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Mapping of *qBK4^T* Derived Bakanae Disease Resistance in Rice

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[Introduction]

Bakanae disease, caused by several *Fusarium* species, is a major threat to the productivity of rice across the globe. The incidence of this disease has been shown to increase, particularly in major rice-growing countries. Thus, the use of highly resistant rice cultivars offers a comparative advantage, such as being cost effective, and could be preferred to the use of fungicides. In this study, we employed a Genome-Wide *As*-sociation Study (GWAS) to investigate novel genetic loci associated Bakanae disease resistance using a population of 145 BC₁F_{7:8} NILs derived from a cross between Ilpum × Tung tin wan hien1.

[Materials and Methods]

The experiments were conducted using a BC₁F_{7:8} population (n = 145) derived from a cross between Tung Ting Wan Hien1 (bakanae disease resistant) and Ilpum (bakanae disease susceptible), and the resultant phenotype was used for QTL analysis. Rice bakanae disease pathogen, CF283, was mainly used inoculation and evaluation of disease was performed with the method of the large-scale screening method developed by Kim et al. (2014). Statistical differences between means were analysed using Duncan's multiple range test in SAS 9.4 program (SAS Institute Inc., Cary, NC, USA).

[Results and Discussions]

A localization of *qBK4^T* was delimited at an approximate 324kb interval in the physical map between AX-116847364 (33.12 Mb) and AX-115752415 (33.44 Mb). Previous studies reported QTLs controlling Bakanae disease on chromosome 4 but different loci, such as *qBK4.1* and *qBK4_31750955*. Therefore, this study provides new insights for R-gene-specific marker development, which could be useful for downstream Bakanae disease-resistant breeding and R-gene pyramiding. Further characterization of the R-gene would be helpful to unveil the mechanism underlying Bakanae disease resistance in rice.

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