FY09 USWBSI Project Abstract

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Research Category: **GDER**	**Duration of Award:** **1 Year**

Project Title: **A Genome Wide Screen to Identify Novel Genes for FHB Resistance.**

PROJECT 1 ABSTRACT

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We have screened the entire collection of yeast deletion mutants for resistance and sensitivity to a trichothecene mycotoxin and identified a valuable collection of novel targets. These results provided a comprehensive picture of cellular processes and molecular components required for trichothecene mechanism of action and metabolism. Since unlike many organisms, yeast is able to survive in the absence of functional mitochondria, this study provided the first in vivo evidence that trichothecene mycotoxins target the mitochondria. To identify the genes involved in trichothecene metabolism, we screened the yeast deletion strains for enhanced sensitivity to a trichothecene mycotoxin and identified the components of pathways that play a role in trichothecene metabolism. The new genes identified from the genome-wide screens will provide novel targets for engineering FHB resistance in cereals and for reducing mycotoxin contamination. Furthermore, this approach will provide important new insights into the mode of action of trichothecene mycotoxins and trichothecene metabolism. The primary goal of this project is to determine if manipulating expression of the orthologs of the genes identified in yeast will confer resistance to trichothecenes in plants.

The specific objectives of this proposal are:

1. Characterize the trichothecene resistance in yeast and determine if trichothecene resistance can be engineered by manipulating expression of the orthologs of the yeast genes in plants. We will use *Arabidopsis* and *Physcomitrella* knockout lines to determine if the genes identified in yeast will confer trichothecene resistance in plants.
2. Determine if genes that confer trichothecene sensitivity when deleted in yeast will confer trichothecene resistance when overexpressed. We will determine if overexpression of the genes identified in the genome-wide screen for trichothecene sensitivity in yeast will confer trichothecene resistance. To obtain a comprehensive picture of the pathways involved in trichothecene metabolism and resistance, the overexpression library, which represents 93% of all coding sequences in yeast, will be screened for trichothecene resistance.

This project fulfills the following research priorities of the GDER: "Increased efficiency of identification of candidate genes for resistance against FHB and reduced DON accumulation" and to "develop effective FHB resistance through transgenic strategies."