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*Fusarium* head blight (FHB; scab), a fungal disease of barley caused by *Fusarium graminearum*, is a major problem for barley growers. My laboratory has conducted a large set of GeneChip experiments to examine the gene expression in barley and wheat during *F. graminearum* infection. These experiments include: barley infected with *F. graminearum*; barley infected with trichothecene-producing and non producing *F. graminearum* strains; three barley near-isogenic line pairs carrying resistant and susceptible alleles for FHB resistance QTL; and a wheat near-isogenic line pair carrying resistant and susceptible alleles for the chromosome 3BS resistance QTL. This proposal aims to identify and characterize barley genes that respond to *F. graminearum* infection and trichothecene accumulation. The specific objectives of this proposal are to: (1) examine variation in genes that respond to *Fusarium graminearum* infection and trichothecene accumulation; (2) genetically map genes that respond to *Fusarium graminearum* infection and trichothecene accumulation; and (3) develop markers for barley breeding programs. In this proposal, we will sequence and map genes derived from our GeneChip experiments that respond to *F. graminearum* infection and trichothecene accumulation. The genes will be sequenced from a set of germplasm that exhibits a range of disease severity. The sequence variation will be used to associate with FHB severity and DON accumulation phenotypes. These genes and map locations will be useful for genetic engineering and molecular breeding applications.