## Molecular Plant-Microbe Interactions (63 ~ 74)

F-63 Development of SCAR Marker Linked to Resistance to *Phytophthora* infestans in Potato. Sang-Pyo Lee<sup>1</sup>, Kwong-Jong Kim<sup>1</sup>, Seung- Hee Eom<sup>1</sup>, Hui-Seon Jeong<sup>1</sup>, Hei-Young Kim<sup>2</sup>, Hyun-muk Cho<sup>3</sup>, Young-Un Park<sup>3</sup>, Hyun-gon kang<sup>1</sup>, Min-Seob Yeo<sup>1</sup>, Hyun-Sik Lim<sup>1</sup>, Sang-Woo Kim<sup>1</sup> and <u>Youn-Su Lee<sup>1</sup></u> College of Agriculture and Life Sciences, Kangwon National University, Chuncheon 200-701, Korea; <sup>2</sup>College of Science, Dongguk National University, Seoul 100-715, Korea; <sup>3</sup>National Institute of Highland Agriculture, Pyeongchang 232-955, Korea

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 overcame 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 resistnace 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