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(1 Page Limit)

Fusarium head blight (FHB) caused by *Fusarium graminearum* is an important disease of wheat and barley. In addition to yield losses, infected grains are reduced in grain quality and contaminated with mycotoxins. Traditional methods for disease control of FHB by plant breeding have been problematic. Therefore, novel methods for the control of the disease or for the amelioration of the effects of toxin accumulation on the plant are desirable. In previous studies, we have identified a transcription factor gene *ZIF1* that plays important roles in pathogenesis and ascospore production. We also have found that no DON production or accumulation is detectable in rice infected with *F. graminearum*. Disease symptoms typically associated with DON are not observed in rice. In this study, we aim to use functional genomics approaches to identify and characterize pathogen genes that are important for plant infection and DON production or accumulation in plant. In objective 1, genes with altered expression patterns in the *zif1* mutant during plant infection and ascospore production will be identified by microarray analysis. This *ZIF1* transcription factor may function downstream from known signaling pathways and regulate genes important for plant infection. Candidate genes will be selected based on expression profiles for further functional characterization. In objective 2, we will compare the gene expression profiles of *F. graminearum* in infected wheat and rice. The transcription levels of the trochothecene biosynthesis genes will be closely examined to determine why DON does not accumulate in infected rice. Microarray data will allow us to identify novel genes that may function as a critical transcriptional repressor or activator for DON biosynthesis or general secondary metabolism.

The objectives of this proposal are relevant to the FY06 Research Priorities of the U.S. Wheat and Barley Scab Initiative, Pathogen Genetics and Genomics (PGG) research area, namely: Identify and characterize important pathogen gene and protein expression profiles, regulatory networks, and developmental or metabolic pathways. To our knowledge, this will be the first work in *F. graminearum* to characterize the genome-wide effect of a transcription factor with a known role in pathogenesis. This work also will examine the role of signal perception on the part of the fungus and how that may be converted into toxin accumulation in the host. If rice contains a factor which suppresses toxin gene expression in the fungus or contains enzymes that rapidly turn over DON during infection, preventing it from accumulating, these factors may be useful targets for introduction into wheat and barley.