

## Project Abstract

<b>Project Title:</b>	<b>Utilizing genomics resources to develop scab resistant wheat</b>	
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Fusarium head blight (FHB, scab), a fungal disease of small grain crops caused by *Fusarium graminearum*, threatens to reduce wheat and barley to economically unviable crops in the United States. Breeders and geneticists have screened large germplasm collections and populations, identified numerous resistant lines and QTL, and introgressed alleles conferring FHB resistance into breeding programs. However, even large effect QTL like *Fhb1* do not provide complete protection under high disease pressure. Thus, there is a need to explore other germplasm and other mechanisms of resistance such as genes that exhibit susceptibility or suppressors of resistance. We plan to take a genomics approach to identify additional genes that encode susceptibility factors and suppressors of resistance that when mutated result in resistance.

Our overall project goal is to identify genetic tools (e.g., mutants and novel germplasm) that will increase FHB resistance. There are two objectives in this proposal: (1) identify and characterize mutations for increased trichothecene and FHB resistance in wheat; and (2) identify mutants for increased trichothecene and FHB resistance in wheat. For objective 1, we will use previous RNA profiling studies to select candidate genes that exhibit upregulation in susceptible genotypes compared to resistant genotypes with the basic premise being that genes that are upregulated in susceptible genotypes may be involved in FHB susceptibility or suppression of resistance. To identify mutations in candidate genes, we will use a sequenced mutagenized population in the tetraploid Kronos background. All sequence data for this population is placed on the web, providing the opportunity to identify mutations in candidate genes. Plants carrying these mutations will be screened for FHB and DON resistance. Independently, we will also screen a subset of the Kronos mutagenized population for FHB and trichothecene resistance and search for mutants exhibiting resistance.

Mapping populations carrying resistance will be developed and QTL mapped and mutants and markers associated with resistance QTL will identified and provided to breeders to increase resistance to FHB and DON accumulation. The proposed research meets the objectives of the USWBSI and fits within the Gene Discovery and Engineering Resistance (GDER) area of research. Stakeholders, breeders and geneticists, will benefit from this research via novel germplasm carrying novel resistance to FHB and trichothecenes.