Project FY22-BA-011: Development of a Multi-parent Population to Enhance FHB Resistance in Barley

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

The overall long-term goal of this research is to facilitate the development of barley cultivars with resistance to FHB and the accumulation of mycotoxins, such as DON. Our proposal directly addresses the primary mission of the USWBSI "to enhance food safety and supply by reducing the impact of FHB on wheat and barley." The specific goals for this research within the four-year timeframe are to: 1) Complete disease and mycotoxin phenotyping of the MAGIC population in 2026 and 2027; 2) Objective 2: Validate QTL for resistance to FHB and DON accumulation in select progeny from the MAGIC and Scarlett/ISR42-8 populations in advanced breeding lines, and 3) Identify agronomically advanced progeny with enhanced resistance to FHB and DON accumulation from the validation populations and distribute them to other researchers for further testing and crossing. Within the Barley Coordinated Project, our proposal aligns closely with Objective 3 (Evaluate and implement modern breeding technologies to further enhance short-term and long-term improvement of FHB resistance in barley, and to efficiently introgress effective resistance genes into barley germplasm) under the Research Area of Variety Development and Host Resistance (VDHR), but is also an important step in advancing Objective 2 (Increase efficiency of coordinated barley breeding programs to develop and release FHB resistant varieties) within VDHR.

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

Objective 1: Complete disease and mycotoxin phenotyping of the MAGIC population in 2026 and 2027

Major activities. We planted the Multiparent Advanced Generation Intercross (MAGIC) population for a second year at Saint Paul and Crookston to assess FHB severity, DON concentration and agronomic traits (heading date, plant height, kernel density, and node density).

Significant results. At St. Paul, we successfully obtained FHB severity data in the MAGIC population despite the hot and dry weather during the heading period. The controls reacted as expected based on many previous years of testing: the susceptible controls of PI 393833 and Stander had severities ranging from 39-89%, whereas the resistant controls of Quest and CIho 4196 had severities ranging from 1 to 26%. In the progeny lines, FHB severity ranged widely from 1-75%. The excessively hot and dry weather at Crookston severely limited disease infection; thus, no FHB severity scores were taken. Even though the disease pressure was low at Crookston, all progeny and controls will still be assayed for DON concentration.

Key outcomes or other achievements. We obtained another year of FHB phenotyping for mapping quantitative trait loci conferring resistance to FHB and the accumulation of DON in the MAGIC population.

Objective 2: Validate QTL for resistance to FHB and DON accumulation in select progeny from the MAGIC and Scarlett/ISR42-8 populations in advanced breeding lines,

Major activities. In 2026, the Scarlett/ISR42-8 population was planted for a fourth time in Crookston and St. Paul in multiple replications to obtain another set of phenotypic data for FHB severity and deoxynivalenol (DON) concentration. During the winter of 2026, crosses were made between four of the most promising Scarlett/ISR42-8 lines for low DON (124, 126, 133 and 176) and the advanced Minnesota breeding lines of S2M184 and 2MW19_3346-014.

Significant results. At St. Paul, we successfully obtained robust FHB severity data in the Scarlett/ISR42-8 population despite the hot and dry weather during the heading period. The controls reacted mostly as expected given the dry weather in 2026. On the susceptible control of PI 383933, FHB severity ranged from 91% to 96%, indicating the potential for high infection levels across the field. The resistant control of Quest ranged in severity from 19% to 33%. The reactions of these controls were as expected based on many past years of data. Although many of the introgression lines suffered partial lodging in St. Paul, disease severity in the Scarlett/ISR42-8 population ranged from 11-41%, allowing for the easy differentiation of lines with and without high levels of FHB resistance. In Crookston, the Scarlett/ISR42-8 population looked much better and did not lodge. However, disease pressure in Crookston was very low due to excessively high temperatures and no precipitation during the month of July. Although disease incidence was not as high as we would like to see, all lines were rated for disease severity and will be harvested and submitted for DON analysis.

All crosses between the four best Scarlett/ISR42-8 lines with low DON (124, 126, 133 and 176) and the advanced Minnesota breeding lines of S2M184 and 2MW19_3346-014 were successful. The F_1 seeds have been planted and will be advanced by single seed descent over the next two years.

Key outcomes or other achievements. We obtained another year of FHB phenotyping for mapping quantitative trait loci conferring resistance to FHB and the accumulation of DON in the Scarlett/ISR42-8 population.

Objective 3: Identify agronomically advanced progeny with enhanced resistance to FHB and DON accumulation from the validation populations and distribute them to other researchers for further testing and crossing.

Major activities. Making crosses between select progeny from the MAGIC and Scarlett/ISR42-8 populations with advanced Minnesota breeding lines.

Significant results. The above-mentioned crosses were successful for nearly all combinations. Those crosses that were not successful will be tried again in the Fall 2026

greenhouse season. Additional crosses are being made with select progeny based on the 2026 field evaluations.

Key outcomes or other achievements. Key outcomes will be achieved once the populations are created and tested for resistance to FHB and DON accumulation.

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

This USWBSI-funded research has provided an excellent training opportunity for many scientists over the past year. The basis for the current research project was part of the Ph.D. thesis of my graduate student Rae Page who submitted her dissertation entitled "Genetics of Fusarium head blight resistance in barley and of rust resistance in the wild wheat relative Aegilops longissima" in May 2023. Other participants in this research included post-doctoral research associates Eric Nazareno, Oadi Matny, and Rebecca Spanner; Researcher 2 scientist Alexis Feist; Researcher 3 scientist James Nesbit; Ph.D. students Reecha Acharya, Yoonjung Lee, and Connor Slawin. Undergraduate students assisting on this project in various capacities include Shelby Dix, Chloe Sandum, Braden Mehle, Carmen Florentz, Carolina Aguiar and Milica Ceperkovic. All these individuals were trained in the methodology for working with FHB, including production and storage of inoculum; inoculation techniques; disease severity scoring; and DON analyses. Moreover, several members of my senior research team gained valuable experience in SNP genotyping, molecular map construction and QTL analysis.

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

Our research results have been disseminated through presentations and publications. A portion of the current research project was based on Rae Page's Ph.D. thesis published in May 2023. She also presented her research at several USWBSI Forums. Two of Rae's thesis chapters were published back-to-back in Crop Science.

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

Our plan is to evaluate the MAGIC population one more time in 2027 to obtain robust phenotyping data for mapping loci conferring resistance to FHB and DON accumulation. We will be analyzing all the data collected for the Scarlett/ISR42-8 population and writing up the results for publication. We will continue to advance the validation populations until the F5 generation. Thereafter, we will evaluate these populations at both St. Paul and Crookston to validate the quantitative trait loci initially identified in the MAGIC and Scarlett/ISR42-8 populations.