

#### 14. Mapping QTLs for deficiency phosphorus response to root-growth of rice seedling

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Phosphorus (P) deficiency has been identified as a major factor limiting grain yield in rice worldwide. In general, rice varieties with tolerance to P deficiency exhibited the root elongation under P deficient conditions, and the relative root length (RRL) were determined as a reliable parameter for tolerance to P deficiency in rice (Shimizu et al., 2004).

In this study, we used a set of recombinant inbred (RI) population from a cross of Asominori with IR24, the molecular data and RFLP map with 375 markers (Tsunematsu et al, 1996), kindly provided by Prof. A. Yoshimura (Kyushu University, Japan) to detect quantitative trait loci (QTLs) for RRL, representing P deficiency response to root-growth seedling. Our experiments were conducted in glasshouse of Shanghai Normal University, Shanghai, China, with three replicates. Six germinated-seeds of each RI line along with its parents were placed into polystyrene floating plates on plastic containers containing running water on 8 July, 2007. After 5d, all seedlings were placed in a pool containing P-deficient (P=0.5 mg/l) and P-sufficient (P=10 mg/l) nutrient solutions (Yoshida et al., 1976), respectively. The pH value of solutions was adjusted to 5.0 using 1 N NaOH or HCl. The nutrient solution was replaced every five days. After 20d, the root length of each RI line was measured, then, RRL were calculated. QTL analysis was performed with QTL Cartographer software (Wang et al., 2003) version 2.0 through composite interval mapping method. The loci with LOD value greater than 2.0 was declared as indicative of the presence of a QTL.

As a result, there was a clear difference of RRL between Asominori (Non-sensitive to elongation) and IR24 (Relatively sensitive to elongation) and continuous distributions for RRL with some transgressive RI lines were observed, suggesting that RRL is quantitatively inherited trait (Fig. 1). Three QTLs, tentatively designated as *qRRL-7*, *qRRL-11*, and *qRRL-12*, were detected for RRL with LOD value of 2.91 (Chr. 7), 2.16 (Chr.11) and 2.30 (Chr. 12) (Table 1 and Fig. 2) and explained 13.3%, 10.7% and 10.3% of total phenotypic variation, respectively. Comparative mapping has shown that *qRRL-12* is allelic to/ tightly linked to the QTL for P efficiency, dry weight and tiller number (Wissuwa et al., 1998) and relative stem and leaf dry-weight, relative root dry-weight and tiller number (Ni et al., 1998) under low phosphorus stress. Interestingly, *qRRL-7* and *qRRL-11* were the first time reported as novel QTLs for P deficiency response in rice. From those results, it can be concluded that there maybe exist more novel QTLs for P deficiency response in rice and the tightly linked molecular markers that flank the QTLs might be useful in improving tolerance to P deficiency in rice.

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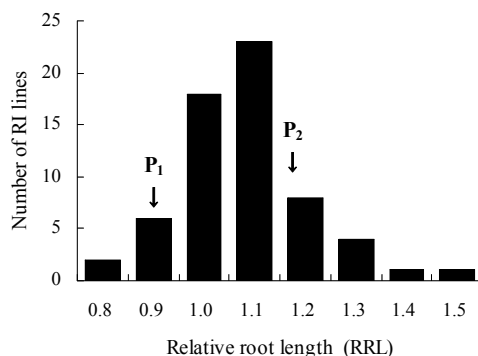


Fig. 1 Frequency distribution of relative root length (RRL) in the RI population derived from Asominori/IR24

Table 1 QTLs for the relative root length (RRL) in low phosphorous level in the RI population derived from Asominori/IR24

QTLs	Chromosome	Marker interval <sup>1)</sup>	LOD Value	Additive effects <sup>2)</sup>	Variance <sup>3)</sup> (%)
<i>qRRL-7</i>	7	<b>XNpb106</b> -C1008	2.91	0.050	13.3
<i>qRRL-11</i>	11	C104B- <b>XNpb52</b>	2.16	0.049	10.7
<i>qRRL-12</i>	12	<b>R3375</b> -R367	2.30	-0.045	10.3

<sup>1)</sup> **Black hold markers** indicate the nearest marker to putative QTL

<sup>2)</sup> Positive values of additive effects indicate Asominori alleles are in the direction of increasing the RRL

<sup>3)</sup> The percentage of explained phenotypic variation

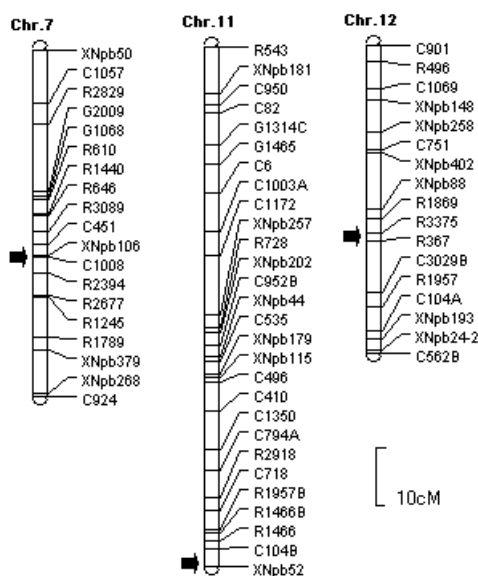


Fig. 2 Location of QTLs for relative root length (RRL) in the RI population derived from the cross between Asominori and IR24  
Black arrowheads indicate the location of peak LOD