

—Full Paper—

Use of Microsatellite Markers to Detect Quantitative Trait Loci in Yorkshire Pigs

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Abstract. To identify genetic markers associated with economic traits in pigs, 157 microsatellite markers were examined in Yorkshire pigs. Thirty eight female Yorkshire pigs were initially examined and six of them were selected as progenitors; half were more than 1.5 standard deviations (SD) above the mean for average daily gain (ADG) and backfat thickness (BFT), and the remaining half were more than 1.5 SD below the mean. These pigs were then mated to male Duroc pigs, and 200 F2 pig offspring were examined for the association of specific alleles with ADG and BFT. To confirm the specific markers identified in the initial analysis, associations of significant markers with economic traits were further examined in 228 additional performance-tested purebred pigs. Twenty-five microsatellite markers were significantly associated with either ADG or BFT, and among these, 17 were associated with both traits. The markers with the highest association to ADG were also associated with BFT. Our study reveals that specific markers could be used to predict economic significance, and confirms several quantitative trait loci (QTL) identified in previous studies. However, further analysis with more closely-spaced microsatellite markers is required to refine predictive values for economic traits and positions of QTL that are reliable for actual phenotypic prediction.

Key words: ADG, BFT, Economic trait, Microsatellite marker, QTL, Swine

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Specific genetic map locations can be identified for quantitative trait loci (QTL) associated with economic traits in pigs. Andersson *et al.* (1994) reported a close connection between growth and fatness at a locus on *Sus scrofa* chromosome (SSC) 4.

Other chromosomal regions containing QTL for economic traits have been identified on SSC 1, 2, 4, 7, 12, and 14. Specific genes and chromosomal regions associated with QTL have been reported previously [6, 10–13, 15, 20].

The chromosomal positions for QTL associated with economic traits in pigs have been studied using association analyses [22], a candidate gene approach [5, 18], and genome scans [1–3, 13, 19]. Most QTL in pigs have been identified using the genome scan method on crosses using wild boar [1, 10] or Chinese Meishan pigs [14, 15, 20]. QTL positions associated with fatness (back fat thickness, BFT) and growth (average daily gain, ADG) were identified on SSC 4 through intercrosses between wild boar and Large White pigs [1]. This QTL on SSC 4 has also been confirmed in other pig strains [13, 21]. Despite these findings, however, many of the QTL identified so far may be specific to the strain of experimental animals evaluated. Instead of relying only on QTLs, in this study, the association between the alleles of microsatellite markers and economic traits, ADG and BFT, was studied in Yorkshire pigs. To avoid pre-determined selection criteria and bias, 157 possible microsatellite markers were evaluated for their association with economic traits.

Materials and Methods

Experimental design and trait analysis

Two hundred female Yorkshire pigs were evaluated as progenitors at the National Livestock Research Institute and Geochang Pig Farm, from which 38 pigs were selected for analysis; half were more than 1.5 standard deviations (SD) above the mean for ADG and BFT, and the remaining half were more than 1.5 SD below the mean. Among the 38 pigs carefully evaluated, 6 pigs 3at (random from the above-average group, and 3at random from the below-average group) were selected and used as the F0 generation for intercross with male Duroc pigs, which are commonly used in breeding programs for swine production in Korea. From these intercrosses, 77 F1 pigs were born. For the F2 generation pigs, 6 male and 12 female pigs from among the 77 F1 hybrids were selected on the basis of ADG and BFT values. Consequently, 200 F2 pigs were born and used in the association study. The

traits measured were birth weight, weaning weight, weight at 21 days, ADG, and BFT [4].

$ADG = (\text{ending weight} - \text{beginning weight}) \div (\text{number of days between measurements})$

$BFT = \text{ending backfat thickness} + \{ (90 \text{ kg} - \text{ending weight}) \times \text{ending backfat thickness} \div (\text{ending weight} - 11.34) \}$

An additional 228 performance-tested purebred pigs from the Second Korea Swine Testing Association were selected and used to confirm the association between measured traits and the markers identified from the crosses.

