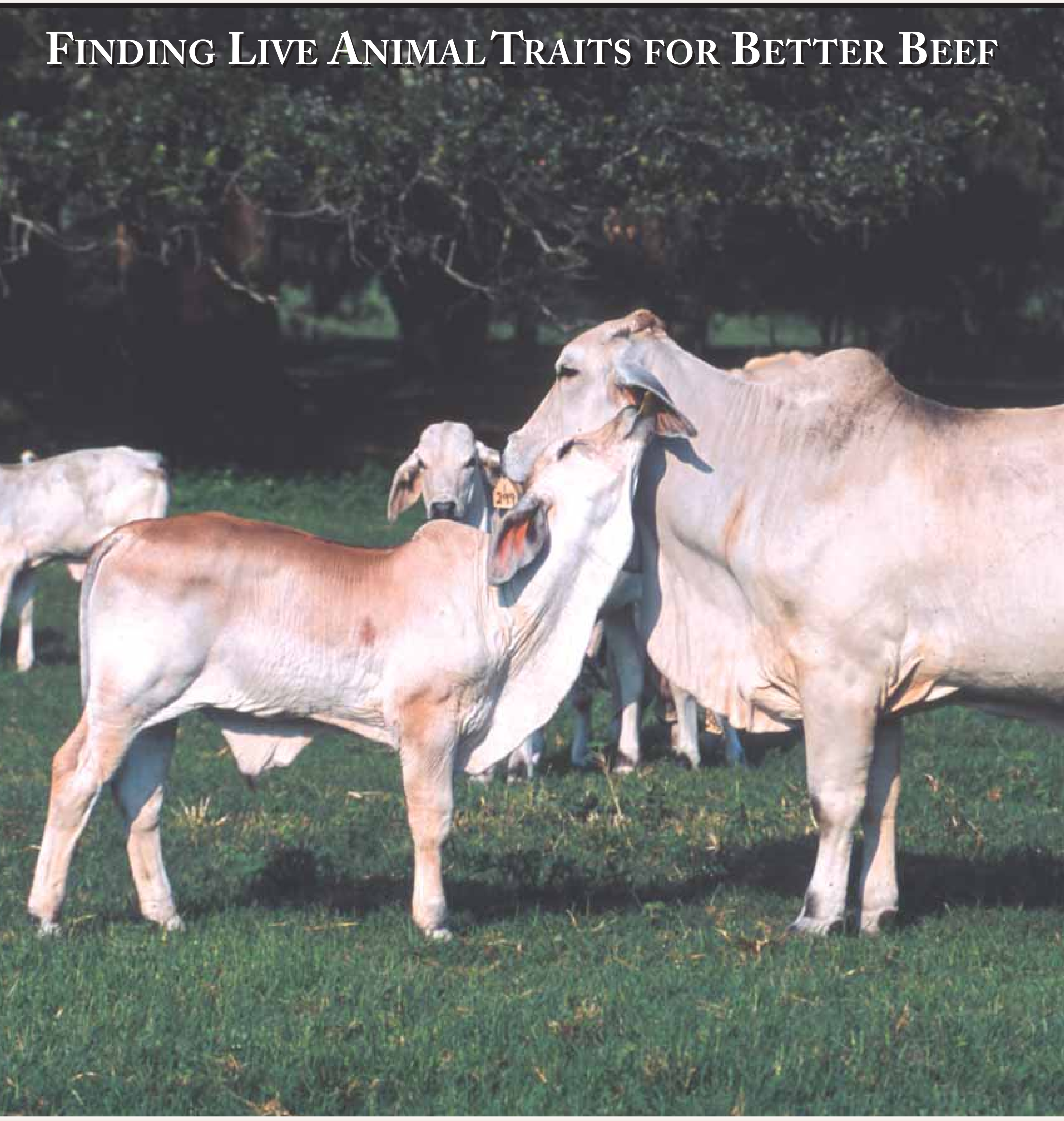
Carcass Merit Project

Finding Live Animal Traits for Better Beef

Research & Knowledge Management

Funded by The Beef Checkoff

Finding Live Animal Traits for Better Beef



RESEARCH R&KM KNOWLEDGE MANAGEMENT

From 1980 to 1997, demand for beef decreased by approximately 50 percent, according to data collected for the Cattlemen's Beef Board (CBB). This dramatic downward decline in the beef demand index heightened the industry's awareness of the need to provide a more consistent product for consumers. Industry efforts, including research, product development and more targeted marketing efforts have helped reverse that downward trend; in fact, between 1998 and 2003, beef demand increased 16.2 percent.

In order that beef demand continues to increase, it is important to identify factors that affect tenderness and beef palatability to achieve maximum consumer satisfaction. Past research conducted by the National Cattlemen's Beef Association (NCBA) and funded with beef checkoff dollars established a link between beef tenderness and consumers' eating satisfaction. However, the National Beef Tenderness study, published in 1999, found that, except for the tenderloin, most beef cuts had considerable variation with regard to tenderness. The study concluded that such variation in quality meant consumers found a significant percentage of beef cuts unacceptable.

While tenderness can be, and often is, improved through technologies applied post-mortem, the entire industry could benefit tremendously from producing cattle proven tender prior to harvest.

> **While post-mortem technology alone could reduce the tenderness failure rate of top sirloin steaks to 18 percent, selective breeding with the top 25 percent of sires with desirable carcass traits combined with post-mortem technology could reduce the failure rate to 5 percent.**

In fact, Colorado State University research indicated that while post-mortem technology alone could reduce the tenderness failure rate of top sirloin steaks to 18 percent, selective breeding with the top 25 percent of sires with desirable carcass traits combined with post-mortem technology could reduce the failure rate to 5 percent (Tatum, 1997). Furthermore, genetic improvements are permanent, whereas most post-mortem interventions add cost perpetually. Therefore, seedstock and commercial producers should be provided selection tools to enable them to consistently identify breeding animals that produce progeny with desirable tenderness traits.

In order to develop these genetic selection tools for tenderness, NCBA initiated the checkoff-funded Carcass Merit Project (CMP) in 1999. The goals of the project were to validate previously discovered Quantitative Trait Loci (QTL) for important carcass and consumer-satisfaction traits such as marbling, tenderness and meat composition, and collect carcass data to enhance existing industry knowledge and build a database from which breeds could develop Expected Progeny Differences (EPDs) for tenderness. In addition, economic analyses were conducted to predict increases in beef consumption, and subsequently beef prices, as a result of tenderness improvement. This information should help fill knowledge gaps that exist between pre-harvest management practices and total product quality.

