Quantitative trait loci affecting growth and carcass composition of cattle segregating alternate forms of myostatin[1,2]

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ABSTRACT: The effects of the bovine myostatin gene on chromosome 2 on birth and carcass traits have been previously assessed. The objective of this study was to identify additional quantitative trait loci (QTL) for economically important traits in two families segregating an inactive copy of myostatin. Two half-sib families were developed from Belgian Blue × MARC III (n = 246) and Piedmontese × Angus (n = 209) sires. Traits analyzed were birth (kg) and yearling weight (kg); hot carcass weight (kg); fat depth (cm); marbling score; longissimus muscle area (cm^2); estimated kidney, pelvic, and heart fat (%); USDA yield grade; retail product yield (%); fat yield (%); and wholesale rib-fat yield (%). Meat tenderness was measured as Warner-Bratzler shear force at 3 and 14 d postmortem. The effect of myostatin on these traits was removed by using phase information obtained from the previous study with six microsatellite markers flanking the locus. Selective genotyping was done on 92 animals from both families to identify genomic regions potentially associated with retail product yield and fat depth, using a total of 150 informative markers in each family. Regions in which selective genotyping indicated the presence of QTL were evaluated further by genotyping the entire population and additional markers. For the family with Belgian Blue inheritance (n = 246), a significant QTL for birth and yearling weight was identified on chromosome 6. Suggestive QTL were identified for longissimus muscle area and hot carcass weight on chromosome 6 and for marbling on chromosomes 17 and 27. For the family with Piedmontese inheritance (n = 209), suggestive QTL on chromosome 5 were identified for fat depth, retail product yield, and USDA yield grade and on chromosome 29 for Warner-Bratzler shear force at 3 and 14 d postmortem. Interactions suggesting the presence of QTL were observed between myostatin and chromosome 5 for Warner-Bratzler shear force at 14 d postmortem and between myostatin and chromosome 14 for fat depth. Thus, in families segregating an inactive copy of myostatin in cattle, other loci influencing quantitative traits can be detected. These results are the initial effort to identify and characterize QTL affecting carcass and growth traits in families segregating myostatin.

Key Words: Beef, Genetic Markers, Quantitative Traits, Carcasses

Introduction

Double-muscled animals have leaner carcasses than those not double-muscled and exhibit greater muscle mass with less fat (Hanset et al., 1987; Arthur, 1995; Wheeler et al., 1997). The locus causing double-muscling in cattle has been mapped to the centromeric end of bovine chromosome 2 (Charlier et al., 1995; Dunner et al., 1997; Casas et al., 1998). Myostatin was identified as the gene responsible for producing double-muscling in mice (McPherron et al., 1997) and has been identified as the gene causing double-muscling in cattle. This gene is located at the centromeric end of bovine chromosome 2 (McPherron and Lee, 1997; Smith et al., 1997; Grobet et al., 1998). Five different myostatin mutations have been detected in cattle segregating the double-muscle phenotype to date. In Belgian Blue, there is an 11-bp deletion causing a frameshift and premature translational termination. In Piedmontese, there is a guanine-to-adenine transition mutation causing a substitution of a critical tyrosine with a cysteine in the signaling portion of the protein. Both mutations produce an inactive myostatin protein (Kambadur et al., 1997; Grobet et al., 1998).

The effect of myostatin on retail product yield and fat thickness has been previously assessed. Animals with a single copy of the inactivated myostatin had a

greater muscle mass and less fat than normal animals (Casas et al., 1998). Casas et al. (1998) established that myostatin accounts for most of the variation observed in the expression of muscle mass and fat deposition in populations of double-muscled cattle. However, the remaining variation is likely attributable to other loci scattered throughout the genome. The objective of this research was to identify these additional quantitative trait loci associated with growth and carcass traits in cattle.

Materials and Methods

Animals

Families used in this study have been previously described (Casas et al., 1998). Briefly, two half-sib families were developed using a Belgian Blue × MARC III (1/4 Angus, 1/4 Hereford, 1/4 Red Poll, 1/4 Pinzgauer) sire and a Piedmontese × Angus sire. A total of 246 1/4 Belgian Blue and 209 1/4 Piedmontese offspring were produced by matings primarily to MARC III dams. Both sires were assumed to be heterozygous at the myostatin gene, and approximately half of the progeny inherited one copy of the inactive allele and the other half inherited an active copy.

Traits Analyzed

Offspring of the two sires were evaluated for growth and carcass traits. Birth (kg) and yearling weight (kg) were recorded. Yearling weight was adjusted for age. Slaughter data were obtained at a commercial facility and the wholesale rib was retrieved from the right side of each carcass for dissection into fat, muscle, and bone (Shackelford et al., 1995). Carcass traits evaluated were hot carcass weight (kg); fat depth (cm); marbling score; longissimus muscle area (cm^2); estimated kidney, pelvic, and heart fat (%); and USDA yield grade. Carcass traits predicted from rib dissection data were retail product yield (%), fat yield (%), and wholesale rib-fat yield (%). Meat tenderness was measured as Warner-Bratzler shear force (kg) at 3 and 14 d postmortem (AMSA, 1995).

Markers Used

The development of the bovine genetic map at the U.S. Meat Animal Research Center (Kappes et al., 1997; http://sol.marc.usda.gov) has resulted in the availability of genetic markers throughout the genome. The goal of this study was to use 150 markers in each family, scanning the genome approximately every 20 centimorgans (cM). Markers were screened for heterozygosity in the two sires and informative markers were chosen based on their location in each chromosome and ease of scoring. Amplification reactions were performed on DNA extracted from blood with a saturated salt procedure (Miller et al., 1988). Amplification conditions have been described elsewhere (Kappes et al., 1997).

