

Identification of a Novel Bakanae Disease Resistance QTL in Zenith Cultivar Rice (*Oryza sativa* L.)

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Bakanae disease, caused by several *Fusarium* species, imposes serious limitations 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 high resistant rice cultivars offers a comparative advantage, such as being cost effective, and could be preferred to the use of fungicides. In this research, we used a tropical *japonica* rice variety, Zenith, a bakanae disease resistant line selected as donor parent. A RIL population (F_{8:9}) composed of 180 lines generated from a cross between Ilpum and Zenith was used. In primary mapping, a QTL was detected on the short arm of chromosome 1, covering about 3.5 Mb region flanked by RM1331 and RM3530 markers. The resistance QTL, *qBKI^Z*, explained about 30.93% of the total phenotype variation (PVE, logarithm of the odds (LOD) of 13.43). Location of *qBKI^Z* was further narrowed down to 730 kb through fine mapping using additional RM markers, including those previously reported and developed by Sid markers. Furthermore, there is a growing need to improving resistance to bakanae disease and promoting breeding efficiency using MAS from *qBKI^Z* region. The new QTL, *qBKI^Z*, developed by the current study is expected to be used as foundation to promoting breeding efficiency with an enhanced resistance against bakanae disease. Moreover, this study provides useful information for developing resistant rice lines carrying single or multiple major QTLs using gene pyramiding approach and marker-assisted breeding.

Key words: Rice, bakanae disease, resistance,

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