Project Abstract

Project Title:	Role of chemotype in aggressiveness and toxigenicity of *Fusarium graminearum* to wheat	
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Numerous reports indicate that 3ADON strains are more aggressive, toxigenic, and competitive than 15ADON strains, constituting higher risk for wheat producers. However, previous work relied on correlations in natural populations, and some studies found no relationship. Our overall goal is to use classical genetics and genomics to test the hypothesis that 3ADON confers higher levels of aggressiveness, toxigenicity, and competitiveness than 15ADON, regardless of genetic background, including with fungicide treatment and in moderately resistant wheat. We will also identify other genetic loci contributing to these phenotypes. Our project aligns with the collaborative PBG and MGMT research priority "Investigate how genotypic and phenotypic diversity in populations of FHB-causing *Fusarium*, and *Fusarium* species complexes, influences the management of FHB. Priority aspects of pathogen diversity include fungicide sensitivity, mycotoxin profiles, and ability to cause severe disease on widely used sources of genetic resistance in wheat and barley". Objectives include: 1) Determine whether trichothecene toxin chemotype, mating type locus, and other genetic makers exhibit Mendelian segregation among progeny from crosses of strains from different *F. graminearum* populations. The primary outcome will be a 15ADON x 3ADON mapping population, but also additional resources to facilitate future genetic studies of other factors related to pathogenicity and fitness in *F. graminearum*. 2) Determine whether individuals and mixtures of progeny from outcrosses differ in aggressiveness, toxigenicity, and competitiveness in susceptible and moderately resistant wheat in the presence and absence of fungicides. Greenhouse trials will be spray-inoculated, disease severity will be evaluated, and tissue collected for mycotoxin analysis and qPCR-chemotyping of surviving strains from strain mixtures. Our hypothesis will be supported if the 3ADON chemotype is statistically associated with high levels of toxigenicity and aggressiveness, and if 3ADON strains are selectively advantaged in mixed inoculations. 3) Identify DNA markers associated with aggressiveness and high toxin production by analyzing whole genome sequence data from pools of progeny that differ in these traits. DNA isolated from selected progeny pools will be Illumina sequenced and mapped to reference genomes. Relative representation of mapped SNPs across the genome will be calculated; linked markers that diverge significantly from the expected 1:1 ratio will identify QTLs for aggressiveness, toxigenicity, and competitiveness under different management regimes. Our long-term goal is to identify conserved markers, including chemotype if our hypothesis is supported, for genotyping pathogen populations and predicting their damage potential. This information could augment next-generation risk assessment models to help growers make profitable management decisions.