Microsatellite markers

We selected 157 microsatellite markers from the USDA-MARC linkage map of the 18 porcine autosomes (Table 1; <http://sol.marc.usda.gov/>). Selection of these microsatellite markers was based on the following considerations: number of available markers per chromosome, interval between markers, and number of alleles. The average interval between the selected markers was 19.2 cM. On SSC 4, there were 26 markers with an average spacing of 3.6 cM. On SSC 7, there were 19 markers with an average spacing of 7.75 cM. On SSC 18, only one marker was used.

PCR and genotype analysis

The 5' end of each forward primer was labeled with fluorescent dye (Fam, Hex, or Ned, Applied Biosystems, USA). PCR amplifications were carried out in a GeneAmp PCR system 9600 or 9700 (Applied Biosystems), with 35 cycles of denaturation at 94 C for 15 sec, annealing at 50–60 C for 1 min, and extension at 72 C for 1 min.

To check the genotype of each microsatellite, 10 μ l from each reaction was precipitated by adding 30 μ l of ethanol. The DNA was resuspended in 12 μ l deionized formamide. Genescan internal size marker (400 HD, Applied Biosystems) was added to 0.5 μ l of DNA (200 ng), and the sample was denatured for 5 min at 95 C. Due to the differences in PCR fragment sizes and the kind of fluorescent dye used, multiple PCR reactions could be carried out simultaneously using multi-injection in a capillary-based Genetic Analyzer (ABI310, Perkin-Elmer, USA). The data was analyzed using the Genescan fragment analysis software (version 2.1) and Genotyper software (version 2.0).

Table 1. 157 Microsatellite markers from the USDA-MARC map

SSC	Marker	RP (cM)	SSC	Marker	RP (cM)	SSC	Marker	RP (cM)	SSC	Marker	RP (cM)	
1	S0316	33.4		SW1089	69.6		SW147	90.1		SW2413	84.9	
	CGA	52.3		SW1996	77.0		SW252	99.4		12	SW2490	0.0
	SW1430	58.5		S0067	102.8		S0115	102.2			S0083	40.2
	SW2185	67.6		SW818	105.0		SW1083	109.5		SW1307	40.2	
	S0313	78.7		SW445	105.8		S0101	134.9		SW60	96.5	
	SWR982	86.2		S0097	120.0		SW2537	139.5		13	SW648	43.1
	SW373	119.5		S0161	121.0		8	SW2611			2.5	SWR1008
SW1301	140.5	SW856	130.1	S0285	20.8	SW1876		66.4				
2	SW256	19.2	5	SW1482	39.9	SW1345	25.2	SW2430	68.0			
	S0141	31.2		DAGK	40.8	SW1702	29.6	S0291	126.2			
	FSHB	53.5		S0005	56.7	SWR1101	38.3	14	SW1918	12.8		
	S0010	77.9		SW310	79.6	SW444	52.5		SW1125	22.2		
	SW2514	104.3		S0018	108.0	SW1843	52.5		SW540	31.5		
SWR308	128.2	SW1200	74.3	S0144	96.3	ATP2	32.8					
3	SWR1637	27.6	6	S0035	7.3	9	SW61	112.3	S0058	33.1		
	SW487	46.0		SW2535	9.5		S0024	27.4	SW210	46.3		
	SW2618	50.8		SW2406	21.4		SW911	32.8	SW1082	53.7		
	SW1315	55.7		SW1841	41.5		SW2401	57.1	SW77	69.4		
	S0164	60.5		SW1067	71.4		SW2094	61.4	15	S0355	1.3	
	SW2570	72.3		SW4	82.1		SW1491	76.5		CHR1-4	16.4	
	SW2408	94.2		SWR987	86.5		SWR915	81.0		SW964	50.7	
SW349	112.6	SW1923	88.6	CALCR	81.0	SW1989	57.9					
4	SW2404	0.0	SW316	89.3	S0019	82.4	S0149	64.2				
	S0227	4.1	SW1823	90.7	SW1435	92.0	SW1983	101.5				
	SW480	4.9	SW353	102.5	S0295	100.5	SWR2121	124.3				
	SW2509	7.4	SW1881	121.1	S0212	141.2	16	SW742	9.3			
	SW489	8.0	SW2419	161.4	SW1349	142.5		FSA	36.5			
	SW919	25.7	7	S0025	3.7	10		S0038	4.3	SW1809	37.3	
	SW2049	27.1		SW1873	10.9		SWR136	7.6	SWR2080	38.0		
	S0301	27.1	SW1354	22.3	SW443	20.4	SW497	39.3				
	SW835	27.1	S0064	30.2	SW173	56.1	SW5	44.2				
	SW2547	29.8	SW1369	48.2	S0070	62.3	SW2517	55.7				
	S0073	40.7	SW1409	57.1	SWR334	67.5	17	SW1891	17.3			
	S0001	41.8	S102	70.1	SWR158	67.5		SW2441	40.6			
	SW1707	48.6	S0078	73.4	SW1708	101.0		END0	42.7			
	SW752	51.2	ANPEP	82.3	SW2067	124.1	SW769	117.5				
SW444	52.5	S0066	82.8	11	S0392	1.9	18	SWR2480	55.7			
SW317	53.5	SWR1121	82.8		S0182	3.3						
S0175	55.9	SW1959	85.4		SW1632	16.6						
S107	66.1	SW2040	90.0	S0230	56.4							

