Update on the Carcass Merit Project

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Introduction

The Carcass Merit Project (CMP) is an industry-wide effort to characterize bulls in U.S. beef breeds for carcass characteristics. Traits of interest include traditional carcass measures, Warner-Bratzler shear force measures, and sensory panel observations. The two preeminent objectives of the CMP are:

1. To generate appropriate data for the estimation of expected progeny differences (EPD's) for tenderness on bulls deemed by each breed to be legacy bulls for the next decade.
2. To seek to validate the segregation of quantitative trait loci (QTL) for selected carcass characteristics within each breed.

Each of fourteen breeds participating in the project were asked to identify bulls that were felt would have the largest genetic impact on the breed over the next decade. Ten of these bulls were then identified as "DNA" bulls for which analysis of the bull and fifty of each bull's progeny would be for validation of the QTL under study in this project. Five of the ten DNA bulls were also designated to obtain sensory panel observations on their progeny. The validation component of this project consists of scoring a bull and his progeny for markers in regions of the bovine chromosomes suspected of containing a QTL based on results from the Texas A & M Angleton project. In that project, QTL were sought using informative families consisting of Angus and Brahman cross and backcrossed cattle. Eleven of the QTL from that project are under investigation in the CMP. Six of the eleven QTL are for Warner Bratzel shear force (WBSF) measures, one for tenderness scores assigned by panelists, three for marbling, and one for rib eye area (REA).

Additional bulls were allocated to each breed in accordance with their number of annual registrations. These additional bulls are referred to as EPD bulls. Twenty-five progeny from each of these bulls were measured for traditional carcass traits and for WBSF. No biological material for DNA analysis of these bulls or their progeny was captured.

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Proceedings of the 54th Reciprocal Meat Conference (2001)

Data

The 14 breeds participating in the project and number of progeny harvested and processed into the CMP database as of June 2001 are shown in Table 1. These numbers do not include a large number of animals (approximately 1,000) harvested in the spring and still in the process of being recorded.

Along with these phenotypic data, genotypic information on 110 bulls for six markers around each of the 11 QTL (three proximal and three distal predicted location of the QTL) has been obtained. Of these bulls, 11 have produced enough harvested progeny to have their progeny genotyped. Each progeny was genotyped for two marker loci around each of the 11 QTL. The markers used for each progeny within a bull family were those found to be heterozygous in their sire, chosen such that one was proximal and one distal to the predicted location of the QTL associated with those markers. As well, a small meat sample was obtained from the carcass to verify that the carcass sample was consistent with the blood sample for the progeny. As such, two types of errors were detectable,

TABLE 1. Breeds Participating in the CMP and Progeny Record Counts by Breed

Breed	EPD Sires	DNA Sires	Total by Breed
Angus	304	426	730
Brahman	9	238	247
Brangus	12	144	156
Charolais	282	229	511
Gelbvieh	80	139	219
Hereford	354	274	628
Limousin	141	49	190
Maine-Anjou		122	122
Red Angus	31	196	227
Salers		188	188
Shorthorn	48	87	135
Simbrah		138	138
Simmental	387	322	709
South Devon		213	213
Total			4413

TABLE 2. Analysis of Bull Progeny Groups for Segregation Within Family of 11 QTL. Probabilities are Those for the Bull in Question to be Heterozygous for the QTL Associated with the Marker Analysis

		Bull								
QTL	**Trait**	**1**	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**
1	WBSF					P<.02				
2	WBSF									
3	WBSF						P<.04			P<.03
4	WBSF	P<.03	P<.01				P<.02			
5	WBSF	P<.01						P<.01	P<.03	
6	WBSF						P<.02			
7	Tenderness					P<.02				
8	Marbling									
9	Marbling									
10	Marbling									
11	REA									

mispaternity (the genotype of the calf blood sample was not consistent with the sire identified in the data for that calf) and misidentity (the meat sample genotyped was not consistent with the calf blood sample genotype). In this update, I will focus on the results of the analysis of the 11 bulls having completed the DNA marker testing.

Results

Mispaternity and Misidentity

Two sires were eliminated from the validation analysis due to large numbers of both mispaternity and misidentity of their calves. Of the nine remaining sires, there was 5.5% mispaternity and 8.6% misidentity among the 396 total progeny analyzed.

Validation

Table 2 shows the results of within-family analysis of the association of markers to the segregation of progeny for QTL. The analysis was to separate the progeny into two groups based on their genotypes at the marker loci and a t-test was run on the phenotype data from the calves across the two groups. Phenotypes were deviated from contemporary group averages for this analysis. The probabilities shown in the table are that there was a statistically significant difference in the means of calves sorted for each QTL based on their marker genotypes for those QTL. This implies that the bull is heterozygous for the QTL, and hence at least two alleles for that QTL are segregating in that breed.

None of the bulls were detected to be heterozygous for any of three marbling QTL or the REA QTL. Reasons for not detecting segregation in these bull half-sib families are:

1. The QTL found in the research phase were false positives.
2. The QTL had a distinct allele in either Angus or Brahman cattle used for discovery.
3. The QTL are segregating but that the sample of bulls completed thus far were simply homozygous.
4. There were heterozygous bulls but the effects were too small to detect with our sample size.

Five of the six QTL for WBSF were found to be segregating in at least one bull (QTL 2 was not), and some were found to be segregating in more than one bull (QTL 3, 4 and 5). Only one bull was implicated as being heterozygous for the tenderness phenotype provided from the sensory panel results. The nine bulls are from four breeds so a more comprehensive breed analysis could not be done at this time. The effect of the QTL found segregating has not been estimated.