Identification of Quantitative Trait Loci (QTL) Affecting Teat Number in Pigs

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ABSTRACT : Quantitative trait loci (QTL) mapping can be applied to detect chromosomal locations that control economic traits in farm animals. Teat number has been considered as one of the most important factors to evaluate mothering ability of sow. Especially, teat number is more important when the number is less than the litter size. This study was conducted to identify QTL affecting teat number in the Korean native pig×Landrace resource family. A total of 240 animals was genotyped for 132 polymorphic microsatellites covering the 18 pig autosomes. Mean and standard deviation of teat number in F_2 animals is 13.46±1.40. QTL was analyzed using F_2 QTL Analysis Servlet of QTL express. A QTL for teat number on SSC9 was significant at the 1% chromosome-wide level and three suggestive QTL were detected on SSC3, 7 and 14. All QTL detected in this study had additive effect and Landrace alleles were associated with higher teat number in comparison with Korean native pig for three of four QTL. *(Asian-Aust. J. Anim. Sci. 2004. Vol 17, No. 9 : 1210-1213)*

INTRODUCTION

Quantitative genetics is concerned with the inheritance of those differences between individuals that are of degree rather than of kind, quantitative rather than qualitative. These differences are usually considered as resulting from the combined effects of many causal factors, some genetic in origin and some environmental. Quantitative trait loci (QTL) refer to gene positions in genetic materials influencing quantitative characteristics. The mapping of QTL is the first step towards the positional cloning and application of marker-assisted selection or marker-assisted introgression in genetic improvement (Soller, 1994). Marker-assisted selection (MAS) may be a method of selecting for traits at a very young age resulting in improving accuracy of selection. Efficiency of MAS relative to phenotypic selection is greatest for lowly heritable and sex-linked traits (Lande and Thompson, 1990). To implement MAS, QTL must be identified and their effects estimated.

The availability of high-density linkage map has made it possible to detect quantitative trait variations and identify individual loci controlling economically important traits. Using a genome-wide scan, Andersson et al. (1994) found evidence of QTL on *Sus scrofa* chromosome 4 (SSC 4) for growth, length of small intestine, and fat deposition.

Following this, QTL for growth and fat deposition traits (Paszek et al., 1999; Rohrer, 2000; Wada et al., 2000; Bidanel et al., 2001; Malek et al., 2001a), for carcass traits (Andersson-Eklund et al., 1998; Rohrer et al., 1998b), and for meat quality (De Koning et al., 1999, 2001; Malek et al., 2001b) have been reported. QTL affecting reproduction traits in swine have been reported by Rathje et al. (1997) and Wilkie et al. (1999).

To date, QTL affecting teat number were reported a significant QTL and a suggestive QTL on chromosomes 1 and 7, respectively, (Wada et al., 2000), one significant and two suggestive QTL on chromosomes 10, 1 and 3, respectively (Rohrer, 2000), and paternally expressed QTL on chromosomes 2 and 12, and Mendelian expressed QTL on chromosome 10 (Hirooka et al., 2001). Because the number of teat is an important trait regarding the mothering ability of sows, the pig industry has traditionally applied selection pressure to teat number (Pumfrey at al., 1980). In particular, teat number plays a significant role when there are more piglets than number of teats (Hirooka et al., 2001).

This study was conducted to identify QTL affecting teat number in the Korean native pig×Landrace resource family that represents a cross between the two divergent pig breeds.

MATERIALS AND METHODS

Resource population

The resource population was constructed from a cross between Korean native boars and Landrace sows. Five boars of Korean native pig and ten sows of Landrace were selected randomly from a herd at the National Livestock Research Institute (NLRI), Rural Development Administration (RDA), Korea. Each boar was mated with two or more different sows to produce F_1 animals. Each F_1

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Table 1. Means and standard deviations of teat number in F2 animals

Side	N	Mean	SD
Left	193	6.80	0.61
Right	193	6.73	0.61
Total	193	13.46	1.40

Table 2. Results of QTL affecting teat number

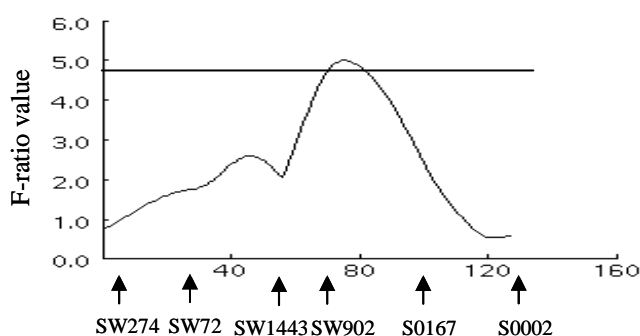| SSC	Locus (cM)	F-ratio	Additive effect	Dominance effect	Threshold
3	76	5.02*	-0.313±0.102	0.134±0.143	4.834
7	67	5.02*	-0.314±0.080	0.109±0.144	4.973
9	136	8.99**	-0.485±0.131	-0.401±0.198	7.169
14	30	5.11*	0.216±0.070	0.079±0.109	4.705