RP: relative position in the USDA-MARC map.

Statistical analysis

The map distance among the microsatellite markers examined in this study had previously been characterized and confirmed. In the present investigation, therefore, linkage analysis using the pedigree was omitted. To verify the relationship between the markers and traits, statistical analysis was performed using the allele appearance ratio of the marker and trait values.

An analysis was performed of the genotypes and

markers associated with ADG and BFT using the SAS software (Statistical Analysis Systems, 1995). The relationship between ADG and BFT and the allele of each of the 157 markers was examined by *t*-test. In the F2 population, the representation rate for the alleles between two groups (pigs >1.5 SD above the average and pigs >1.5 SD below the average) was checked by χ^2 analysis. The *t*-test was used to correlate each microsatellite marker to ADG and BFT in the 228 performance-tested pigs

Table 2. Microsatellite marker alleles associated with significantly different ADG in F2 pigs (n=200)

C	Marker	ADG Mean \pm SE (g)		<i>t</i> -value	A
		N	P		
1	SW373	928.47 \pm 6.73	875.65 \pm 26.73	1.99*	6
	SW2185	921.25 \pm 6.54	1004.46 \pm 29.21	-2.11*	5
2	SW256	946.00 \pm 9.47	909.10 \pm 8.55	2.86**	4
	SWR308	920.20 \pm 6.61	1079.40 \pm 45.13	3.00**	6
4	SW2547	931.20 \pm 7.79	900.06 \pm 11.69	2.07*	4
	SW2404	922.03 \pm 6.44	1054.95 \pm 56.61	-2.88**	4
5	SW310	930.40 \pm 6.98	888.50 \pm 16.20	2.23*	5
6	SW353	933.99 \pm 8.01	903.73 \pm 10.81	2.25*	5
	SW1881	923.16 \pm 6.41	1141.52 \pm 48.55	-3.15**	6
7	S0102	914.50 \pm 7.49	956.10 \pm 12.56	-2.73**	4
9	SW911	911.20 \pm 8.79	938.90 \pm 9.36	-2.15*	4
	SW1349	929.45 \pm 6.69	857.83 \pm 26.48	3.04**	5
10	S0019	926.10 \pm 6.58	834.40 \pm 41.90	2.33*	4
	SW497	928.11 \pm 6.64	850.40 \pm 28.57	2.67**	8
13	S0038	929.25 \pm 7.00	886.50 \pm 16.15	2.14*	5
	SW864	929.30 \pm 6.90	886.00 \pm 15.00	2.60*	6
15	S0291	917.50 \pm 6.80	968.58 \pm 16.54	-2.87**	4
	S0355	924.90 \pm 6.55	872.86 \pm 6.51	5.63**	4

N/P indicates the absence/presence of alleles in markers. C, chromosome; SE, standard error; A, number of alleles detected.