By establishing linkages between research areas, and unearthing discoveries related to genetic selection for tenderness, the Carcass Merit Project is arguably one of the most important projects undertaken by the beef industry in recent years.

Project Objectives

The CMP project first sought to determine how highly influential sires of various breeds performed in tenderness and sensory panel tests by collecting carcass data on their progeny. This allowed breed associations to begin to develop tenderness EPDs. Concurrently, the project validated previously discovered QTL for tenderness. An analysis of the costs and benefits of developing and implementing such EPDs helped put the study's results in economic perspective.

Specifically, project objectives included:

1. Develop procedures for collection of information necessary to develop EPDs for carcass merit traits, particularly tenderness EPDs.

2. Collect carcass data and measure tenderness of the longissimus thoracis using Warner-Bratzler shear force (WBSF) of contemporary groups of progeny from multiple sires within each breed.

3. Measure sensory attributes of striploins (longissimus dorsi) from a sample of contemporary groups included in DNA marker validation.

4. Validate DNA markers to be used in marker-assisted selection programs for improvement of carcass merit traits.

5. Measure direct costs of implementing EPDs for carcass merit traits to the existing genetic selection programs and combinations of management and genetic improvement of carcass merit traits.

6. Measure opportunity costs and returns of implementing EPDs for carcass merit traits to the existing genetic selection programs and combinations of management and genetic improvement of carcass merit traits.

Materials and Methods

Selection and testing of progeny

Thirteen breed associations (representing 14 breeds) provided over 8,500 progeny of the most widely used sires within their respective breeds, primarily from commercial cowherds, for this research. The final analysis excluded data from 883 progeny because of incorrect animal or carcass identification. One or more reference sires of each breed were used in each test herd to tie contemporary groups together within breeds. The number of progeny included in the study from each breed was dependent on registration numbers, where breeds with larger numbers of animals registered had a greater number of progeny. Each breed association coordinated the following aspects of the study for its respective breed:

1. *Sire selection*
2. *Progeny testing*
3. *Synchronization and breeding*
4. *Collection of blood samples*
5. *Selection of feedlots and feedlot regimen*
6. *Slaughter endpoint designation*
7. *Tenderness EPD development*

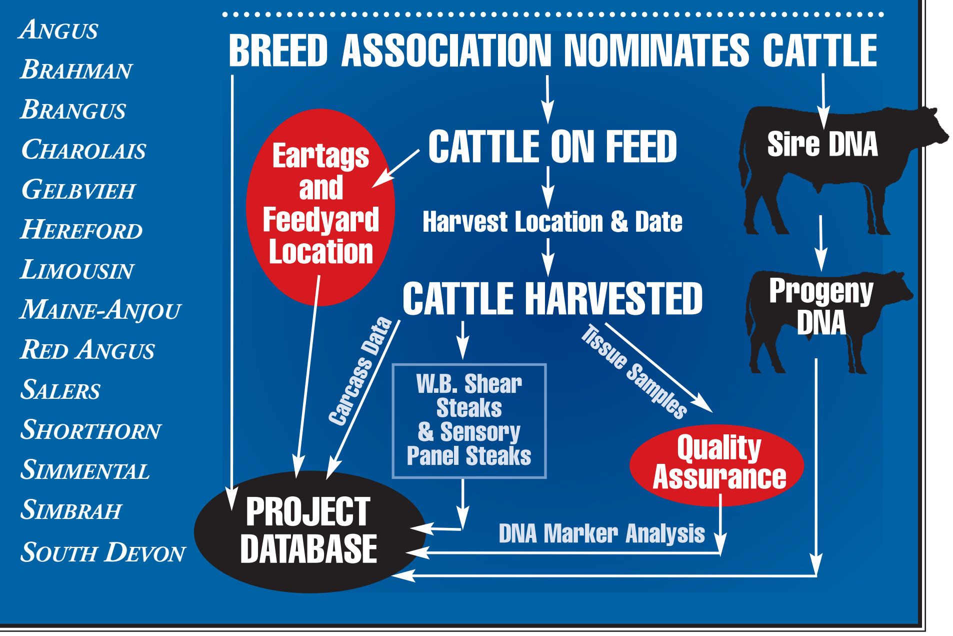
Selection and testing of sires

Each breed association entered sires for both the DNA and EPD portions of the project. The total number of sires per breed with progeny data in the study, ranged from seven to 79.

Breed associations designated DNA sires, with the objective of selecting bulls that were used widely and expected to have a lasting impact on the breed. To ensure analytical power for an accurate test of QTL segregation, project guidelines specified first, that each breed designate 10 bulls as DNA sires and secondly, that each DNA sire have 50 progeny by the conclusion of the five-year study period. For EPD sires, the target number of progeny per sire was 25.

FIGURE 1:
CARCASS MERIT PROJECT OVERVIEW, AND PARTICIPATING BEEF BREEDS.

Note: All U.S. beef breed associations were invited to participate.



Researchers obtained carcass data and WBSF values for steaks from progeny of all sires. Steaks from progeny of up to five of the bulls designated as DNA sires within each breed were also evaluated by trained sensory panels.

Prior to, or upon entering the feedlot, two blood samples of each progeny of DNA sires were obtained and sent to Texas A&M University and MMI Genomics for DNA analysis. One set of samples was stored as a back up and for quality assurance purposes, with the remainder of the sample to be available for future validation projects as the industry discovers additional carcass merit QTL. Project managers advised breed associations to collect additional blood samples to keep on file for their own future validation studies; many associations have thus compiled samples for independent validation of other tests.