Genomic Screen

Genotyping of extreme phenotypes, or selective genotyping, reduces the cost without losing much power for QTL detection (Lander and Botstein, 1989). The initial genomic screening was performed by genotyping individuals with the highest retail product yield and lowest fat depth or the lowest retail product yield and highest fat depth. Individuals were selected within each family based on residuals from a model that included the fixed effects of sex, dam line, and days on feed and the probability of inheriting the inactive myostatin allele from the sire as covariates. A total of 92 animals were used in this procedure. Forty-six animals from each family were selected, 23 from each selected group. F-statistics were generated at 1-cM intervals by regression of phenotypes on the conditional probability of inheriting the allele from the Belgian Blue or the Piedmontese sire (Haley et al., 1994). A region was further evaluated if it was nominally significant (F = 7; $P < .01$) for retail product yield, fat depth, or both.

Markers in the vicinity of the maximum F-statistic were typed in all members of the family. An F-statistic profile was generated at 1-cM intervals for each genomic region. The probability of inheriting the Belgian Blue or the Piedmontese allele at each centimorgan was calculated using the approach suggested by Haley et al. (1994). Data were analyzed using SAS (1988) with a model that included the effects previously mentioned and the conditional probability of inheriting the Belgian Blue or the Piedmontese allele from the sire at each position of the genomic region under study as a covariate. This last probability was also included as an interaction with the probability of inheriting the inactive copy of myostatin when significant, to account for the interaction between myostatin and the QTL.

The experiment-wise threshold value was calculated according to Lander and Kruglyak (1995). An F-statistic was considered suggestive of linkage to a QTL if it exceeded a value of F = 10.2 (one expected false positive per genomic scan) and significant if it exceeded a threshold value of F = 17.2 (one expected false positive in 20 genomic scans). These values correspond to a nominal P-value of $P = .002$ and $P = .00005$, respectively.

Power of identifying a QTL in the study was approximated by simulations of each family. Simulation was repeated 100,000 times for a range of QTL effects where differences between offspring inheriting alternative sire alleles were .4, .5, .6, .7, or .8 phenotypic standard deviations (SD). Targeted QTL had an effect of at least .4 SD. The marker used to compute F-statistics was located 0 cM from the QTL. F-statistics were calculated using either the 46 extreme progeny (selective genotyping) from the phenotypic distribution (23 high and 23 low) or the entire family (n = 246). The only fixed effect in the analysis was the mean for either the selective genotyping or the entire family set. Thresholds corresponding to the expected fraction of false positives of < .05 (1 expected false positive per 20 scans), from .05 to

< 1, from 1 to < 2, from 2 to < 3, and > 3 were 20.7, 11.5, 9.9, and 8.4, respectively, for selective genotyping and 17.1, 10.2, 8.5, and 7.6, respectively, for the entire family. Thresholds were calculated according to Lander and Kruglyak (1995).

Results

Based on selective genotyping, several regions were initially associated with retail product yield and fat depth in both families. Marker information suggested that QTL were segregating on regions of chromosomes 5, 6, 7, 13, 14, 17, 19, 22, 27, and 29 for the traits under study. In the family with Belgian Blue inheritance, nominally significant QTL were identified on chromosomes 5 (hot carcass weight), 6 (retail product yield, birth weight), 7 (14-d Warner-Bratzler shear force), 19 (fat depth, retail product yield, birth weight), 22 (retail product yield), 27 (marbling score), and 29 (fat depth, retail product yield, marbling score). In the family with Piedmontese inheritance, putative QTL were identified on chromosomes 5 (fat depth), 7 (fat depth, 14-d Warner-Bratzler shear force), 13 (fat depth, retail product yield), 14 (fat depth retail product yield), 17 (fat depth), 19 (birth weight), 22 (fat depth, retail product yield, kidney, pelvic, and heart fat), and 29 (fat depth, retail product yield).

Including genotypes of the entire family for markers used in selective genotyping and the addition of other markers in the analysis resulted in the exclusion of several regions in both families from further consideration. Quantitative trait loci segregating in these families were identified on regions of chromosomes 5, 6, 14, 17, 27, and 29. From the beginning of each linkage group, the maximum F-statistic for all traits was detected between 62 and 72 cM on chromosome 5, between 48 and 51 cM on chromosome 6, at 15 cM on chromosome 14, at 21 cM on chromosome 17, at 60 cM on chromosome 27, and between 56 and 65 cM on chromosome 29. Table 1 shows the QTL for growth and carcass composition traits that were identified in each family and chromosome.

