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QTL Analysis of the $qBK1^Z$, a Major QTL for Bakanae Disease Resistance in Rice

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[Introduction]

Bakanae disease is one of the most serious problems in rice production in Korea, and has become serious in the hybrid rice growing area, worldwide, where involves increased use of seed beds for the raising platelets. In a previous research, we identified $qBK1$, a major QTL for bakanae disease resistance, from indica variety (Shingwang) as the donor and a japonica variety (Ilpum) as the recurrent parent (Hur et al, 2015). Beside another bakanae disease resistance discovered major QTL for qBK^{WD} , and identify gene pyramiding effect harboring both $qBK1$ and qBK^{WD} (Lee et al, 2018).

[Materials and Methods]

A tropical japonica rice variety, Zenith, was selected as resistant donor to bakanae disease. One hundred eighty RILs (F_{8,9}) were generated from a cross between Ilpum and Zenith. Rice bakanae disease pathogen, *F. fujikuroi* isolate CF283, was used inoculation. Evaluation of disease was performed with the method of the large-scale screening method developed by Kim et al. (2014). QTL analyses were performed by composite interval mapping with QTL ICIM mapping program (Li et al. 2008).

[Results and Discussions]

In primary mapping, a QTL was found on short arm chromosome 1 was 3.5 Mb region between RM1331 and RM3530 markers. The resistance QTL, $qBK1^Z$, explained 30.93% of the total phenotype variation with an LOD score of 13.43. Location of $qBK1^Z$ was further narrow-downed to 730kb by finer mapping by using additional RM markers and those of previous study developed by lee et al.,(2017). further more, augment resistance of bakanae disease and promoting breeding efficiency using MAS from $qBK1^Z$ region. The new QTL, $qBK1^Z$, developed in current study are expected to provide promoting breeding efficiency with to enhance resistance against bakanae disease resistance.

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