

## Project Abstract

<b>Project Title:</b>	Genome sequences for mapping <i>Fusarium</i> head blight traits	
<b>USWBSI Project ID:</b>	FY24-PB-004	
<b>Principal Investigator:</b>	Christopher Toomajian	Kansas State University

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### Project Summary

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. Additionally, we aim to generate important genomics resources for *Fusarium* researchers.

Project objectives and approaches:

1. Perform additional years of greenhouse head inoculation experiments on susceptible and resistant wheat backgrounds, continuing the phenotyping of 150 *Fg* isolates from the NA1 population that we have used in our current USWBSI project for aggressiveness and amount of DON produced, for the purpose of performing genome-wide association studies (GWAS) of these traits.
2. Vastly expand the set of genetic markers segregating in this sample of 150 *Fg* isolates and available for GWAS analysis by performing inexpensive, high-throughput whole genome sequencing of this sample using an inexpensive DNA library preparation protocol to be offered by K-State's Integrated Genomics Facility.

Outcomes from Objective 1 will include more accurate estimates of disease severity and *in planta* DON production on the different wheat backgrounds for these 150 *Fg* isolates our lab is currently studying, and subsequent mapped genome regions identified as underlying the natural genetic variation in the traits. In Objective 2, the outcome of producing greater than an order of magnitude more genetic variants than we currently have for our sample will result in a more complete and higher resolution GWAS mapping. Our project targets PBG goal 1, characterize plant-fungal interactions to identify important genes that may be used to develop FHB resistance or reduce DON contamination in barley and wheat. The objectives of our project will support PBG's intended long-term output of establishing a national, curated collection of FHB-associated *Fusarium* strains, and a national, curated database for genomic and population genetic information relevant to FHB-associated *Fusarium* spp. Stakeholders will benefit from our project and longer-term objectives since knowledge of novel genetic variants that lead to greater aggressiveness and higher DON contamination can be used for disease surveillance, informing management strategies, and as targets for managing the FHB pathogen and its mycotoxins.