A suggestive QTL affecting fat depth, yield grade, and retail product yield was identified on a region of chromosome 5 in the family of Piedmontese inheritance (Figure 1). Differences between the Piedmontese and Angus alleles inherited from the sire are shown in Table 2. Individuals inheriting the Piedmontese allele had less fat, lower yield grade, and higher retail product yield than those inheriting the Angus allele (differences between alleles of −.18 cm, −.32, and 1.6%, respectively). This region on chromosome 5 affected d-14 Warner-Bratzler shear force (Figure 2) and there is evidence of an interaction with myostatin on chromosome 2. Shown in Figure 3 are the differences in performance among all four genotypic groups. Among animals with active myostatin (+/+), those that inherited the Piedmontese allele in this region of chromosome 5 had greater 14-d Warner-Bratzler shear force than those inheriting the

Table 1. Secondary screening on double-muscled resource populations[a,b]

	Sire	
Chromosome	(Piedmontese × Angus)	(Belgian Blue × MARC III)
5	FAT, RPYD, YG, (WBS14)	—
6	—	BWT, W365, LMA, HCW
14	(FAT)	—
17	—	MARBLE
27	—	MARBLE
29	WBS14, WBS3	—

[a]FAT = fat depth (cm), RPYD = retail product yield (%), YG = USDA yield grade, WBS3 = Warner-Bratzler shear force at d 3 postmortem (kg), WBS14 = Warner-Bratzler shear force at d 14 postmortem (kg), BWT = birth weight (kg), W365 = yearling weight (kg), LMA = longissimus muscle area (cm^2), HCW = hot carcass weight (kg), and MARBLE = marbling score.
[b]Quantitative trait loci detected at least at the suggestive level according to Lander and Kruglyak (1995). Traits within parentheses were suggestive ($P < .002$) for the interaction between the chromosome and myostatin on chromosome 2.

Angus allele from the paternal granddam (3.7 and 3.3 kg, respectively). Conversely, in animals inheriting the inactive myostatin allele (*mh*/+), cattle inheriting the Angus allele on chromosome 5 had a higher 14-d Warner-Bratzler shear force than those inheriting the Piedmontese allele (3.5 and 3.1 kg, respectively).

There was evidence supporting the presence of a QTL for growth and carcass traits on chromosome 6. Quantitative trait loci for birth and yearling weights were found in the family of Belgian Blue inheritance (Figure 4). There was evidence suggesting the presence of QTL
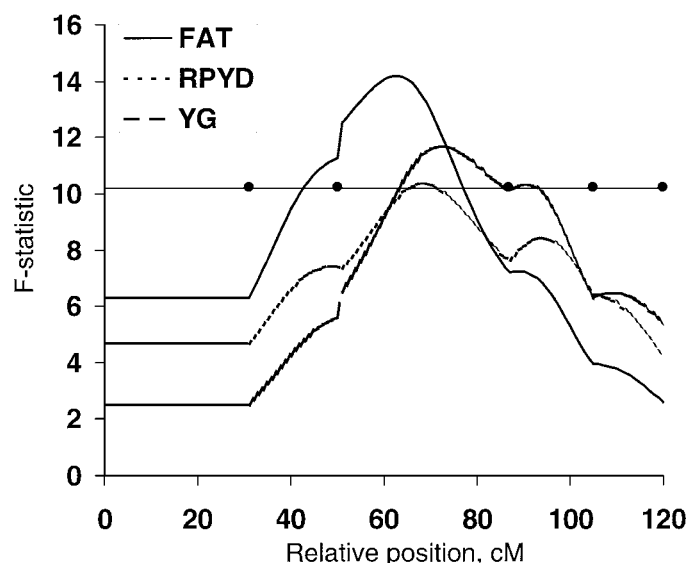

Figure 1. F-statistic profile for bovine chromosome 5. Profile for fat depth (FAT), retail product yield (RPYD), and USDA yield grade (YG) for the family from the Piedmontese × Angus sire. The horizontal line represents the suggestive threshold (F = 10.2) and dots on the line indicate the relative position of markers AGLA293, BL4, BMS1248, BMS772, and BM2830.

Table 2. Allelic effects of putative QTL detected with at least suggestive level on the family from the Piedmontese × Angus sire

Chromosome and trait[a,b]	Effect (P − A)[c]	F	P[d]	Genome[e]
5				
FAT	−.18 cm	14.2	.0002	.18
YG	−.32	11.7	.0007	.53
RPYD	1.6%	10.4	.0014	.93
(WBS14)	—	13.3	.0003	.27
14				
(FAT)	—	12.0	.0006	.47
29				
WBS3	.62	11.2	.0009	.66
WBS14	.42	15.3	.00011	.11

[a]FAT = fat depth (cm), RPYD = retail product yield (%), YG = USDA yield grade, WBS3 = Warner-Bratzler shear force at d 3 postmortem (kg), WBS14 = Warner-Bratzler shear force at d 14 postmortem (kg).
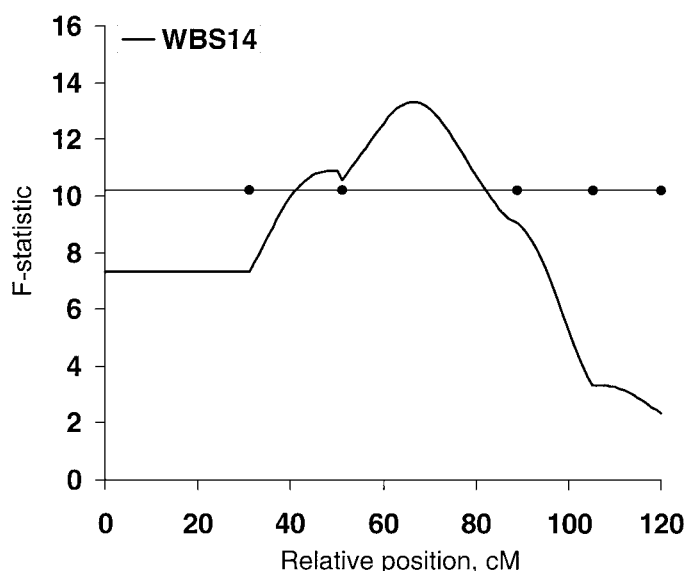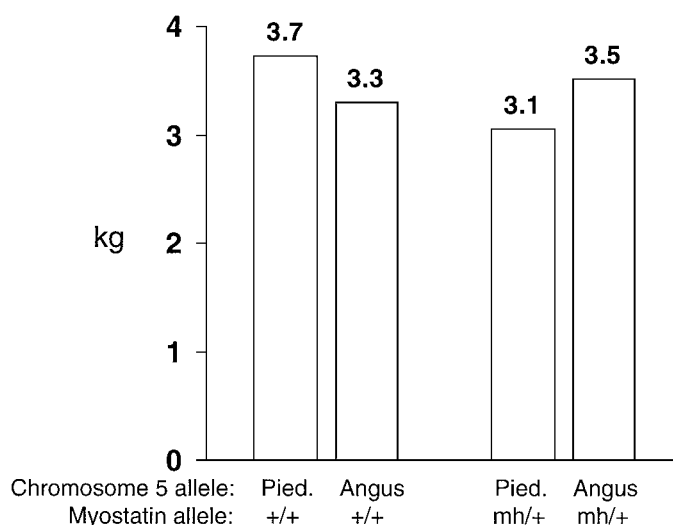[b]Quantitative trait loci detected at least at the suggestive level according to Lander and Kruglyak (1995). Traits within parentheses were suggestive ($P < .002$) for the interaction between the chromosome and myostatin on chromosome 2.
[c]P = Piedmontese, A = Angus.
[d]Probability of false positive for a single test.
[e]Expected number of false positives per genome-wide scan (Lander and Kruglyak, 1995).

