Project FY22-GD-015: Manipulating a Conserved Susceptibility Factor for Developing FHB Resistant Wheat

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

   Project Goals: Genetic resistance is the most sustainable approach for managing Fusarium Head Blight (FHB) in wheat and barley. As most of the resistance genes are sourced from un-adapted germplasm, linkage drag and variable penetrance in different genetic backgrounds limits their deployment in cultivars. The goal of this project is to characterize and manipulate a conserved susceptibility factor present in wheat cultivars for enhancing their FHB resistance. The project builds-up on three-years of work done by PI Rawat (Chhabra et al. 2021), which mapped a susceptibility factor in the peri-centromeric region of wheat chromosome 7AS. In this project, we will fine-map and isolate the susceptibility factor using Radiation Hybrid (RH) mapping. Collaborator Vijay Tiwari is an expert on RH mapping and will be vital in the SF-7AS fine mapping. After fine mapping we will perform VIGS, TILLING, and genome editing to validate the gene function and utilize the loss-of-function variants to enhance the FHB resistance in wheat cultivars. In the fourth year, PI will test the lines in field conditions for yield evaluation and FHB resistance.

   Specific objectives of this project over a 4-year period are:
   1. Fine mapping and isolation of 7AS susceptibility factor using RH mapping.
   2. Validation of candidate genes using TILLING and Genome-editing.
   3. Transfer of FHB resistant variants in wheat cultivars
   4. Field Testing of the variant lines for yield evaluation.

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

   What were the major activities?

   Chinese Spring radiation panels were developed using 35kRad gamma radiation. As the deletion of the susceptibility factor is expected to provide resistance in homozygous condition, generation advancement was done for the irradiation panel. Considering R7 generation to have majority of deletions in homozygous state, we have been able to advance the population upto R6 generation so far. A total of 700 individual strong population at R6 generation has been developed. Work on characterizing the deletions in the targeted interval progress using genome-specific markers from Chhabra et al. and using GBS is in. In the meanwhile, phenotyping of the whole population at R6 generation was performed with 3 spikes per plant data points. We have obtained ~20 lines that showed resistance response. Phenotyping of these lines is in progress.

   In the meanwhile, we also generated Radiation Hybrid panels with irradiated pollens of Chinese Spring crossed with deletion line #4 to achieve homomzygous deletions in the F1 hybrids and their progeny. Characterization of these RH plants is in progress.

   We also developed an irradiated seed population in the wheat cultivar Jagger. Genotyping by skim-sequencing has identified some deletions in the region of interest. Phenotyping of these lines is in progress.

Additionally, we are trying genome-editing to create targeted deletions in the region of interest. Transformation is in progress currently. Plants with the desired deletions will be phenotyped in the Fall 2024 and Spring 2024 seasons in the greenhouse.

What were the significant results?
Development of populations and characterization of deletions is the significant results. Confirmation of the phenotypes is in progress.

List key outcomes or other achievements.
Key outcomes include: Development of irradiated panels, and generation advancement up to R6, genotyping of the deletion panels in Chinese spring and Jagger.

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

The project has enabled training of 1 PhD student and a PostDoc, plus two undergrad students and 3 high school students.

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

The results have been disseminated via oral and poster presentations at National FHB forum, Mid-Atlantic ASPB meeting, and University level presentations by the graduate student and PostDoc involved in the project.

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

We plan to complete the phenotyping of the selected homozygous deletion lines generated via the different methods listed above.