Project Abstract

Project Title:	Genetic Mapping of Genes Underlying Variation in Fusarium Head Blight Traits	
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The project goal is to identify genes harboring functional variation that contributes to variation in critical pathogen traits within *Fusarium graminearum* (*Fg*) populations to provide targets for pathogen management and control, and toxin reduction. This proposal leverages the genotyping of our FY14-15 USWBSI project, and continues our FY16-17 aims to determine the underlying genetic basis of naturally occurring phenotypic variation in *Fg* populations.
Project objectives and approaches:

1. In *in vitro* laboratory experiments with controlled environments, phenotype approximately 150 *Fg* isolates from the over 500 isolates genotyped in our FY14-15 project for the following measures: amount of DON produced in culture, fungicide sensitivity, ascospore discharge, and mycelial growth at different temperatures.
2. In greenhouse experiments on susceptible and resistant wheat backgrounds, phenotype 150 *Fg* isolates for aggressiveness and amount of DON produced via head inoculations.
3. Perform genome-wide association studies (GWAS) of the above traits to identify individual SNPs or genome regions statistically associated with variation in the traits.

Outcomes from Objective 1 will include estimates of fitness traits, including DON production and propiconazole sensitivity, and those from Objective 2 will include estimates of disease severity and *in planta* DON production for the isolates on the different wheat backgrounds. Based on previous work we expect to obtain high quality phenotypic data. The trait measures will be used in Objective 3 to map the genetic basis of natural variation in the traits. Based on patterns of association between linked variants, we expect gene-level mapping resolution, and we can validate key variants with follow-up QTL mapping. Our project targets PBG research priority 1, as we will identify genes that can be used to develop FHB resistance and reduce DON contamination. We also overlap with priorities 2 and 3, as our mapping may identify variation in pathogen regulators, and by screening a diverse sample we may identify variants contributing to pathogen adaptation to crops. Our project will establish a connection between the genotypic and phenotypic diversity in *Fg* populations, and soon we hope to collaborate with MGMT researchers to examine a broader sample of recently collected isolates to inform FHB management. Stakeholders will benefit from our project and longer-term objectives since knowledge of genetic variants that lead to greater aggressiveness, higher DON contamination, and greater resistance to fungicides can be used for disease surveillance, informing management strategies, and as targets for the control of the pathogen and its mycotoxins.