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Quantitative trait loci with additive effects on growth and carcass traits in a Wagyu–Limousin F_2 population

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Summary

A whole-genome scan for carcass traits [average daily gain during the pre-weaning, growth and finishing periods; birth weight; hot carcass weight and longissimus muscle area (LMA)] was performed on 328 F_2 progeny produced from Wagyu × Limousin-cross parents derived from eight founder Wagyu bulls. Nine significant ($P \leq 0.05$) and four suggestive ($P \leq 0.1$) QTL affecting seven growth and carcass traits were identified. Significant QTL were located on bovine chromosomes 2, 4, 7, 9, 12, 16, 17 and 29. A QTL previously reported on chromosome 2 for LMA was also detected in this study. These results provide insight into genetic differences between the Wagyu and Limousin breeds.

Keywords carcass, cattle, Limousin, myostatin, quantitative trait loci, Wagyu.

Many QTL have been identified in bovine populations (http://bovineqtlv2.tamu.edu/index.html; http://www.animalgenome.org/QTLdb). Experimental comparisons of Limousin and Wagyu germplasm indicate decisive breed differences with respect to carcass attributes (Kuber *et al.* 2004; Pitchford *et al.* 2006). These differences make Limousin and Wagyu candidate breeds from which to develop populations for mapping QTL for carcass traits. Here, we report the results of a genome scan for carcass traits using a Wagyu × Limousin F_2 population.

Eight Wagyu bulls were mated to 108 Limousin females to produce 121 females over a 3-year period. Three of the eight Wagyu bulls also sired six F_1 males. The Wagyu–Limousin F_1 bulls and females used in this study were purchased from Washington State University and moved to Miles City, MT in October 1999. The F_1 males and females were *inter se* mated, except that matings of known relatives were avoided. These matings produced 328 F_2 progeny between 2000 and 2003.

The F_2 calves were weighed at birth (BWT), reared by their dams and weighed again at weaning at an average age of 175 days (SD: 14 days). Pre-weaning growth rate (ADG_p) was the difference between weights at weaning and birth divided by the animal's age at weaning. Age-adjusted weaning weight (180-day weight) was calculated as BWT plus ADG_p multiplied by 180. After weaning, the calves were managed in a two-phase system: a growing phase with a ration composition of 50–54% DM, 14.4–15.6% CP and 1.06–1.18 Mcal/kg NEg and a finishing phase with a ration composition of 68–70% DM, 11.6–13.4% CP and 1.26–1.31 Mcal/kg NEg. All calves were fed the growing ration for approximately 207 days from weaning until they were switched to the finishing ration. The finishing ration was fed a minimum of 113 days until the calves were harvested. Post-weaning ADG was computed within the growing and finishing phases (ADG_g and ADG_f respectively) by regression of weight (measured at 28-day intervals) on age. Within year and sex, calves were randomly assigned to groups of 8–11 animals, to be harvested at 2- to 3-week intervals. Thus, the final group harvested each year had been fed the finishing ration at least 210 days. At 450–641 days of age (average 561 days), calves were transported to the abattoir the afternoon prior to harvest and held overnight with water but no feed. Hot carcass weight (HCW) was measured the day of harvest and LMA was assessed after 48 h of storage at 2 °C using a planer grid at the interface of the 12th and 13th ribs.

Initially, 156 markers covering the 29 bovine autosomes were chosen from http://www.marc.usda.gov/genome/cattle/cattle.html based on marker position, suitability for multiplex reactions, ease of scoring and number of alleles (Table S1). Genotypes on all animals in the population were collected on a LiCor 4200 DNA Analysis System and independently scored by two individuals. Markers with discrepancies in scoring and genotypic errors detected using GENOPROB (Thallman *et al.* 2001a,b) that could not be

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resolved between the two scorers were re-amplified. A linkage map of each chromosome was constructed using CRI-MAP (Green *et al.* 1990; http://compgen.rutgers.edu/multimap/crimap/). Average marker spacing was 17.1 cM, and the information content for detection of additive effects averaged 0.3. Loci shown to harbour QTL in preliminary analyses were fine-mapped by adding 44 markers across eight regions of interest (Table S1). After adding these markers, the inter-marker interval in the regions of interest was reduced to 6.8 cM.

