Detection of QTL in a Wagyu x Limousin cross

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Introduction

These lines were chosen due to extremes of marbling. Wagyu (Japanese Black) are heavily marbled while Limousin are lightly marbled. Also, relative to other breeds, Wagyu beef has an increased ratio of monounsaturated fat (MUFA) to saturated fat (SFA). A whole genome scan for carcass traits was performed on 328 F_2 progeny produced from Wagyu x Limousin cross parents derived from eight founder Wagyu bulls.

Carcass QTL

Average genetic marker spacing was 17.1 cM. Loci shown to harbor QTL in preliminary analyses were fine mapped by adding 44 marker areas across regions of interest reducing the average interval to 6.8 cM.

Significant QTL (genome-wide threshold $P \leq 0.05$) were found for Longisimus Muscle Area (BTA2; F= 45.39), Birth Weight (BTA12; F=11.92: BTA29; F=11.1), Average Daily $Gain_{growing\ phase}$ (BTA4; F=10.51), Average Daily $Gain_{finishinig}$ phase (BTA9; F=16.3: BTA17; F=11.63) and Hot Carcass Weight (BTA7; F=9.73; BTA16; F=10.09; BTA29; F=13.8). Positive effects indicate that substitution of a Wagyu allele for a Limousin allele increased the phenotype shown in Table 1. Conversely, negative effects indicate substitution of a Limousin allele for a Wagyu allele increased the phenotype.

The QTL affecting LMA (Figure 1) has been described by other researchers and is near the myostatin locus (*GDF8*) which has been previously associated with double muscling (muscular hypertrophy). Limousin have been shown to have almost exclusively a mutation in this gene that changes the amino acid sequence in the protein. (Phenylalanine to Leucine). The increase in LMA effect of the GDF8 gene has been confirmed by SNP analyses of this region.

Table 1. Location of QTL affecting growth and carcass traits in a Wagyu x Limousin cattle population

BTA	Trait[1]	Position (cM)	*F*-statistic	Additive effect + S.E.[2]	Flanking markers[3]
2	LMA	4	45.39	-6.19 ± 0.92	*ILSTS026*, 9.7; *TGLA431*, 12.6
4	ADG_g	93	10.51	0.044 ± 0.013	*IDVGA-51*, 84.1; *CA088*, 93.7
7	ADG_g	2	7.68*	0.031 ± 0.011	*BM7160*, 0; *DIK2870*, 3; *BL1067*, 18.3
7	HCW	0	9.73	9.48 ± 3.04	*BM7160*, 0; *DIK2870*, 3
9	ADG_f	60	16.3	0.076 ± 0.019	*ILSTS013*, 53.8; *BMS1724*, 78.1
12	180 d wt	8	8.36	5.15 ± 1.78	*BMS410*, 0; *DIK2916*, 7.9; *BM6108*, 20.9
12	ADG_p	8	7.9*	0.027 ± 0.010	*BMS410*, 0; *DIK2916*, 7.9; *BM6108*, 20.9
12	BWT	125	11.92	-2.08 ± 0.60	*BMS1316*, 111; *BMS2724*, 125.3
12	LMA	11	9.06	2.79 + 0.92	*BMS410*, 0; *DIK2916*, 7.9; *BM6108*, 20.9
16	180 d wt	79	9.02	-8.47 ± 2.82	*CSSM028*, 56.5; *BM719*, 79.4
16	ADG_p	79	9.43	-0.046 ± 0.015	*CSSM028*, 56.5; *BM719*, 79.4
16	HCW	65	10.09	-14.10 ± 4.51	*CSSM028*, 56.5; *BM719*, 79.4
17	ADG_f	30	11.63	-0.059 ± 0.017	*BMS1825*, 0.9; *BMS1101*, 24.4
29	BWT	11	11.1	1.56 ± 0.47	*BMS1857*, 3.8; *ILSTS057*, 10.6; *DIK5269*, 12.2; *BMS764*, 15.3
29	HCW	1	14.17	11.62 ± 3.13	*TGLA86*, 0; *BMS1857*, 3.8

1 ADGf- average daily gain finishing, ADGg - ADG growth, ADGp - ADG pre-weaning, BWT - birth weight, HWC - hot carcass weight, LMA - longissimus muscle area .
2 Units are kg except for LMA (cm2). Effect resulting from a Wagyu allele replacing an allele from Limousin.
marker is shown.
* Approaching suggestive value.

