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Dissection of QTLs for Hull Silicon Content on the Short Arm of Rice Chromosome 6

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Abstract: The QTL *qHUS6* for hull silicon content in rice was previously located on the short arm of rice chromosome 6. By using an $F_{2:3}$ population segregating in the RM587–RM19784 region harboring *qHUS6* in an isogenic background, two QTLs for hull silicon content were detected, of which *qHUS6-1* was located in the distal region and *qHUS6-2* in the region proximal to the centromere. Three rice plants carrying small heterozygous segments in the target region were selected, of which two covered the *qHUS6-1* region and the other covered the *qHUS6-2* region. Three $F_{2:3}$ populations were derived from the selfed seeds of the three plants, respectively. QTL mapping was performed using the two populations segregating in the *qHUS6-1* region, and *qHUS6-1* was delimited to a 147.0-kb region flanked by the markers RM510 and RM19417. Five groups of F_3 lines with different genotypic compositions in the *qHUS6-2* region were selected from the other $F_{2:3}$ population. Two QTLs were separated with two-way ANOVA, of which *qHUS6-2a* was located in the interval defined by RM19706–RM19795 and *qHUS6-2b* in the interval RM314–RM19665.

Key words: rice (*Oryza sativa*); quantitative trait locus; residual heterozygous line; hull silicon content; gene mapping

Silicon plays an important role during rice growth and development. High levels of silicon correlate with biotic and abiotic stress resistance as well as high yield and good quality of rice [1-4]. Numerous studies concerning the absorption, accumulation and distribution of silicon in rice have been performed and three genes controlling silicon transport have been cloned [5-7]. Several studies of QTL (quantitative trait locus) mapping of traits pertaining to silicon in rice have also been performed [8-10].

Lsi1 and *Lsi2* genes that control the transport of silicon in rice were located on chromosomes 2 and 3, respectively. *Lsi6*, which shares 77% homology with *Lsi1*, was localized to chromosome 6 using homology-based cloning and it participates in the process of silicon distribution in rice shoot [7]. QTL mapping for silicon-based traits in rice is underway. Three QTLs were located on chromosomes 3, 5 and 9, respectively, by using a population containing 98 backcross recombinant inbred lines (BILs) derived from Nipponbare and Kasalath [8]. Seven QTLs were located on chromosomes 1, 3, 7, 8, 9, 10 and 11, respectively, with a recombinant inbred line (RIL) population derived from Kinmaze and DV85 [9]. In our previous study, 10 QTLs controlling silicon content in hull (4 QTLs), flag leaf (4 QTLs) and stem (2 QTLs) were mapped respectively with an RIL population derived from Zhenshan 97B and Milyang 46 [10]. *qHUS6*, a QTL for hull silicon content, can be detected with different populations in different locations and years [11].

In the present study, several different QTLs were detected in the region of *qHUS6*. Two QTLs for hull silicon content were found in the *qHUS6* region with a population that has a homozygous genetic background. Individuals having a smaller segregating region were then constructed and finally three QTLs were detected in the *qHUS6* region and one of them was delimitated to a 147.0-kb region.

MATERIALS AND METHODS

Rice materials

Four different populations were used in this study. The first $F_{2:3}$ population named RHL6 was derived from a residual heterozygous line (RHL) and segregating

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in the region RM587–RM19784 on the short arm of chromosome 6 (Fig. 1). RHL6 was adopted for QTL mapping for rice yield and related traits and the linkage map has been constructed [12-13]. Three other populations were derived from RHL6.

Two individuals heterozygous in the regions of RM587–RM5815 and RM510–RM225 were selected from RHL6 and two selfed inbred F_2 populations named FM3 and FM4 were constructed with six simple sequence repeat (SSR) markers in the region RM587–RM5815 (Fig. 2). A total of 26 recombinant plants in the region RM587–RM5815 and 36 non-recombinant plants were selected from the F_2 population of FM3, and an $F_{2:3}$ population was constructed with these plants with nine SSR markers in the region RM510–RM225 (Fig. 2). Also, 10 recombinant plants in the region RM510–RM225 and 30 non-recombinant plants were selected from the F_2 population of FM4, and an $F_{2:3}$ population was constructed with these plants.

