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Project ID: FY11-TU-010

FY10 ARS Agreement #: 59-0790-6-069

Research Category: GDER

Duration of Award: 1 Year

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

PROJECT 1 ABSTRACT

(1 Page Limit)

My laboratory has screened the entire collection of yeast deletion mutants for altered sensitivity to trichothecenes and identified a valuable collection of novel targets for trichothecene resistance. These genome-wide studies in yeast identified mitochondria as a prominent target. More recently, using isolated mitochondria from yeast, we showed that trichothecenes have a direct effect on mitochondrial translation and mitochondrial membrane potential. To identify novel plant genes for trichothecene resistance, we screened Arabidopsis T-DNA insertion lines representing orthologs of the yeast genes and identified loss-of-function mutations in three genes that showed enhanced resistance to Tcin. All three were nuclear encoded genes whose products were localized in mitochondria, demonstrating the importance of mitochondria in trichothecene sensitivity in plants. The primary goal of this application is to use high throughput approaches in Arabidopsis and barley for identification of novel plant genes that confer resistance to DON. We will determine if silencing homologs of one of the identified Arabidopsis genes in barley will lead to reduced sensitivity to DON and increased resistance to FHB. We screened the activation tagged Arabidopsis library and identified 15 Arabidopsis lines that showed high level of resistance to Tcin. These plants were able to form roots on 4 μ M Tcin and were indistinguishable from the untreated wild type plants. Sequence analysis of two of the activation tagged lines by TAIL-PCR identified T-DNA insertions in two novel genes. We plan to characterize the novel loci and determine if loss-of-function of these genes confers resistance to Tcin. Using a similar approach, we will screen the activation tagged barley population against trichothecenes. The specific objectives are:

1. Screen the Arabidopsis T-DNA insertion lines for resistance to Tcin and determine whether silencing homologous genes in barley will confer resistance to trichothecenes.
2. Utilize activation tagging to identify candidate Arabidopsis and barley genes for resistance to FHB and reduced DON accumulation.

The activation tagging approaches along with the analysis of yeast-Arabidopsis orthologs led to the identification of novel genes that conferred high level of resistance to DON. Characterization of these novel loci and identification of DON resistant barley lines proposed here fit very well with all three FY11 research priorities of GDER: 1) Characterization of novel loci for FHB resistance; 2) Identification of candidate genes for resistance against FHB; 3) Development of effective FHB resistance and/or reduced DON accumulation through transgenic strategies.