

# Meeting Consumer Demands Through Genetic Selection: The NCBA Carcass Merit Project

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## Introduction

It is well documented that tenderness is one of the most important attributes of higher-value beef cuts. Equally well documented is that genetic variation exists both between and within breeds for this important trait. However, tenderness is difficult and expensive to measure, and market incentives to improve tenderness are limited. Accordingly, it has been ignored in most selection programs. Left purely to chance, the beef industry is fortunate that a majority of cattle harvested have acceptable tenderness, but the fact remains that a significant portion of the population is unacceptable. It is hard to imagine that any industry would ignore the primary criterion by which their product is evaluated by consumers.

In 1998, the US cattle industry initiated the Carcass Merit Project (CMP), a large multi-breed study to evaluate the genetics of tenderness in the US beef cattle population. The project was jointly funded by the \$1 per head beef checkoff, and the participating breed associations. The objectives of the project were:

- Generate data from which genetic evaluations for tenderness and sensory traits can be computed.
- Develop methodology and procedures for collection of information necessary for further development of EPDs for carcass traits.
- Validate DNA markers discovered in previous checkoff-funded research for use in industry-wide marker-assisted selection programs for improvement of carcass traits.
- Measure costs and returns of implementing EPDs for carcass traits for the alternative genetic selection programs and combinations of management × genetic improvement of carcass traits.
- Breed comparison was strictly precluded from being an objective.

## Project Design

All US beef breeds were invited to participate in CMP, and the following chose to do so:

Angus	Maine-Anjou
Brahman	Red Angus
Brangus	Salers
Charolais	Shorthorn
Gelbvieh	Simmental
Hereford	Simbrah
Limousin	South Devon

Commercial cows were inseminated to several of the most widely used AI sires of each of the breed associations cooperating and supporting the research project. Each breed association selected the sires and provided the leadership and all costs associated with nominating cattle for the study, including semen, AI, collecting feedlot performance data, blood sampling/collection, carcass data collection, shipping of blood samples and the development of EPDs for their respective breeds. Breed identity was coded to prevent breed associations and/or breeders from comparing breeds.

Ten bulls from each breed were designated as “DNA sires.” Fifty progeny of each of these sires were used for DNA analysis and shear force observations. Five of those DNA sires were further designated as “Sensory Sires”, and all fifty of their progeny were also used in sensory panel assessments of tenderness, juiciness and flavor. In addition to the sensory sires, breeds were allocated a number of “EPD sires”, of whom 25 progeny would be evaluated for shear force, but no DNA samples would be collected. The number of EPD sires allocated was based on the historical number of registrations by the respective breed associations.

Progeny were fed at numerous commercial feedyards and ultimately slaughtered at several cooperating packers. Breed associations were encouraged to minimize the number of contemporary groups and harvest each group in its entirety, whenever possible. Decisions on days fed, rations, implant and health protocols, and other management considerations were made by the breed associations in consultation with feedlot personnel, and were uniform within contemporary group.

The project was not designed to provide comparisons between breeds and consequently, no valid breed comparisons can be made from these data. A breed's average relative to the overall project average can be due to

management of that breed's groups as much as genetics. Furthermore, some breed associations bred their sires to cows of the their breed, while other breeds used cows of breeds believed to excel for tenderness. There is no reasonable statistical approach to adjust for the nesting of contemporary group effects within breeds, nor for the differences in genetics of the dams.

## Phenotypic Results

Analysis of the phenotypic data showed significant variation among all breeds for shear force. Ranges of sire progeny means for shear force within breed varied from 1.90 to 6.62 lb., indicating that every breed has significant variation in tenderness, and opportunity to improve. Warner-Bratzler shear force was strongly correlated with trained sensory panel tenderness scores, but the relationship between shear force and marbling score was weak at best. These results indicate that Warner-Bratzler shear force is an excellent predictor of consumer experience for tenderness, and that selection for marbling alone will not significantly improve tenderness. Heritability estimates for shear force were variable across breeds, but were moderate or higher in some breeds, consistent with other studies. If adequate amounts of phenotypic shear force data can be collected, significant improvement in tenderness is possible through selection.

Greater than 7200 progeny of 279 sires representing 14 breeds were harvested for collection of carcass and meat quality data. There were 7015 progeny used in carcass and WBSF analyses and 2401 progeny with sensory panel data. Carcass traits of the project cattle were representative of the beef industry with average hot carcass weight of 771 lb, fat thickness of 0.48 in, ribeye area of 13.2 in<sup>2</sup>, yield grade of 2.8 and marbling score of Small<sup>20</sup>. Although the cattle were young, mostly from AI sires, and managed optimally, 26% of the steaks had WBSF values > 11.0 lb (considered tough) and 19.4% had sensory panel tenderness scores of < 5.0 (5 = slightly tender; 4 = slightly tough).

Data from four of the breeds for shear force and marbling were used to estimate heritabilities and genetic correlations (Minick et al., in press). In these data, the phenotypic correlation between shear force and sensory score overall tenderness is high, indicating shear force is a useful predictor of consumer satisfaction. Furthermore, shear force is a heritable characteristic, and hence, will respond to selection. Therefore, EPDs for shear force can be computed for all sires in the CMP and can be generated on an ongoing basis if new phenotypic information is generated.

