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Association of Microsatellite Markers on Bovine Chromosomes 5 and 6 with Carcass Traits[1]

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Summary

The objective of this study was to identify chromosomal regions associated with phenotypic variation in carcass traits in three crossbred families. Three half-sib families were developed from crossbred sires. Families 1, 2, and 3 comprised 29, 25, and 77 offspring, respectively (n = 131). The genetic background of the sires, dams, and offspring was 1/3 Angus, 1/3 Hereford, 1/3 Simmental. Carcass traits collected were finished weight, hot carcass weight (HCW), marbling score, Quality Grade, Longissimus muscle area (LMA), rib fat, percent kidney pelvic, and heart fat (KPH), and Yield Grade. Microsatellite markers on chromosomes 5 and 6 were selected based on their relative position. Markers used on chromosome 5 were BM6026, RM103, BM321, RM084, BMS1216, BM315, and BM597. Markers used on chromosome 6 were ILSTS093, ILSTS090, BM1329, BMS518, ILSTS035, BM8124, and BMC4203. Individual marker analysis was conducted because homozygosity of the bulls for some markers hindered interval mapping. Family 1 exhibited allelic affects for finished weight, hot carcass weight, and marbling score on chromosome 5. Markers RM103 and BM321 were associated with finished ($P < 0.01$) and carcass ($P < 0.05$) weights. An association with marbling score was identified with BM6026 ($P < 0.05$), RM103 ($P < 0.01$), and BM321 ($P < 0.01$). On chromosome 6, BMC4203 was associated with Longissimus muscle area in family 1 ($P < 0.05$) and family 2 ($P < 0.001$). No association was detected ($P > 0.05$) on family 3.

Introduction

LMA has been identified as an economically important trait, as the Longissimus dorsi is located in the most valuable carcass regions and is used to calculate USDA Yield Grade and total retail product yield (Tatum, 1997). LMA was correlated with a QTL on chromosome 6 in the Belgian Blue X MARC III sired cattle (Casas et al., 2000). The identification of a QTL for LMA on chromosome 6 was supported by a study involving Brahma X Hereford sired cattle (Casas et al., 2003). In the same study, another QTL for the same trait was located on chromosome 5 with significance (Casas et al., 2003).

LMA was selected as the trait of interest for this study, leading to the selection of microsatellite markers on bovine chromosomes 5 and 6. The objective was to identify chromosomal regions associated with phenotypic variation in carcass traits in three crossbred half-sib families.

Materials and Methods

A reference population of 162 offspring born from 2001 to 2004 from three sires was developed at the South Dakota State University Beef Breeding Unit, Brookings, SD. The three sires and all offspring were comprised of 1/3 Angus, 1/3 Hereford, and 1/3 Simmental genetic material. The offspring and mated dams of each sire were identified as families 1, 2, and 3. Family 1 corresponds to sire 988083, family 2 corresponds to sire 999114, and family 3 corresponds to sire 988042.

Cattle were weaned at approximately 185 days of age. Following weaning, cattle were fed a corn based diet consisting of 12.5% crude protein and 94.2 Mcal/cwt NE_m for about 110 days. Harvest criteria included an average ultrasound determined rib fat measurement of 0.30 inches and average finished weight of at least 1,000 pounds for the group.

Cattle were marketed to Tyson Fresh Meats, Dakota City, NE or PM Beef, Windom, MN. Animal identification numbers were matched to plant carcass identification numbers at the time of harvest for cross-referencing pre- and post-mortem phenotypes. Phenotypic data was

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collected for finished weights and post-mortem measures of HCW, marbling score, Quality Grade, LMA, rib fat, percent KPH, and Yield Grade. Finished weight was determined just prior to harvest, while HCW was determined at the time of harvest. Carcasses were chilled for at least 24 hours prior to collection of the additional carcass data. LMA and rib fat measures were taken by South Dakota State University personnel, while marbling score, Quality Grade, percent KPH, and Yield Grade were determined by a USDA grader.

Whole blood was collected from each calf by jugular or tail vein venapuncture at weaning and again at 5 to 6 months into the feeding period. Samples of about 10 ml were collected in evacuated tubes with 15% EDTA. Blood was stored at 4°C for no more than 24 hours prior to buffy coat (white blood cell) extraction by centrifugation. DNA was extracted from the isolated buffy coats using a saturated salt DNA extraction procedure (Miller et al., 1988).

Seven microsatellite markers were selected on each of the two chromosomes, approximately 20 cM apart. Markers used on chromosome 5 were BM6026, RM103, BM321, RM084, BMS1216, BM315, and BM597. Markers used on chromosome 6 were ILSTS093, ILSTS090, BM1329, BMS518, ILSTS035, BM8124, and BMC4203. Genotyping was completed by polymerase chain reaction (PCR) amplification of the microsatellite markers with incorporated radioactive phosphorus (^{32}P). PCR products were loaded on 8% polyacrylamide gels for electrophoresis. Electrophoresed gels were fixed to blot paper and dried in a gel dryer, prior to being placed on autoradiography film in radiography cassettes. Films were exposed for two days and then developed. Films were read over a transluminator, and genotypes were determined independently by two researchers and reconciled or excluded from analysis. Assigned genotypes were also verified against sire and dam genotypes, with those not in agreement excluded from the analysis (excluded $n = 31$).