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

Figure 1. F-ratio curve for teat number on chromosome 3. The x-axis indicates the relative position on the linkage map. The y-axis represents the F-ratio value. The horizontal line indicates the 5% chromosome-wise significance level from the permutation test.

Figure 2. F-ratio curve for teat number on chromosome 7. 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-wise significance level from the permutation test.

Figure 3. F-ratio curve for teat number on chromosome 9. The x-axis indicates the relative position on the linkage map. The y-axis represents the F-ratio. Two lines present the 5% chromosome-wise (—) and 1% chromosome-wise (---) significance level from the permutation test.

sire was randomly selected from each litter, and mated with full-sib sows. That is, ten sires and 31 dams were used to produce 240 F_2 animals. The number of morphologically normal teats was counted at 12 weeks of age.

DNA isolation, marker selection, and genotyping

Blood samples were collected from all F_2 animals and their parents (F_1) and grandparents (F_0), and DNA was isolated with Wizzard Genomic DNA Purification Kit (Promega, USA).

Totally 132 polymorphic microsatellite markers were selected and used for genotyping the animals in the resource pedigree. An average marker interval was approximately 19 cM based on USDA-MARC Pig Map (Rohrer et al., 1996).

The PCR was carried out in a GeneAmp PCR System 9600 (Applied Biosystems, USA). PCR products of up to 9 markers were pooled, and analyzed simultaneously using an automated DNA sequencer (ABI 310 Genetic Analyzer, Applied Biosystems, USA). Fragment length of the PCR product was determined with Genescan software version 2.1 (Applied Biosystems, USA), and marker genotypes were assigned to the animals using Genotyper software version 2.5 (Applied Biosystems, USA).
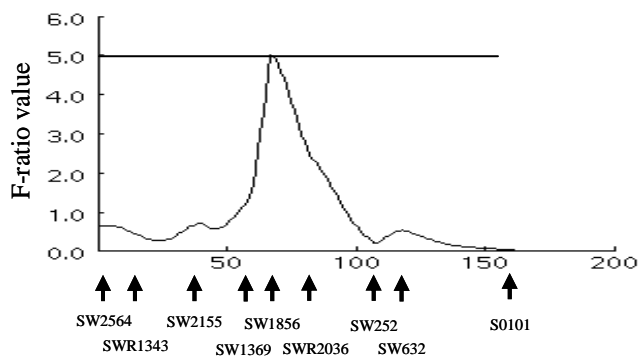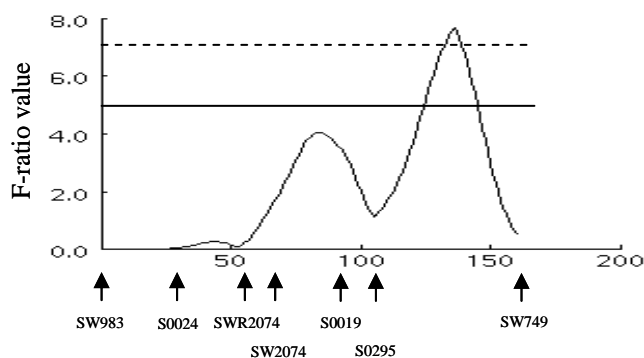
Statistical analysis

Linkage analysis was performed using CRIMAP software version 2.4 (Green et al., 1990). For the QTL analysis, the F_2 QTL Analysis Servlet of QTL express which is a web-based QTL mapping tool was used (http://qtl.cap.ed.ac.uk/).

RESULTS

The mean of total teat number of F_2 individuals was 13.46±1.40 (Table 1). Mean teat number of Korean native pigs was 12.10±1.2, whereas Landrace have 13.78±1.3 of mean teat number (Seo et al., 1996). Mean teat number of F_2 animals was similar to that of Landrace pure breed.