* $p < 0.05$, ** $p < 0.01$.

from the Second Korea Swine Testing Association.

Results

Statistical analyses of the markers' relationships to ADG and BFT was carried out under the assumption that they were in accordance with their respective positions on the existing USDA linkage map. In this research, we concentrated our efforts on finding relationships between economic traits and identified microsatellite markers throughout the genome, rather than on confirming linkage mapping already demonstrated by many other studies.

First, we determined the genotypes of 157 microsatellite markers in the 6 F0 pigs that were more than 1.5 SD above or below the mean. Among the 157 microsatellite markers, we identified 60 markers in which one allele or genotype appeared at a significantly higher frequency between the two groups. These 60 markers identified on the basis of F0 pig screening were further tested through analysis in the genotypes of 200 F2 pigs.

For each marker tested, all 200 F2 pigs (from both above-average and below-average parents) were

sorted by allele. For each allele of each marker, we calculated the mean ADG for that group of pigs. We identified specific alleles of 18 markers for which ADG was significantly different in pigs with or without these alleles (Table 2). Using the same method, we identified specific alleles of 24 markers for which the mean BFT was significantly different in pigs with or without these alleles (Table 3). In addition, 17 out of 18 microsatellite markers related to ADG value were also associated with BFT value. One marker was associated with only ADG, and 7 markers were associated with only BFT. All markers with alleles identified in this screening were marked according to their chromosomal map location (Table 1).

We reanalyzed the represented genotypes of each microsatellite marker. The analysis of genotype was carried out with a *t*-test, as in Tables 2 and 3, dividing the negative group, in which the allele/genotype did not appear, and the positive one, in which it did appear. Most of the genotype results were similar to those from analysis by allele (data not shown).

We tested whether the same result was found by dividing the 200 F2 pigs into two groups based on their lineage from the two groups of F0 pigs. In the

Table 3. Microsatellite marker alleles associated with significantly different BFT in F2 pigs (n=200)

C	Marker	BFT Mean ± SE (cm)		t-value	A
		N	P		
1	SW373	1.22 ± 0.00	1.09 ± 0.02	5.14**	6
	SW2185	1.16 ± 0.00	1.30 ± 0.01	-7.85**	5
2	SW256	1.26 ± 0.01	1.18 ± 0.01	4.57**	4
	SWR308	1.23 ± 0.00	1.12 ± 0.01	6.95**	6
4	SW835	1.19 ± 0.00	1.30 ± 0.01	-5.10**	6
	SW919	1.18 ± 0.00	1.31 ± 0.01	-6.39**	4
	SW2404	1.20 ± 0.00	1.46 ± 0.03	-7.12**	4
5	SW310	1.18 ± 0.01	1.24 ± 0.01	3.64**	5
6	SW353	1.25 ± 0.01	1.15 ± 0.01	6.86**	5
	SW1881	1.99 ± 0.00	1.33 ± 0.02	-6.95**	6
7	S0102	1.17 ± 0.00	1.34 ± 0.01	-8.79**	4
	SW2537	1.20 ± 0.00	1.37 ± 0.02	-6.31**	4
	SW2040	1.19 ± 0.00	1.32 ± 0.01	-6.65**	6
9	SW911	1.23 ± 0.01	1.17 ± 0.01	4.14**	4
	SW1349	1.23 ± 0.01	1.15 ± 0.01	4.39**	5
	S0019	1.16 ± 0.00	1.28 ± 0.01	7.18**	4
10	S0038	1.17 ± 0.00	1.30 ± 0.01	-7.17**	5
	SW497	1.22 ± 0.00	1.13 ± 0.01	4.32**	8
11	SW1632	1.24 ± 0.01	1.17 ± 0.01	4.19**	6
13	SW864	1.22 ± 0.00	1.09 ± 0.03	4.10**	6
	S0291	1.20 ± 0.00	1.31 ± 0.02	-4.98**	4
14	SW210	1.16 ± 0.00	1.33 ± 0.01	-10.12**	9
15	SW964	1.19 ± 0.00	1.13 ± 0.01	5.94**	6
	S0355	1.23 ± 0.00	1.10 ± 0.02	5.22**	4

