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Response to Bakanae Disease in Korean Rice Varieties

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[Introduction]

Bakanae disease is one of the major constraints factor in rice production in Korea, and has become serious in rice growing areas worldwide, where the use of seed beds is predominant. The incidence of this disease has been shown to increase, particularly in major rice-growing countries. In this study, 66 rice varieties cultivated in Korea were screened and assessed for their resistance to Bakanae disease. The output of this study will provide a basic data of Bakanae resistance level to rice growers as well as rice research field.

[Materials and Methods]

This study was carried out to evaluate the degree of resistance of 75 domestic breeding rice varieties and abroad genetic resources owned by the National Institute of Crop Science towards Bakanae disease. The rice bakanae disease pathogen, CF283 strain, was used to inoculate plants. The evaluation of the disease severity and symptoms development were done following the large-scale screening method developed by Kim et al. (2014).

[Results and Discussions]

Currently, domestic identified rice bakanae disease resistance genes include *qBK1*, *qBK1^{WD}*, *qBK1^Z*, and *qFfR1* mapped on chromosome 1, and *qFfR6* on chromosome 6. In this study, we tried to evaluate the genetic diversity using previously reported 14 DNA markers linked to *qBK1*, *qBK1^Z*, *qBK1^{WD}*, *qFfR1* and *qFfR6*. The results of the bioassay identified 27 rice varieties showing a moderate or high degree of resistance, accounting for about 36% of the total publicly available varieties, and the remaining varieties showed low or weak resistance towards bakanae disease. The discrepancy between the results of the bakanae disease bioassay and the genotype based on molecular markers was 17.7% (SN2 for *qBK1*) - 52.3% (KJ06_059 for *qFfR6*). This was lower than the discrepancy rate (38%) of the molecular marker RM9 (linked to *qBK1*) used in the previous study. These cultivars require further evaluation in order to identify new bakanae disease resistance genes through genetic mapping, and may be used for gene pyramiding as a countermeasure to increase resistance or breakdown of resistance in rice Bakanae disease.

[Acknowledgements]

This work was conducted with the support of the Cooperative Research Program for Agriculture Science & Technology Development (Project No. PJ01477401), Rural Development Administration, Republic of Korea.

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