Marker-Assisted Selection for Bacterial Blight Resistant Lines of Rice[1]

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ABSTRACT

Rice bacterial blight caused by *Xanthomonas oryzae* pv. *oryzae*. is an important rice infectious disease in Taiwan. More than 30 bacterial blight resistance genes have been discovered during the past few decades. The International Rice Research Institute (IRRI) has successfuly bred several near isogenic lines with the IR24 genetic background that contain different bacterial blight resistance genes. IRBB66 is one of them. The present study reveals the distribution of *xa5*, *Xa7*, and *Xa21* genes in the F_2 populations derived from the two corsses of Tai-Ken 9 × IRBB66 and Taichung-Shien 10 × IRBB66. The three genes were dectected by closely linked molecular markers blonging to STS, SSR, and CAPS types. The results show that the above molecular markers worked efficient discrimination of various genotypes in progenies. The proportion of homozygous resistant genotypes of *xa5*, *Xa7*, and *Xa21* loci are 27.95%, 20.88%, and 24.08% respectively in the F_2 population of TCS10 × IRBB66. On the other hand, the proportion of homozygous resistant genotypes of *xa5*, *Xa7*, and *Xa21* loci are 25.0%, 18.95%, and 24.28% respectively in the F_2 population of TK9 × IRBB66. The distributions of most examined genotypes are following Mendel's segregation law except *Xa7* locus in the F_2 population of TK9 × IRBB66, which showing bias distritubion. The results of our study provide the information of inheritance behaviors of these three resistance genes, and the information will be helpful for the proper strategies design of breeding. Marker-assisted selection (MAS) approach utilized in this study can provide clear and difinite evidences for targeted traits selection. We believe that this strategy can enhance the efficiency and shorten the period of breeding. In general, MAS will be a valuable and practicable model for crop breeding in the future.

Key words: rice bacterial blight, *Xanthomonas oryzae* pv. *oryzae*, marker-assisted selection.