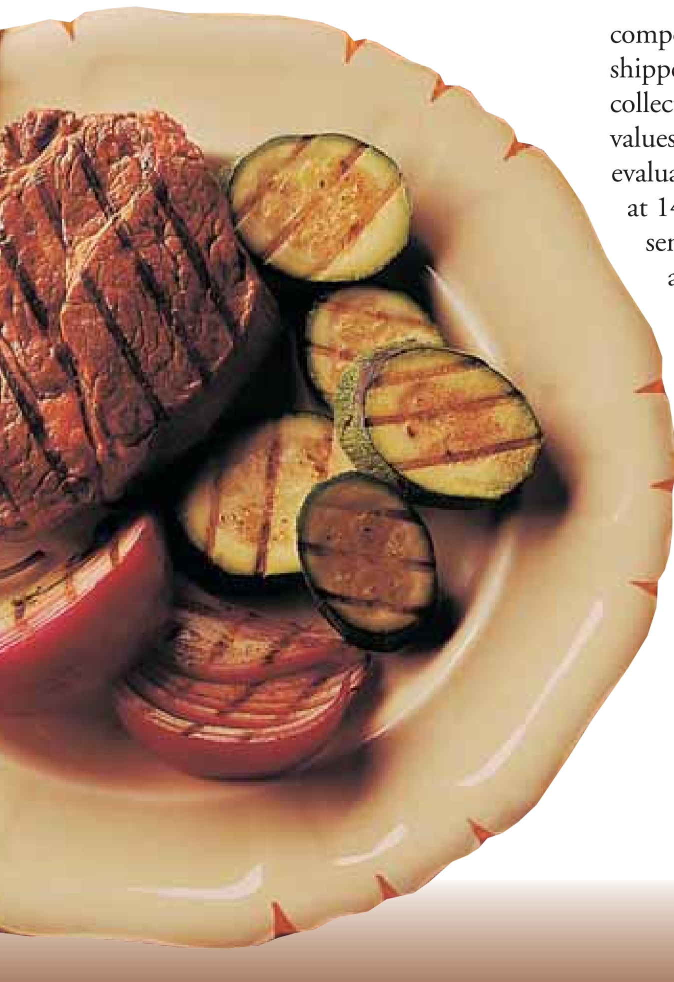
Researchers also analyzed semen samples from the DNA sires to identify DNA markers that would efficiently track segregation of the QTL within their progeny. The DNA markers were used to validate the association of particular QTL with shear force measures, sensory panel traits and carcass traits as identified at Texas A&M University Experiment Station, USDA-Cooperative State Research, Education and Education Service (CSREES), Texas A&M and check-off funded "Angleton" Genome Mapping project.

The project's design did not allow for any across-breed comparison, as genetic differences between commercial cow breeds and the different environments in which calves produced; did not allow for it. This was in accordance with the original agreement with the breed associations.

Phenotypic analysis

Researchers obtained muscle tissue samples from individual progeny at the time of harvest for backup DNA analyses and animal identity verification. Carcass data, including carcass weight, ribeye area, fat thickness, marbling, and percent internal fat were collected. In addition, researchers obtained one steak from each progeny of every sire and two steaks from each progeny of the DNA sires designated for the sensory panel component of the project. Steaks were shipped to Kansas State University to collect Warner-Bratzler shear force values and for trained sensory panel evaluation. Shear steaks were cooked at 14 days post-mortem, whereas sensory panel steaks were frozen and later thawed for trained sensory panel evaluations.

Considerable variation in Warner-Bratzler shear force exists between individual strip loin steaks taken from young cattle.



Database maintenance

Cornell University researchers created and maintained a secure database to ensure accessibility to the information collected. Breed associations took responsibility for developing carcass, shear force and/or sensory panel EPDs. Several breed associations have already used project data toward this end. The breed associations, NCBA, and the checkoff program own all carcass, shear force and sensory panel data. Although the marker identities, genotypes produced by scoring the markers and protocols for marker identification remain the property of Texas A&M University, NCBA, and the checkoff program, this information, as well as the phenotypic data, continues to be provided to cooperating breed associations for use in computing EPDs for related carcass merit traits.

Economic analysis

Colorado State University researchers conducted the project's economic analysis in three steps, with two distinct research outputs–an estimation of the increase in prices and increase in beef consumption following improvements in tenderness.

The percentage change in the price of beef when tenderness changes by a given amount; also known as price flexibility with respect to tenderness was determined. Secondly, the research generated an estimate how consumer beef expenditures are affected when demand for beef changes, also known as elasticity of expenditures with respect to demand. Finally, the economic analysis combined the first two pieces of information to calculate the net effect of improving tenderness on market prices in a partial equilibrium model.

Results from Phenotypic Studies

The industry measures tenderness by WBSF and sensory analysis testing. Overall tenderness is directly related to myofibrillar and connective tissue content. The WBSF test measures tenderness by the force required to shear through the cooked muscle, the higher the shear value the less tender the product. Sensory panel analysis factors in other palatability traits such as juiciness and flavor as a measure of the overall palatability.

Research has shown that a WBSF value of ≥ 10.00 lb. results in a sensory panel score of "slightly tough or tougher." Data from the Carcass Merit Project demonstrated that a WBSF value of ≥11.0 lb. generally resulted in a sensory panel tenderness score of slightly tough or tougher. In this analysis, 26.2 percent of study cattle had WBSF values ≥11.0 lb. and 19.4 percent had sensory panel tenderness scores of slightly tough or tougher.

- The phenotypic range of WBSF means for sires ***within*** breeds ranged from 1.7 lb. in the least variable breed to 6.6 lb. in the most variable breed.
- The phenotypic range in the mean WBSF values ***across*** breeds was quite large at 8.9 lb.
- The range in the mean WBSF values ***among*** sires ***across*** breeds was a dramatic 13.8 lb.

These results indicate that considerable variation in Warner-Bratzler shear force exists between individual strip loin steaks taken from young cattle, even though those cattle have been managed optimally.

Sensory panel

On an eight-point scale with eight being extremely tender and one being extremely tough, the range in sensory panel tenderness means:

- for sires within breeds ranged from 0.47 in the breed with the least variation to 1.24 in the breed with the most variation.
- across breeds was 2.96
- among sires across breeds the range was 3.22.

The range for sensory panel flavor scores for sires within breeds was quite small, except for one breed. The range for sensory panel juiciness scores for sires within breeds was slightly larger than for flavor, but not as great as for tenderness. The rankings of breeds for sensory panel tenderness, flavor and juiciness from most tender, most flavorful, and most juicy were quite dissimilar, except that two breeds ranked last for almost all traits.

