Carcass Merit Project: Development of EPDs and Genetic Marker Validation

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Introduction

The Carcass Merit project is an extensive 3½ year research project involving four universities, 16 beef cattle breed associations, and Celera AgGen. The project is funded and coordinated by NCBA and the Cattlemen's Beef Board, the breed associations, and Celera AgGen. The objectives of the project are:

1. Develop procedures for collection of information necessary for further development of Expected Progeny Differences (EPDs) for carcass merit traits.
2. Collect carcass data and measure longissimus lumborum Warner-Bratzler shear force of contemporary groups of progeny of multiple sires within each breed.
3. Measure longissimus lumborum sensory attributes on a sample of contemporary groups included in DNA 'marker' validation.
4. Validate DNA markers to be used in industry-wide 'marker-assisted' selection programs for improvement of carcass merit traits.
5. Determine DNA genotypes of these progeny for previously identified carcass merit 'markers.'
6. Measure 'direct' costs and 'opportunity' costs and returns of implementing EPDs for carcass merit traits for genetic selection programs and combinations of management x genetic improvement of carcass merit traits.

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**Ronnie Green has left CSU and will be the breed association liaison only until summer of 2000; Scott Davis and Jerry Taylor have formed a new company called GenomicFX and will be involved in the project only until fall of 2000.*

Experimental Procedure

The 16 breed associations are providing approximately 11,000 AI progeny of the more popular sires within their respective breeds, primarily from commercial cow herds. One or more reference sires of each breed must be used in a test herd in which a breed is being tested. BIF guidelines for sire evaluation must be followed. The number of progeny from each breed is determined by the number of registrations of the respective breeds calculated as a proportion of the total number of cattle registered by the cooperating breed associations. It is the responsibility of each breed association to provide leadership for progeny testing; costs of synchronizing and mating cows; progeny testing; blood sampling; feeding; carcass data collection; and the development of EPDs for their respective breed. Consequently, the breed associations are funding approximately 50% of the total costs of the research project. The NCBA is providing funds for shear force and sensory panel evaluation, graduate student assistantships, and one-half of the DNA analyses. Celera AgGen is funding the other one-half of the DNA analyses. Sires will be **compared only within breed** and **NOT across breeds**. Breed identity is coded to prevent associations or breeders from comparing breeds. Dr. Ronnie Green is the facilitator and liaison to the breed associations.

The selection of test herds, feedlots and feedlot regimen, slaughter endpoint, and beef processing plants are at the discretion of the breed associations. Breed associations are strongly encouraged to keep the number of contemporary groups to a minimum by slaughtering the cattle in as narrow a time frame as possible.

Each breed association is allocated a minimum of 10 sires plus additional sires based on the number of registrations for each respective breed. The range for the number of allocated sires for the different breed associations is from 10 to 54. Ten sires within each breed will be designated as DNA sires, with a target of 50 progeny/sire. For the other sires within each breed, the minimum number of progeny/sire is 15. Carcass data and Warner-Bratzler shear force are obtained on all progeny from all sires. For five of the DNA sires, trained sensory panel evaluations will be conducted on all progeny. Progeny can be accumulated over the 3½ year period, as long as reference sires are repeated. Prior to, or upon entering the feedlot, blood is obtained and sent to both Texas A&M and to Celera

AgGen for analyses. Semen samples are also analyzed for the DNA sires. The DNA analyses are to validate the presence of 'markers' for shear force, sensory panel traits, and carcass traits that have been identified by Jerry Taylor and Scott Davis at Texas A&M University through the checkoff and Texas A&M funded Genome Mapping project.

A small muscle tissue sample from all progeny is obtained at the time of slaughter for backup DNA analyses and verification of the identity of animals. Detailed carcass data are obtained after carcasses are chilled. One steak is obtained from the progeny of every sire and two steaks are obtained from DNA sires and shipped overnight to Kansas State University for Warner-Bratzler shear force and sensory panel evaluation, respectively. Shear steaks are cooked at 14 days postmortem whereas sensory panel steaks are frozen and later thawed for trained sensory panel evaluations.

The database is maintained by John Pollak and researchers at Cornell University. This database is secure and updated almost daily. The development of carcass, shear force, and sensory panel EPDs is the responsibility of the breed associations, although John Pollak will be conducting analyses for at least two breeds. The NCBA and breed associations own all carcass, shear force, and sensory panel data. The marker identities, genotypes produced by scoring the markers, and protocols for marker identification remain the property of Texas A&M and NCBA. However, this information as well as the phenotypic data will be provided to the breed associations for their use in computing EPDs for related carcass merit traits.

Economic analyses will be conducted by Steve Koontz at Colorado State University. The first phase will measure direct costs of developing carcass merit EPDs and implementing management systems necessary to use the information. The second phase will measure the expected returns for implementation of a carcass-merit-based production system. The third phase addresses the marketing system for cattle, carcasses, and meat.

Elizabeth Wescott is the NCBA project coordinator who is responsible for implementation and oversight of the project. An NCBA Producer Steering Committee consists of Kathy Hawkins, chair, from MI; Rob A. Brown from TX; Dave Nichols from IA; James Bradford from IA; John Grande from MT; and James Bennett from VA. The Producer Steering Committee has the responsibility to give oversight as needed and to provide insight on future use of the DNA information.

Preliminary Results

At the time of writing this manuscript, carcass data and Warner-Bratzler shear force data have been collected on over 3,000 cattle. Sensory panel evaluations have been conducted on steaks from over 800 cattle. There have been enough progeny slaughtered from two breeds so that the heritability of Warner-Bratzler shear force has been calculated to be .55 for one breed and .67 for the other. These are considerably higher than those reported in the literature and it is anticipated that, as the remaining portions of the progeny are slaughtered, the heritability estimate will decrease somewhat. Even with a modest decrease, the heritability will still clearly be high enough so that useful EPDs can be developed and progress can be made through selection. Within breed analysis, the high group and low group of sires were .36 kg different in shear force. One breed association will be publishing EPDs for Warner-Bratzler shear force in September of this year. That will be a first.

Two breeds have provided enough progeny to date for complete DNA analyses on two sires. A minimum of 44 markers are to be screened for each sire (11 QTLs). There are seven QTLs for shear force and sensory panel tenderness; three for marbling, and one for ribeye area. The markers are not genes, but are random segments of DNA found at specific locations. Validation determines if the heterozygotes segregate from sire to progeny.

Much of the DNA in a chromosome is not in the form of genes, but is present in several repeated sequences that frequently are different among individuals. These segments of repeated short sequences are found scattered throughout the chromosomes and are used by molecular biologists as 'markers.' Markers from different chromosomes can be used for a DNA "fingerprint" or identity test. Those that flank a quantitative trait locus (QTL), an area of a chromosome that contains a gene affecting a certain trait, can be used to select for the QTL (the trait) even before the actual gene involved is identified and isolated. In an example where a sire is heterozygous for a marker, such as Warner-Bratzler shear force, the progeny with one marker that flanks the QTL on one of the pair of chromosomes will have a lower or higher shear force value than those with the other marker. Therefore, DNA marker analysis could be used in selection, if a sire is heterozygous for the marker(s) of interest.

Preliminary results show that some markers identifying QTLs have been validated in three sires of the two breeds where DNA analysis is complete. This suggests that the markers can be used as a selection tool for at least some traits for sires of some breeds.

Results obtained to date are very encouraging. EPDs can be developed for carcass traits, shear force, and sensory traits for several breeds in the very near future. In addition, the DNA marker validation on a few sires show that marker analysis can be used in selection.