

PI: Kistler, H. Corby**PI's E-mail:** hckist@umn.edu**Project ID: FY08-KI-118****FY07 ARS Agreement #:** NA**Research Category: PBG****Duration of Award:** 1 Year**Project Title: Fungal Genes involved in DON Accumulation in Wheat.****PROJECT 1 ABSTRACT**

(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. In addition to factors reducing the impact of FHB, novel methods for reduction of toxin accumulation in grain are desirable. In previous studies, we have found that little or no DON is produced or accumulates in wheat infected with *F. graminearum* mutants for the genes *Tri6* and *Tri10*. Disease symptoms typically associated with DON in wheat, such as blighting, spread within the head and tissue bleaching are not observed in these mutants. We also have found that no DON is produced or accumulates in rice infected with *F. graminearum*. Disease symptoms typically associated with DON are not observed in rice. **The objective of this project is to identify and characterize fungal genes involved in DON accumulation in wheat.** This will be done by 1) comparing fungal microarray data from wheat infected with wild type or trichothecene defective mutants and 2) comparing fungal microarray data from *Fusarium* infected wheat (toxin accumulates) with *Fusarium* infected rice (toxin does not accumulate). For objective 1, gene expression profiles of *F. graminearum* in wheat infected with wild type, as well as *Tri6* and *Tri10* mutants have been compared and several novel, differentially regulated genes, potentially involved in toxin accumulation *in planta*, have been identified. Gene deletion analysis may allow us to identify novel genes that may mediate critical steps in DON biosynthesis and/or accumulation *in planta*. In objective 2, we will compare the gene expression profiles of *F. graminearum* in infected wheat and rice. The transcription levels of the trichothecene biosynthesis genes will be closely examined to determine why DON does not accumulate in infected rice. The objectives of this proposal are relevant to the FY08 Research Priorities of the U.S. Wheat and Barley Scab Initiative, Pathogen Biology and Genetics (PBG) research area. Both objectives deal with whole plant research aimed to develop toxin reduction strategies which are consistent with PBG Research Priority 3: Develop new strategies for reducing the impact of FHB and associated mycotoxin accumulation in barley and wheat. 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.