Quantitative trait loci for litter size and prenatal loss in a White Duroc × Chinese Erhualian resource population

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Summary

To detect quantitative trait loci (QTL) for litter size related traits, the total number of born piglets (TNB), the number of born alive piglets (NBA), the number of stillborn piglets (NSB) and the number of mummies (NM) at the first parity were recorded in 299 F₂ sows in a White Duroc × Chinese Erhualian intercross resource population. A whole genome scan was performed with 183 microsatellites distributed across 19 porcine chromosomes in the resource population, and the QTL analysis was performed with a least-squares method. A 5% genome-wide significant QTL was detected at 88 cM on pig chromosome (SSC) 15 for NBA, which also showed suggestive effect on TNB. In addition, four suggestive QTL were detected on SSC 6, 7, 8 and 15 for TNB, NBA or NSB. Two of the five QTL detected showed accordance with previous reports. No QTL was found for NM.

Keywords litter size, pig, prenatal loss, quantitative trait loci.

Litter size related traits, including the total number of born piglets (TNB) and the number of born alive piglets (NBA), are economically important in the pig industry. Litter size is controlled by many factors such as ovulation rate, number of corpora lutea, uterine capacity and prenatal survival. The number of stillborn piglets (NSB) and the number of mummies (NM) are two main parameters reflecting prenatal loss. As a result of these characteristics being of low heritability and sex-limited, litter size and prenatal loss traits are suitable for marker-assisted selection on the basis of causative genes or closely linked markers. The whole genome scan and the candidate gene approach are two main strategies to identify genetic markers for complex traits. Until now, a total of 18 suggestive (5% chromosome-wide significant) quantitative trait loci (QTL) have been reported for TNB or NBA on pig chromosomes (SSC) 6, 7, 8, 12, 14 and 17 (Yasue et al. 1999; Cassady et al. 2001; de Koning et al. 2001; King et al. 2003), for NSB on SSC 4, 5 and 13 (Wilkie et al. 1999; Cassady et al. 2001), for ovulation rate on SSC 3, 8, 9, 10 and 15 (Rathje et al. 1997; Rohrer et al. 1999; Wilkie et al. 1999; Campbell et al. 2003), and for uterine capacity and prenatal loss on SSC 8 (Rohrer et al. 1999; King et al. 2003). No QTL for NM has been detected. Numerous genes have been evaluated as candidate genes affecting litter size, such as oestrogen receptor (ESR) (Rothschild et al. 1996), osteopontin (OPN) (Korwin-Kossakowska et al. 2002), gonadotrophin-releasing hormone receptor (GNRHR) (Jiang et al. 2001) and retinol binding protein 4 (RBP4) (Rothschild et al. 2000). However, associations of these genes with litter size are always population specific, and the causative mutations underlying litter size remain unexplored.

Erhualian pigs are a subpopulation of the Chinese Taihu breed, which is well known for prolificacy, with an average litter size of 16.0 (Zhang et al. 1986). We have developed a four-generation intercross resource population using Erhualian and White Duroc as founder breeds (Guo et al. 2009). The objective of this study was to identify QTL for TNB, NBA, NSB and NM at the first parity of F₂ sows from the White Duroc × Erhualian resource population. In this population, 229 gilts from the first and second batches were transferred to three breeding farms in Yichun (n = 59), Dongxiang (n = 52) and Shangyou (n = 118) counties (Jiangxi province). Gilts at the age of 7–10 months were naturally mated to 53 Western purebred or crossbred boars (Table 1). In addition, 70 gilts of 11–18 months old from the fifth and sixth batches were kept on the original farm and were naturally mated to 34 mature F₂ boars (Table 1). All experimental pigs at the four farms were provided with an identical feed. TNB, NBA, NSB and NM were recorded in all experimental populations, showing remarkably
phenotypic segregation (Table 2). All the procedures involving animals followed the guidelines for the care and use of experimental animals established by the Ministry of Agriculture of China.

A whole genome scan was performed with 183 informative microsatellite markers in the resource population as described by Guo et al. (2009), and a comprehensive map with a total length of 2344.7 cM and an average interval of 13.40 cM was constructed (Guo et al. 2009). The QTL analysis was performed with QTL express at http://qtl.cap.ed.ac.uk/ based on a least-squares method (Haley et al. 1994). The GLM process of SAS9.1 (SAS Institute Inc) was employed to determine fixed effects and covariates used in the QTL model. In this study, farm and batch were included as the fixed effects. Thresholds at 1% and 5% genome-wide significance levels and suggestive levels, respectively, were estimated using a permutation analysis with 1000 random data shuffles as described by Churchill & Doerge (1994). Bootstrap analysis was carried out to determine 95% confidence intervals (CI95) for each QTL detected (Visscher et al. 1996). Percentage of variance explained by each QTL was calculated using the following formula:

\[
\text{Var} \% = \frac{(\text{MS}_{\text{reduce1}} - \text{MS}_{\text{full}})}{\text{MS}_{\text{reduce}}} \times 100,
\]

where \(\text{MS}_{\text{full}},\ \text{MS}_{\text{reduce1}}\) and \(\text{MS}_{\text{reduce}}\) were the residual mean squares of the models with all detected QTL, with all QTL except the currently focused one, and with no QTL respectively.

