

from *F. graminearum*, two representative strains (SCKO4 from rice and Z03643 from wheat) were mutagenized using restriction enzyme-mediated integration (REMI). In total, 20,000 REMI transformants have been collected from the two strains. So far, 63 mutants for several traits involved in disease development such as virulence, mycotoxin production, and sporulation have been selected from 3,000 REMI transformants. Now, selected mutants of interest have been genetically analyzed using a newly developed outcross method (See Jungkwan Lee et al poster). In addition, cloning and characterization of genomic DNA regions flanking the insertional site in the genome of the mutants are in progress.

1-44. Analysis of genes expressed during pepper-*Phytophthora capsici* interaction

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Phytophthora capsici is a pathogen on several economically important crops including pepper. In pepper growing areas in Korea, Phytophthora blight caused by *P. capsici* has been considered as the most serious problem in pepper production. The Oomycete attacks the roots, stems, leaves and fruits of the plant. To understand the molecular mechanisms involved in the disease development, the genes expressed during pepper *P. capsici* interaction were explored by analyzing expressed sequence tags (ESTs). A complementary DNA (cDNA) library was constructed from total RNA extracted from pepper leaves challenged with *P. capsici* for 3 days resulting in early stage of symptom development. The comprehensive analysis on the single pass sequencing of over 4000 randomly selected cDNA clones with contig assembly, unique gene extraction, sequence comparison, and functional categorizing will be presented with an emphasis on the genes involved in plant defense and pathogenicity during disease development of the pepper Phytophthora blight.