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**Research Category: BAR-CP**

**Duration of Award: 1 Year**

**Project Title: Next Generation Approaches to Characterize Barley FHB Resistant QTL.**

### **PROJECT 1 ABSTRACT**

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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. Previous work has resulted in mapping quantitative trait loci that confer resistance in barley to FHB. To gain an increased understanding of the genetics of FHB resistance and the response to infection in barley, my laboratory seeks to identify genes that are expressed in barley during infection of *F. graminearum* and differentially expressed between near-isogenic genotypes carrying contrasting alleles for FHB resistance and susceptibility. In addition, we seek to identify novel markers for key QTL carrying resistance. There are three major objectives in the proposed work including: (1) identify all genes in barley spikes expressed during *F. graminearum* infection; (2) identify and test candidate genes for scab resistance; and (3) identify markers linked to major barley scab resistant QTL.

To identify all barley genes that are expressed in response to *F. graminearum* infection and to identify genes that are specifically expressed in FHB resistant and susceptible genotypes, we will conduct RNA-seq of three near-isogenic line pairs carrying resistance and susceptible alleles for three FHB resistance QTL (chromosome 2H bin 8, 2H bin10, and 6H bin 6) in barley. Each of these pairs will be inoculated with *F. graminearum*, RNA isolated, libraries prepared, sequenced on an Illumina sequencer, and the sequencing reads will be aligned to the emerging barley reference genome. Two sets of differentially expressed genes will be identified including: (1) genes expressed during *F. graminearum* infection; (2) and genes differentially expressed between plants carrying the resistant and susceptible alleles in the NIL pairs. Candidate genes for each of the QTL will be identified and tested for trichothecene resistance. Differentially expressed genes will be mapped on standard mapping populations.

This proposed project addresses the USWBSI research area “Gene discovery and engineering resistance” (GDER) to “characterize the genetic function of existing and novel loci for FHB resistance” and “to identify candidate genes for resistance against FHB and/or reduced DON accumulation”, and Objective 5 of the Barley CP to “identify barley genes differentially regulated in the barley-*Fusarium* interaction”.