

PI: Muehlbauer, Gary

PI's E-mail: muehl003@umn.edu

Project ID: FY07-MU-068

FY06 ARS Agreement #: 59-0790-4-116

Research Area: HGG

Duration of Award: 1 Year

Project Title: Mechanisms and Essential Genes for Resistance to Fusarium Head Blight.

PROJECT 2 ABSTRACT

(1 Page Limit)

Fusarium head blight (FHB; scab), a fungal disease of wheat and barley caused by *Fusarium graminearum*, threatens to reduce these small grains to economically unviable crops in the United States. This proposal aims to identify the mechanisms, signaling pathways and genes that are involved in FHB resistance, and markers linked to resistant QTL. The specific objectives of this proposal are to (1) identify genes potentially involved in FHB resistance; (2) generate markers linked to FHB resistant QTL; and (3) develop viral induced gene silencing to functionally test potential resistance genes.

We have conducted six RNA profiling experiments on barley and wheat during *F. graminearum* infection. We used the Barley1 and Wheat Affymetrix GeneChips to collect the data from five and one experiment, respectively. We will conduct a meta-analysis of the five barley-profiling experiments. In addition, we will compare the RNA profiles between the barley and wheat experiments. Our goal is to identify signaling pathways and genes that are potentially involved in FHB resistance. These analyses will be completed by the summer of 2007.

We will map genes that exhibit single feature polymorphisms (SFPs) between resistant and susceptible alleles for the barley chromosome 2H BIN8 FHB resistant QTL. SFPs are genetic differences that can be detected using GeneChips. We have detected 265 SFPs between the resistant and susceptible alleles for the chromosome 2H BIN8 QTL. This is the first FHB resistance QTL in barley that has been uncoupled genetically from a deleterious agronomic trait. Thus, adding more markers to this QTL region will facilitate marker-assisted selection and map-based cloning. We will develop markers from the SFPs and map them in barley mapping populations developed by Dr. Kevin Smith. This is a powerful approach to identify additional markers in a QTL region. This work will be ongoing throughout the funding period.

Genes identified in the GeneChip experiments that are potentially involved with FHB resistance will be functionally tested in a virus-induced gene silencing (VIGS) system in collaboration with Dr. Steve Scofield (USDA-ARS, West Lafayette, IN). My laboratory has provided Dr. Scofield a list of 76 genes that are potentially involved with FHB resistance. Members of my laboratory will visit Dr. Scofield's laboratory in the spring-summer of 2007 to learn the VIGS system and help with the functional testing of a select group of genes. Subsequent to this visit we will establish VIGS in my lab.

The proposed research meets the objectives of the U.S. Wheat and Barley Scab Initiative and fits within the host genetics and genomics area of research because we will identify molecular mechanisms, signaling pathways and genes that are potentially involved in FHB resistance, and we will identify novel markers for molecular breeding and map-based cloning.