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Identification of QTLs for Flooding Tolerance Using RIL Population in Rice (*Oryza Sativa* L.)

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[Introduction]

Rice (*Oryza sativa* L.) is one of the most important staple food crops grown worldwide. In rainfed lowlands and flood-prone areas worldwide, rice farmers commonly encounter flooding after seeding, which results in partial to complete crop failure because the high sensitivity of rice to the flooding conditions caused considerable losses in grain production each year by flooding during germination. In this study, we identified candidate quantitative trait loci (QTLs) associated with flooding tolerance during germination using recombinant inbred lines (RILs).

[Materials and Methods]

To analyze QTLs for flooding tolerance, we evaluated the survival rate under flooding conditions of RIL populations with their parental lines. Genotypic analyses were performed using single nucleotide polymorphisms (SNPs) markers.

[Results and Discussion]

A linkage map of 1134.9 cM was constructed using 1313 polymorphic SNPs markers. Five putative QTLs were detected on chromosomes 1 (*qSUB1*), 3 (*qSUB3*), 4 (*qSUB4*), 7 (*qSUB7*), and 11 (*qSUB11*), explaining from 5.3 to 15.4% of the phenotypic variation, and with LOD scores of 2.82–7.53.

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