Heritabilities & Genetic Correlations

Data from 2,615 progeny of 70 sires were used to estimate heritabilities and genetic and phenotypic correlations **(Table 1)** using an animal model accounting for relationships among sires (dams were assumed to be unrelated). The identity and paternity of these carcasses were verified by DNA marker data. The genetic correlations between WBSF and the sensory panel tenderness scores were highly negative. This negative correlation is favorable, indicating that lower WBSF measures are indicative of higher sensory panel scores for tenderness. Thus, Warner-Bratzler shear force values are a useful predictor of consumer satisfaction. The genetic correlations between marbling and sensory tenderness were also favorable, but of less magnitude. Furthermore, WBSF is a heritable characteristic, and hence, it will respond to selection. As a result, EPDs for WBSF can be computed for all sires in the research and can be generated on an ongoing basis if new phenotypic information is generated.

TABLE 1

Heritabilities and Genetic and Phenotypic Correlations.

Trait Name	Trt	WBSF	MT	CT	CL	FL	JC	MB	FT	KPH	HCW	REA
Shear Force	WBSF	**0.43**	0.99	0.79	0.41	-0.65	-0.65	-0.56	-0.28	0.47	0.02	0.23
Myofib Tnd	MT	-0.68	**0.29**	0.92	-0.26	0.79	0.74	0.38	0.14	-0.86	0.20	-0.51
Cn Tiss Tnd	CT	-0.63	0.82	**0.25**	-0.24	0.74	0.62	0.19	0.22	-0.82	0.38	-0.53
Cooking Loss	CL	0.27	-0.06	-0.04	**0.14**	-0.16	-0.21	-0.72	-0.16	-0.02	0.16	0.28
Flavor	FL	-0.14	0.24	0.23	-0.03	**0.18**	0.98	0.35	-0.23	-0.61	-0.17	-0.63
Juiciness	JC	-0.05	0.26	0.14	0.02	0.43	**0.29**	0.56	-0.11	-0.39	-0.14	-0.66
Marbling	MB	-0.23	0.21	0.13	-0.14	0.14	0.20	**0.76**	0.20	-0.19	-0.27	-0.36
Fat Thick	FT	-0.10	0.07	0.09	-0.08	0.05	0.02	0.22	**0.24**	0.37	0.27	-0.19
Internal Fat	KPH	0.01	-0.03	-0.02	-0.04	-0.06	-0.08	0.03	0.13	**0.42**	0.76	0.37
Hot Carc Wt	HCW	-0.07	0.12	0.15	0.02	0.03	-0.01	0.10	0.31	0.19	**0.24**	0.24
Ribeye Area	REA	0.07	-0.06	-0.04	0.08	-0.05	-0.08	-0.04	-0.11	0.06	0.41	**0.30**

Genetic correlations are above the diagonals in black. Heritabilities are on the diagonals in bold black. Phenotypic correlations are below the diagonals in blue.

Results from DNA Marker Validation

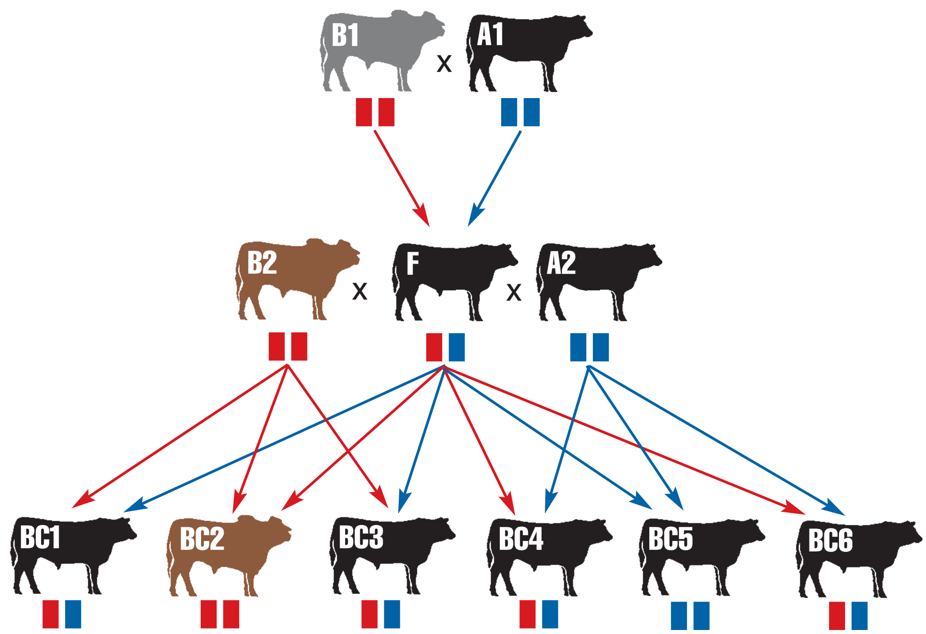
The objectives of the DNA component of the CMP were to validate and characterize 11 QTL for carcass and meat quality traits that were discovered in previous research. The checkoff funded Angleton Project conducted at Texas A&M University used a resource population of greater than 600 progeny in large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

Validation of QTL discovery projects is necessary due to the substantial risk of false positive results, even in large, well-designed studies. However, failure to validate a QTL does not necessarily imply that the QTL was a false positive; it may simply have been segregated in the resource population used for discovery, but not in the population used for validation.

Characterization of QTL involves:

1. **Determining which QTL are segregating in each breed**
2. **How many sires per breed appear to be segregating each QTL**
3. **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 loci. As stated previously, the QTL analysis involved 70 sires with 2,615 progeny with DNA marker data and phenotypes in 210 contemporary groups. There were 1,458 progeny with sensory data and DNA marker data.

To test the significance of the QTL effects, traits were grouped into pairs according to their biological relationships. A two-trait random regression model that accounted for sire and contemporary group effects in addition to the QTL effect was used in this analysis. Initially, textbook values for significance were used, but when significant results were found, permutation tests were used to more accurately determine level of significance. Significance levels are the probabilities that the variation accounted for by the QTL are is due to chance (probability of obtaining a spurious result). Therefore, smaller numbers indicate stronger evidence supporting the effect of the QTL on a trait.

