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Research Area: EDM

Duration of Award: 1 Year

Project Title: Genomics of *Gibberella zeae*, the Head Scab Fungus.

PROJECT 1 ABSTRACT

(1 Page Limit)

Fusarium graminearum lineage 7 (*Gibberella zeae*) is the major fungal species causing *Fusarium* head blight of small grains in North America. With the previous support of USWBSI, we have been able to generate EST data for the fungus that allowed us to propose, fund externally, and carry out a whole genome shotgun sequence assembly of one strain of *F. graminearum*. Previous support of USWBSI for pilot studies on cDNA based microarrays also has allowed us to be able to propose for external funding, an Affymetrix Genechip based on the whole genome gene set. We now seek funding for pilot studies to test the feasibility of whole genome mutagenesis based on the gene set derived from the whole genome sequence. By this approach we could gain comprehensive knowledge of the suite of genes and regulatory networks essential for sporulation and disease causing ability in the fungus. As such, this work is a FY04 research priority for the EDM Research Area under the category of “genes and gene expression involved in the *Fusarium* life cycle and disease processes.” Specifically we propose to mutagenize by site-directed gene replacement, genes falling into three large classes: 1) molecular motors and ascospore discharge proteins, 2) non-ribosomal peptide synthase genes and 3) transporter genes involved in drug or fungicide resistance. Each class of gene potentially contains members that are essential for plant pathogenicity. Importantly, the results we obtain for the efficiency of mutagenizing cells, identifying and purifying mutants and screening for altered pathogenicity or sporulation will test and potentially validate methods for genome-wide mutagenesis. This approach ultimately may be the most rapid way for identifying potential targets for novel disease control methodologies.