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(1 Page Limit)

*Fusarium* head blight or scab caused by *Fusarium graminearum* is a destructive disease on wheat and barley. Infested cereals are reduced in yield and contaminated with harmful mycotoxins. Better understanding of *F. graminearum* pathogenesis is critical because effective fungicides and highly resistant plant varieties are not available. Previous studies have shown that the Gpmk1 MAP kinase is a key component of a well conserved signal transduction pathway that is essential for plant infection in *F. graminearum*. The goal of this study is to identify and characterize genes that are regulated by the Gpmk1 pathway and important for plant infection. One objective of this research is to determine the biological functions of ten putative transcription factor genes identified by microarray analyses with the *gpmk1* mutant. Targeted deletion mutants of selected genes will be examined for phenotypic changes in toxin production, different plant infection and developmental stages will be examined. Some of these transcription factors may regulate the expression of genes that are important virulence factors in *F. graminearum*. The other objective is to identify genes with similar expression profiles in the *gpmk1*, *fst11*, and *fst7* mutants. Comparative analysis with microarray data of the *gpmk1*, *fst11*, and *fst7* mutants will be helpful to identify *F. graminearum* genes that are truly up- or down-regulated by the Gpmk1 MAP kinase pathway.

Overall, the proposed research will utilize available functional genomic resources to identify and characterize genes that are regulated by the Gpmk1 pathway and important for *F. graminearum* pathogenicity. To our knowledge, the Gpmk1/Pmk1 MAP kinase pathway is the most important signal transduction pathway in plant pathogenic fungi for controlling different infection and development processes. Therefore, the objectives of this proposal are relevant to the FY06 research priorities of the Pathogen Genetics and Genomics (PGG) research area on 'Identify and characterize important pathogen gene and protein expression profiles, regulatory networks, and developmental or metabolic pathways'. In the long run, results from this study will be helpful to understand molecular mechanisms of fungal-plant interactions in scab disease development, and may ultimately lead to the development of more effective fungicides or disease control strategies.