four markers.

- For CRCI and CRCII tropical breeds, the markers explained none of the sire or phenotypic variance. Similar results were obtained for the two progeny test datasets, except the direction of the effect was in the unfavourable direction (but not significant).

- Markers FE3 and FE4 were significant in the CRCI temperate breed populations (that also included the discovery animals) for net feed intake and daily feed intake, but they did not validate in any other set of information. The direction of effects for NFI was not consistent across populations. The high gene frequencies of the 2-star form of the gene, especially in the tropical breeds, also limit their usefulness for breeding purposes.

- The effects of the markers on other traits associated with feed efficiency (e.g. daily feed intake and feed conversion ratio) were very similar to the effects on NFI.

Glossary of technical terms

DNA marker - A unique DNA sequence genetically associated with a particular trait and used to identify an individual or cell carrying that marker.

Genotype - The genetic makeup of an animal (at one gene, a series of gene markers or for all its genes).

Phenotype - Measured performance. The observable or measurable properties of an animal. The combination of genetic and environmental effects on performance.

Allele - A specific form of a gene or gene marker.

Gene - The functional sequence of DNA that codes for a specific protein.

Tender-stretch - A method of hanging a carcase employed at the processing level. It involves hanging carcases by the pelvis as opposed to the traditional Achilles tendon and is known to improve beef tenderness.

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