

QUANTITATIVE TRAIT LOCI MAPPING AFFECTING GROWTH TRAITS IN PIGS

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INTRODUCTION

Quantitative trait loci (QTL) mapping is a basic tool for positional cloning, and application of marker-assisted selection or marker-assisted introgression in genetic improvement. Comprehensive genetic maps of the porcine genome were developed during the last decade (Marklund et al., 1996; Rohrer et al., 1996). These genetic maps can be used to search for individual locus affecting quantitative traits of economic importance. On the base of these linkage maps and data from F₂ breed cross resource population, several reports have been published on genomic scans for quantitative trait loci in pigs (Andersson *et al.*, 1994; Knott *et al.*, 1998; Paszek *et al.*, 1999; Rohrer, 2000). Recently, using whole genome scans, Malek *et al.* (2001) reported significant QTL affecting growth traits on SSC1, 2, and 4, and also Bidanel *et al.* (2001) also reported highly significant QTL for growth on SSC1, 4, 6 and 7.

This study was conducted to map QTL for growth traits in pigs through interval mapping on SSC1 to 10 using Korean native pig × Landrace resource family developed from a cross between the two phenotypically divergent swine breeds.

MATERIALS AND METHODS

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

Body weight of piglets was measured at birth, 3 weeks, and 5 weeks of age. Pigs were weighed and transferred to performance testing pens at 12 weeks of age. They were weighed and slaughtered at 210 days of age. Average daily gain was calculated from birth to 5 weeks of age, from 5 to 12 weeks of age, and from 12 to 30 weeks of age.

Blood samples were collected from all F₂ animals and their parents (F₁) and grandparents (F₀), and DNA was extracted with Wizzard Genomic DNA Purification Kit (Promega, USA). Markers were selected based on ease of scoring, informativeness, and location in the genome. Finally, eighty markers from chromosome 1 to 10 were selected to genotype our resource population. Intervals between adjacent markers were less than 20 cM whenever possible.

Fragment length of the PCR products was 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 FIXED option to obtain the map distances. The maps were then used for QTL analysis of the 10 autosomes from SSC 1 to 10. For QTL analysis, interval mapping procedure using least squares regression method was applied under line cross concept, where founder breed or lines are assumed to be fitted for alternative alleles at the QTL affecting the traits of interest.

RESULTS AND DISCUSSION

Quantitative trait loci for growth traits were analyzed using a three generation resource population constructed from a cross between Korean native boars and Landrace sows. The results of QTL that were detected at least 5% chromosome-wide level are listed in Table 1. Ten suggestive QTL were identified on chromosome 1 to 10 as affecting growth traits studied. Two suggestive QTL for birth weight were identified between *sw2443* and *sw1650* on SSC2, and between *sw61* and *s0178* on SSC8. The additive effect suggested that Korean native pig alleles were associated with lower birth weight on SSC2, and higher birth weight on SSC8 compared to Landrace pig alleles. The phenotypic variances accounted for by the QTL were 16.26 and 18.68%, respectively. There are no previous reports of QTL for birth weight on SSC2 and SSC8. So far, QTL affecting birth weight were found on SSC3 (Malek *et al.*, 2001), on SSC4, SSC5, SSC9, and SSC16 (Paszek *et al.*, 1999), on SSC1 (Wada *et al.*, 2000), and on SSC1, SSC12, and SSC13 (Knott *et al.*, 1998). Also, Bidanel *et al.* (2001) reported that QTL for birth weight were identified on SSC4 and SSC7 using a line-cross regression method, and on SSC11 using a half-/full-sib maximum likelihood methods. Suggestive evidences for body weight at 5 and 30 weeks of age were identified on SSC6 and SSC8, respectively. A suggestive QTL for body weight at 5 weeks of age was located between *sw1057* and *sw1067* on SSC6. Korean native pig alleles were associated with lower body weight. This QTL accounted for 14.36% of phenotypic variance in F₂ animals. QTL for body weight at 30 weeks of age were located between *s0098* and *sw268*. The additive effect for the QTL suggested that Korean native pig alleles are associated with lower body weight compared to alleles of Landrace pigs. The phenotypic variance accounted by the QTL was 8.02%. Moreover, three suggestive QTL for body weight at 12 weeks of age were found on SSC5, SSC6 and SSC8. These QTL contributing body weight at 12 weeks of age accounted for 6.24 to 14.76% of phenotypic variance. For these QTL, the additive effects suggested that Korean native pig alleles were associated with lower body weight compared to alleles of Landrace pigs. Average daily gain between 12 to 30 weeks of age was suggestively affected on SSC2 and SSC4, which were located between marker *sw1650* and *sw1686* on SSC2, and between marker *sw1678* and *sw35* on SSC4. The phenotypic variances explained by these QTL were 26.15% on SSC2 and 9.14% on SSC4. The additive effect suggested that Korean native pig alleles were superior to Landrace pig allele on SSC2, and inferior to Landrace pig alleles on SSC4. In addition, a suggestive QTL for average daily gain between birth to 5 weeks of age was detected between *sw1057* and *sw1067* on SSC6. Korean native pig alleles were associated with higher growth rate compared to Landrace pigs alleles. The QTL accounted for 12.5% of phenotypic variance. The QTL for late growth in similar chromosomal region of SSC4 were reported by Andersson *et al.* (1994), Knott *et al.* (1998), Paszek *et al.* (1999), Bidanel *et al.* (2001), and Malek *et al.* (2001). Also, QTL affecting growth rate of SSC2 were identified by Knott *et al.* (1998), and Malek *et al.* (2001). These results were almost consistent with results of this study. Rohrer *et*

