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Project ID: FY08-MU-136

FY08 ARS Agreement #: 59-0790-4-116

Research Category: BAR-CP/GDER

Duration of Award: 1 Year

Project Title: Characterize and Map Barley Genes that Respond to *Fusarium graminearum* Infection.

PROJECT 1 ABSTRACT

(1 Page Limit)

Fusarium head blight (FHB; scab), a fungal disease of barley caused by *Fusarium graminearum*, is a major problem for barley growers. My laboratory has conducted a large set of GeneChip experiments to examine the gene expression in barley and wheat during *F. graminearum* infection. These experiments include: barley infected with *F. graminearum*; barley infected with trichothecene-producing and non producing *F. graminearum* strains; three barley near-isogenic line pairs carrying resistant and susceptible alleles for FHB resistance QTL; and a wheat near-isogenic line pair carrying resistant and susceptible alleles for the chromosome 3BS resistance QTL. This proposal aims to identify and characterize barley genes that respond to *F. graminearum* infection and trichothecene accumulation. The specific objectives of this proposal are to: (1) examine variation in genes that respond to *Fusarium graminearum* infection and trichothecene accumulation; (2) genetically map genes that respond to *Fusarium graminearum* infection and trichothecene accumulation; and (3) develop markers for barley breeding programs. In this proposal, we will sequence and map genes derived from our GeneChip experiments that respond to *F. graminearum* infection and trichothecene accumulation. We have identified a large set of germplasm that exhibits a range of FHB severity and genetic variation. The genes will be sequenced from this set of germplasm. The sequence variation will be used to associate with FHB severity and DON accumulation phenotypes. These genes and map locations will be useful for genetic engineering and molecular breeding applications.

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Project ID: FY08-MU-053

FY08 ARS Agreement #: 59-0790-4-116

Research Category: BAR-CP/GDER

Duration of Award: 1 Year

Project Title: Identify Barley Genes that Respond to Deoxynivalenol.

PROJECT 2 ABSTRACT

(1 Page Limit)

Fusarium head blight (FHB; scab), a fungal disease of barley caused by *Fusarium graminearum*, is a major problem for barley growers. Grain quality is reduced primarily due to the fungal biosynthesis of trichothecene mycotoxins such as deoxynivalenol (DON), 3-acetyl-deoxynivalenol (3-ADON), and 15-acetyl-deoxynivalenol (15-ADON). This proposal aims to identify and characterize barley genes that respond to DON accumulation. The specific objective of this proposal is to: (1) identify barley genes that respond to DON. We plan to use the Barley1 Genechip to examine transcript accumulation in barley spikes inoculated with DON and mock inoculated with water. We will analyze the data and identify the genes that respond to DON treatment. To refine the set of genes that respond to DON, we will compare the data obtained from the proposed GeneChip experiment with our previous GeneChip experiments. We have identified a large set of genes that we will continue to characterize for their role in providing resistance to DON. The outcomes from this work will be a novel set of barley genes that respond to DON accumulation. These genes will be useful for genetic engineering and molecular breeding applications.

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Project ID: FY09-MU-001

FY08 ARS Agreement #: 59-0790-4-116

Research Category: GDER

Duration of Award: 1 Year

Project Title: Rapidly Identify and Test Scab Resistance Genes.

PROJECT 3 ABSTRACT

(1 Page Limit)

Fusarium head blight (FHB, scab), a fungal disease of small grain crops caused by *Fusarium graminearum*, threatens to reduce wheat and barley to economically unviable crops in the United States. During infection the fungus produces trichothecene mycotoxins that have been shown to increase fungal virulence. To complement the current breeding efforts, my laboratory seeks to functionally characterize a large set of genes with the potential to provide resistance to FHB. There are two major objectives in the proposed work including: (1) rapidly test genes for FHB resistance/susceptibility; and (2) develop transgenic wheat with genes with potential to exhibit FHB resistance.

We have conducted a wide array of RNA profiling experiments on barley and wheat during *F. graminearum* infection and identified potential resistance/susceptibility genes, including a large set of regulatory genes. We will test a subset of these potential resistance genes in two functional assays including: (1) virus-induced gene silencing (VIGS); and (2) a yeast screen. From these functional assays we will identify genes that we will use to develop transgenic wheat. These transgenic plants may result in wheat with enhanced resistance.

The proposed research meets the objectives of the USWBSI and fits within the Gene Discovery and Engineering Resistance (GDER) area of research. The proposed research has specific reference to the priorities of characterizing genes that provide FHB resistance, identification of FHB resistance genes and reduced DON accumulation, and developing transgenic wheat exhibiting FHB resistance.