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Enhancing durable resistance of rice cultivars to Korean rice blast fungus

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1) Breakdown of blast resistance and change of *Magnaporthe grisea* population structure in Korea

Host resistance, for its economical benefits, has been used most extensively as a tool for crop disease management. Extensive pathogenic differentiation of rice blast fungus, *Magnaporthe grisea*, has been reported in many countries resulting in the breakdown of resistant cultivars of rice. Therefore, selection of resistance source and deployment of resistance genes should be based on the pathotypic structure of pathogen populations in the field. Most of the Korean commercial cultivars planted during the early 1960s were regarded to have the resistance gene, *Pi-a*, for blast. Since severe incidence of blast had been frequently observed, a new resistant variety Kwanok possessing R gene *Pi-k* from Kanto 55 was released into farmers' field in 1966. However, the variety was unfortunately severely infected in 1969 by a new race at the panicle stage.

A semi-dwarf gene from indica type rice, TN1, was introduced into japonica rice Yukara in 1965. Since then, indica rices have been extensively used to develop Tongil-type varieties by crossing with japonica lines. There have been no severe blast epidemics during the 7 years since 1970 when Tongil-type varieties were released to farmers. However, panicle blast occurred regionally on rice cultivars, Tongil and Yushin in Jeonbug province in 1976. Severe blast epidemics were observed in all provinces in 1977 and 1978. Breakdown of resistance of Tongil-type varieties was due to the pathogenic differentiation, change of population structure and favorable environmental

conditions.

Resistant cultivars, such as Youngpunbyeo and Gayabyeo, became susceptible to the new pathogenic races KI-315a and KI-315b in 1983. Race KI-401 was a newly identified race which could infect resistant cultivars Seonambyeo and Cheonmabyeo. There have been no resistant cultivars showing overall resistance to all the races distributed in the field since 1983. The race KI-409 was first identified from Namyangbyeo in 1985 and has been rapidly built up since 1990. Most commercial cultivars having *BL1* and *BL7* pedigrees, Jinmibyeo and Ilpumbyeo were susceptible to race the KI-409. The race KI-409 was isolated from 47 rice varieties and became a predominant race with 23.7% of distribution ratio in 1995.

The cultivars Daesan, Ilmi and Dongan-byeo have shown wide spectrum of resistance to many races including KJ-301, however, their resistance were broken-down by new races such as KI-1117a, KI-1113a and KJ-105a in 1999 and 2000.

2) Virulence spectrum of Korean *M. grisea*

Twenty-seven monogenic rice lines harboring major resistant gene for blast were screened to analyze their resistance spectrum to Korean blast fungus population using 190 isolates collected from 1985 to 2002. Especially, the monogenic line containing *Pi-9* gene was screened using 320 isolates. Based on the monogenic lines-blast isolate interactions, the 27 rice lines were classified into 9 groups. The Chinese rice cultivar LTH showed susceptible to all the tested isolates. These lines IRBLZ-Fu, IRBL5-M and IRBL9-

W harboring *Pi-z*, *Pi-5*, and *Pi-9*, respectively showed broader spectrum of resistance than those rice lines having *Pi-19*, *Pi-7* etc. Interestingly, the *Pi-9* gene (IRBL9-W) showed resistance to most isolates collected before 2000, but showed susceptible reactions to 5% and 20% of blast fungus population in 2001 and 2002, respectively. Population of virulent isolates to *Pi-ta*, *Pi-b*, and *Pi-7* also increased in 2002.

3) Enhancing durable resistance to blast disease

a. Selection of durable resistant cultivars to blast fungus through sequential planting method; Sequential planting method was conducted to identify durable blast resistance in Korean rice cultivars by a simple greenhouse assay. First planting of monogenic rice lines, harboring different major resistance genes for blast developed at International Rice Research Institute (from Dr. Fukuta of IRRI), *Pi-a*, *Pik-s*, *Pk-h*, *Pi-ta*, *Pi-b*, *Pi-sh*, *Pi-7(t)*, *Pi-z*, *Pi-i*, *Pi-3*, *Pi-5(t)*, and *Pi-9(t)*, in a seedling box (57x30cm) was inoculated by sprayer with a mixture of 27 blast isolates consisted of genetically different lineages (23 races).