N/P indicates the absence/presence of alleles in markers. C, chromosome; SE, standard error; A, number of alleles detected.

* p<0.05, ** p<0.01.

Table 4. Microsatellite alleles with significantly different representations in F2 pigs that were >1.5 SD below (lo) or above (hi) the average for ADG

C	Marker		No. of pigs (%)		χ ²
			0	1	
4	SW2404	lo	32 (100.00)	0 (0.00)	3.91*
		hi	18 (81.82)	4 (18.18)	
5	SW310	lo	24 (75.00)	8 (25.00)	4.63*
		hi	22 (100.00)	0 (0.00)	

Lo/hi indicates pigs that were >1.5 SD below/above average for ADG.

0/1 indicates the absence/presence of alleles in markers.

case of ADG, most of the markers were not significantly different when we compared the F2 pigs derived from the -1.5 SD group versus the +1.5 SD group (Table 4). This indicates that most of the markers that affected ADG were not represented differently between the two groups, 1.5 SD above or below average. However, in the case of BFT, we found that 19 out of 24 markers showed significantly different representations between the

two groups (Table 5).

It is possible that the relationship between these microsatellite markers and the economic traits might apply only to the small number of animals chosen for breeding in these experiments. We therefore confirmed the relationship between the selected markers and traits using 228 performance-tested pigs randomly chosen from the Second Korea Swine Research Institute.

Table 5. Microsatellite alleles with significantly different representations in F2 pigs that were >1.5 SD below (lo) or above (hi) the average for BFT

C	Marker	No. of pigs (%)		χ^2	C	Marker	No. of pigs (%)		χ^2	
		0	1				0	1		
1	SW2185	lo	23 (82.14)	5 (17.86)	18.93**	SW2537	lo	22 (100.00)	0 (0.00)	6.059*
		hi	5 (19.23)	21 (80.77)			hi	18 (69.23)	8 (30.77)	
2	SW256	lo	6 (20.00)	24 (80.00)	13.80**	SW2040	lo	26 (100.00)	0 (0.00)	12.30**
		hi	19 (73.08)	7 (26.92)			hi	12 (54.55)	10 (45.45)	
	SWR308	lo	17 (60.71)	11 (39.29)	6.42*	SW919	lo	2 (70.00)	9 (30.00)	7.20**
		hi	16 (100.00)	0 (0.00)			hi	26 (100.00)	0 (0.00)	
	SW835	lo	24 (92.31)	2 (0.69)	5.17*	S0019	lo	20 (71.43)	8 (28.57)	19.96**
		hi	12 (60.00)	8 (40.00)			hi	1 (4.55)	21 (95.45)	
	SW919	lo	27 (90.00)	3 (10.00)	9.05**	10 S0038	lo	26 (86.67)	4 (13.33)	13.96**
		hi	13 (50.00)	13 (50.00)			hi	9 (34.62)	17 (65.38)	
	SW2404	lo	30 (100.00)	0 (0.00)	14.99**	11 SW1632	lo	11 (42.31)	15 (57.69)	4.22*
		hi	14 (53.85)	12 (46.15)			hi	18 (75.00)	6 (25.00)	
5	SW310	lo	13 (43.33)	17 (56.67)	9.57**	14 SW210	lo	24 (100.00)	0 (0.00)	25.69*
		hi	1 (3.85)	25 (96.15)			hi	6 (25.00)	18 (75.00)	
6	SW353	lo	15 (53.57)	13 (46.43)	8.24**	15 SW964	lo	28 (93.33)	2 (6.67)	5.24*
		hi	24 (92.31)	2 (7.69)			hi	17 (65.38)	9 (34.62)	
	SW1881	lo	23 (88.46)	3 (11.54)	11.94**	S0355	lo	20 (66.67)	10 (33.33)	8.40**
		hi	9 (37.50)	15 (62.50)			hi	26 (100.00)	0 (0.00)	
7	S0102	lo	29 (96.67)	1 (3.33)	17.59**					
		hi	11 (42.31)	15 (57.69)						