for longissimus muscle area and hot carcass weight in the same region (Figure 4). Differences between the Belgian Blue and the MARC III allele inherited from the sire are shown in Table 3. Individuals inheriting the MARC III allele were heavier at birth and at 1 yr of age (differences of −3.8 and −20 kg, respectively),

Figure 3. Interaction for meat tenderness measured as Warner-Bratzler shear force at 14 d postmortem (kg), between myostatin (+/+ or *mh*/+) and chromosome 5 (Piedmontese or Angus) for the family from the Piedmontese × Angus sire.

and there was evidence indicating a heavier carcass and greater longissimus muscle area (differences of −12 kg and −3.22 cm^2, respectively).

A region on chromosome 14 affected fat depth (Figure 5), and there is evidence of an interaction of this region

Figure 2. F-statistic profile for bovine chromosome 5. Profile for meat tenderness measured as Warner-Bratzler shear force at 14 d postmortem (WBS14) for the family from the Piedmontese × Angus sire. The horizontal line represents the suggestive threshold (F = 10.2) and dots on the line indicate the relative position of markers AGLA293, BL4, BMS1248, BMS772, and BM2830.
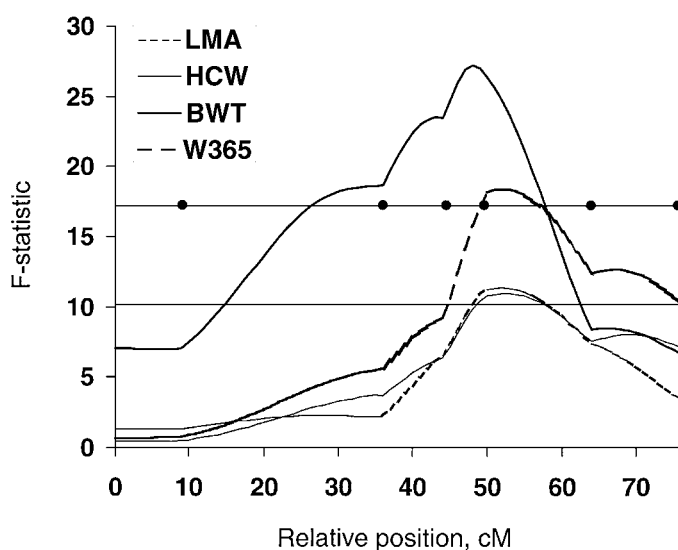

Figure 4. F-statistic profile for bovine chromosome 6. Profile for birth weight (BWT), yearling weight (W365), hot carcass weight (HCW), and longissimus muscle area (LMA) for the family from the Belgian Blue × MARC III sire. The upper horizontal line represents the significant threshold (F = 17.2) and the lower horizontal line represents the suggestive threshold (F = 10.2). Dots on the upper horizontal line indicate the relative position of markers INRA133, BM1329, BMS2508, BM3026, BMS483, and BM415.

Table 3. Allelic effects of putative QTL detected with
at least suggestive level on the family from
the Belgian Blue × MARC III sire

Chromosome and trait[a,b]	Effect (BB − MIII)[c]	F	P[d]	Genome[e]
6				
BWT	−3.8 kg	27.2	.0000004	.0006
W365	−20 kg	19.8	.00002	.019
(LMA)	−3.22 cm^2	11.4	.0008	.61
(HCW)	−12 kg	10.9	.0011	.75
17				
(MARBLE)	−32.77	12.8	.0004	.33
27				
(MARBLE)	29.82	15.5	.0001	.1

[a]BWT = birth weight (kg), W365 = yearling weight (kg), LMA = longissimus muscle area (cm^2), HCW = hot carcass weight (kg), and MARBLE = marbling score.
[b]Quantitative trait loci detected at least at the suggestive level according to Lander and Kruglyak (1995). Traits within parentheses were suggestive ($P < .002$) and all other traits were significant ($P < .00005$).
[c]B = Belgian Blue, MIII = MARC III.
[d]Probability of false positive for a single test.
[e]Expected number of false positives per genome-wide scan (Lander and Kruglyak, 1995).