An individual heterozygous in the region RM111–RM19784 was selected from RHL6 and an $F_{2:3}$ population containing 499 lines was constructed. Five groups of F_3 lines with different genotypic compositions in the target region were selected from the other $F_{2:3}$ population (Fig. 3).

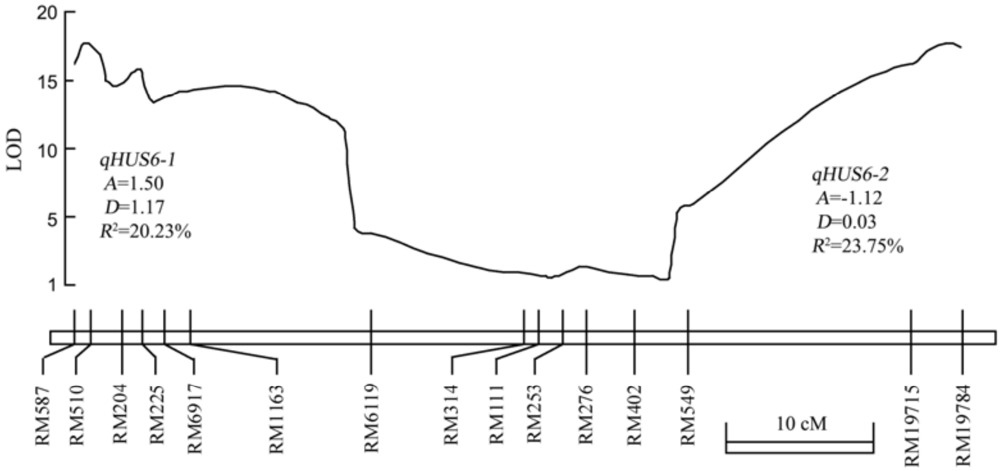

Fig. 1. Detection of QTLs for hull silicon content in the interval RM587–RM19784 on the short arm of rice chromosome 6 by using an RHL6 $F_{2:3}$ population.

A, Additive effect. The genetic effect when a maternal allele is replaced by a paternal allele. D, Dominance effect. R^2, The proportion of phenotypic variance accounted for by the given QTL.

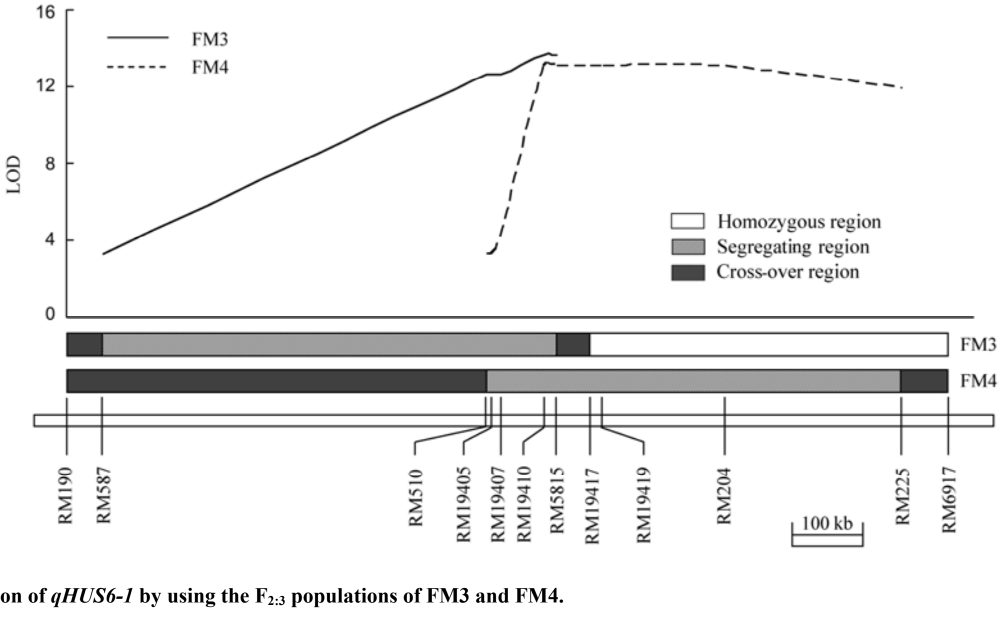

Fig. 2. Validation of *qHUS6-1* by using the $F_{2:3}$ populations of FM3 and FM4.