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Identification of rice blast major resistance genes in Korean rice varieties using molecular marker

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Abstract

Rice blast caused by *Magnaporthe oryzae* is one of the most serious diseases that affect the quantity and quality of rice production. The use of resistant rice varieties would be the most effective way to control the rice blast. However R gene incorporation into the rice variety takes time and pathogen could overcome the R gene effects after for a while. For monitoring the rice blast resistance gene distribution in Korean varieties, the four major blast resistance genes against *M. oryzae* were screened in a number of Korean rice varieties using molecular markers. Of the 120 rice varieties tested, 40 were found to contain the *Pi-5* gene, 25 for the *Pi-9* gene, 79 for *Pi-b* and 40 for the *Pi-ta* gene. None of these rice varieties includes tested 4 R genes. 3 R genes combination, *Pi-5/ Pi-9/Pi-b*, *Pi-5, Pi-9.Pi-ta*, or *Pi-9/Pi-b/Pi-ta* were found in 12 varieties, the rice blast disease severity were showed as resistant in the rice varieties containing *Pi-9/Pi-b/Pi-ta* R genes combination, respectively. Also pathogenic diversity of *M. oryzae* isolates collected in the rice field from 2004 to 2015 in rice field in Korea were analyzed using rice blast monogenic lines, each harboring a single blast resistance gene. Compatibility of blast isolates against rice blast monogenic lines carrying the resistance genes *Pi5*, *Pi9*, *Pib*, and *Piz* showed dynamic changes by year. It indicates that pathogen has high evolutionary potential adapted host resistances to increase fitness and would lead to rice blast resistance bred into the cultivar becoming ineffective eventually.

Keywords: Rice blast, *Magnaporthe oryzae*, Resistance gene, R gene combination, Compatibility

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