Figure 6. Interaction for fat depth (cm), between myostatin (+/+ or *mh*/+) and chromosome 14 (Piedmontese or Angus) for the family from the Piedmontese × Angus sire.

with myostatin on chromosome 2. Figure 6 indicates the performance of all four genotypic groups at the maximum of the F-statistic profile for this interaction. Within progeny that inherited the active myostatin allele, those that inherited the Piedmontese allele on chromosome 14 were leaner than those inheriting the Angus allele (.74 and .85 cm, respectively). In the animals inheriting an inactive myostatin allele, those inheriting the Angus allele on chromosome 14 were leaner
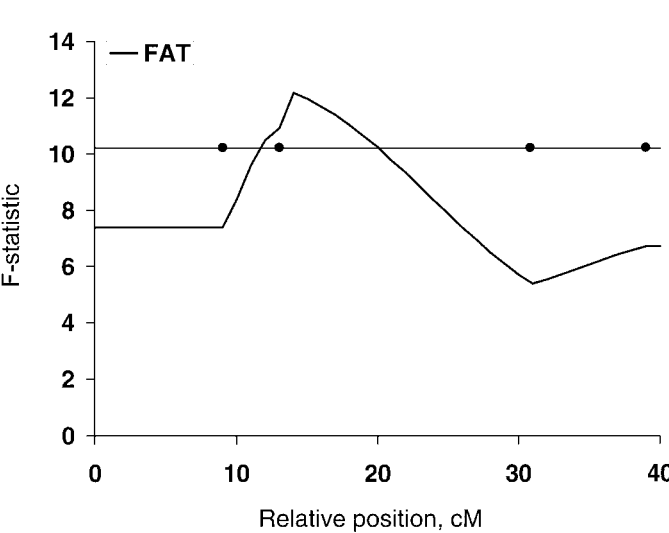
than those inheriting the Piedmontese allele (.46 and .72 cm, respectively).

There was evidence suggesting the presence of QTL affecting marbling on chromosomes 17 and 27 in the Belgian Blue family (Figures 7 and 8). On chromosome 17, individuals inheriting the allele from the MARC III grandparent had more marbling than those inheriting the Belgian Blue allele (Table 3). However, an opposite effect was observed on chromosome 27, where individuals inheriting the Belgian Blue allele had more marbling than those inheriting the MARC III allele (Table 3).

Figure 5. F-statistic profile for bovine chromosome 14. Profile for fat depth (FAT) for the family from the Piedmontese × Angus sire. The horizontal line represents the suggestive threshold (F = 10.2) and dots on the line indicate the relative position of markers BMS1678, RM180, RM011, and BMC 1207.
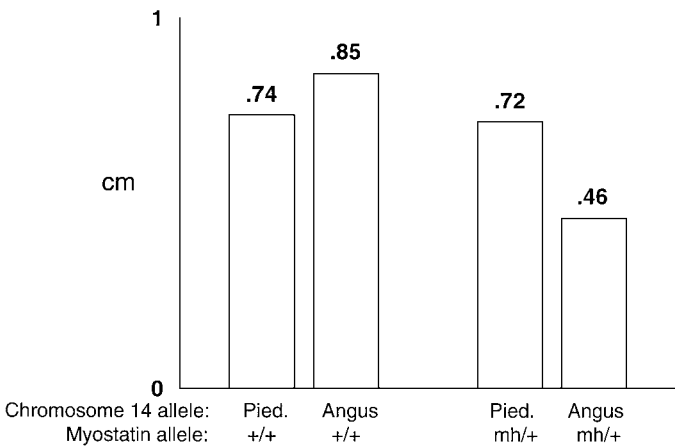

Figure 7. F-statistic profile for bovine chromosome 17. Profile for marbling (MAR) for the family from the Belgian Blue × MARC III sire. The horizontal line represents the suggestive threshold (F = 10.2) and dots on the line indicate the relative position of markers BMS1825, BMS2780, BM9138, BM8125, and BM1862.
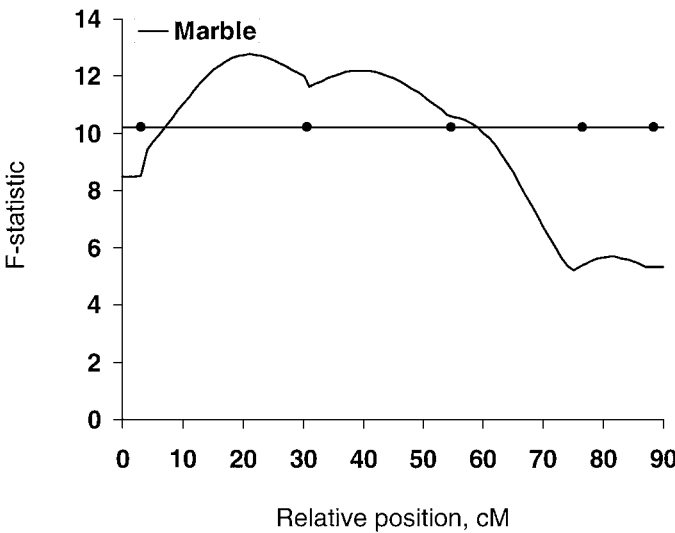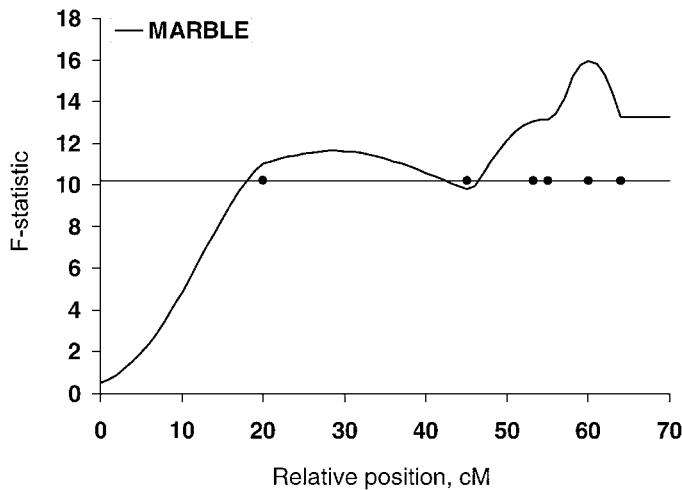
Figure 8. F-statistic profile for bovine chromosome 27. Profile for marbling (MAR) for the family from the Belgian Blue × MARC III sire. The horizontal line represents the suggestive threshold (F = 10.2) and dots on the line indicate the relative position of markers BMS2137, INRA134, BMS2116, HUJI13, BM17052, and BM203.

