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Genomics, the powerful tool for identifying genes involved in the pathogenesis of plant pathogenic fungi

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The ascomycete *Magnaporthe grisea*, the causal agent of rice blast, is one of the most destructive plant pathogens in rice production worldwide. It penetrates the host cuticle directly by way of a highly melanized, specialized infection structure called an appressorium. Appressorium formation has been considered as a rational target for disease control. Environmental factors and genes involved in appressorium formation have been studied intensively during last decades. cAMP and signal transduction pathways have been shown to be involved in appressorium formation. To further understand the cellular mechanisms, adenylate cyclase gene (*MAC1*) was cloned and the function was characterized. Transformants lacking *MAC1* were unable to form appressoria on an inductive surface and were unable to penetrate rice. These results confirm that cell signaling involving cAMP plays a central role in the development and pathogenicity of *M. grisea*. Genes expressed during appressorium formation in the rice blast fungus *M. grisea* were identified by sequencing the cDNA clones prepared from conidia forming appressorium. A total of 2325 expressed sequence tags (ESTs) corresponding to 1430 unique sequence sets (307 contigs and 1123 singletons) were generated. ESTs showing significant homology to known genes were assigned to 10 functional categories. Differential and subtractive hybridization approaches were used to identify genes showing appressorium stage specific expression. High density cDNA microarrays were employed to examine the expression profile of a large number of genes associated with appressorium formation. Microarrays containing 4582 cDNAs derived from cDNA libraries of the appressorium formation stage and the vegetative stage were constructed. From preliminary experiments, comparing appressorium forming cells and vegetative cells, 30 genes including *MPG1*, *THNR*, and *PKS1* were found to be up-regulated during appressorium formation. Some of these genes were already known to be involved in appressorium formation or

pathogenicity in *M. grisea* and other plant pathogenic fungi. Twenty nine genes including those encoding glucose repressible protein 1 and glyceraldehyde-3-phosphate dehydrogenase were highly expressed in vegetative cells. At July 2002, the whole genome of *M. grisea* was completely sequenced and publicly available by the joint work of NCSU/Whitehead Institute (MIT). This achievement is waiting for post-sequence exploring by using functional and comparative genomics, proteomics, and pathogenomics.