normally but in pectin and complex media, it grew slower than wild type. Expression of various CWDEs in *MgSnf1* mutant was investigated and found that expression of some CWDEs is repressed. However, no significant difference was observed in conidial germination, appressorium formation, and pathogenicity in *MgSnf1* mutant. However, *MgSnf1* functionally complemented a yeast *Snf1* mutant. These results suggest that *MgSnf1* is involved in regulation of CWDEs and *MgSnf1* is dispensable in pathogenicity of *M. grisea*.

1-42. Shifting reproductive mode of a mycotoxin producing-fungus by manipulation of mating-type genes

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In most ascomycetes, a single mating type locus, *MAT*, with two alternate forms (*MAT1-1* and *MAT1-2*) called idiomorphs, controls mating ability. In heterothallic ascomycetes these alternate idiomorphs reside in different nuclei. In contrast, most homothallic ascomycetes carry both *MAT1-1* and *MAT1-2* in a single nucleus, usually closely linked. An example of the latter is *Gibberella zeae*, a producer of mycotoxins such as trichothecene and zearalenone that threaten human and animal health. We asked if *G. zeae* could be made strictly heterothallic by manipulation of *MAT*. Targeted gene replacement was used to differentially delete *MAT1-1* or *MAT1-2* from a wild type haploid *MAT1-1*;*MAT1-2* strain, resulting in *MAT1-1*;*mat1-2*, *mat1-1*;*MAT1-2* strains that were self-sterile, yet able to cross to wild type testers and more importantly, to each other. These results indicated that differential deletion of *MAT* idiomorphs eliminates selfing ability of *G. zeae*, but the ability to outcross is retained. To our knowledge, this is the first report of complete conversion of fungal reproductive strategy from homothallic to heterothallic by targeted manipulation of *MAT*. Practically, this approach opens the door to simple and efficient procedures for obtaining sexual recombinants of *G. zeae* that will be useful for genetic analyses of mycotoxin production and other traits, such as ability to cause disease.

1-43. Insertional mutagenesis of *fusarium graminearum* for characterization of genes involved in disease development and mycotoxin production

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Fusarium graminearum is an important pathogen of cereal crops in many areas of the world causing head blight and ear rot of small grains. In addition to serious economic losses, this fungus produces mycotoxins, such as trichothecenes and zearalenone on diseased crops and has been a potential threat to human and animal health. To massively identify pathogenesis-related genes

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 being 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.