A putative QTL for meat tenderness was identified on chromosome 29 in the family of Piedmontese inheritance (Figure 9). The F-statistic profile of both measures of meat tenderness (3- and 14-d Warner-Bratzler shear force) suggest the presence of a QTL at the telomeric end of this chromosome. In both measurements, differences in meat tenderness indicate that those individuals inheriting the Piedmontese allele were tougher than those inheriting the Angus allele (.62 and .42 kg, respectively).
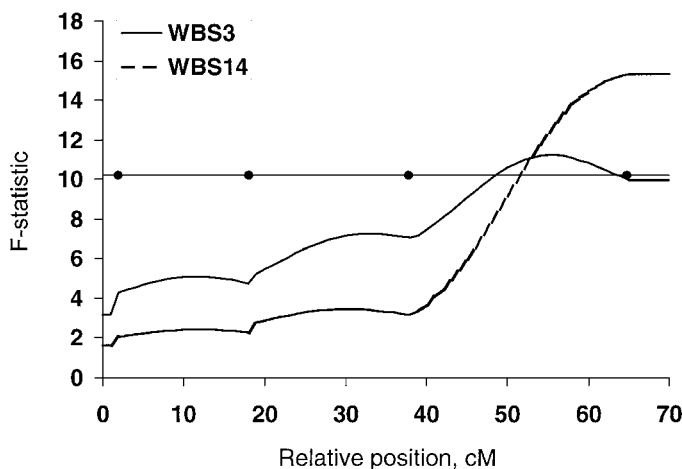

Figure 9. F-statistic profile for bovine chromosome 29. Profile for meat tenderness measured as Warner-Bratzler shear force at 3 (WBS3) and 14 (WBS14) d postmortem for the family from the Piedmontese × Angus sire. The horizontal line represents the suggestive threshold (F = 10.2) and dots on the line indicate the relative position of markers BMS1244, BMS1787, BMS2149, and BMS1948.

The power of detecting QTL is shown in Table 4. Using selective genotyping, the power of detecting a significant (expected fraction of false positives < .05) QTL was .0602, .1612, .3364, .5606, and .7603 for QTL with effects of .4, .5, .6, .7, and .8 SD, respectively. The power of identifying a significant QTL using the entire family after using selective genotyping for preidentification of QTL with effects of .4, .5, .6, .7, and .8 SD was .1145 (i.e., from Table 4 it can be calculated as .1641 − .0196), .3768, .6662, .8783, and .9682, respectively. The power to detect suggestive QTL that were not significant was .1694, .1971, .1299, .0484, and .0113 for QTL with effects of .4, .5, .6, .7, and .8, respectively.

Discussion

A putative QTL on chromosome 5 for fat depth, retail product yield, yield grade, and 14-d Warner-Bratzler shear force was detected. While the evidence for a QTL on chromosome 5 affecting these characteristics was only suggestive for individual traits, the fact that several traits were apparently pleiotropically associated with the same chromosomal region increases the confidence that a gene or cluster of genes affecting growth and carcass traits resides in the region. Quantitative trait loci have been identified previously for carcass traits in this region of chromosome 5 in cattle. Stone et al. (1999) found evidence for a dressing percentage and wholesale rib-bone yield QTL segregating in a half-sib family from a *Bos indicus* × *Bos taurus* cross in the same chromosome 5 region. Furthermore, Stone et al. (1999) found evidence that wholesale rib fat yield is influenced by the same region. In the present study, a QTL for wholesale rib fat yield was nominally significant (*P* = .005) in the same region, supporting the existence of a locus associated with carcass traits. It is not possible to ascertain whether it is a pleiotropic effect of one gene or different genes closely linked with quasi-independent effects on all traits.

