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Fusarium head blight (FHB, scab), caused by *Fusarium graminearum*, is a major disease problem in wheat and barley worldwide. An understanding of the genetic control of the host responses and defense mechanisms in barley to *F. graminearum* infection and trichothecene accumulation is limited. To gain an initial understanding of these processes, my laboratory has conducted a large set of gene expression experiments aimed at identifying barley and wheat genes that respond to *F. graminearum* infection, trichothecene accumulation and deoxynivalenol (DON) treatment. We have identified genes that are involved in the barley-*F. graminearum* and wheat-*F. graminearum* interaction and that respond to trichothecenes. We have employed functional approaches to identify two genes that play a role in the host defense to *F. graminearum* infection. One gene appears to detoxify trichothecenes and transgenic Arabidopsis expressing this gene exhibits clear resistance to DON. The other gene appears to act as a negative regulator of trichothecene defense responses. We have also initiated association genetics and mapping approaches to identify genes that play a role in the genetic control of defense response and resistance. To this end, we DArT genotyped a set of 102 barley genotypes that exhibit a range of resistance/susceptibility to FHB. We used the DArT genotyping information to identify a core set of genotypes that will serve as a representative set for sequencing genes that have the potential to exhibit resistance or susceptibility. We have also sequenced portions of 40 genes from six mapping population parents and identified polymorphisms for mapping. In this proposal, we seek to leverage our prior gene expression, sequencing and DArT genotyping work to further characterize and map genes that exhibit the potential to exhibit resistance. Our specific objectives are: (1) examine variation in genes that respond to *F. graminearum* infection and trichothecene accumulation; (2) genetically map genes that respond to *Fusarium graminearum* infection and trichothecene accumulation; and (3) identify expression QTL for trichothecene accumulation. This proposed project addresses the USWBSI research area "Gene discovery and engineering resistance" (GDER) and Objective 4 of the Barley CP to "identify and validate genes with potential anti-fungal or anti-DON activity in barley".