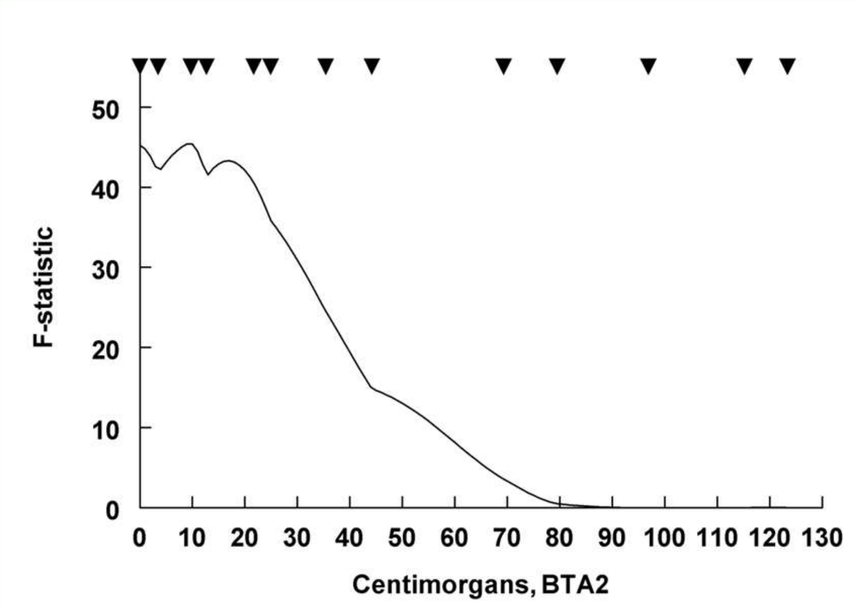

Figure 1. QTL scan of chromosome 2 for LMA

Lipid QTL

As consumers become more health conscience, they are more concerned about levels of saturated fat (SFA) in their diet. Fatty Acids with 16 and 18 carbon units make up most of the lipid in meat. Saturated fats are represented as C16:0 and C18:0 whereas mono-unsaturated fats are represented as C16:1 and C18:1. Flavor has been positively correlated with the mono-unsaturated fatty acid oleate (C18:1). Another type of fat implicated in health is conjugated linoleic acid (CLA) which has been shown to decrease fat and total body weight, total and LDL cholesterol in animal models while in humans there are conflicting data on the positive effects of CLA.

A QTL with multi-faceted significant effects on CLA (F = 12.01), marbling (F = 11.76), mono-unsaturated fat (F = 21.37), saturated fat (F = 12.52), R2 (ratio of C16:0 to C16:1) (F = 19.44), R3 (ratio of C18:0 to C18:1) (F = 25.18) and a suggestive effect on flavor (F = 7.91) was observed towards the centromere of BTA2 (Figure 2). These QTL effects are seemingly consistent with a unified biological model supportive of a gene or genes segregating between Wagyu and Limousin in this region that confer greater lipid content and a more desirably flavored steak derived from Wagyu genes. Other QTL were spread around the genome with the exception of a number of suggestive QTL on chromosome 7 (Figure 3).

Table 2. Location of QTL affecting lipid deposition, profile and meat characteristic traits in a Wagyu x Limousin cattle population.

