

Project FY22-NW-003: Accelerating the Development of FHB-Resistant Soft Red Winter Wheat Varieties.

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

1) Breed and release improved scab resistant varieties; 2) Develop and release improved scab resistant germplasm; 3) generate new knowledge on the inheritance of FHB resistance to expedite the breeding process and 4) communicate the importance of best management practices to all stakeholders in the wheat industry: growers, crop consultants, extension agents, millers, bakers and consumers.

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

What were the major activities?

- 1) Screening: More than 3500 individual headrows were planted to be screened in the scab nursery at Lexington, KY. Material screened included released cultivars, breeding lines, uniform scab nurseries, other cooperative nurseries, segregating populations and genetic studies. During the nursery season covered by this report – April through July of 2023, dry weather was prevalent so once again infection levels, though better than the previous year were not as high as desired.
- 2) Breeding: Approximately 560 crosses were made during this period, all of which involved at least one scab resistant parent. Many parents were selected through the app Popvar based on predicted FHB resistance and known QTL. Breeding populations from F₂ through F₅ were selected for advancement. Preliminary lines were selected for testing based on genomic predictions. Advanced lines were tested in KY and multi state nurseries and tests.
- 3) Collaboration – We participated in three uniform scab nurseries (Northern, Prelim Northern and Southern soft winter wheat FHB nurseries) and other collaborative nurseries such as the Mason Dixon. This allows for germplasm sharing and making diverse parents available to other breeders. At meetings we shared genomic selection ideas and information with breeders in the region.
- 4) Outreach – We communicated findings and observations to stakeholders through newsletters, our website and at meetings and field days

What were the significant results?

- We observed significant differences among breeding lines in the resistance to FHB as indicated by FHB index. The DON data ranged from < 1 ppm to 23 ppm, but it was heavily skewed toward the lower value. Due to dry weather, DON values were very likely underestimated.
- We obtained genomic FHB resistance predictions for all of our preliminary lines: DON, rating, FDK which were part of the selection criteria we used in choosing lines to continue testing in agronomic trials and in the scab nursery.

List key outcomes or other achievements.

- Identified new moderately resistant lines based on genomic predictions and to a limited extent in a dry year, phenotypic data.
- Predicted FHB resistance was validated in some breeding lines, particularly those in the uniform scab nurseries grown in other states
- Several breeding lines had the lowest level of scab symptoms in the uniform scab nurseries

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

Two graduate students, Joyce Morris and Maggie Gillum attended the 2023 National FHB Forum in Cincinnati, OH in December. They interacted with PI's and fellow graduate students.

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

I have shown the FHB results at meetings with the Kentucky Small Grain Growers at Field Days and have made them available on our website.

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

The next reporting period is that one that is actually occurring now in real time. One thing we did was doublecheck the virulence and aggressiveness of our Fusarium strains by inoculating in the greenhouse over the winter. The strains that we use in our scab nursery inoculum were effective in causing the disease in the greenhouse. The weather finally cooperated this summer (2024) to give us some decent levels of infection.

It became clear that although the genomic predictions are helpful, there is no substitute for actual phenotyping. Fortunately, when our weather was bad and infection levels were low, we had at least some of our material in the Uniform Northern and Uniform Preliminary Northern scab nurseries, and some of the locations provided good scab data we could rely on.