There was a difference in time and quantity of susceptible response among cultivars. IRBL9-W harboring *Pi-9* produced very small and few lesions in the 1st inoculation. The size and number of susceptible lesions increased as planting time increased from 2nd to 7th. At the 3rd planting set, the IRBL9-W already showed abundant big size susceptible lesions and disease severity became severe at the 5th planting time. The isogenic line harboring *Pi-ta* and *Pi-b* etc showed more than 40% of DLA at the 1st planting time and continuously showed high incidence of disease. Some commercial cultivars or isogenic lines including Palgongbyeo, IRBL5-M (*Pi-5(t)*) and IRBL3-M (*Pi-3*) showed less than 40% DLA during the whole time until 7th planting. The sequential planting method in this experiment used enough number of compatible isolates under favorable condition for disease development, suggesting that this method might be useful to evaluate durability of blast resistance

b. Cloning and characterization of resistance gene *Pi-5* potentially broad spectrum resistance to blast in Korea; Three dominant DNA markers JJ80-T3, JJ81-T3 and JJ113-T3 were developed on the basis of physical map of the *Pi5(t)* locus. In the phenotype evaluation, almost all the selected cultivars were resistant to the rice blast PO6-6 and Korean isolates, indicating

that the resistance matched perfectly with PCR-positive genotypes. The disease evaluation results suggest that the three DNA markers could be used as markers for marker-aided selection of rice blast resistance to PO6-6. Through similarity searches of sequence data in public databases, it was found that the deduced amino acid sequences of three genes in the *Pi5(t)* region showed similarity to the conserved NB-and/or LRR motifs. These data indicate that the *Pi5(t)* locus contains a cluster of NB-LRR sequences. These three genes, *Pi5-1*, *Pi5-2*, and *Pi5-3*, are good candidates for *Pi5(t)* and may constitute part of a natural pyramid of resistance genes that confer the broad-spectrum resistance.

c. Field performance of multi-lines to blast disease; Performance of rice blast resistant multilines targeting the M. grisea race KJ-301, KJ-201, KJ-101 and KI-313 was investigated in the experimental field at Icheon and Suwon Gyeonggi province using Chuchoengbyeo and its multilines, Suwon (S) 433I and 433II and Suwon 345 and its multilines, Suwon (S) 443I and 443II in 1998~1999. Although incidence of leaf blast was not severe in the experimental field, there was a significant difference in leaf blast when measured by percentage of lesion area between susceptible parent Chuchoengbyeo and its multilines; leaf blast incidence in the multilines S433I and S433II was 0.14 and 0.06%, respectively, while it was 2.14% in Chuchoengbyeo. Multilines S443I and S443II showed 0.16 and 0.26% of leaf blast, respectively, while Suwon 345 showed 0.23%. Incidence of panicle blast was severe in the experimental field, which made it clear to see a significant difference disease severity between susceptible parent and its multilines; panicle blast incidence in the multilines S433I and S433II was 0.5 and 1.2%, respectively, while it was 21.5% in Chuchoengbyeo. Multilines S443I and S443II showed 6.8 and 9.6% of panicle blast incidence, respectively, while Suwon 345 showed 21.45%. Cultivation area of the first commercial multiline cultivar Saechuchoengbyeo was 31,000ha in 2003 and has been increased fast in farmer's field. Popularity of the cultivar is mainly from high quality of rice grain similar to the parent cultivar Chuchoengbyeo and resistance to blast disease. Enhancing development of resistant multilines would be deemed necessary in resistant breeding program against rice blast disease.