A total of five QTL were detected on SSC6, SSC7, SSC8 and SSC15 (Table 3). The most significant QTL was observed at 88 cM on SSC15 for NBA (Fig. 1), which reached the 5% genome-wide significance level and explained 4.96% of the phenotypic variance. This region also showed a suggestive effect on TNB. Heterozygous sows at this locus produced 1.83 more live piglets per litter than those homozygous for the Erhualian allele and 2.73 more than those homozygous for the White Duroc allele, showing an overdominant effect. Two additional suggestive QTL for NBA and TNB were identified on SSC6 and SSC7. For NSB, two suggestive QTL were detected on SSC7 and SSC8. No QTL for NM was detected in this study.

The two QTL on SSC6 and SSC7 showed accordance with the previous report. On SSC6, Wilkie et al. (1999) found a suggestive QTL for TNB. Yasue et al. (1999) also evidenced a region of 7-cM affecting TNB on this chromosome, and the pregnancy-specific beta-1-glycoprotein gene was proposed as a positional candidate gene. In the TNB QTL region on SSC7, a suggestive QTL has been previously suggested in a Meishan × Dutch commercial breed resource population (de Koning et al. 2001).

Before this study, no evidence has been shown for QTL or candidate genes affecting the two traits in the most significant QTL region associated with both NBA and TNB on SSC15. However, QTL for ovulation rate that are highly correlated with litter size have been reported in this region in two experimental populations (Rathje et al. 1997; Rohrer et al. 1999). It is well known that sperm quality is associated with litter size. Nevertheless, we did not find QTL for sperm quality related traits in the QTL region in the current population (data not shown).

It has been reported that polymorphisms of several candidate genes including ESR, PRLP, FSHb, RBP4, GNRHR, LEP, LEPR, OPN, BF, FUT1 and EPOR (for a review, see Buske et al. 2006) could be associated with litter size in different pig populations. In this study, the NBA QTL region on SSC6 harbours LEPR and FUT1 genes, and the NSB QTL region on SSC8 contains OPN and GNRH genes. However, genomic regions harbouring ESR, PRLP, RBP4, LEP, FSHb and EPOR genes were not associated with litter size traits in this study.

Few QTL, especially genome-wide significant QTL, have been detected for litter size related traits. In this study, we detected only one 5% genome-wide significant QTL for these traits. Considering that sample sizes of resource populations for mapping QTL affecting litter size are relatively small because of phenotyping difficulty and cost, we speculated that

Table 1: The White Duroc × Erhualian F2 sows from four experimental farms and their mating partners.

<table>
<thead>
<tr>
<th>Farm</th>
<th>No. of sows</th>
<th>Batch</th>
<th>Boar breed</th>
<th>No. of boars</th>
</tr>
</thead>
<tbody>
<tr>
<td>Yichun</td>
<td>59</td>
<td>1</td>
<td>Duroc, large white</td>
<td>5</td>
</tr>
<tr>
<td>Dongxiang</td>
<td>52</td>
<td>1</td>
<td>Duroc, large white, landrace</td>
<td>12</td>
</tr>
<tr>
<td>Shangyou</td>
<td>118</td>
<td>2</td>
<td>Large white, landrace</td>
<td>36</td>
</tr>
<tr>
<td>Nanchang</td>
<td>36</td>
<td>5</td>
<td>F2 boars</td>
<td>19</td>
</tr>
<tr>
<td></td>
<td>34</td>
<td>6</td>
<td>F2 boars</td>
<td>15</td>
</tr>
<tr>
<td>Total</td>
<td>299</td>
<td></td>
<td></td>
<td>87</td>
</tr>
</tbody>
</table>

1The maternal birth batch of F2 sows in the White Duroc × Erhualian resource population.
2F2 boars from the 4th birth batch of the White Duroc × Erhualian resource population.
3F2 boars from the 5th birth batch of the White Duroc × Erhualian resource population.

Table 2: Phenotype data of litter size related traits at the first parity in F2 sows from the White Duroc × Erhualian intercross.

<table>
<thead>
<tr>
<th>Trait</th>
<th>Range</th>
<th>Mean ± SE</th>
<th>SD</th>
</tr>
</thead>
<tbody>
<tr>
<td>NBA</td>
<td>1–17</td>
<td>8.77 ± 0.23</td>
<td>4.01</td>
</tr>
<tr>
<td>NM</td>
<td>0–3</td>
<td>0.08 ± 0.02</td>
<td>0.40</td>
</tr>
<tr>
<td>NSB</td>
<td>0–16</td>
<td>1.58 ± 0.16</td>
<td>2.83</td>
</tr>
<tr>
<td>TNB</td>
<td>1–19</td>
<td>10.48 ± 0.20</td>
<td>3.39</td>
</tr>
</tbody>
</table>

NBA, the number of born alive piglets; NM, the number of mummies; NSB, the number of still born piglets; TNB, the total number of born piglets.
one of the limiting factors for the detection of significant QTL for litter size is limited informative meiosis. Another limiting factor is the complex genetic architecture of litter size-related traits and environmental factors. It is well known that litter size is affected by a set of factors such as farm, feeds, season and mating boars, which account for a large part of the phenotype variance. From a genetic point of view, litter size is affected by a set of factors such as farm, feeds, season and mating boars, which account for a large part of the phenotype variance. Moreover, interaction between QTL may substantially contribute to complex traits. Further searches for epistatic QTL could reveal chromosomal regions with significant effects on the measured traits.

In conclusion, we detected one 5% genome-wide significant and four suggestive QTL for litter size and prenatal loss traits in the White Duroc × Erhualian resource population. Two of the five QTL identified confirmed those found in previous reports and the other QTL were reported for the first time. Caution should be taken when considering the suggestive QTL because of the possibility of false positive results.

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References


