

GWAS-BASED IDENTIFICATION OF LOCI FOR BAKANAE DISEASE RESISTANCE IN RICE

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Bakanae disease is one of the most serious and oldest problems of rice production, caused by one or more seed-borne *Fusarium* species, mainly *F. fujikuroi*. The disease may infect rice plants from the pre-emergence stage to the mature stage. Although management practices such as thermal seed treatment using hot water or fungicides are adopted to control bakanae infection, its incidence is increasing, leading to a serious concern in the main rice-producing areas worldwide. Identification and cultivation of rice resistant cultivars represent efficient procedures for bakanae disease control. However, only few accessions were reported to have high resistance to the infection. Similarly, the availability of mapped genes conferring resistance to bakanae is very restricted. In the present study, japonica rice collection comprising 142 accessions were screened for bakanae resistance after an artificial inoculation with *F. fujikuroi*. A large variability was observed, with few lines showing low levels of disease symptoms, indicating that genetic determinants for the trait are segregating in the collection under analysis. Molecular variation between the same rice accessions was evaluated by a Genotyping-by-Sequencing approach, which yielded a total of about 31.000 informative SNPs with a Minor Allele Frequency above 10%. Genome Wide Association Scan performed with the GAPIT R-package resulted in the identification of new genomic regions on chromosomes Os1 and Os3, that are involved in the resistance to the bakanae disease in the rice japonica background.

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