

# MARKER-ASSISTED SELECTION IN BEEF CATTLE

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Marker-assisted selection allows for the accurate selection of specific DNA variations that have been associated with a measurable difference or effect on complex traits. It is important to realize that markers for complex traits like marbling are associated with only one of the many genes that contribute towards that trait. The presence or absence of the numerous other “unmarked” genes and the production environment will determine whether an animal actually displays the desired phenotype (e.g. large weaning weight, increased marbling). When making selection decisions Expected Progeny Differences (EPDs) should be considered, even in the presence of marker data, as they estimate the breeding value of all the “unmarked” genes that contribute to a given trait. **Marker assisted selection should be seen as a tool to assist with, and not as a replacement for, traditional selection techniques.**

Potential benefits from marker assisted selection are greatest for traits that

- 1) have low heritability (traits with observed or measured values that are a poor predictor of breeding value).
- 2) are difficult or expensive to measure (disease resistance).
- 3) cannot be measured until after the animal has already contributed to the next generation (carcass data) .
- 4) are currently not selected for as they are not routinely measured (tenderness).
- 5) are genetically correlated with a trait that you do not want to increase (most likely because associated genes affects one trait of the pair but not the other) (e.g. a marker that is associated with increased marbling but that is not also associated an increase backfat thickness).

In order of greatest to least degree of benefit, the following categories of traits are likely to benefit the most from marker-assisted selection:

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- 1) simply inherited traits (coat color, genetic defects),
  - 2) carcass quality and palatability attributes,
  - 3) fertility and reproductive efficiency,
  - 4) carcass quantity and yield,
  - 5) milk production and maternal ability, and
  - 6) growth performance.



This ranking is due to a combination of considerations including: 1) relative difficulty in collecting performance data, 2) relative magnitude of the heritability and phenotypic variation observed in the traits, 3) current amount of performance information available, and 4) when performance data becomes available in the life cycle.

Recently genetic tests for DNA markers associated with marbling and tenderness have become commercially available. These markers are associated with only one of the genes that contribute towards marbling or tenderness. Other “unmarked” genes, in conjunction with the production setting, will determine whether an animal marbles or has tender meat. Cattle can be genotyped for the desirable form of the marker by analyzing DNA collected from hair, tissue, blood, or semen samples.

Marker information can be used to increase the frequency of the marker that is positively associated with the trait of interest by selecting for animals carrying two copies of that marker, and against those carrying no copies of the marker. Validation studies and the effect of these markers in commercial herds should be evaluated to determine the cost:benefit ratio of these tests, and the emphasis that should be placed on these markers versus all of the other “unmarked” genes that contribute towards marbling or tenderness. In the future it is likely that EPDs and marker loci will be combined into a selection index for the trait of interest, and this will be superior to selection on EPDs or markers alone. The challenge will be to ensure that the cost of obtaining marker data for marbling and tenderness, or any other trait, is in line with the expected long-term return based on the accelerated cumulative and permanent genetic improvement of the herd.

The commercially available markers for carcass quality traits that have been validated by the NBCEC (National Beef Cattle Evaluation Consortium) and related websites as of 8/1/06 are:

**GeneSTAR® Quality** (<http://www.bovigensolutions.com>) is a DNA genetic marker panel test comprised of two markers (TG5 and M2) that have been associated with increased quality grade (% choice and prime). The TG5 DNA variation is in the 5’ leader sequence of the thyroglobulin gene. This enzyme is involved in the pathway that creates fat cells within muscle fibers as energy stores. Favorable forms of these markers (★) have been associated with quality grade in company trials, and this finding was validated by National Beef Cattle Evaluation Consortium (NBCEC) on Simmental x Angus fed cattle. They found an insignificant increase in marbling score, but estimated that a TG5 “star” was associated with an 8.6% increase in the number of cattle grading choice or prime, and a M2 “star” was associated with a 2.9% increase in the number of cattle grading choice or prime. The average effect of a GeneSTAR® Quality Grade star estimated to be a 6.2% increase in the number of cattle grading choice or better. See the NBCEC Validation Study data at the following website: <http://www.nbcec.org>.

**Igenity TenderGENE™** (<http://www.igenity.com>) is a DNA genetic marker panel test comprised of three markers (UoGCAST1, Calpain 4751 and Calpain 316). An increase in “tenderness” is associated with substituting a “C” allele at calpastatin (UoGCAST1) and a “C” allele at both  $\mu$ -calpain loci (Calpain 4751 and Calpain 316). This gene produces an enzyme which weakens muscle fibers thus increasing tenderness during the post-mortem aging process. The  $\mu$ -calpain DNA variations are located close together on the same gene and hence must be considered as a haplotype (a set of closely linked alleles inherited as a unit). Validation studies by the NBCEC confirmed an association between these three markers and meat tenderness in commercial cattle. Each calpastatin “C” was associated with a decrease of 0.4 lb of Warner-Bratzler Shear force, and substituting the Calpain 4751 “C”-316 “C” haplotype for the Calpain 4751 “T” - 316 “G” haplotype was associated with a decrease of 0.7 lb of Warner-Bratzler Shear force. See the NBCEC Validation Study data at the following website. <http://www.nbcec.org>.

**GeneSTAR® Tenderness** (<http://www.bovigensolutions.com>) is a DNA genetic marker panel test comprised of three markers (CAST-T1, Calpain 316-T2, and Calpain 4751-T3). An increase in “tenderness” is associated with substituting a “T” allele at calpastatin (CAST-T1) and a “C” allele at both  $\mu$ -calpain loci (Calpain 316-T2, and Calpain 4751-T3). Calpastatin is a naturally occurring enzyme that inhibits the normal tenderizing of meat as it ages post-mortem through the regulation of Calpain (see above). Favorable forms of these markers (★) have been associated with tenderness in company trials, and this finding was validated by National Beef Cattle Evaluation Consortium (NBCEC). Each calpastatin “T” was associated with a decrease of 0.3 lb of Warner-Bratzler Shear force, and substituting the Calpain 316-T2 “C”- 4751-T3 “C” haplotype for the Calpain 316-T2 “G” - 4751-T3 “T” haplotype was associated with a decrease of 0.8 lb of Warner-Bratzler Shear. See the NBCEC Validation Study data at the following website <http://www.nbcec.org>.