Statistical analysis of associations between the gene markers and phenotypic traits was conducted using the General Linear Model (GLM) procedure of SAS (SAS Institute Inc., 2001). Individual marker analysis was conducted because homozygosity of the sires for some markers inhibited interval mapping. Differences in sex, year, age at finishing, and the specific marker were accounted for in the model, with age at finishing used as the adjustment factor. Representative *P*-values and Least-squares means were determined.

Results and Discussion

A total of 131 offspring from families 1 ($n = 29$), 2 ($n = 25$), and 3 ($n = 77$), were included in the analysis of allelic affects on carcass traits. Informative markers for family 1 were BM6026, RM103, BM321, BMS1216, and BM315 on chromosome 5, and ILSTS093, ILSTS090, BMS518, ILSTS035, and BMC4203 on chromosome 6. Informative markers for family 2 were BM321, RM084, and BM597 on chromosome 5, and ILSTS090, BM1329, and BMC4203 on chromosome 6. Informative markers for family 3 were BM6026, RM103, BM321, RM084, and BM315 on chromosome 5, and ILSTS093, BM8124, and BMC4203 on chromosome 6.

Significant associations between sire allele and phenotype were shown for finished weight, HCW, marbling score, and LMA. Tables 1 and 2 exhibit the associations between the markers and carcass traits where significance ($P < 0.05$) was detected.

Table 1. BM6026, RM103, and BM321 allelic effects on carcass phenotypes in family 1

BM6026

	Sire allele 1		Sire allele 2		
Trait	*n*	LS Mean	*n*	LS Mean	*P*-value
Finished weight, lb	14	996	8	924	0.1765
HCW, lb	14	613	8	578	0.3199
Marbling score [a]	14	427	8	355	0.0124
Choice [b]	14	0.71	8	0.43	0.1481
LMA, in^2	14	12.7	8	12.2	0.3344
Fat, in	13	0.32	8	0.26	0.3054
YG [c]	12	1.75	8	1.58	0.5109
KPH, %	13	2.55	5	2.73	0.3316

RM103

	Sire allele 1		Sire allele 2		
Trait	*n*	LS Mean	*n*	LS Mean	*P*-value
Finished weight, lb	12	960	11	1074	0.0063
HCW, lb	12	602	11	677	0.0119
Marbling score [a]	12	372	11	451	0.0040
Choice [b]	12	0.47	11	0.77	0.1222
LMA, in^2	12	12.7	11	13.3	0.2034
Fat, in	12	0.33	11	0.42	0.0895
YG [c]	10	1.35	10	1.49	0.5386
KPH, %	9	2.34	10	2.56	0.1668

BM321

	Sire allele 1		Sire allele 2		
Trait	*n*	LS Mean	*n*	LS Mean	*P*-value
Finished weight, lb	7	1092	6	912	0.0072
HCW, lb	7	682	6	564	0.0144
Marbling score [a]	7	477	6	361	0.0061
Choice [b]	7	0.74	6	0.42	0.2617
LMA, in^2	7	14.0	6	12.6	0.0780
Fat, in	7	0.38	6	0.24	0.0657
YG [c]	6	1.54	5	1.37	0.6851
KPH, %	6	2.38	3	1.95	0.0849

[a] slight = 300-399, small = 400-499; [b] choice = 1, not choice = 0; [c] USDA 1, 2, 3, 4, 5

Table 2. BMC4203 allelic effects on carcass phenotypes in families 1 and 2

	Family 1					Family 2				
	Sire allele 1		Sire allele 2			Sire allele 1		Sire allele 2		
Trait	*n*	LS Mean	*n*	LS Mean	*P*-value	*n*	LS Mean	*n*	LS Mean	*P*-value
Finished weight, lb	9	960	8	1016	0.3155	7	1022	10	1043	0.6534
HCW, lb	9	596	8	629	0.4045	7	596	10	638	0.1033
Marbling score [a]	9	387	8	391	0.9029	7	365	10	364	0.9813
Choice [b]	9	0.61	8	0.72	0.6755	7	0.29	10	0.40	0.3130
LMA, in^2	9	11.7	8	13.1	0.0359	7	9.8	10	12.1	0.0004
Fat, in	9	0.29	7	0.35	0.5196	.	.	.	.	.
YG [c]	9	1.94	7	1.47	0.1613	7	2.27	10	1.94	0.1782
KPH, %	7	2.38	7	2.43	0.7753	7	2.76	10	2.36	0.0662

[a] slight = 300-399, small = 400-499; [b] choice = 1, not choice = 0; [c] USDA 1, 2, 3, 4, 5

Only 2 offspring from family 2 had rib fat data, so analysis of that trait was not possible. Family 1 exhibited allelic affects for finished weight, HCW, and marbling score on chromosome 5. Markers RM103 and BM321 were associated with finished ($P < 0.01$) and carcass ($P < 0.05$) weights. An association with marbling score was identified with BM6026 ($P < 0.05$), RM103 ($P < 0.01$), and BM321 ($P < 0.01$). BMS1216 showed an association with rib fat in family 1 ($P < 0.05$). On chromosome 6, BMC4203 was associated with LMA in family 1 ($P < 0.05$) and family 2 ($P < 0.001$). No significant association between sire alleles and phenotypes were detected ($P > 0.05$) on family 3. Quality Grade, rib fat, percent KPH, and Yield Grade were not found to be associated with any of the markers in any of the families analyzed.

Implications

The markers found to be significantly associated with carcass traits could be utilized in MAS applications. The consistency of the results of this study with other studies indicates that these microsatellite markers may be useful for assessing a wide variety of populations with varying characteristics. Based on the results for the informative markers identified, further exploration in an attempt to make interval mapping possible is warranted.

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