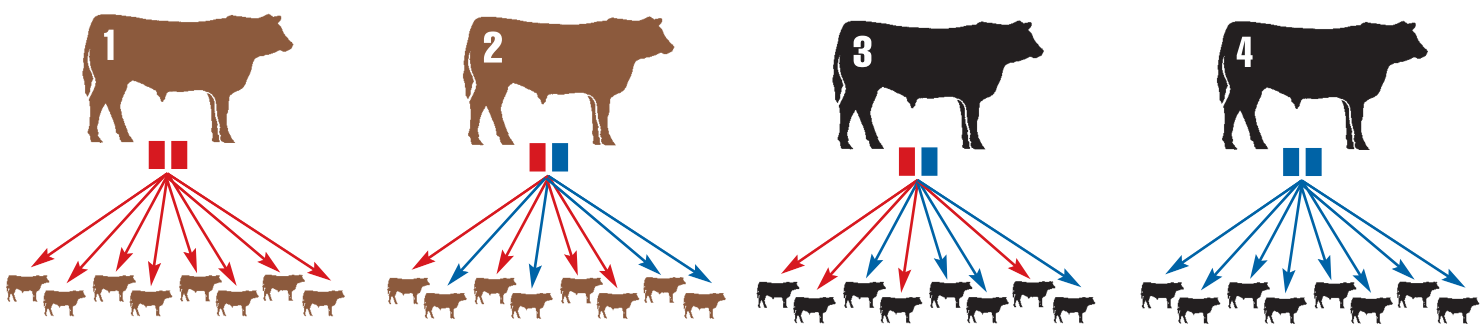


TABLE 2

Significance levels of QTL effects from multiple trait hypothesis tests.[a]

Trait	Q1	Q2	Q3	Q4	Q5	Q6	Q7	Q8	Q9	Q10	Q11
Shear Force	0.5	0.5	0.5	0.32	0.25	**0.008**	0.5	**0.040**	0.16	0.49	0.5
Overall Tnd	0.5	0.5	0.5	0.37	0.44	**0.001**	0.5	**0.030**	0.49	**0.004**	0.5
Fat Thickness	0.1	0.5	0.48	**0.043**	**0.030**	0.12	0.2	0.5	0.1	0.34	0.33
Marbling	0.15	0.4	0.44	0.31	0.32	0.11	0.12	0.5	0.06	0.37	**0.002**
Ribeye Area	0.5	0.5	0.18	0.44	0.32	**0.011**	**0.008**	**0.037**	0.5	0.5	0.5
Hot Carc Wt	0.5	0.5	0.19	0.47	0.5	0.47	**0.006**	**0.002**	0.5	0.5	0.49
Flavor	0.5	0.45	0.5	0.5	0.28	0.3	0.34	**0.022**	0.32	0.11	0.33
Overall Tnd	0.5	0.29	0.5	0.5	0.45	**0.01**	0.35	**0.015**	0.5	0.24	0.5
Juiciness	0.5	0.33	0.46	0.11	0.5	0.107	**0.024**	0.49	0.5	**0.050**	0.41
Overall Tnd	0.5	0.37	0.49	0.31	0.5	**0.021**	0.45	0.09	0.5	0.14	0.46

[a] ***Significance levels expressed to one or two decimal places are textbook values, those expressed to three decimal places are from permutation tests.***

Several QTL showed significant effects for two or more traits. QTL 6 had significant effects on shear force, overall tenderness, and ribeye area. QTL 7 was significant for ribeye area, hot carcass weight, and juiciness. QTL 8 had significant effects on shear force, overall tenderness, ribeye area, hot carcass weight and flavor. QTL 10 had significant effects on overall tenderness and juiciness. In addition, QTL 4 and 5 had significant effects on fat thickness, and QTL 11 had noteworthy effects on marbling.

Random QTL analysis can also explain the amount of variance in phenotypes attributable to the QTL. This can be most easily interpreted as the proportion of phenotypic variance explained by the QTL, just as heritability is the proportion of phenotypic variance explained by breeding value. The amount of variance explained indicates the magnitude and practical significance of the QTL effect.

Table 3 contains the estimated percentages of phenotypic variance accounted for by each of the 11 QTL for each trait. As is the case for all analyses reported herein, each QTL was analyzed separately; no multiple QTL analyses have been performed. Values greater than four percent are indicated in blue. As expected, most of the QTL with significant evidence of segregation account for some of the variance in a number of traits. Typically, one or a few closely related traits will be most influenced by a QTL and a number of other traits will be influenced to a lesser extent.

TABLE 3

Percentage of phenotypic variance accounted for by each QTL.

Trait Name	Q1	Q2	Q3	Q4	Q5	Q6	Q7	Q8	Q9	Q10	Q11
Shear Force	1	0	1	3	3	**12**	0	**6**	3	1	0
Overall Tnd	0	1	1	1	0	**10**	2	**8**	0	4	0
Myofib Tnd	1	2	0	1	0	**9**	2	**8**	0	4	0
Cn Tiss Tnd	3	1	0	0	0	**12**	4	**8**	0	2	0
Cooking Loss	4	2	**5**	0	3	1	0	**0**	2	2	1
Flavor	1	1	0	3	2	1	3	3	2	**5**	3
Juiciness	0	4	1	**6**	0	**6**	**7**	0	0	**5**	3
Marbling	1	2	2	2	1	4	4	1	4	1	**8**
Fat Thick	3	1	3	**5**	**6**	4	3	2	2	2	2
Internal Fat	0	**7**	0	3	**5**	2	0	1	2	1	1
Hot Carc Wt	1	0	2	0	0	2	**6**	**10**	0	1	3
Ribeye Area	0	0	4	2	3	**7**	**7**	3	0	1	1

Whenever QTL appear to have effects on multiple traits, it is useful to know whether the allele that is favorable for one trait is favorable or unfavorable for others. To answer this question, correlations among the effects of QTL 6, 7, and 8 are reported in Tables 4, 5, and 6, respectively.

QTL 6 was shown in **Table 2** to have significant effects on shear force, overall tenderness, and ribeye area. In **Table 4**, the correlation between the effects of QTL 6 on shear force and overall tenderness is –0.96. This means the allele that increases shear force decreases tenderness score, where higher tenderness scores indicate greater tenderness. Therefore, selecting for the favorable allele at QTL 6 for shear force will also improve overall tenderness. In contrast, the correlation between QTL 6 effects on shear force and ribeye area is 0.17. Thus, the allele that decreases shear force also decreases ribeye area, but only to a minor extent. This suggests that the effect of QTL 6 on ribeye area may be due to a different gene, in the same chromosomal region as, but some distance away from the gene that causes the effect of QTL 6 on tenderness. If this is the case, it should be possible to select for favorable effects of both genes.

TABLE 4

Correlations among effects of QTL 6 (proportion of phenotypic variance accounted for by QTL 6 on the diagonals).

