DNA technology or more specifically Gene markers have been available to the Beef producer for a number of years. Initially this technology was utilized in the areas of parent verification (e.g identify actual sires of calves from multiple sire groups) or to identify carriers of genetic diseases such as mannosidosis or pompes disease. More recently this technology has moved into the area of production traits with the aim to offer the Beef producer a tool to increase the rate of genetic gain for certain traits by enabling superior genetics to be identified within “young” animals i.e before the trait could be measured on the animal itself or its’ progeny.

Going back a step, a gene marker identifies the location, or proximity on the chromosome of individual genes that influence a trait. Current genetic research into beef cattle has aimed at finding markers that identify the genes that control economically important traits and particularly those that are difficult and/or expensive to measure. By identifying the markers, a simple DNA test would identify if the animal in question was carrying favourable genes or not for the required trait.

At present there are 12 gene markers being marketed to the beef industry – four markers for each of the traits of Tenderness, Marbling and Net Feed Intake (NFI) with each being identified on the scale of 0 to 2 stars. With each trait having 4 markers, an animal could be described as having a range from 0 to 8 stars.

Results recently released by the SmartGene for Beef project which tested these markers against well recorded cattle populations i.e Beef CRCI and CRCII, have shown that:

- of the 4 gene markers for Tenderness, three (T1, T2 and T3) have significant effect on improving meat tenderness in Tropical breeds and explain 6% of the phenotypic (or observed) variation while two (T1 and T2) were shown to have a significant effect in the Temperate breeds and explain 4% of the phenotypic variation.
- of the 4 gene markers for Marbling, none had a significant effect on IMF or marble score in any of the breeds tested.
- of the 4 gene markers for NFI, two markers had a significant effect on NFI in the population they were discovered (CRC1) but not in any other population tested.

While the results for Tenderness are encouraging (particularly for Tropical breeds), the markers still only explain a small portion of the genetic variation for Tenderness and, as such, currently offer limited scope to select superior animals for the purpose of genetic improvement of this trait.

Initially it was thought that a few markers would be sufficient to identify a significant portion of the genetic variation in economically important traits. It is now apparent that this concept was oversimplified and many i.e hundreds, possibly thousands, of markers will be required to adequately identify enough of the genes that account for a significant portion of the genetic variation. Genetic technologies are advancing rapidly to accommodate this need and already have the ability to scan DNA samples to identify a very large number of DNA sequence variations that may be associated with respective traits. The key will be to validate these markers on well recorded current cattle populations to determine how much of the genetic variation they explain within and between breeds for economically important traits. If they account for a significant amount of the variation (i.e individually or collectively), Gene markers can be used in isolation to confidently select genetically superior cattle.

It is worth noting that validation of the currently marketed gene markers did not include the Gelbvieh breed. The temperate breeds represented in the validation study were Angus, Hereford, Murray Grey and Shorthorn. The adapted breeds represented were Brahman, Santa Gertrudis, Belmont Red and Tropical composites. European breeds were not represented. With results suggesting that Gene markers are breed, and possibly production system, specific i.e markers that work in one population
may not necessarily work in another, it appears that there would be exploring the benefits of validating current markers within a well recorded Gelbvieh population. This would also potentially be a valuable resource in validating new markers as they are made available.

It is becoming more apparent that Gene markers, were possible, will best be used to add additional information to the current available BREEDPLAN Estimated Breeding Values (EBVs) calculated from performance and pedigree information. Through the SmartGene for Beef project, this has already been achieved for one trait with the release of the Trial Tenderness marker assisted EBV (EBV\textsuperscript{M}) for Brahman. The Trial Tenderness EBV\textsuperscript{M} incorporates the animals pedigree, performance measures for shear force and flight time and Gene markers (figure 1) to provide an estimate of the animals’ breeding value. The resulting marker assisted EBV can be used in the same way as any of the other existing EBVs for selection.

![Information used to calculate Trial Tenderness EBV\textsuperscript{M}s](image)

**Figure 1. Information used to calculated Trial Tenderness EBV\textsuperscript{M}s**

For further information regarding this article, please contact Christian Duff, SBTS – ph (02) 6773 2472 or email: christian@sbts.une.edu.au. Full scientific results from the SmartGene for Beef project are available on the AGBU website [http://agbu.une.edu.au](http://agbu.une.edu.au).

\* Smartgene for Beef was a collaborative R&D project between Catapult genetics, CRC for Beef Genetic Technologies, the Animal Breeding and Genetics Unit (AGBU), the Agricultural Business Research Institute (ABRI), Meat and Livestock Australia (MLA), Cornell University and Breedlink Pty Ltd with co-funding from the Queensland Government.

\+ Cattle used for the Marbling validation were grain fed for up to 180 days. Longer feeding times may provide more variation in Marbling and a better correlation to the Gene Markers.

*Article compiled by Christian Duff for the Australian Gelbvieh Association, February 2009*