



Detection of Quantitative Trait Loci Affecting Fat Deposition Traits in Pigs

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ABSTRACT: Quantitative trait loci (QTL) associated with fat deposition traits in pigs are important gene positions in a chromosome that influence meat quality of pork. For QTL study, a three generation resource population was constructed from a cross between Korean native boars and Landrace sows. A total of 240 F₂ animals from intercross of F₁ were produced. 80 microsatellite markers covering chromosomes 1 to 10 were selected to genotype the resource population. Intervals between adjacent markers were approximately 19 cM. Linkage analysis was performed using CRIMAP software version 2.4 with a FIXED option to obtain the map distances. For QTL analysis, the public web-based software, QTL express (<http://www.qtl.cap.ed.ac.uk>) was used. Two significant and two suggestive QTL were identified on SSC 6, 7, and 8 as affecting body fat and IMF traits. For QTL affecting IMF, the most significant association was detected between marker *sw71* and *sw1881* on SSC 6, and a suggestive QTL was identified between *sw268* and *sw205* on SSC8. These QTL accounted for 26.58% and 12.31% of the phenotypic variance, respectively. A significant QTL affecting IMF was detected at position 105 cM between markers *sw71* and *sw1881* on SSC 6. (**Key Words:** Quantitative Trait Loci, Pig, Intramuscular Fat, Body Fat, Microsatellite Marker)

INTRODUCTION

Quantitative trait loci (QTL) are gene positions in a chromosome that influence multifactorial traits that are determined by several genes as well as environmental factors and the interactions between them. Comprehensive genetic maps of the porcine genome have been developed during the last decade (Marklund et al., 1996; Rohrer et al., 1996). These genetic maps can be used to search for individual loci affecting economically important traits. Andersson et al. (1994) identified QTL for fat deposition traits in pigs on SSC 4 via a genome-wide scan. Several other QTL for fat deposition traits have subsequently been reported (Knott et al., 1998; Paszek et al., 1999; Rohrer, 2000). Recently, Grindflek et al. (2001) identified a QTL affecting intramuscular fat (IMF) content on SSC 6, which was supported by additional studies (De Koning et al., 1999; Ovilo et al., 2000). Here we mapped QTL for fat traits in pigs using interval mapping on chromosomes 1 to

10 using a Korean native pig×Landrace resource family constructed from a cross between the two phenotypically divergent swine breeds.

MATERIALS AND METHODS

The resource population was developed by a cross between Korean native boars and Landrace sows. Specifically, five boars of the Korean native pig and 10 sows of Landrace were selected randomly from a herd at the National Livestock Research Institute, Rural Development Administration, Korea. Each boar was mated naturally with two different sows to produce F₁ animals. An F₁ sire was selected randomly from each litter and mated naturally with all sows of the same litter. Thus, 10 sires and 36 dams overall were used to produce 240 F₂ animals.

After slaughtering, the body fat, comprising abdominal fat and fat trimmed from cut meat, was weighed. The intramuscular fat content (IMF) was determined from a sample of *longissimus* muscle using the CEM technique.

Blood samples were collected from all F₂ animals and their parents (F₁) and grandparents (F₀), and DNA was isolated using the Wizzard Genomic DNA Purification Kit (Promega, Madison, WI, USA).

Markers were selected based on ease of scoring,

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informativeness, and location in the genome. In total, 80 markers covering chromosomes 1 to 10 were selected to genotype the resource population. Intervals between adjacent markers were less than 20 cM whenever possible, and the average marker interval was approximately 19 cM based on the USDA-MARC map (Rohrer et al., 1996). Microsatellite markers were amplified by PCR using 10 ng pig genomic DNA as a template. PCR was performed in 10 µl reactions with 10 mM Tris-HCl (pH 8.3), 50 mM KCl, 1.5 mM MgCl₂, 200 µM each dNTP, 3 pmole each primer, 0.5 units Taq DNA polymerase (TaKaRa Shuzo Co., Shiga, Japan). Thermal cycling conditions included an initial denaturation for 5 min at 94°C, followed by 35 cycles of 30 s at 94°C for denaturation, 30 s at optimum temperature depends on markers for annealing and 1 min at 72°C for extension, and a final extension of 10 min at 72°C in GeneAmp PCR System 9600 (Perkin-Elmer Co., USA). The fragment lengths of the PCR products were determined with Genescan software version 2.1 (Perkin-Elmer Co., USA), and marker genotypes were assigned to the animals using Genotyper software version 2.5 (Perkin-Elmer Co., USA).

