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

---

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 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. Finding reliable candidate susceptibility genes has been difficult due to the confounding mutations throughout the genome. 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 have narrowed our search down to a biosynthetic pathway and a key gene that is integrated with other biosynthetic pathways. We identified three mutant lines with mutations in the same gene which exhibit increased FHB susceptibility, and another five mutant lines carrying mutations in five genes in the same biosynthetic pathway which have shown increased FHB 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 to verify their resistance/susceptibility to FHB. Six lines consistently exhibited very high FHB severity, and another six lines consistently exhibited low disease severity. To generate the mapping populations, four Kronos mutant lines which showed high levels of FHB resistance were crossed to Langdon and F_2 populations generated. Twenty plants of each F_2 population were screened in the greenhouse and at least one individual line segregated for the resistant genotype. To initiate genetic mapping of FHB resistance, the four F_2 populations will be re-grown in larger numbers during the fall 2025 greenhouse season and F_3 lines derived for additional phenotyping. We plan to continue to create additional mapping populations with the other two resistant Kronos lines.

Other related activities

Developing elite wheat germplasm carrying the *HvUGT13248* transgene

We introgressed the *HvUGT13248* transgene (Bobwhite background) into the elite cultivar ‘Rollag’ that carries the *Fhb1* resistance gene. We developed BC1F3 and BC1F4 families from three 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-. Phenotyping experiments have been moved from the greenhouse to growth chambers to better control environmental conditions which confounded previous phenotyping experiments. Testing of disease severity of one of the three independent transgenic families (#14-14) has been completed. The results of this family indicate

that expression of the *HvUGT13248* transgene significantly reduced the variability of disease severity between individual plants, and numerically albeit non-significantly reduced total disease susceptibility compared to plants only expressing *Fhb1*. Plants expressing both *Fhb1* and *HvUGT13248* were the most resistant to FHB, with an average percent disease of 3.6% of the entire head. Trichothecene levels and glycosylated-trichothecene levels of each genotype for this experiment are currently being analyzed. Disease screening of the other two independent families will be completed by the end of the summer.

What were the significant results?

We used two approaches to identify mutants that exhibit increased resistance and increased susceptibility. F_2 families have been created with four of the increased resistance mutants and are in the process of being evaluated for resistance. We introgressed the *HvUGT13248* transgene into elite cultivar Rollag that carries *Fhb1* and created families that contain all four genetic combinations of the *HvUGT13248* transgene and *Fhb1*: (1) *Fhb1*+/*Fhb1*+,*UGT*+/*UGT*+; (2) *Fhb1*+/*Fhb1*+,UGT-/UGT-; (3) *Fhb1*-/*Fhb1*-,*UGT*+/*UGT*+; and (4) *Fhb1*-/*Fhb1*-,UGT-/UGT-. We showed that lines carrying the *HvUGT13248* transgene in combination with *Fhb1* (*Fhb1*+/*Fhb1*+,*UGT*+/*UGT*+) exhibited less than 4% disease severity and individuals carrying the *HvUGT13248* transgene (*Fhb1*+/*Fhb1*+,*UGT*+/*UGT*+; and *Fhb1*+/*Fhb1*+,UGT-/UGT-) exhibited reduced variation for disease severity.

List key outcomes or other achievements.

We used two approaches to identify mutants that exhibit increased resistance and increased susceptibility. F_2 families have been created with four of the increased resistance mutants and are in the process of being evaluated for resistance. We introgressed the *HvUGT13248* transgene into elite cultivar Rollag that carries *Fhb1* and created families that contain all four genetic combinations of the *HvUGT13248* transgene and *Fhb1:* (1) *Fhb1*+/*Fhb1*+,*UGT*+/*UGT*+; (2) *Fhb1*+/*Fhb1*+,UGT-/UGT-; (3) *Fhb1*-/*Fhb1*-,*UGT*+/*UGT*+; and (4) *Fhb1*-/*Fhb1*-,UGT-/UGT-. We showed that lines carrying the HvUGT13248 transgene in combination with *Fhb1* (*Fhb1*+/*Fhb1*+,*UGT*+/*UGT*+) exhibited less than 4% disease severity and individuals carrying the *HvUGT13248* transgene (*Fhb1*+/*Fhb1*+,*UGT*+/*UGT*+; and *Fhb1*+/*Fhb1*+,UGT-/UGT-) exhibited reduced variation for disease severity.

3. What opportunities for training and professional development has the project provided?

One postdoctoral research associate worked on this project. The postdoc meets with me weekly and attends my weekly lab meeting where recent research results are presented and current journal articles discussed. The postdoc attended the National Scab Forum in December 2024 and presented a poster.

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

Two posters were presented at the National Scab Forum. A paper will be written in the upcoming year that describes the introgression and characterization of the *HvUGT13248* transgene into an elite wheat cultivar carrying *Fhb1*.

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

We will continue to genetically characterize the Kronos mutants that exhibit low disease severity. We will initiate genetic mapping of FHB resistance derived from the Kronos mutants. We will complete the characterization of the lines carrying the *HvUGT13248* and *Fhb1* genetic combinations and prepare a manuscript for submission.