

Molecular Plant-Microbe Interactions (63 ~ 74)

F-63 Development of SCAR Marker Linked to Resistance to *Phytophthora infestans* in Potato. Sang-Pyo Lee¹, Kwong-Jong Kim¹, Seung-Hee Eom¹, Hui-Seon Jeong¹, Hei-Young Kim², Hyun-muk Cho³, Young-Un Park³, Hyun-gon kang¹, Min-Seob Yeo¹, Hyun-Sik Lim¹, Sang-Woo Kim¹ and Youn-Su Lee¹
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Late blight resistance is demanding the attention of potato breeders worldwide following recent migrations of aggressive metalaxyl-resistant isolates of *Phytophthora infestans* in potato production areas. Resistance to late blight was controlled by a few major genes (R gene) which can be easily overcome by new races of *Phytophthora infestans* and an unknown number of genes expressing a quantitative type of resistance which may be more durable. In this study, we used AFLP method to identify markers linked to resistance trait. Based on AFLP method, primer combination of E+AT/M+CTC was selected out of eighty primer combinations. The specific fragment was isolated and ligated into a T-vector, followed by transformation into *E.coli*. Plasmid DNA was extracted from transformants, and the target product was harvested. The whole sequence of 127 bp were determined using T-vector and designated on LBR-1 primer set. We employed the PCR with LBR-1 of the SCAR primer. As a result, 127 bp fragment was observed only on HR lines but not in S lines. The DNA sequences of AFLP fragment from highly resistant potato clone showed high levels of homology with the PGECO93P17 sequences of the AT/CTC-196 revealed 86% nucleotide identity of *S. demissum*.

F-64 Effectiveness of avr-pita in *Magnaporthe grisea* isolated in Korea. Hyun-Kyung Kim, Sunggi Heu, Seungdon Lee, and Dongsoo Ra. Division of Plant Pathology, NIAST, Rural Development Administration, Suwon, Korea

Rice blast disease, caused by the fungus *Magnaporthe grisea*, is one of the severe diseases, resulting in plant damage and reduced yield. Rice plants have evolved defense systems to resist constant attacks from pathogens such as *M. grisea*. Apart from the preformed defenses such as antimicrobial secondary compounds, plant defenses can be induced by effectors such as avirulence (AVR) proteins, which are the products generated by pathogen during infection. These effectors can be recognized by plant

disease resistance (R) proteins in a specific manner, referred as gene-for-gene interaction, and activating defense responses. The interaction between blast pathogen and rice follows the “gene-for-gene” theory in which r genes interacts a corresponding avr gene, and induces defense responses. The presence of *avr-pita*, an avirulence gene originated from *M. grisea*, was analyzed for the 80 strains of *M. grisea*, which were collected nationwide in 2003. Using the same strains, pathogenicity tests were carried out on a monogenic rice cultivar, IRBLta-K1, which carried the corresponding resistance (R) gene, *pita*. All strains, except 2, carried the *avr-pita* gene, however, lots of strains showed virulence and brought about disease symptoms, such as formation of typical disease lesions. Expression level of *avr-pita* gene was analyzed for the virulent and avirulent strains using RT-PCR.

F-65 Functional characterization of SA- and JA- inducible OsWRKY. Jae-Soon Seo, Ji-Young Lee, Jee-Eun Kim, Seok-Cheol Suh, Duk-Ju Hwang. National Institute of Agricultural Biotechnology, Suweon, 441-707, Korea.

Plants have the ability to defend themselves against pathogens by activating a series of defense responses. The activation of a series of plant defense responses is known to be through varieties of transcription factors. WRKY proteins are known to regulate defense response in plants. WRKY proteins are defined by the presence of highly conserved WRKY domain characterized by the hallmark heptapeptide WRKYGQK and a zinc-finger structure distinct from other known zinc finger-type motif. The WRKY domain binds to the W box ((T)TGAC(C/T)) in the promoter of wound- and pathogen-responsive genes. In this study we have isolated an OsWRKY gene from rice plants. This OsWRKY belongs to group III member that contains a C₂-HC motif instead of a C₂-H₂ pattern. The OsWRKY was induced by salicylic acid (SA) and jasmonic acid (JA) highly at 24hr respectively, suggesting that this OsWRKY might be involved in plant defense response. To determine whether this OsWRKY act as transcriptional activator, a transactivation assay of OsWRKY in yeast were carried out. It reveals that OsWRKY acts a transcriptional activator in yeast. Whether OsWRKY regulate defense signaling in rice will be discussed in detail.

F-66 Disruption of *hrp*-related genes by homologous recombination in *Xanthomonas oryzae* pathovar *oryzae*. Cho, Hee Jung, Young Jing Park, Eun-Sung Song, Dong-Hee Lee¹ and Byoung-Moo Lee. National Institute of Agricultural Biotechnology, R.D.A., Suwon, 441-707, Korea, ¹Department of Life Science, Ewha Womans University, Seoul, 120-420, Korea