Trait Name	Trt	WBSF	OT	MT	CT	CL	FL	JC	MB	FT	KPH	HCW	REA
Shear Force	WBSF	**0.12**											
Overall Tnd	OT	-0.96	**0.10**										
Myofib Tnd	MT	-0.99	1.00	**0.09**									
Cn Tiss Tnd	CT	-0.89	0.95	0.96	**0.12**								
Cooking Loss	CL	0.67	-0.86	-0.84	-0.76	**0.01**							
Flavor	FL	0.31	0.62	0.32	0.57	-0.57	**0.01**						
Juiciness	JC	0.11	0.04	0.04	0.27	-0.74	0.79	**0.06**					
Marbling	MB	0.23	-0.57	-0.41	-0.62	0.90	-0.85	-0.24	**0.04**				
Fat Thick	FT	-0.40	0.43	0.28	0.03	0.18	0.85	0.70	0.84	**0.04**			
Internal Fat	KPH	-0.79	0.93	0.99	0.70	-0.90	-0.43	-0.66	-0.19	0.41	**0.02**		
Hot Carc Wt	HCW	-0.23	0.18	0.02	-0.16	-0.51	-0.35	-0.45	0.87	0.54	1.00	**0.02**	
Ribeye Area	REA	0.17	0.09	0.14	0.06	0.47	-0.57	-0.77	0.35	0.91	0.21	-0.02	**0.07**

For QTL 7, shown in **Table 5,** the significant effects of increased ribeye area and carcass weight were the result of the same allele, but the allele that increased those traits tended to decrease juiciness. Especially encouraging was that correlations among effects of QTL 8 were all favorable, shown in **Table 6**. The allele that decreased shear force also improved overall tenderness, as expected, but was also associated with increased flavor, increased carcass weight and increased ribeye area.

TABLE 5

Correlations among effects of QTL 7 (proportion of phenotypic variance accounted for by QTL 7 on the diagonals).

Trait Name	Trt	WBSF	OT	MT	CT	CL	FL	JC	MB	FT	KPH	HCW	REA
Shear Force	WBSF	**0.00**											
Overall Tnd	OT	-0.99	**0.02**										
Myofib Tnd	MT	-0.99	1.00	**0.02**									
Cn Tiss Tnd	CT	-1.00	1.00	0.99	**0.04**								
Cooking Loss	CL	0.41	-0.33	-0.27	-0.98	**0.00**							
Flavor	FL	0.98	0.83	0.76	0.84	0.99	**0.03**						
Juiciness	JC	0.99	0.57	0.60	0.58	0.99	0.97	**0.07**					
Marbling	MB	-0.84	0.75	0.50	0.70	0.96	0.73	0.55	**0.04**				
Fat Thick	FT	0.95	1.00	0.92	1.00	0.99	1.00	1.00	0.81	**0.03**			
Internal Fat	KPH	0.95	1.00	1.00	1.00	0.99	0.99	1.00	0.54	0.98	**0.00**		
Hot Carc Wt	HCW	-0.98	0.48	0.24	0.60	-0.99	-0.23	-0.23	0.70	0.43	0.20	**0.06**	
Ribeye Area	REA	-0.99	0.20	-0.09	0.34	-0.99	-0.52	-0.52	0.56	0.12	-0.13	0.96	**0.07**

TABLE 6

Correlations among effects of QTL 8 (proportion of phenotypic variance accounted for by QTL 8 on the diagonals).

Trait Name	Trt	WBSF	OT	MT	CT	CL	FL	JC	MB	FT	KPH	HCW	REA
Shear Force	WBSF	**0.06**											
Overall Tnd	OT	-0.97	**0.08**										
Myofib Tnd	MT	-1.00	1.00	**0.08**									
Cn Tiss Tnd	CT	-0.81	0.97	0.99	**0.08**								
Cooking Loss	CL	0.90	-0.14	0.00	0.46	**0.00**							
Flavor	FL	-1.00	1.00	1.00	0.93	-0.99	**0.03**						
Juiciness	JC	-0.99	0.93	0.99	0.67	-0.99	0.83	**0.00**					
Marbling	MB	-0.99	0.95	0.87	0.67	-0.92	0.95	0.99	**0.01**				
Fat Thick	FT	-0.35	0.67	0.15	0.67	-0.58	1.00	0.99	0.78	**0.02**			
Internal Fat	KPH	0.69	-0.44	0.24	-0.63	0.85	-1.00	-0.99	-0.47	-0.87	**0.01**		
Hot Carc Wt	HCW	-0.49	0.66	0.61	0.70	-0.14	0.61	-0.60	0.97	0.18	0.01	**0.10**	
Ribeye Area	REA	-0.81	0.86	0.88	0.91	-0.52	0.55	-0.65	0.98	-0.30	0.48	0.93	**0.03**

Economic Analysis

The ultimate goal of the economic analyses was to estimate the increase in prices and the increase in consumption of beef following improvement in tenderness. In short, the research estimated the economic value of improving beef tenderness, without considering costs associated with making the improvements initially.

Beef tenderness valuation

Results of this portion of the Carcass Merit Project indicated a positive relationship between quality grade and retail price. Retail price also shows implicit responsiveness to WBSF measurements. Lower shear force values resulted in higher price. According to the model, variation in tenderness explains variation in actual retail price. Prices predicted by this research are shown with corresponding WBSF in **Figure 1**.

A 10 percent difference in the WBSF steaks is predicted to garner a 1.41 percent higher price in the Prime grade, a 2.49 percent higher price in CAB, a 3.55 percent higher price in Choice and a 4.20 percent higher price in Select.

A 1 percent improvement in tenderness is predicted to garner a 0.14 percent higher price for beef grading USDA Prime, a 0.25 percent higher price for Certified Angus Beef (CAB) products, a 0.36 percent higher price for USDA Choice products and a 0.42 percent higher price in Select steaks. A 10 percent difference in the WBSF steaks is predicted to garner a 1.41 percent higher price in the Prime grade products, a 2.49 percent higher price in CAB, a 3.55 percent higher price in Choice and a 4.20 percent higher price in Select.

The research also sought to determine if quality grades are adequate predictors of tenderness. The model indicated that quality grade does not appear to be an adequate predictor of WBSF / tenderness, although products labeled as CAB, when compared to quality grade itself, may have been more tender, on average. A low number of Prime-grade observations and the absence of cut specification may have biased these particular results.

