

## Systems Biology Initiatives in the Rice Blast Fungus, *Magnaporthe grisea*

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*Magnaporthe grisea*, the causal agent of rice blast, is one of the representatives of fungal plant pathogens. Whole genome sequence data is released and over 8,800 uniESTs of this fungus are available in the public databases. Recently we generated 20,000 mutants using *Agrobacterium tumefaciens*-mediated transformation (ATMT) and developed a high-throughput phenotype assay system. Thus far, over 1,000 loss of virulence and several hundreds of transformants including auxotrophs, development-defective and oleate-nonutilizing mutants were obtained from ATMT mutant library. The T-DNA tagged sequences from the mutants are being rescued by TAIL-PCR technology. As the first step to establish fungal systems biology in this fungal pathogen, we developed the databases to manage all phenomics and genomics data of these transformants. Furthermore, a web-based portal system is established for efficient data acquisition and analyses such as BLAST and INTERPRO searches, gene ontology (GO) classification, expression profiling, phylogenetic and comparative analyses, and tools for further functional genomics research. Fungal systems biology initiatives would provide the platform for system-level understanding of the biology not only for *M. grisea*, but also is applicable for other fungal pathogens.