al. (2000) also found QTL for growth on SSC2 using genome-wide scan. QTL on SSC5 was suggestively affected for growth in this study. Only Paszek *et al.* (1999) reported QTL for growth on SSC5. QTL on SSC6 were associated with body weight at 5 weeks and 12 weeks of age, and ADG between birth to 5 weeks of age. This QTL was same chromosomal region affecting growth traits of SSC6 reported by Rohrer *et al.* (2000) and Bidanel *et al.* (2001). Malek *et al.* (2001) reported a QTL affecting ADG on test on SSC8. Also, Bidanel *et al.* (2001) found QTL for early growth on SSC8. QTL for body weight at 12 weeks and 30 weeks of age was found at the similar position of SSC8 in the present study.

Table 2. Chromosome-wide significant and suggestive associations of chromosomal regions with growth, carcass and meat quality traits

SSC	Trait	Loc. (cM)	F	Additive		Dominance		var %
				estimate	S.E	estimate	S.E	
2	B0W ^a	25	4.88	-0.084	0.036	-0.119	0.067	16.26
2	ADG ^b (12 to 30wks)	155	6.03	0.016	0.020	0.098	0.029	26.15
4	ADG (12 to 30wks)	56	5.09	-0.012	0.014	-0.057	0.019	9.14
5	B12W ^c	77	4.90	-1.500	0.510	-0.765	0.805	6.24
6	B5W ^d	77	5.58	-0.037	0.245	1.228	0.373	14.36
6	ADG (birth to 5 wks)	76	5.07	0.001	0.001	0.033	0.01	12.50
6	B12W	78	6.31	-1.213	0.861	4.410	1.337	14.76
8	B30W ^e	0	6.57	-5.055	2.122	6.080	2.895	8.02
8	B12W	0	5.88	-1.235	0.792	2.818	1.081	7.25
8	B0W	140	4.75	0.078	0.035	-0.142	0.070	18.68

^abirth weight, ^baverage daily gain, ^cbody weight at 12 weeks of age, ^dbody weight at 5 weeks of age, ^ebody weight at 30 weeks of age

CONCLUSION

In this study, the data of F₂ individuals from a cross between the Korean native boars and landrace sows were analyzed using interval mapping procedure of least squares regression method under line cross concept. We detected 10 QTL affecting growth traits at least 5% level of chromosome-wide scans. It was suggested that QTL on SSC6 effected early growth, 5 weeks and 12 weeks of age, whereas QTL on p arm of SSC8 controlled late growth. However, a significant QTL was not found for growth traits at 1% level of chromosome-wide. Although a few of the detected QTL may be false positives, the results of QTL at this level of significance will provide further our knowledge on the inheritance of QTL for growth traits.

Additional markers should be genotyped for detected regions to obtain more precise estimates of the position of QTL.

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