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Fine-mapping of Pre-harvest Sprouting Quantitative Trait Locus through the Whole-Genome Sequencing in Rice (*Oryza sativa* L.)

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[Introduction]

Rice (*Oryza sativa* L.) is one of the most important food crops as it is the main staple food for more than half of the world's population. Climate change entails higher temperatures, and the predicted above-average temperatures will diminish rice crop yields. Pre-harvest sprouting (PHS), one of the adverse effects of climate change on crops, was reported to become a serious threat to rice production. In this study, we identified candidate genes associated with PHS using segregation populations.

[Materials and Methods]

To analyze quantitative trait loci (QTLs) and fine-mapping for PHS tolerance, we evaluated PHS under field and growth chamber conditions of F_{2:3} and F_{3:4} populations with their parental lines. Genotypic analyses were performed using single nucleotide polymorphisms (SNPs) and InDel (Insertion & deletion) markers designed in re-sequencing data.

[Results and Discussion]

qPHS^{FC} and *qPHS^{GC}* were detected on chromosome 1, and the QTL regions were narrowed down from 237 Kbp to 50 Kbp. The five candidate genes *Os01g0111200*, *Os01g0111300*, *Os01g0111400*, *Os01g0111500*, and *Os01g0111600* were detected in this 50 Kbp region, and *Os01g0111400* and *Os01g0111600* were confirmed to contain SNP and an InDel.

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