QTL were identified by least-squares regression analysis using the F_2 analysis option of QTL EXPRESS (Seaton *et al.* 2002; http://qtl.cap.ed.ac.uk/). A profile of *F*-statistics was generated at 1-cM intervals for each chromosome. For BWT, ADG_p and 180-day weight, a single additive QTL was modelled with simultaneous adjustment for a contemporary group effect (year–sex–age of dam combinations). For post-weaning growth and carcass traits, the effect of a single additive QTL was modelled with simultaneous adjustment for classification effects of year and sex, and the continuous linear effect of age at harvest. For QTL that had not been previously reported, the observed significant level was adjusted to a genome-wide basis following Cheverud (2001). The observed nominal significance level was used to confirm QTL previously identified in other studies. Dominance QTL effects were not detected.

Seven new QTL involved in growth and carcass traits were found in our study. Chromosomal locations, flanking markers, *F*-statistics, 95% confidence intervals, significance levels and effect sizes are shown in Table 1. QTL influencing fatty acid metabolism, fat deposition and palatability are reported elsewhere (L.J. Alexander *et al*., unpublished data). Significant QTL (genome-wide threshold $P \leq 0.05$) were found for LMA (BTA2, $F = 45.39$), BWT (BTA12, $F = 11.92$; BTA29, $F = 11.1$), ADG_g (BTA4, $F = 10.51$), ADG_f (BTA9, $F = 16.3$; BTA17, $F = 11.63$) and HCW (BTA7, $F = 9.73$; BTA16, $F = 10.09$; BTA29, $F = 13.8$). Positive additive effects in Table 1 indicate that the substitution of a Wagyu allele for a Limousin allele increased the phenotype. Conversely, negative additive effects in Table 1 indicate that the substitution of a Limousin allele for a Wagyu allele increased the phenotype.

The QTL on BTA2 affecting LMA (Fig. 1) has been described previously by Casas *et al.* (1998) and is near the *myostatin* locus (*GDF8*), which has been previously

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

BTA	Trait[1]	Position (cM)	95% CI[2]	Start CI	End CI	*F*-statistic	Significance		Additive effect ± SE[3]	Flanking markers[4]
							Nominal	Genome-wide		
12	180-day weight	8	69	0.0	42.4	8.36	0.004	0.09	5.15 ± 1.78	*BMS410*, 0; *DIK2916*, 7.9; *BM6108*, 20.9
16	180-day weight	79	25	66.4	end	9.02	0.003	0.084	−8.47 ± 2.82	*CSSM028*, 56.5; *BM719*, 79.4
9	ADG_f	60	15	52.4	67.7	16.3	6.94E-05	0.002	0.076 ± 0.019	*ILSTS013*, 53.8; *BMS1724*, 78.1
17	ADG_f	30	26	17.2	42.8	11.63	0.001	0.024	−0.059 ± 0.017	*BMS1825*, 0.9; *BMS1101*, 24.4
4	ADG_g	93	29	78.4	end	10.51	0.001	0.043	0.044 ± 0.013	*IDVGA-51*, 84.1; *CA088*, 93.7
7	ADG_g	2	60	0.0	31.9	7.68	0.006	0.122[5]	0.031 ± 0.011	*BM7160*, 0; *DIK2870*, 3; *BL1067*, 18.3
12	ADG_p	8	73	0.0	44.3	7.9	0.005	0.113[5]	0.027 ± 0.010	*BMS410*, 0; *DIK2916*, 7.9; *BM6108*, 20.9
16	ADG_p	79	24	66.9	end	9.43	0.002	0.068	−0.046 ± 0.015	*CSSM028*, 56.5; *BM719*, 79.4
12	BWT	125	24	112.8	end	11.92	0.001	0.014	−2.08 ± 0.60	*BMS1316*, 111; *BMS2724*, 125.3
29	BWT	11	49	0.0	35.6	11.1	0.001	0.037	1.56 ± 0.47	*BMS1857*, 3.8; *ILSTS057*, 10.6; *DIK5269*, 12.2; *BMS764*, 15.3
7	HCW	0	39	0.0	19.6	9.73	0.002	0.043	9.48 ± 3.04	*BM7160*, 0; *DIK2870*, 3
16	HCW	65	21	54.6	75.5	10.09	0.002	0.037	−14.10 ± 4.51	*CSSM028*, 56.5; *BM719*, 79.4
29	HCW	1	33	0.0	17.6	14.17	0.0002	0.008	11.62 ± 3.13	*TGLA86*, 0; *BMS1857*, 3.8
2	LMA	4	12	0.0	9.8	45.39	8.55E-11	1.91E-09	−6.19 ± 0.92	*ILSTS026*, 9.7; *TGLA431*, 12.6
12	LMA	11	57	0.0	39.6	9.06	0.003	0.063	2.79 ± 0.92	*BMS410*, 0; *DIK2916*, 7.9; *BM6108*, 20.9

[1]ADG_f, average daily gain finishing; ADG_g, ADG growth; ADG_p, ADG pre-weaning; BWT, birth weight; HWC, hot carcass weight; LMA, longissimus muscle area.