Trait[1]	BTA[2]	Position cM	F-statistic	Additive effect ± S.E[5]	Flanking marker
fat_d	1	58	9.7	-0.053 + 0.017	*BMS4030, 48.7; DIK2121, 62.4*
CLA	2	2	12.01	5.265 ± 1.519	*TGLA44*, 0.00; *DIK4469*, 3.50; *ILSTS026*, 9.7
Flavor	2	0	7.91	0.096 ± 0.035	*TGLA44*, 0.00; *DIK4469*, 3.50
KPH	2	25	9.33	0.105 ± 0.034	*DIK1172*, 21.7; *CSFM050*, 24.90; *TEXAN-2*, 35.40
Marbling	2	3	11.76	0.400 ± 0.117	*DIK4469*, 3.50; *ILSTS026*, 9.7
MUFA	2	5	21.37	1374.7 ± 297.3	*TGLA44*, 0.00; *DIK4469*, 3.50; *ILSTS026*, 9.7
SFA	2	10	12.52	919.8 ± 260.0	*DIK4469*, 3.50; *ILSTS026*, 9.7
R_2	2	3	19.44	0.778 ± 0.176	*DIK4469*, 3.50; *ILSTS026*, 9.70; *TGLA431*, 12.7
R_3	2	4	25.18	22.445 ± 4.473	*TGLA44*, 0.00; *DIK4469*, 3.50; *ILSTS026*, 9.7
Myo-fibral tenderness	5	0	12.66	-0.246 ± 0.069	*BMS1095*, 0; *BM6026*, 10.4
Overall tenderness	5	0	10.17	-0.216 ± 0.068	*BMS1095*, 0; *BM6026*, 10.4
CLA	7	131	8.24	-5.195 ± 1.810	*CST*, 122; *BMS1979*, 133.4
KPH	7	40	8.16	-0.090 ± 0.031	*BMS713*, 21.1; *BM6105*, 40.3; *TGLA303*, 42.2
MUFA	7	125	10.76	-1095.8 ± 334.0	*CST*, 122; *BMS1979*, 133.4
SFA	7	125	8.93	-848.5 ± 283.9	*CST*, 122; *BMS1979*, 133.4
R_2	7	110	9.17	-0.547 ± 0.181	*BM9065*, 99.7; *DIK4838*, 110.5; *CST*, 122
R_3	7	108	8.62	-13.4 ± 4.58	*BM9065*, 99.7; *DIK4838*, 110.5; *CST*, 122
CLA	7	131	8.24	-5.195 ± 1.810	*CST*, 122; *BMS1979*, 133.4
WBSF	10	95	7.9*	-0.316 ± 0.112	*BMS2641*, 79.2; *BL1134*, 110.9
MUFA	12	0	7.66*	-766.7 ± 277.0	*BMS410*, 0; *DIK2916*, 7.90
SFA	12	0	9.43	-718.7 ± 234.0	*BMS410*, 0.00; *DIK2916*, 7.90
R_2	28	50	9.29*	1.247 ± 0.409	*BM7246*, 33.4; *MB023*, 50.5 (end)
Cholesterol	ND				
Connective tissue	ND				
Juiciness	ND				
PUFA	ND				
R_1	ND				

[1] fat_d - subcutaneous fat depth; CLA- conjugated linoleic acid; KPH - kidney, pelvic and heart fat; MUFA amount of monounsaturated fat; R_1 ratio of C14:1 to C14:0, R_2 ratio of C16:1 to C16:0, R_3 ratio of C18:1 to C18:0, SFA - amount of saturated fat; WBSF - Warner–Bratzler shear force.
[2] ND -No suggestive or significant association detected.
*approaching suggestive value.
[5] Effect resulting from a Wagyu allele replacing an allele from Limousin.

