E-P-5

The Gene Pyramiding Effect of *qBK1* and *qFfR1* Genes of Major Resistance Genes in Bakanae Disease

Sais-Beul Lee[1], Sumin Jo[1], Jun-Hyun Cho[1], Nkulu Rolly Kabange[1], Ji-Yoon Lee[1], Yeongho Kwon[1], Ju-Won Kang[1], Dongjin Shin[1], Jong-Hee Lee[1], You-Cheon Song[1], Jong-Min Ko[1], Kyung-Min Kim[2] and Dong-Soo Park[1,3]*

[1]National Institute of Crop Science, Milyang 50424, Korea
[2]School of Applied BioSciences,College of Agriculture and Life Science,
Kyungpook National University, Daegu, 41566, Korea;
[3]International Rice Research Institute, Pili Drive, Los Baños, Laguna 4031, Philippines

Bakanae disease, caused by *Gibberella fujikuroi*, is one of the most devastating diseases threatening rice production in Korea. In recent years, the incidence of bakanae disease became alarming due to the mechanical transplanting practice where the spread of bakanae can be amplified during accelerating seeds growth, due to the use of seeding boxes. The development of resistant rice cultivars could be the primary and effective method for controlling bakanae disease. However, the effects of individual resistance genes are relatively small. Therefore, pyramiding of bakane R genes in rice breeding is a promising strategy having a high potential to mitigate the advert effects of bakanae disease. This study employed a gene pyramiding approach to develop bakanae disease resistant rice lines carrying *qBK1*, *qFfR1* introduced from rice line MY299BK and cv. Nampyeong, respectively. The MY299BK carries *qBK1* introduced from cv. Shingwang, which was found to have a high resistance compare to Nampyeong. In addition, the pyramiding effect of the *qBK1* and *qFfR1* resistance genes were investigated, and the presence or absence of these genes helped us investigate their interaction through bioassay method and MAS. Furthermore, the distribution of resistance in the population showed a biased distribution toward resistance in the $F_{6:7}$ populutions. However, we could not confirm the accumulation effect of the resistance gene, but the difference between the two genes by the SN2 marker was confirmed. Therefore, the *qBK1* gene harbored by MY299BK appears to be different from the *qFfR1* carried by Nampyeong, suspected to possess a different bakanae disease resistant gene different from those found in MY299BK and Nampyeong.

Key words: Rice, bakanae disease, resistance, *qBK1*, MY299BK

[This work was carried out with the support of "Cooperative Research Program for Agriculture Science and Technology Development (Project title: QTL mapping and development of functional rice with bakanae disease resistance in rice, Project No. PJ01477401)'', Rural Development Administration, Republic of Korea.]

*(Corresponding author) parkds9709@korea.kr, Tel: +82-55-350-1184