Linkage analysis was performed using CRIMAP software version 2.4 (Green et al., 1990) with a FIXED option to obtain the map distances. The maps were then used for QTL analysis of the 10 autosomes, which was conducted using the interval mapping procedure with the least squares regression method under the outbred line cross concept, in which founder breeds or lines are assumed to be fitted for alternative alleles at the QTL affecting the traits of interest. The statistical model included sex and slaughter data as fixed effects and live weight as covariable. A single QTL was fitted in all cases by regression on additive and dominance coefficients for the QTL at each 1 cM putative position. Additive and dominance coefficients at a given position of the QTL were derived from marker data using the procedure of Haley et al. (1994).

RESULTS AND DISCUSSION

QTL affecting fat deposition traits were analyzed using a three-generation resource population constructed between Korean native boars and Landrace sows in Table 1. The QTL detected at a minimum chromosome-wide level of 5%

Table 1. Means and phenotypic standard deviations of fat traits

Trait	Number of pigs	Mean	Standard deviation
Backfat thickness (mm)	240	21.62	8.08
Total body fat content (kg)	240	10.13	5.24
Intramuscular fat content (%)	240	2.47	3.08

are listed in Table 2. Two significant and two suggestive QTL were identified on SSC 6, 7, and 8 as affecting body fat and IMF traits in Figure 1, 2, 3 and 4. For QTL affecting IMF, the most significant association was detected between marker *sw71* and *sw1881* on SSC 6, and a suggestive QTL was identified between *sw268* and *sw205* on SSC8. These QTL accounted for 26.58% and 12.31% of the phenotypic variance, respectively. The former QTL was significant at a 1% chromosome-wide level. The Korean native pig alleles were responsible for the higher intramuscular fat content. Additionally, a significant and a suggestive QTL for body fat were identified on SSC 7 and SSC 6. For the QTL on SSC 7, Korean native pig alleles were associated with higher body fat. The QTL for body fat on SSC 6, however, was positively affected by the alleles of Landrace pigs, which were detected between the same markers that identified QTL for IMF. These QTL accounted for 18.38% and 12.87% of the phenotypic variance, respectively.

A significant QTL affecting IMF was detected at position 105 cM between markers *sw71* and *sw1881* on

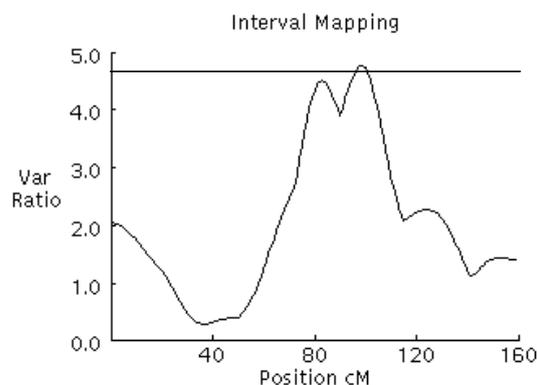


Figure 1. F-ratio curves for body fat on chromosome 6. The x-axis indicates the relative position on the linkage map. The y-axis represents the F-ratio. The horizontal line indicates the 5% chromosome-wide significance level from the permutation test.

Table 2. Chromosome-wide significance and suggestive associations of chromosomal regions with fat deposition traits

SSC	Trait	Loc. (cM)	F	Additive		Dominance		var %
				Estimate	SE	Estimate	SE	
6	Body fat ^a	98	4.78	-1.498	0.726	2.811	1.119	12.87
6	IMF ^b	105	9.34	1.513	0.455	-2.329	0.705	26.58
7	Body fat	23	8.30	1.860	0.525	-3.282	1.065	18.38
8	IMF	38	5.84	1.225	0.474	-1.300	0.819	12.31

^a Body fat, including abdominal and trimmed fat from cut meat. ^b Intramuscular fat content.

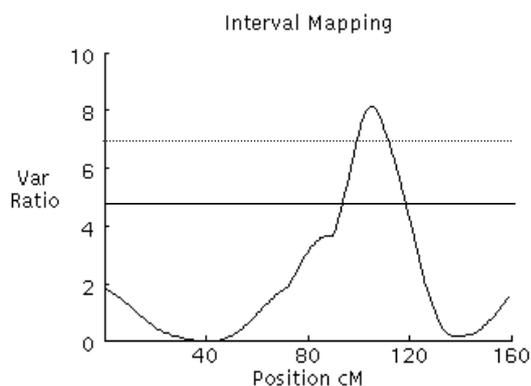


Figure 2. F-ratio curves for intramuscular fat on chromosome 6. The x-axis indicates the relative position on the linkage map. The y-axis represents the F-ratio. The two lines represent the 5% chromosome-wide (—) and 1% chromosome-wide (···) significance levels from the permutation test.