By April 2004, four breeds (Simmental, Simbrah, Shorthorn, and Hereford) had calculated and publicly released shear force EPDs on over 200 sires. Breeds not calculating or not releasing shear force EPDs report several reasons for not doing so. The most common reason cited is that there appears to be limited opportunity to collect shear

force data on progeny of new sires. While three of the four largest packers, as well as many smaller plants were very accommodating of this project, there seems to be less willingness by packers to allow steak retrieval for shear force analysis in the future. Accordingly, a release of shear force EPDs might be limited to mostly project sires, with the many of the newest sires in the breed unevaluated. However, such an analysis would describe the amount of variation in the breed, and identify sire lines that are more or less favorable for this important, heritable trait. While some project sires may be past the time when they are widely used, their sons and grandsons are now some of the most important sires in their respective breeds. Some project sires have thousands of recorded progeny in their respective breed associations.

## Evaluation of Marker Data

The objectives of the DNA component of the CMP were to validate and characterize 11 quantitative trait loci (QTL) for carcass and meat quality traits that were discovered in previous beef checkoff-funded research at Texas A&M University (the Angleton Project). The Angleton Project used a resource population comprised of greater than 600 progeny in large full-sib families (produced by embryo transfer) of a double reciprocal backcross design between Angus and Brahman.

Validation of QTL discovery projects is necessary because of the substantial risk of false positive results, even in large, well-designed projects. However, failure to validate a QTL does not necessarily imply that the QTL was a false positive; it may simply have been segregating in the resource population used for discovery, but not in the population used for validation. In other words, it is possible that in the Angleton population, all Angus were homozygous for one allele, and all Brahmans were homozygous for a different allele, so segregation was found in the designed crosses, but might not be found in any single breed in the CMP. Characterization of QTL involves determining which QTL are segregating in each breed, how many sires per breed appear to be segregating each QTL, and which traits are affected by each QTL. In other words, characterization seeks to determine the potential utility of the QTL in genetic improvement programs.

Segregation of QTL occurs within paternal half-sib families. Some sires segregate QTL, but many are homozygous at the QTL. The QTL analysis involved 70 sires with 2516 progeny with DNA marker data and phenotypes in 210 contemporary groups. There were 1458 progeny with sensory data and DNA marker data.

While preliminary analyses appear promising, at the time this article was written, the marker data collected in CMP was undergoing final analysis. Those results will be presented in the Thursday morning general session, with details to follow in the Emerging Technologies committee meeting. As that information becomes available, this

document will be updated with that information and will be available on the BIF website.

## **Economic Considerations**

The economic portion of the project also revealed useful findings. Improvement of tenderness has the potential to significantly increase market price, quantity and revenue of fresh beef sales. Improvement of tenderness both increases the value of beef and stimulates greater demand leading to higher consumer expenditures. A ten percent improvement in tenderness would result in approximately a one percent improvement in industry revenue, although the cost of such an improvement is unknown.

## **How Can Cattle Breeders Use the Results?**

The most direct and immediate way is for breed associations to compute and publish EPDs for shear force and sensory traits from the data generated by the CMP. Use of the DNA results is contingent on a partner commercializing tests based on the QTL. This could be done either in the form of direct tests or linked markers.

The existing linked markers could be used to select among progeny and grandprogeny of the 70 legacy bulls that were evaluated in the DNA component of the CMP. While this may seem to be a small number of bulls, these 70 bulls were very influential in their respective breeds and have produced a tremendous number of progeny and grandprogeny.

Linked markers could be commercialized quickly with relatively little development cost and could be used to improve accuracy of selection among progeny of the CMP sires. The technology would probably be used effectively by only a small proportion of the breeders in any breed, but the improved selection response in those herds would likely benefit the entire breed. Some additional development of statistical/computational methods would be required to include marker information in national cattle evaluation.

This approach would also require continued collection of phenotypes and marker data on progeny groups for the approach to be sustainable long term. However, fewer phenotypes would be required than without the markers and accurate genetic evaluations could be obtained earlier in life (prior to breeding decisions).

Although there are several scenarios under which the CMP QTL could be used as linked markers, most commercial interest is in association or functional tests. Therefore, the most promising QTL should be converted into association tests based on single nucleotide polymorphisms. While this is no small task, the large number of animals measured with DNA samples represents an excellent population for further discovery and refinement.

## **Conclusions**

The primary objectives of the NCBA Carcass Merit Project were to collect data for carcass merit EPDs, including tenderness, and to attempt to validate previously discovered QTL for carcass merit in the U.S. cattle population. Both of those objectives were accomplished, but much work remains to be done in these areas.

Besides the stated objectives, several other benefits have resulted from the Carcass Merit Project, both tangible and intangible. The project represents a considerable cooperative effort among U.S. beef breed associations. Experiences gained and goodwill generated in this project will facilitate further cooperative research by breeds, benefiting the entire beef industry. The project has raised the awareness of marker-assisted selection and genomics in the beef industry, and has tested and refined methodology to evaluate results of such studies. The considerable publicity received and educational efforts undertaken by the project have moved the industry closer to embracing selection aided by DNA tests, and have improved the understanding of issues with these technologies. In addition, the project has revealed the considerable cost and coordination required for shear force data collection.

Likely the most significant result of the Carcass Merit Project is the sizeable database of phenotypic information and DNA samples stored for a wide cross section of US beef germplasm. Already, data and samples stored by breed associations are being used to validate gene tests marketed to cattle producers. The potential to further mine this resource to refine the positions of QTL and create association tests for them should accelerate the genetic improvement of carcass merit in beef cattle. The building of a large unbiased multi-breed database to use in discovery and validation alone justifies the industry's investment in this project, and stands to be the project's greatest legacy.