Lo/hi indicates pigs that were >1.5 SD below/above average for BFT.

0/1 indicates the absence/presence of alleles in markers.

Table 6. Microsatellite markers associated with significantly different ADG in 228 performance-tested purebred Yorkshire pigs (n=228)

C	Marker	ADG Mean \pm SE		t-value	A
		N	P		
2	SW256	919.14 \pm 6.64	874.98 \pm 12.08	2.88**	8
4	SW2404	913.73 \pm 6.01	847.81 \pm 28.25	2.10*	11
6	SW353	917.18 \pm 6.8	888.58 \pm 9.69	2.42*	8
7	S0102	918.69 \pm 6.29	881.35 \pm 15.32	2.45*	7
9	SW911	892.12 \pm 7.18	938.63 \pm 12.06	-3.47**	8
15	SW964	9021.77 \pm 6.55	948.88 \pm 12.91	-3.22**	8

N/P indicates the absence/presence of alleles in markers. C, chromosome; SE, standard error; A, number of alleles detected.

* p<0.05, ** p<0.01.

Among the 18 markers related to ADG value, the relationships of the SW256, SW2404, SW353, and S0102 markers to ADG value were reconfirmed in the performance-tested pigs (Table 6). Among the 24 markers related to BFT value, the relationships of the SW373, SW256, SW835, SW2404, SW353, SW864, SW964, and S0355 markers to BFT value were also reconfirmed in the performance-tested pigs (Table 7). To increase the accuracy of the markers related to ADG and BFT values, we

identified the relationship between the microsatellite markers and traits in the F0 to F2 pedigrees, and the relationships of the selected markers were then reconfirmed in the performance-tested pigs.

Discussion

By selecting 6 female Yorkshire pigs above and

Table 7. Microsatellite markers associated with significantly different BFT in 228 performance-tested purebred Yorkshire pigs (n=228)

C	Marker	BFT Mean \pm SE		t-value	A
		N	P		
1	SW373	1.29 \pm 0.01	1.23 \pm 0.02	2.24*	6
2	SW256	1.26 \pm 0.01	1.31 \pm 0.01	-2.08*	8
4	SW835	1.30 \pm 0.01	1.23 \pm 0.02	2.42*	9
	SW2404	1.28 \pm 0.01	1.34 \pm 0.02	-2.00**	11
6	SW353	1.28 \pm 0.01	1.35 \pm 0.02	-2.59**	8
13	SW864	1.33 \pm 0.01	1.28 \pm 0.01	2.35*	4
15	SW964	1.31 \pm 0.01	1.23 \pm 0.02	3.36**	8
	S0355	1.29 \pm 0.01	0.87 \pm 0.00	43.60**	9

N/P indicates the absence/presence of alleles in markers. C, chromosome; SE, standard error; A, number of alleles detected.

* $p < 0.05$, ** $p < 0.01$.

below the mean for ADG and BFT and genotyping microsatellite markers, this study was able to test the heredity of specific alleles in an F2 population produced by intercross with male Duroc pigs. We tested if the markers found in the F0 population would show the same result in the F2 generation, and then identified independent succession of alleles from F0 to F2. Based on these analyses, we found that 18 and 24 markers were closely related to ADG and BFT, respectively. While concentrating our efforts on SSC 4 and 7, known to have a close relationship to ADG and BFT, we did analyze markers on all 18 autosomes. One or more markers on SSC 1, 2, 4, 5, 6, 9, 10, 11, 13, 14, and 15 were shown to have some correlation with these traits, but no linkage was found on the remainder of the chromosomes. As ADG and BFT are often positively correlated with each other, 17 of the markers that were linked to either trait turned out to be related to both traits. There was only 1 marker associated with ADG, and 7 markers were associated with BFT only.

