FY16 USWBSI PROJECT ABSTRACT

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Project ID: FY16-TO-027 **ARS Agreement #: New 5-yr (FY15 -59-0206-1-113)**

Research Category: **PBG** **Duration of Award: 1 Year**

Project Title: Population Genomics to Identify *Fusarium graminearum* Genes to Target.

PROJECT 1 ABSTRACT

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The goal of our project is to identify genes harboring functional variation that contributes to variation in important pathogen traits (pathogenicity, mycotoxin production, measures of fitness) within *F. graminearum* (*Fg*) populations to provide targets for pathogen control. This goal is a natural extension of our FY14-15 project, through which we are densely genotyping hundreds of *Fg* isolates with genotyping-by-sequencing (GBS) and performing population genetic analyses to infer genes affected by natural selection that could be targeted for pathogen control. While the FY14-15 project identifies candidate pathogen genes indirectly by inferring their evolutionary history, the current proposal uses a more direct method of finding genetic variants statistically associated with pathogen traits. Our current results from FY14-15 indicate that levels of linkage disequilibrium (LD), or the nonrandom association between alleles at different genetic loci, in *Fg* populations are appropriate for performing the genotype-phenotype association scans and also indicate that the specific methods used must control for population structure. This proposal leverages the genotyping results of our previous project and aims to clarify the connection between naturally occurring genotypic and phenotypic variation in *Fg*.

Project objectives:

1. Phenotype isolates from two sets from the over 500 isolates genotyped in our FY14-15 project, one set from a small geographic region (New York state), and a second set composed of isolates chosen to represent the full genetic diversity of the previously genotyped isolates from the US.
2. Perform genome-wide association studies (GWAS) of the above traits, taking into account population structure. Polymorphisms associated with pathogen traits will be compared to the results of the scans for natural selection from our FY14-15 project as well as aggressiveness or mycotoxin production QTL identified by other groups through biparental mapping strategies.

Based on the levels of LD observed between our GBS loci, we expect that our GWAS approach can identify genes important in trait variation even when the causative variant is between GBS loci. Our project targets research priority 2 for the FY16-17 PBG program. Our GWAS of pathogen aggressiveness, mycotoxin levels, and fitness traits will identify genes with natural functional variation that is critical for fungal fitness against which we can develop strategies for toxin reduction and FHB control. Our results will also characterize the diversity of US *Fg* isolates, both genetically and phenotypically, which can be used in the choice of *Fg* isolates used to screen for FHB resistance in breeding programs.