Project FY22-GD-005: Utilizing Genomic Resources to Develop Scab Resistant Wheat

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1. What are the major goals and objectives of the research project?

The major goal of this project is to develop genetic tools for increasing FHB resistance in wheat. There are two major objectives that will be addressed including: (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.

2. What was accomplished under these goals or objectives? *(For each major goal/objective, address these three items below.)*

What were the major activities?

Objective 1. Identify and characterize mutations for increased trichothecene and FHB resistance in wheat. We are using a mutagenized Kronos population (Krasileva et al., 2017) and identifying mutations in candidate susceptibility genes and testing plants carrying those mutations for FHB and trichothecene resistance. Kronos is a tetraploid exhibiting susceptibility to FHB. This objective is a targeted approach to identify susceptibility genes that when mutated result in resistant plants, and resistance genes that when mutated result in susceptible plants. Using previously generated and published transcriptome data from wheat and barley inoculated with *F. graminearum* and literature searches of papers published on plant-pathogen interactions, we identified a gene family that is a good candidate for studying in more detail. We have identified Kronos lines that contain mutations in members of this gene family and screened 37 mutant families and 18 exhibited increased susceptibility.

Objective 2. Identify mutants for increased tricothecene and FHB resistance in wheat. We phenotypically screened over 400 individuals from the Kronos mutagenized population. Fifty-five mutagenized Kronos lines were re-screened during the Fall 2023 greenhouse season to verify their resistance/susceptibility to FHB. Six lines consistently exhibited very high FHB symptoms, and another six lines consistently exhibited low disease severity. The six low FHB lines were selected to cross to cultivar Langdon in the Winter 2024 greenhouse. Efforts at crossing were made difficult by the vastly different maturation rates of Kronos and Langdon, and the vastly different plant heights of the cultivars. F_1 seeds from the crosses will be grown out in the fall 2024 greenhouse.

Other related activities

Developing elite wheat germplasm carrying the *HvUGT13248* transgene

We introgressed the *HvUGT13248* transgene (Bobwhite background) into the elite cultivar 'Rollag'. Rollag carries the *Fhb1* resistance gene. Thus, we developed BC1F3 and BC1F4 families from two independent transgenic events crossed to Rollag. These families contain four genotypic combinations: (1) *Fhb1*+/*Fhb1*+,*UGT*+/*UGT*+; (2) *Fhb1*+/*Fhb1*+,UGT-/UGT-; (3) *Fhb1*-/*Fhb1*-,*UGT*+/*UGT*+; and (4) *Fhb1*-/*Fhb1*-,UGT-/UGT-. In a single disease screen, our results show that the lines carrying the *HvUGT13248* transgene (*Fhb1*+/*Fhb1*+,*UGT*+/*UGT*+; *Fhb1*-/*Fhb1*-,*UGT*+/*UGT*+) are very resistant to FHB, the UGT-/FHB1-R genotype is moderately to strongly resistant, and the UGT-/FHB1-S genotype is the most susceptible.

What were the significant results?

We identified wheat mutants that exhibit increased FHB resistance and susceptibility. We also have an initial disease screen that shows that the *HvUGT13248* transgene exhibits a high level of resistance that is comparable to or better than *Fhb1*.

List key outcomes or other achievements.

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3. What opportunities for training and professional development has the project provided? A postdoc has worked on this project. He meets with me regularly and attends and presents results in weekly lab meetings.

4. How have the results been disseminated to communities of interest?

The postdoc presented some results of this work at the USWBSI GDER zoom meeting. We have not generated enough results that have been validated to disseminate them widely.

5. What do you plan to do during the next reporting period to accomplish the goals and objectives?

We plan to begin to genetically characterize the Kronos mutants that exhibit low disease severity. We will also continue to characterize the lines carrying the *HvUGT13248* and *Fhb1* genetic combinations.