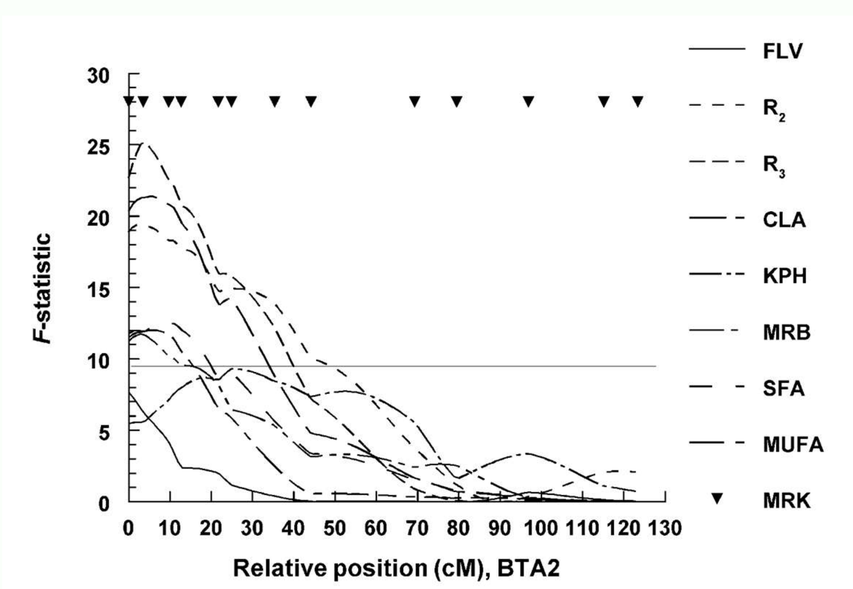

Figure 2. QTL scan for fatty acids and flavor

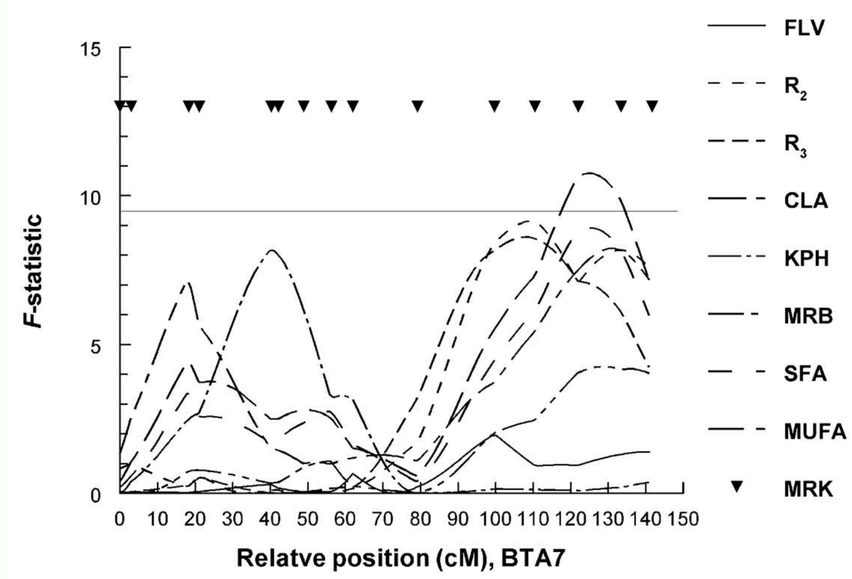

Figure 3. QTL scan for fatty acids and flavor

In summary, we have identified seven new QTL regions on five chromosomes that influence tenderness, fatty acid deposition and profiles, and meat quality in a F2 Wagyu x Limousin population. Further investigation of these QTL will promote our understanding of lipid metabolism and fat deposition in cattle. As the consumer becomes more health conscious they have increased concerns about the levels of SFA in their diet. Therefore, CLA and the ratio of MUFA to SFA have human health implications in terms of overall health and coronary heart disease. It still remains to determine if it is GDF8 that is effecting the fatty acids ratios or if it is a nearby gene and what the mechanism of action maybe.