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E.J. Pollak

R.D. Green

J. Taylor

See next page for additional authors

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Carcass merit project: development of EPDS and genetic marker validation (2001)

Authors

E.J. Pollak, R.D. Green, J. Taylor, S. Davis, T. Holm, S. Koontz, C. Gill, Daniel W. Moser, E.A. Westcott, and Michael E. Dikeman

CARCASS MERIT PROJECT: DEVELOPMENT OF EPDS AND GENETIC MARKER VALIDATION

M. E. Dikeman, E. J. Pollak[1], R. D. Green[2], J. Taylor[3], S. Davis[3], T. Holm[4], S. Koontz[5], C. Gill[6], D. Moser, and E. A. Westcott[7]

Summary

Carcass and Warner-Bratzler shear force data on strip loin steaks have been obtained on over 4,200 cattle from contemporary progeny groups from the most widely used sires in 15 beef cattle breed associations (16 breeds). Trained sensory panel evaluations have been conducted on over 1,500 strip loin steaks from a sample of contemporary progeny groups from sires included in the QTL (quantitative trait loci) validation component of the project. One breed association has published Warner-Bratzler shear force Expected Progeny Differences (EPDs) for 57 sires of two breeds. DNA analyses and screening have been completed for 11 QTL on eight sires from several breeds. EPDs for carcass traits, Warner-Bratzler shear force, and sensory panel traits may be completed for several breeds within the year 2001. Information from this project should allow seedstock producers to improve carcass traits, tenderness, and other palatability traits through classical genetic selection or through DNA marker-assisted selection.

Introduction

Consumers eat beef primarily for its great flavor, but there have been complaints about its palatability associated with unacceptable tenderness. The National Beef Tenderness Study published in 1987 found that, except for the tenderloin, tenderness varies considerably, and significant proportions of nearly all beef cuts were unacceptable in tenderness. Tenderness is generally measured on the longissimus (loin-eye) muscle because it has the most total value, and is almost always cooked by dry heat. It is expected by consumers to be tender, juicy, and flavorful. Recent market studies have shown that consumers are willing to pay more for beef of known tenderness. Although consumers are the ultimate judges of tenderness, Warner-Bratzler shear force is a highly repeatable and economical method for measuring tenderness. Reviews of published literature on the genetic control of tenderness show that the heritability of Warner-Bratzler shear force is moderately high (29%) and that of marbling is high (38%), indicating that progress can be made through selection. However, selecting for palatability is difficult and expensive. EPDs have become "user friendly" tools for cattlemen to use in selecting for numerous traits, but until the implementation of this project, no cattle breed association had EPDs for Warner-Bratzler shear force or sensory-evaluated palatability traits. Recently, the American Simmental Association published Warner-Bratzler shear force EPDs as a result of this project. DNA markers have been identified at Texas A & M University for tenderness and other quality traits and, if

[1]Professor of animal breeding , Cornell University.
[2]R. D. Green, formerly Colorado State University.
[3]Genomics FX.
[4]Celera AgGen.
[5]Agricultural economist, Colorado State University.
[6]Molecular geneticist, Texas A & M University.
[7]Associate Director for Research & Technical Services, National Cattlemen's Beef Association.

validated in this project, could be used in 'marker-assisted' selection. With EPDs and(or) DNA marker-assisted selection, the beef cattle industry then can make significant progress toward improving meat palatability through genetic selection.

The Carcass Merit Project is an extensive 3½ year project involving four universities, 15 beef cattle breed associations (16 breeds), and Celera AgGen. The project is funded and coordinated by NCBA and the Cattlemen's Beef Board, the breed associations, and Celera AgGen. Its objectives are:

1. Collect information to develop EPDs for carcass merit traits.

2. Measure longissimus lumborum (strip steak) Warner-Bratzler shear force of contemporary groups of progeny from multiple sires within each breed.

3. Measure longissimus lumborum sensory attributes on a sample of contemporary groups of progeny from sires 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 and opportunity costs and returns of implementing EPDs for carcass merit traits.

Experimental Procedures

The 15 breed associations (16 breeds) are providing approximately 11,000 AI progeny of their more widely used sires, primarily from commercial cow herds. One or more reference sires of each breed is used in a test herd in which a breed is being tested (reference sires are used to tie contemporary groups together for the breeds 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 each breed calculated as a proportion of the total number registered by the cooperating breed associations. Each breed association is responsible for providing leadership for progeny testing; costs of synchronizing and mating cows; coordinating progeny testing; blood sampling; feeding; carcass data collection; and the development of EPDs for their breed. Consequently, the breed associations are funding about 50% of the total costs. The NCBA is providing funds for shear force and sensory panel evaluation, graduate student assistantships, travel for carcass data collection, and one-half of the DNA analyses. Celera AgGen is funding the other 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. Dan Moser is the facilitator and liaison to the breed associations.

The selection of test herds, sires, feedlots and feedlot regimen, slaughter endpoint, and processing plants are at the discretion of each breed association.

Each association is allocated a minimum of 10 sires plus additional sires, based on the number of registrations for each breed, resulting in 10 to 54 sires per association. Ten sires within each breed will be designated as DNA sires, with a target of 50 progeny per sire. For non-DNA sires, the target is 15 progeny per sire, although this is at the discretion of each breed association. Carcass and Warner-Bratzler shear force data are obtained on all progeny from all sires. For five of the DNA sires within each breed, trained sensory panel evaluations will be conducted on all progeny. Progeny data can be accumulated over the 3½ year period, as long as reference sires are repeated. Prior to or upon entering the feedlot, blood samples are sent to both Clare Abbey at Texas A & M and to Tom Holm at 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 through the checkoff and the 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 animal identity. Detailed carcass data are obtained after chilling. One steak from each progeny of every sire and two steaks from progeny DNA sires are obtained and shipped overnight to Michael Dikeman at Kansas State University for Warner-Bratzler shear force and sensory panel evaluation. Shear steaks are cooked at 14 days postmortem. Sensory panel steaks are frozen and later thawed for trained sensory panel evaluations.

The database maintained by John Pollak at Cornell University 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 those analyses for at least two breeds. The NCBA and breed associations own all carcass, shear force, and sensory panel data. 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.

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 implementing a carcass merit-based production system. The third phase addresses the marketing system for cattle, carcasses, and meat.

Elizabeth Westcott, the NCBA project coordinator, 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. That Committee is responsible for giving oversight as needed and providing insight on future use of the DNA information.

Preliminary Results

To date, carcass and Warner-Bratzler shear force data have been collected on over 4,300 cattle. Sensory panels have evaluated steaks from over 1,500 cattle. Warner-Bratzler shear force EPDs have been developed and published for 47 Simmental and 10 Simbrah sires and are reported in the following paper in this report. Publishing EPDs for shear force is a first for the beef industry. Several other breeds may be developing EPDs within the year 2001. For breeds in which sufficient progeny have been slaughtered, variation appears sufficient to allow for genetic progress.

Several breeds have provided enough progeny to date for complete DNA analyses on several sires. A minimum of 66 markers are to be screened for each sire (11 Quantitative Trait Loci, QTL). 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 will determine if the QTL discovered in the Texas A & M experiment using Angus and Brahman cross cattle segregate within the various breeds in this project and, if so, which are heterozygous. In an example where a sire is heterozygous for a marker, such as Warner-Bratzler shear force, the progeny with markers that flank the QTL on one of the pair of chromosomes will be associated with having a lower or higher shear force value than those with the other markers. Therefore, DNA marker analysis could be used in selection, if a sire is heterozygous for the QTL of interest.

Some markers identifying QTL have been validated in several sires of the 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.