Other studies have also identified QTL for growth composition in homologous regions of chromosome 5. The QTL for carcass traits on chromosome 5 is located near the *insulin-like growth factor I* gene (*IGF1*). Moody et al. (1996) found an association between *IGF1* and growth in Hereford cattle, suggesting the possibility that this or a neighboring gene could be associated with growth. Davis et al. (1998), using information from families obtained from a *Bos indicus* × *Bos taurus* cross, reported a QTL for birth weight in the same chromosome 5 region. Similar associations have been observed in other species. Collins et al. (1993), using markers closely linked to *IGF1*, detected a QTL associated with growth in mice. Horvat and Medrano (1995), using a population of mice segregating the high growth (*hg*) locus, mapped the gene to a region near *IGF1*; however, the 500-kb deletion presumably responsible for the high growth phenotype does not include *IGF1*. Casas-Carrillo et al. (1997) also found a potential QTL associated with growth rate in pigs near *IGF1*. Thus,

Table 4. Power of detecting quantitative trait loci from one half-sib family with 246 progeny using the entire family and selective genotyping (n = 46)

ENFP for entire family	ENFP[a] for selective genotyping					
	< .05	.05 to < 1	1 to < 2	2 to < 3	≥ 3	Total
			.4 SD[b]			
<.05	.0466	.0716	.0144	.0119	.0196	.1641
.05 to 1	.0125	.0824	.0345	.0399	.1465	.3159
1 to 2	.0006	.0109	.0076	.0104	.0754	.1049
2 to 3	.0002	.0043	.0032	.0053	.0522	.0652
>3	.0003	.0063	.0060	.0100	.3273	.3498
Total	.0602	.1755	.0657	.0776	.6210	1.0000
			.5 SD			
<.05	.1448	.1741	.0314	.0265	.0390	.4158
.05 to 1	.0156	.0978	.0388	.0449	.1514	.3485
1 to 2	.0005	.0078	.0051	.0074	.0515	.0723
2 to 3	.0002	.0027	.0021	.0028	.0318	.0395
>3	.0001	.0027	.0025	.0045	.1141	.1238
Total	.1612	.2851	.0799	.0861	.3877	1.0000
			.6 SD			
<.05	.3248	.2669	.0417	.0328	.0456	.7118
.05 to 1	.0114	.0650	.0252	.0283	.0908	.2207
1 to 2	.0002	.0033	.0021	.0029	.0205	.0291
2 to 3	.0000	.0009	.0007	.0010	.0099	.0125
>3	.0000	.0005	.0006	.0014	.0234	.0259
Total	.3364	.3366	.0703	.0664	.1903	1.0000
			.7 SD			
<.05	.5559	.2641	.0333	.0250	.0308	.9091
.05 to 1	.0046	.0248	.0093	.0097	.0307	.0791
1 to 2	.0000	.0006	.0004	.0006	.0044	.0060
2 to 3	.0000	.0002	.0001	.0002	.0018	.0023
>3	.0000	.0001	.0001	.0001	.0032	.0035
Total	.5606	.2898	.0432	.0355	.0710	1.0000
			.8 SD			
<.05	.7593	.1791	.0176	.0123	.0130	.9812
.05 to 1	.0011	.0061	.0019	.0022	.0063	.0176
1 to 2	.0000	.0000	.0001	.0001	.0004	.0006
2 to 3	.0000	.0000	.0000	.0000	.0002	.0002
>3	.0000	.0000	.0000	.0000	.0003	.0004
Total	.7603	.1852	.0196	.0146	.0202	1.0000

[a]ENFP = expected number of false positives: < .05 = genome-wide significance (one false positive expected per 20 scans; $P < .00005$); .05 to 1 = evidence suggestive of linkage (one false positive expected per scan; $P < .002$); 1 to 2 = nominally significant results (one to two false positives expected per scan; $P < .004$); 2 to 3 = nominally significant results (two to three false positives expected per scan; $P < .006$); > 3 = nominally significant results (more than three false positives expected per scan; $P > .006$).
[b]SD = standard deviations.

to date, there are several independent lines of evidence to support the existence of a QTL for growth and carcass traits on bovine chromosome 5 in a region closely linked to *IGF1*. Further studies will be needed to ascertain whether the same gene or genes is(are) responsible for the expression of the traits in different species.

An interaction for 14-d Warner-Bratzler shear force between myostatin on chromosome 2 and a locus on chromosome 5 was identified. The maximum F-statistic is in the same region of chromosome 5 where QTL for fat depth, retail product yield, and yield grade were located. Shackelford et al. (1994) found that F_1 offspring obtained from Piedmontese sires had higher 14-d shear force values than offspring obtained from Angus sires. A similar pattern was observed in ani-

mals inheriting the inactive myostatin allele and chromosome 5: F_1 animals of Piedmontese inheritance had a higher 14-d shear force values than animals with Angus inheritance. The interaction between these genomic regions could explain results observed by Shackelford et al. (1994). However, there is no previous study in which animals with Piedmontese inheritance with active myostatin alleles are compared with other breeds. Further studies are required to verify the existence of this interaction.

The presence of a QTL for growth and carcass traits was observed on chromosome 6. Davis et al. (1998) reported a QTL for birth weight on chromosome 6. Furthermore, an estimated effect of 2 kg in one family and 3.8 kg in a second family is very similar to the

estimated effect of 3.8 kg observed in the present study. Given that the study by Davis et al. (1998) focused on birth weight, no other information is available on the effect of this region on subsequent weights or for carcass traits. Results from the present study suggest that this region of chromosome 6 is associated with yearling weight and hot carcass weight and longissimus muscle area. Animals inheriting the MARC III allele instead of the Belgian Blue allele from the sire were heavier and expressed a greater longissimus muscle area. The comparison between alternative alleles inherited from the sire favors the MARC III allele in all traits. Alleles inherited from MARC III animals can be from any of the four breeds involved in the composite breed (Hereford, Angus, Red Poll, or Pinzgauer), so these results highlight the need to characterize allelic variation of quantitative trait loci in several breeds and breed crosses to enable effective marker-assisted selection implementation.