The association of each marker with both ADG and BFT was confirmed using three different methods of correlation, by allele, genotype, and group. Thus, a relation to economic traits was found regardless of the analysis method. Comparing the results of markers in the backcrossed lines (Tables 2, 3) with those of markers using performance-tested pigs (Tables 6, 7), the latter group usually included more alleles for each marker because it did not compose a family line. Most of the 25 markers associated with ADG and BFT (1 related only to ADG, 7 related

only to BFT, and 17 associated with both ADG and BFT) were confirmed in their relationship to economic traits by the results from performance-tested pigs. Several markers were associated with economic traits in a similar pattern at the same allele and genotype in the 228 performance-tested pigs compared to those of the backcrossed line. There were 6 markers for ADG and 8 markers for BFT.

Examining the chromosomal regions that had some relation to economic traits, we found that even though 26 markers were used on SSC 4, only 3 markers affected ADG and BFT. On SSC 7, we discovered that 4 markers were associated with 2 QTL. There were fewer markers related to traits on these two chromosomes than had been anticipated. In addition, the results for SSC 4 pointed to a relation to ADG and BFT at a position different from previous results. In this investigation, we found a strong association between ADG and BFT and microsatellite markers at SW2404 (0.0 cM) and SW2547 (29.8 cM). However, Andersson *et al.* (1994) and Walling *et al.* (2000) found that QTL for fat and BFT traits was localized between 60 cM and 80 cM. Knott *et al.* (1998) clarified that the strongest correlation was between S0175 (61 cM) and S0107 (65 cM), not at the position between S0001 (45 cM) and S0175 (65 cM), which had been formerly known as the QTL position for fatness traits on SSC 4.

In the case of SSC 7, the relation to ADG and BFT was confirmed at positions 70 cM, 90 cM, and 139 cM. Although previous studies discovered QTL at the position of 40–70 cM [6, 13, 16, 17, 20], a novel correlation to BFT was found at 90 cM and 139 cM

in this study. In the case of SSC 1, previous studies found an association with BFT at various positions [6, 17]. In this study, it was clear that two markers—SW2185 (67.6 cM) and SW373 (119.5 cM)—had a strong relationship with the traits studied. Paszek *et al.* (1999) reported an important QTL for ADG at weaning and at 56 kg between SW373 and SW1301 in SSC 1. The relationship to ADG at SW373 was also confirmed. In the case of SSC 6, previous studies have correlated a region of this chromosome to meat quality, including intramuscular fat (IMF) content [7, 8]. In this study, a relationship was found for this region to ADG and BFT at SW353 (102.5 cM) and SW1881 (121.1 cM). Recent research by Ovilo *et al.* (2000) also showed a connection with IMF and BFT at 97–98 cM, near SW1881, the same position found in other studies.

Studies of chromosomal regions related to economic traits always exhibit some differences in the positions identified because of differences in the experimental animals used and potential experiment error even though many genetic researchers have made great efforts to pinpoint the positions with the highest relationship to traits. In addition to the candidate genes that are found thus far in this study, further efforts should be made to investigate the exact QTL regions related to

economic traits, and to search for the markers and genes that are most closely associated with economic traits. By using polymorphic microsatellite markers in this research, the effect of a specific inherited allele on two traits in a family line was examined. While analyzing markers across the entire genome, some markers were correlated at the same positions found in previous studies, and we also obtained some novel correlation results at totally different positions. Considering how many QTL positions are related to actual economic traits, in this investigation, 25 out of 157 microsatellite markers in pigs were determined to have some relation to the economic traits examined.

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