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

PROJECT 2 ABSTRACT

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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. To complement the breeding efforts for FHB resistance, several laboratories have established genetic engineering approaches. However, the genetic engineering efforts are limited due to the lack of useful resistance genes. In addition, there are limited numbers of molecular markers linked to resistance QTL for use in marker-assisted selection (MAS) and map-based cloning. This proposal aims to identify the mechanisms, signaling pathways and genes that are involved in FHB resistance, and markers linked to resistant QTL.

By the start of the funding period, we will have conducted six RNA profiling experiments focused on barley and wheat during *F. graminearum* infection. We used the Barley1 and Wheat Affymetrix GeneChips to collect the data. These experiments will result in approximately 4.5 million data points. Thus, to extract the maximum amount of information from this dataset, we propose to carefully analyze the data. Bioinformatics analysis of the profiling experiments will be employed to identify genes that are differentially expressed in each experiment. In addition, we will compare the RNA profiles between experiments and between barley and wheat. Our goal is to identify signaling pathways and genes that are potentially involved in FHB resistance. Genes potentially involved with FHB resistance will be functionally tested for resistance in a virus-induced gene silencing system in collaboration with Dr. Steve Scofield (USDA-ARS).

We will map genes that exhibit differential expression between resistant and susceptible alleles for barley QTL. These expression differences may be due to allelic differences in the QTL region. We will develop markers from these genes and map them in barley mapping populations developed by Dr. Kevin Smith. We have already mapped two genes to a FHB resistant QTL region in this fashion. We believe this is a powerful approach to identify additional markers in the FHB resistant QTL regions.

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 involved in these small grains-pathogen interactions and are potentially involved in FHB resistance, and we will identify novel markers for MAS and map-based cloning.