IMPLICATIONS

The current beef quality grades, represented in this research by classification of products into USDA Prime, CAB, USDA Choice and USDA Select do not effectively segregate steaks by levels of tenderness, although CAB appears to be more tender on average than USDA Choice and Select. Retail prices respond to differences in quality grades, tenderness levels and the interaction of these two classification techniques. USDA Prime product was represented with few observations in the data set, which may have biased the results of Prime variables in the models.

This study determined that an improvement in average WBSF should add value to beef products. Improvement in tenderness of USDA Choice and Select beef has the potential to be especially valuable. When combined with tenderness measurements, the price flexibilities for USDA Choice and Select grades were the least inelastic.

Beef demand and consumer expenditures

Over time, the Beef Demand Index and real annual per capita beef expenditures appear to follow the same trends. Both the Beef Demand Index and real beef expenditures increased from the 1960s until the late 1970s and then declined into the 1990s, but at a decreasing rate. Models suggest that per capita real beef expenditures and the Beef Demand Index move in the same direction. In the long run, per capita real beef expenditures are related to changes in the Beef Demand Index.

Median age and median income were also used as co-variates in the time-series model. Changes in the beef demand index and real beef expenditures can be explained in part by an aging and wealthier U.S. population. An aging population demands less beef, while an increasingly wealthy population spends more on beef.

Improving beef quality should result in consumers spending more of their hard-earned dollars on beef.

A 10 percent improvement in beef tenderness results in approximately a 1 percent improvement to industry revenue. This translates to $150 to $170 million increase in revenue.

The models examining the dynamics between changes in the Beef Demand Index and real beef expenditures are relatively fragile. However, the models do suggest that, after accounting for increases in consumer income and changes in age demographics, a strong link between the strength of consumer demand for beef and the amount of income consumers are willing to spend on beef exists. The implication is that improving beef quality should result in an improved Beef Demand Index and consumers spending more of their hard-earned dollars on beef.

Market effects of improving tenderness

This study determined that tenderness has an implicit marginal value in beef, and consumer expenditures on beef are related to demand as measured by the Beef Demand Index. All of the results indicated an increase in the equilibrium price, quantity, and industry revenue given a percentage increase in average tenderness. By improving the average tenderness level of beef available to consumers, the industry should see an increase in the price of beef and an overall increase in consumer expenditures.

The final portion of this study examined how improving tenderness might affect the industry. The study developed an empirical model to determine possible impacts of a change in average tenderness level on market price, quality and industry revenue. Previous research related the percentage change in the Beef Demand Index to a one percent change in WBSF values. This study calculated the percent change in price, quantity and revenue, as well as the dollar change in revenue for four combinations of supply and demand scenarios.

Results indicated that improving average tenderness level increased average price of products. Improvement in tenderness resulted in both improvement in average value of Choice and Select products and increases in consumer expenditures. **Figure 2** illustrates the maximum percent price and quantity increases in USDA Choice and Select fresh beef expected for given percent improvements in WBSF. The maximum percent and dollar revenue improvement to Choice and Select fresh beef expected for a given percent increase in tenderness can be found in **Figure 3**. A 10 percent improvement in average tenderness yields approximately 1 percent, or a $150 to $170 million increase in revenue.

This research determined that improvements to average tenderness levels would create significant improvements in market equilibrium price, quantity and revenue of Choice and Select fresh beef. The market benefits from two surges when tenderness is improved. First, the value of more tender products increases, and second, demand increases, leading to higher consumer expenditures. A 10 percent improvement in beef tenderness results in approximately 1 percent improvement to industry revenue. This translates to approximately $150 to $170 million.

Further sensitivity analysis on each variable used in this simulation could be productive. This analysis also ignored any costs involved in improving tenderness. Many methods to improve tenderness exist, and further research on how costs of preferred strategies would affect these results is also recommended.

FIGURE 1: Prices predicted with corresponding WBSF

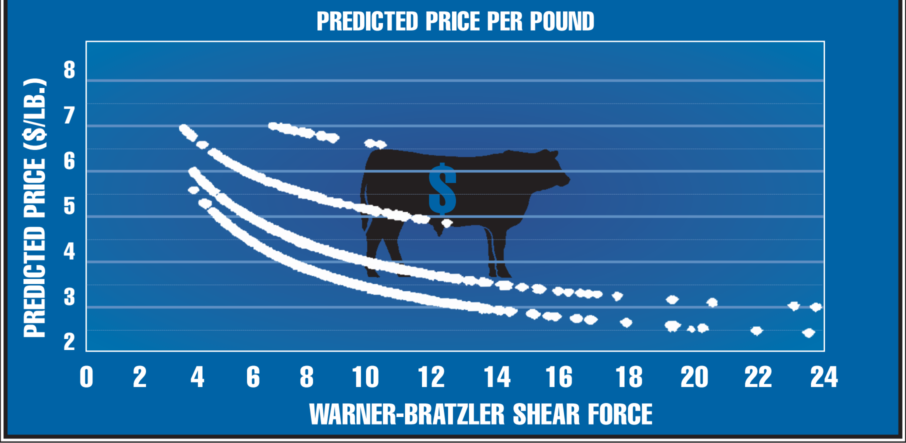


FIGURE 2: Price Flexibility Illustration

Maximum percent and dollar revenue improvement for a given percent improvement in tenderness

