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## Studies on QTLs for Bakanae Disease Resistance with Populations Derived from Crosses between Korean *japonica* Rice Varieties

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### [Abstract]

Rice bakanae disease is a serious global threat in major rice-cultivating regions worldwide causing high yield loss. It is caused by the fungal pathogen *Fusarium fujikuroi*. Varying degree of resistance or susceptibility to bakanae disease had been reported among Korean *japonica* rice varieties. We developed a modified in vitro bakanae disease bioassay method and tested 31 Korean *japonica* rice varieties. Nampyeong and Samgwang varieties showed highest resistance while 14 varieties including Junam and Hopum were highly susceptible with 100% mortality rate. We carried out mapping QTLs for bakanae disease resistance with four F2:F3 populations derived from the crosses between Korean *japonica* rice varieties. The Kompetitive Allele-Specific PCR (KASP) markers developed in our laboratory based on the SNPs detected in Korean *japonica* rice varieties were used in genotyping F2 plants in the populations. We found four major QTLs on chromosome 1, 4, 6, and 9 with LOD scores of 21.4, 6.9, 6.0, and 60.3, respectively. In addition, we are doing map-based cloning of the QTLs on chromosome 1 and 9 which were found with Junam/Nampyeong F2:F3 population and Junam/Samgwang F2:F3 population, respectively. These QTLs will be very useful in developing bakanae disease resistant high quality rice varieties.

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