[2]CI, confidence interval calculated by the method of Darvasi & Soller (1997).

[3]Units are kg except for LMA (cm^2). Effect resulting from a Wagyu allele replacing a Limousin allele.

[4]Flanking marker, position (cM). In cases where the flanking marker is 1 cM or less from the QTL peak, the next flanking marker is shown.

[5]Approaching suggestive value.

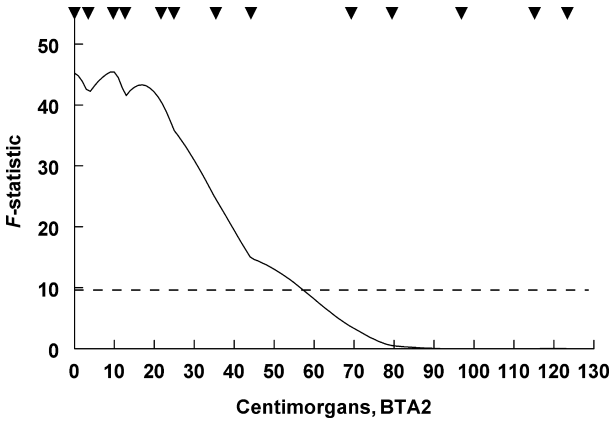

Figure 1 *F*-statistic profile for longissimus muscle area on BTA2. Marker positions are indicated by triangles above the graph. Marker order is *TGLA44, DIK4469, ILSTS026, TGLA431, DIK1172, CSFM050, TEXAN-2, TGLA377, RM356, ILSTS050, BMS1866, BMS2267* and *BM2113*. *Myostatin* (*GDF8*) is located close to *DIK4469*. The genome-wide significance threshold of 9.46 is shown as a dashed line.

associated with muscular hypertrophy (Grobet *et al.* 1998). Grobet *et al.* (1998) and Dunner *et al.* (2003) found that Limousin were almost fixed for the *GDF8* F94L substitution. Grobet *et al.* (1998) classified this mutation as a conservative amino acid change and suggested that the Limousin allele had at most a minor role in muscular hypertrophy. However, we suggest that a hydrophobic aromatic (Phe) replaced by an aliphatic side chain (Leu) is not conservative and that the effect on LMA we found on BTA2 is due to the L94 allele from the Limousin breed on the Wagyu background. The confirmation of the presence of the L94 allele in this population and its effect on LMA in this population is the focus of future research.

Suggestive QTL (genome-wide threshold $P \leq 0.10$) were found for LMA (BTA12, $F = 9.06$), 180-day weight (BTA12, $F = 8.36$; BTA16, $F = 9.02$) and ADG_p (BTA16, $F = 9.43$). An additional QTL affecting ADG_p ($F = 7.9$, $P = 0.113$), with a probability level approaching the suggestive threshold of $P = 0.10$, was observed in the region of BTA12 where the suggestive QTL for LMA and 180-day weight were detected, and on BTA7 where ADG_g ($F = 7.68$, $P = 0.122$) and HCW were present. On BTA16, the suggestive QTL for ADG_p, 180-day weight and HCW were coincident.

Mizoguchi *et al.* (2006) identified QTL in a genome scan for carcass weight in a purebred Wagyu population on BTA14. QTL for LMA and carcass yield were not found. In an earlier study, Mizoshita *et al.* (2004) found QTL for LMA on BTA4 and a group of body weight, carcass weight and ADG QTL on BTA14 in Wagyu cattle. However, these QTL were not detected in the Wagyu × Limousin crosses used in this study.

In conclusion, we found nine significant and four suggestive QTL affecting seven growth and carcass traits in this population. These results lead to a better understanding of genetic differences between the Wagyu and Limousin breeds. These results also contribute to a broader understanding of the genetic architecture of associated phenotypes.

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Supplementary Material

The following supplementary material is available for this article online from http://www.blackwell-synergy.com/doi/full/10.1111/j.1365-2052.2007.01616.x

Table S1 Mapping positions of the markers used in this study.

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