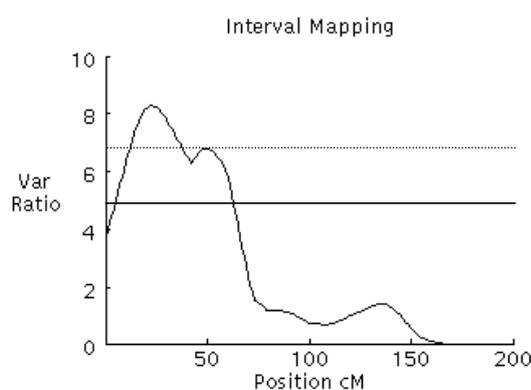


Figure 3. F-ratio curves for body fat on chromosome 7. The x-axis indicates the relative position on the linkage map. The y-axis represents the F-ratio. The two lines indicate the 5% chromosome-wide (—) and 1% chromosome-wide (···) significance level from the permutation test.

SSC 6. This QTL is well supported by previous reports in the literatures (De Koning et al., 1999; Ovilo et al., 2000; Grindflek et al., 2001). Ovilo et al. (2000) reported that a highly significant QTL affecting IMF and back fat thickness was located between 97 and 98 cM on SSC6, which is close to the marker *sw1881*. Similarly, a QTL affecting IMF was located between markers *sw1823* and *s0003* (Grindflek et al., 2001), and marker *s0003* and *sw2419* (De Koning et al., 1999) on SSC 6. Finally, a genetic variant of the porcine heart fatty acid binding protein (HFABP) was associated with IMF in Duroc pigs (Gerbens et al., 1999), which was mapped to marker interval *sw316-s0003* (Gerbens et al., 2000). The marker *s0003* was located between *sw71* and *sw1881* genotyped in the present study. Therefore, the marker intervals for the QTL affecting IMF are almost identical between the present results and previous reports (De Koning et al., 1999; Ovilo et al., 2000; Grindflek et al., 2001). Additionally, Grindflek et al. (2001) suggested that

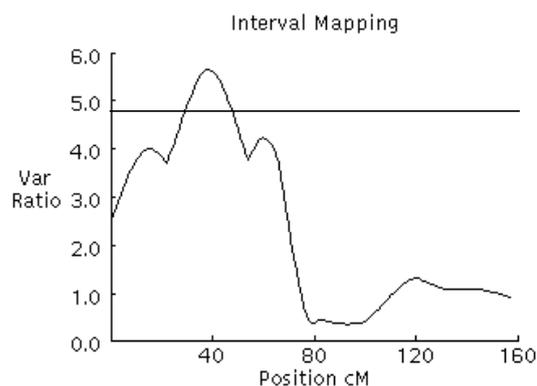


Figure 4. F-ratio curves for intramuscular fat on chromosome 8. The x-axis indicates the relative position on the linkage map. The y-axis represents the F-ratio. The horizontal line indicates the 5% chromosome-wide significance level from the permutation test.

HFABP and the melanocortin-receptor 5 (MC5R) may constitute positional candidate genes for QTL affecting IMF. On the other hand, a suggestive QTL for IMF was detected and located in the *FABP4-s0073* interval (De Koning et al., 1999; Rattink et al., 2000). No QTL for IMF, however, was detected on SSC 4 in the present study.

CONCLUSION

Highly marbled meat is generally considered ideal given that it is associated with greater flavor, increased meat tenderness, and desirable cooking properties. The marbling score reflects the intramuscular fat content. IMF is one of the most economically important traits in modern pig breeding.

In this study, F_2 animals from a cross between Korean native boars and Landrace sows were analyzed using an interval mapping procedure with the least squares regression method. We identified two significant and two suggestive QTL affecting body fat and IMF traits. Specifically, a QTL associated with IMF on SSC 6 strongly suggested that SSC 6 contains genes affecting IMF. The detected regions, however, should be narrowed to obtain more precise estimates of the QTL locations using additional markers. In addition, commercially relevant populations of pigs should be examined for the QTL to identify whether variants for these regions exist, which could be used for marker-assisted selection or marker-assisted introgression for breeding in pigs. Further studies should also examine interactions between the QTL identified herein and other QTL.

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