Locates in the Nucleus and Mediates Pathogenesis-Related Gene Expression by Activation of a Transcription Factor. Plant Physiology (2003). 132: 1961-1972.

Zanke, B. W., Boudreau, K., Rubie, E., Winnett, E., Tibbles, L. A., Zon, L., Kyriakis, J., Liu, F.-F., and Woodgett, J. R. The stress-activated protein kinase pathway mediates cell death following injury induced by cis-platinum, UV irradiation or heat. Curr. Biol. (1996). **6**, 606–613.

Zhang, S. & Klessig, D. F. Resistance gene N-mediated de novo synthesis and activation of a tobacco mitogen-activated protein kinase by tobacco mosaic virus infection. Proc. Natl Acad. Sci. USA 95, 7433–7438 (1998).

Zhang, S., Du, H. & Klessig, D. F. Activation of the tobacco SIP kinase by both a cell-wall-derived carbohydrate elicitor and purified proteinaceous elicitins from Phytophthora spp. Plant Cell 10, 435– 449 (1998).

Zhang, S.&Klessig,D. F.MAPKcascades in plant defense signaling. Trends Plant Sci. 6, 520–527 (2001).

SIV-3

How the plant disease resistance genes can continue to recognize pathogen's infection.

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Most of plant R-gene's function is based on its recognizing ability, directly or indirectly, of the pathogen's corresponding avirulence gene products. Not to be overcome by the rapid mutation of pathogen's genome, plant R-genes also need to have some diversification mechanism, in addition to its maintenance mechanism in population. In order to analyze the mechanism of plant R-genes diversification, we have compared the base changes in the neighborhood region of rather isolated resistance genes, between the resistant and susceptible cultivars in rice and then in *Arabidopsis*. At the first search on the rice blast resistance gene *Pi-b*, the mutation rate was found to be more than ten times higher than the average of the genome, in about 60-80 kb region around the gene. This high-variability was not confined within the R-gene, of which LRR domain, the specificity determining factor, may have been subject to some diversification selection. Major types of the mobilization were accumulation of less than a few bases of small substitutions and insertion-and-deletions (indels). Density of small transposable elements like mites was about the same level as the other regions.

This tendency of high genome mobilization around R genes or its analogues was confirmed in *Arabidopsis* too, by comparing their sequences between ecotypes Columbia and Landsberg. Analysis about 15 kb around some rather isolated R gene and analogues revealed that the variability of the genome in this region is about 5 times higher than the average of the total genome, although there are variatons in the extent of this variability, from the normal level to more than ten times of that. Hypothesis that the mutations of *Arabidopsis* are explained as biallelic origins was refuted for R-genes that are experiencing high rate of genome mobilization.

To further characterize the R-gene analogue in the genome, more than 1000 R-gene analogues (RGA) were fine mapped in the rice genome by a combination of HEGS (High Efficiency Genome Scanning) system and RGA-scanning, both of them were developed by us. These systems can be readily applied for any other crops irrespective of the presence of genome sequence database.

SIV-4

Molecular marker assisted breeding for blast resistance in rice

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Rice blast disease caused by the fungal pathogen *Magnaporthe grisea* is one of the most serious and widespread diseases of rice worldwide. The deployment of resistant cultivars is the most effective and economical way of controlling blast disease, so breeding for resistant cultivars continues to be a priority in rice improvement (Kim *et al.* 1994). Comprehensive genetic studies on blast resistance have been conducted. At least 20 dominant genes conferring complete resistance to rice blast and 10 quantitative trait loci associated with partial resistance have been identified and several have been located via linkage to molecular markers (McCouch *et al.* 1994) and two of them, *Pi-b* and *Pi-ta*, have been cloned (Wang *et al.* 1999, Bryan *et al.* 2000).

Ilpumbyeo is an elite line widely cultivated in Korea. However, this cultivar has become increasing susceptible to blast, resulting in a decline of the area planted to this cultivar. The objectives of this study were to improve the blast resistance of Ilpumbyeo by introgressing the blast resistance gene(s) of *Moroberekan* by molecular marker-assisted selection in the backcrossing process; and to evaluate the effects of such improvement on the agronomic performance of Ilpumbyeo and the

introgression lines under both blast inoculated and non-inoculated conditions.

An advanced backcross population consisting of 279 BC3F3 lines from the cross between Ilpumbyeo as a recurrent parent and Moroberekan as a donor, was analyzed for blast resistance and traits of agronomic importance including days to heading and culm length. Also, the population was genotyped with 102 SSR markers evenly distributed on the rice chromosome. Most of the lines displayed similar phenotypes compared to Ilpumbyeo in evaluated traits. However, several lines showed differences compared to Ilpumbyeo and these differences might be due to the Moroberekan chromosome segments introgressed into Ilpumbyeo.

Out of 279 BC3F3 lines, 140 lines were analyzed for blast resistance. Two SSR markers (RM560 and RM3701) were associated with partial blast resistance. These two markers each accounted for 23.9% and 26.5% of the phenotypic variation of the diseased leaf area under natural infection. Three SSR markers (RM317, RM7269, and RM144) were significantly associated with resistance to three single pathogen isolates, respectively.

SSR genotyping analysis indicated that some lines have only one or two chromosome fragments from Moroberekan. Thirty-seven out of the 279 BC3F3 lines which had a minimum length of introgressed Moroberekan DNA fragment in the Ilpumbyeo background, were identified to cover all chromosomes of Moroberekan. The number of integrated fragments was in the range of 3-16. The genetic distance of integrated fragment was in the range of 7.2-79.1 cM. These ILs (introgression lines) developed here, which have improved resistance to blast resistance in the background of Ilpumbyeo, will be useful for breeding resistant cultivars and characterization of blast resistance. Additional backcrosses and selections are underway to purify the candidate ILs with a few independent introgressions and to construct a complete set of ILs. The results will be discussed.

References

Bryan G et al. 2000. A single amino acid difference distinguishes resistant and susceptible alleles of the rice blast resistance gene *Pi-ta*. Plant Cell 12:2033-2045.

Kim KH, Cho SY, Moon HP, Choi HC 1994. Breeding strategy for improvement and diversification of grain quality in rice. Korean J. Breeding 26 (Supp. 2): 3-19.

McCouch SR, Nelson RJ, Thome J, Zeigler RS 1994. Mapping of blast resistance genes in rice. In: Zeigler RS, Leong SA, Teng PS (eds) Rice Blast Disease, pp. 167186. Cab Int'l and IRRI, Wallingford, Oxon,UK.

Wang ZX et al. 1999. The *Pib* gene for rice blast resistance belongs to the nucleotide binding and leucine-rich repeat class of plant disease resistance genes. Plant J. 19:55-64.