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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. To develop FHB resistant varieties, large-scale wheat and barley breeding programs have been established. To complement these efforts, several laboratories have established genetic engineering approaches to enhance resistance to FHB. 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 and map-based cloning. This proposal aims to continue our gene discovery effort for FHB resistance genes and to develop novel markers for marker-assisted selection and map-based cloning. We will use the Barley1 and Wheat1 Affymetrix GeneChips to study the barley-*F. graminearum* and wheat-*F. graminearum* interactions and to identify the mechanisms, pathways and genes that are involved in FHB resistance, and markers linked to resistant QTL. RNA profiling experiments using these GeneChips will be conducted on resistant and susceptible barley and wheat genotypes infected with *F. graminearum*. In particular, we will examine barley and wheat near-isogenic line (NIL) pairs carrying contrasting resistant and susceptible alleles at the barley 3HS, barley 2HL and wheat 3BS QTL. Also, we will examine the RNA profiles in barley infected with trichothecene-producing and non-producing strains of the fungus. These experiments will identify differences in transcript accumulation in these resistant and susceptible interactions and genes that are expressed upon trichothecene accumulation. Bioinformatics analysis of the profiling experiments will be employed to identify genes that are up and down regulated as well as clusters of genes that are coordinately regulated over the course of infection. Additional bioinformatics will include comparing the RNA profiles in barley and wheat. Due to the different FHB disease phenotypes in wheat and barley, comparing transcript accumulation in wheat and barley will identify differences in gene expression that underlie the different disease phenotypes. We will also work with Drs. James Anderson and Kevin Smith (University of Minnesota) to map genes that are differentially expressed in genotypes carrying resistant and susceptible alleles for the NIL pairs. Many of these genes will be linked to FHB resistant QTL. All potential resistance genes will be provided to the genetic engineering groups for transformation. Markers that are tightly linked to the QTL will be made available to interested parties for marker-assisted selection and map-based cloning. The proposed research meets the objectives of the U.S. Wheat and Barley Scab Initiative and fits within the biotechnology area of research because we will identify molecular mechanisms, 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 marker assisted selection and map-based cloning.