One significant and three suggestive QTL affecting teat number were found at the chromosome-wide level. A significant QTL on chromosome 9 was identified around 136 cM between markers S0295 and SW749 (Table 2 and Figure 3). Three suggestive QTL on SSC3, SSC7 and SSC14 were founded at position 76 cM (SW902-S0167), 67 cM (SW1856-SWR2036) and 30 cM (SW857-SW210), respectively (Table 2; Figures 1, 2 and 4). Table 2 shows the
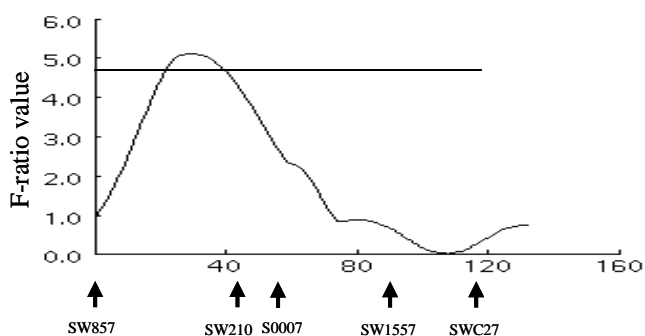
Figure 4. F-ratio curve for teat number on chromosome 14. The x-axis indicates the relative position on the linkage map. The y-axis represents the F-ratio. The horizontal line indicates the 5% chromosome-wise significance level from the permutation test.

estimated effects for significant QTL affecting teat number. The mode of gene action for all QTL detected in present study was additive nature. Landrace alleles for the QTL on SSC3, SSC7 and SSC9 increase teat number. The QTL affecting teat number on SSC9 was 0.485 of additive effect which indicates that animals having two alleles of Landrace at this locus had more 0.97 teats than those that transmitted both alleles for Korean native pig.

However, in the QTL affecting teat number on SSC14, alleles of Landrace have negative effect, which is opposite to the general expectations based on the mean teat numbers of the breeds used for our reference pedigree. It would be suggested that Landrace breed still have alleles that express an unfavorable effect on teat trait, as compared with the alleles existing at the corresponding locus in Korean native pigs.

DISCUSSION

During the suckling period, a sow must provide a fair opportunity to access nipple for all its piglets, thus teat number has been considered as one of the most important factors to evaluate mothering ability of swine. The markers associated with the significant QTL which were detected in this study can be used in marker-assisted selection for teat number.

Up to date, a few studies on QTL affecting mothering abilities have been performed in pigs. Wada et al. (2000) reported two QTL affecting teat number on SSC1 and SSC7, of which the identified QTL on SSC1 had highly significant additive effects. Rohrer (2000) reported a significant QTL for teat number on SSC10 and two suggestive QTL on SSC1 and SSC3. Hirooka et al. (2001) reported QTL three highly significant QTL affecting teat number, of which two were imprinted. Paternally expressed QTL were found on SSC2 and SSC12. A Mendelian expressed QTL was found on SSC10. In addition, they reported a suggestive QTL for teat number on SSC3, which has its best position at 90 cM

in S0216-S0002 interval. Cassady et al. (2001) reported two suggestive and three putative QTL for teat number were found on SSC8, SSC11, SSC1, SSC6 and SSC7, respectively. The first genomewide significant imprinted QTL for teat number on SSC2 and SSC12 reported by Hirooka et al. (2001).

In this study, a suggestive QTL affecting teat number was detected on SSC 3 at position 76 cM between SW902 and S0167. The region is close to those of the reports by Rohrer (2000) and Hirooka (2001). QTL for teat number on SSC7 reported by Wada et al. (2000) and Cassady et al. (2001) also are in close proximity to the QTL in our study. A significant QTL detected in present study at position 136 cM between markers SW295 and SW749 on SSC9 was same chromosomal region as a suggestive QTL for gestation length reported by Wilkie et al. (1999). In addition, we found another QTL for teat number on SSC14 which has not been reported previously. However, we could not find highly significant QTL affecting teat number on SSC1 (Wada et al., 2000), SSC2 (Hirooka et al., 2001), SSC10 (Rohrer, 2000; Hirooka et al., 2001), SSC11and SSC12 (Hirooka et al., 2001).

In conclusion, we found a significant and three suggestive QTL affecting teat number on SSC9, SSC3, SSC6 and SSC14, respectively. However, it is apparent that expending this study to include larger resource population will probably be necessary to increase the power to verify our current results and to confirm the validity of our suggestive observation. Furthermore, construction of high-resolution maps of the region containing the QTL will be important for identifying additional markers more close to linked to the QTL and cloning trait genes.

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