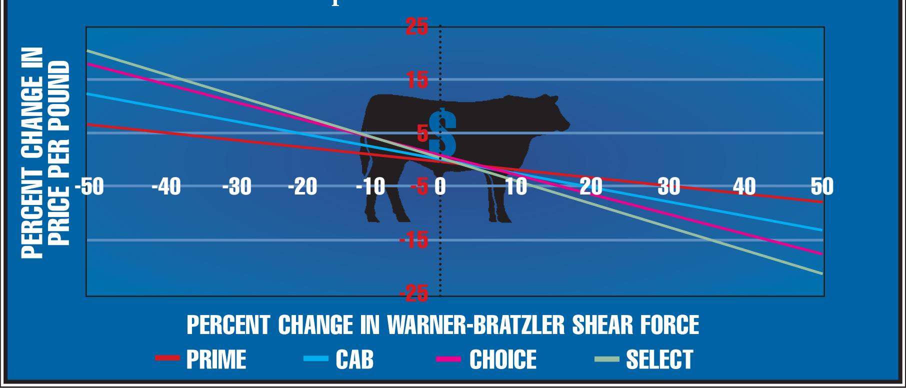
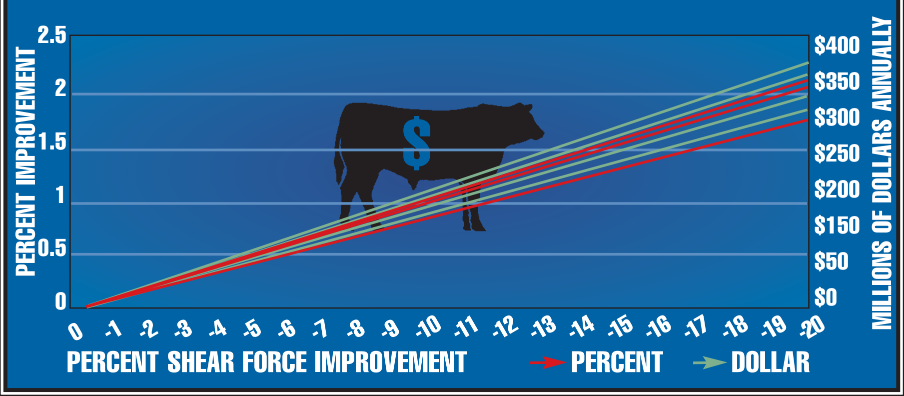
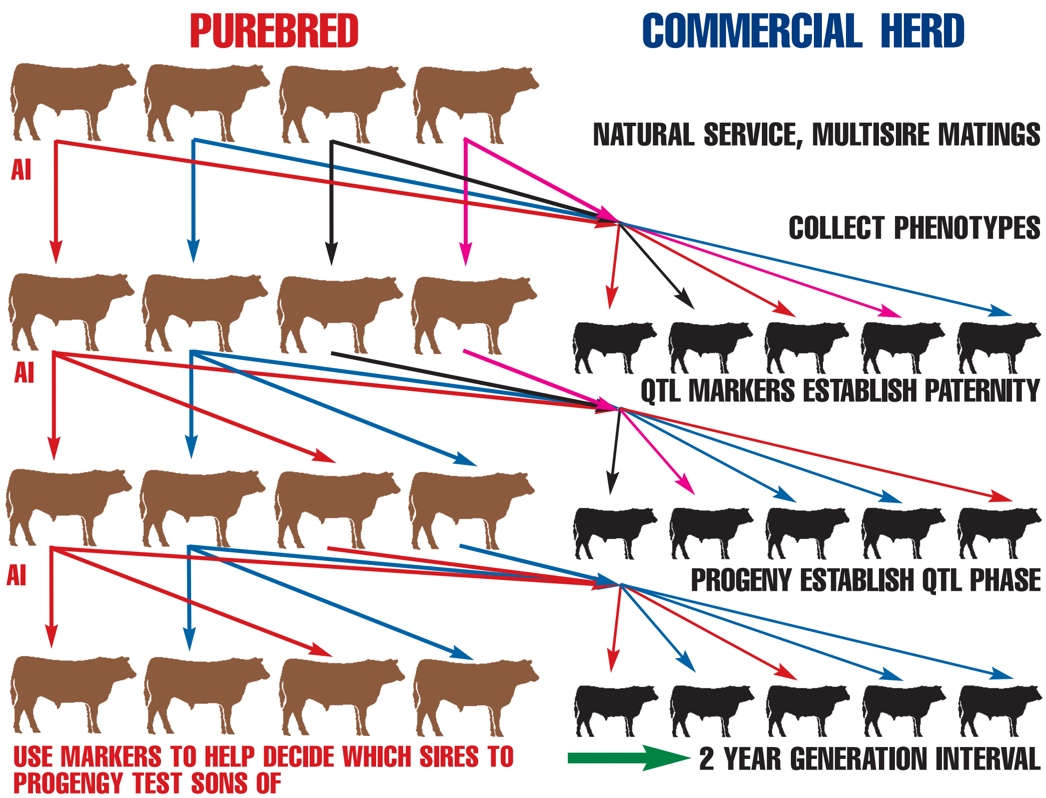


FIGURE 3: Maximum percent and dollar revenue improvement for a given percent improvement in tenderness



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 Carcass Merit Project.

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. For example, in two breeds, the total number of sons, daughters and grandprogeny left by the 20 legacy bulls in those breeds is currently 81,000, 103,000 and 385,000, respectively.

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 Evaluations.

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).

The linked markers from the CMP could be used effectively in intensive breeding programs for tenderness. Young bulls would be progeny tested in multiple sire matings to commercial cows and, at the same time, would be mated to seed-stock cows to produce the next generation of herd sire candidates. Some of the CMP markers would be used to determine paternity of the multiple sired calves. This would not necessarily be any more expensive than a paternity test based on anonymous DNA markers and should be cost-competitive with progeny testing by artificial insemination matings. The QTL effects of the sires for the markers used in paternity testing could be estimated at no additional cost and those estimates could be used with marker data on seedstock progeny of the tested sires to select the next generation of bulls to be progeny tested. Provided that phenotypes could be collected by about 14 months of age, this approach would allow marker assisted progeny testing at a two-year generation interval with the existing markers.

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 this area.

Besides the stated objectives, several other benefits have resulted from the Carcass Merit Project, both tangible and intangible. The project perhaps represents the greatest cooperative effort ever, among U.S. beef breed associations. Experiences gained and goodwill generated in this project will allow further cooperative research by breeds, which will benefit the entire beef industry. The project has also raised the visibility of marker-assisted selection and genomics in the beef industry. The considerable publicity received and educational efforts undertaken by the Carcass Merit 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 industry-wide tenderness data collection. Furthermore, the CMP has resulted in greater understanding of, and development of methods to address, statistical issues in the validation of quantitative trait loci.

The most significant result of the Carcass Merit Project is the sizeable database of phenotypic information and DNA samples collected from a wide cross section of U.S. beef germplasm. Already, data and samples stored by breed associations are being used to validate gene tests marketed to U.S. cattle producers. These resources could be extremely valuable tools for converting QTL (both those developed in the Angleton project and in public research) into more easily used diagnostic tests. Having a large unbiased resource population, representative of the U.S. beef cattle population, justifies the industry's investment in this project, and stands to be the project's greatest legacy.

For more information contact:
NATIONAL CATTLEMEN'S BEEF ASSOCIATION
9110 East Nichols Avenue • Centennial, CO 80112-3450 • 303-694-0305 • www.beef.org

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