Suggestive QTL for fat deposition traits have been detected on chromosome 14. The putative QTL for fat depth resulted from the interaction between myostatin on chromosome 2 and a gene or genes located on chromosome 14, closely linked to the marker RM180. Animals inheriting the Piedmontese allele on chromosome 14 had a similar fat depth regardless of what allele was inherited on chromosome 2 (.74 and .72 cm, respectively, for individuals inheriting active and inactive myostatin alleles), but those individuals inheriting the Angus allele on chromosome 14 deposited different amounts of fat. Individuals inheriting the Angus allele on chromosome 14 deposited more fat when inheriting the active myostatin allele on chromosome 2, compared to animals that inherited the inactive allele. The location of the maximum F-statistic for this fat deposition interaction is similar to that identified for fat percentage and fat yield in dairy cattle (Zhang et al., 1998). Zhang et al. (1998) confirmed results from Ron et al. (1998), who reported a suggestive QTL for fat percentage and fat yield in the same chromosomal region. These results suggest the presence of genes on chromosome 14 that influence fat production in bovines.

Two putative QTL for marbling were detected on chromosomes 17 and 27. A false QTL of the magnitude observed on chromosome 17 would be observed by chance once in every three scans, and the magnitude of the one on chromosome 27 would be observed once in every 10 scans. Other studies have reported QTL on chromosome 27, in the same region where the putative QTL for marbling is located. Ashwell et al. (1998) reported that dairy form and dairy capacity, both conformational-type traits used to evaluate Holstein cows, were associated with a QTL near the marker BM203. Dairy form and dairy capacity are indirect fat deposition measurements. Furthermore, Zhang et al. (1998) indicate a nominally significant association between this region of chromosome 27 with fat percentage and fat yield in dairy cattle. The combined results of these studies suggest that a putative QTL associated with fat deposition is located in this genomic region in cattle. However, more studies using additional phenotypic measurements for fat deposition would be necessary to establish whether the same genes influence these traits in bovines.

Meat tenderness, expressed as Warner-Bratzler shear force, is an economically important trait in the beef industry. A putative QTL was detected on the telomeric end of bovine chromosome 29. Tenderness of meat is determined by the rate and extent of postmortem proteolysis. The calpain proteolytic system has a major role and is perhaps responsible for meat tenderization during postmortem storage (Shackelford et al., 1994). The calpain proteolytic system consists of μ-calpain (requires micromolar Ca^{2+} for activity), m-calpain (requires millimolar Ca^{2+} for activity), and calpastatin (endogenous inhibitor of calpains). Pang et al. (1996) mapped μ-calpain to the region 11q13 of human chromosome 11. A single nucleotide polymorphism was developed from a partial cDNA bovine sequence of μ-calpain and mapped at 54 cM from the most centromeric marker on bovine chromosome 29 (T.P.L. Smith, personal communication). This makes μ-calpain a positional candidate gene for the QTL identified on this chromosome.

Quantitative trait loci with an effect of < .4 SD, in which the sire is heterozygous, are probably undetected. Unidentified QTL could be the result of low power. It is expected to detect QTL with effects of .4 SD with a power of .38. Quantitative trait loci with smaller effects would have a lower power of detection. The power to detect QTL with effects of .7 SD with selective genotyping, followed by the inclusion of information from the entire family, is .87. The power to detect QTL with effects > .7 SD is high, suggesting that selective genotyping as a prescreening procedure is an effective tool to identify QTL with large effects.

Additional chromosomal regions harboring QTL need to be examined. In the present study, 2,850 cM were evaluated for putative QTL using 150 markers in 92 individuals (46 from each family). In the second phase, the entire progeny from both families was evaluated in regions with putative QTL, based on the information obtained from selective genotyping. Forty-eight markers on 10 chromosomal regions were used, covering 598 cM. The coverage evaluated in the entire population is 21% of the genome. It is likely that QTL with moderate effects (< .6 SD) are located in regions unevaluated with the entire population. Further screening in the entire progeny of both families needs to be pursued to identify these QTL in other chromosomal regions.

Selective genotyping for two correlated traits was used to identify putative regions where QTL for these traits may reside. Bovenhuis and Spelman (1998) indicated that the benefit of selective genotyping diminishes rapidly as the number of traits increases. This is especially the case if correlations between traits are low. Although putative QTL for other traits were

identified, loci for traits uncorrelated with retail product yield and fat depth could have been missed. Further studies are required to identify additional quantitative trait loci segregating in the families under study for traits of economical importance.

It was possible to identify additional QTL in two families segregating the locus that causes double-muscling in cattle. Myostatin is considered a major gene because of its extreme effect in expression of growth and carcass traits (Arthur, 1995). However, it was possible to assess that other regions in the genome contribute to the expression of these traits. The magnitude of the identified QTL effects was mostly suggestive, indicating that the effects of these loci may be so subtle that in order to identify them the number of progeny studied should be increased.

Implications

Findings have advanced the understanding of inheritance of quantitative characters. In families with allelic segregation of myostatin in cattle, other loci also influence quantitative traits. Putative interactions for economically important traits between myostatin and other regions of the genome have been detected. Some of the detected QTL fall within the chromosomal regions reported in other studies. Further studies are necessary to assess whether other regions harbor genes associated with growth and carcass traits in families segregating myostatin. Regions reported here to contain quantitative trait loci must be assessed in other populations to determine the extent of their usefulness.

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