

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

- 1) *Introgress a minimal Sumai 3 Fhb1 segment in elite germplasm.*
- 2) *Develop mapping populations to evaluate specific background effects.*
- 3) *Evaluate background gene expression effects on Fhb1.*

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

Objective 1:

a) What were the major activities?

Generated BC₄F₆ lines that introgress *Fhb1* and *Fhb5* (from ND2710) into adapted germplasm (NDHRS13-0273, MT1621, MN15005-4, SD5103) not carrying *Fhb1*. Lines with MN, ND and MT recurrent parents were evaluated for FHB disease in the Prosper, ND Field nursery in 2025 and lines better than the recurrent parent were screened in the greenhouse with point inoculations in the Fall of 2025. SD introgressions were added to the other selections and evaluated again in the field in 2026. The best candidates are currently being increased for distribution to the breeders.

b) What were the significant results?

Molecular marker genotyping works well to rapidly identify the lines that maintain heterozygous state after crossing and selfing. Unfortunately, *Fhb 1/5* carrier status was not globally predicted of disease. However, we did identify several lines (28) with consistently lower disease scores than the recurrent parent. Additionally, 21 SD lines with good scores were selected for evaluation in the next year.

c) List key outcomes or other achievements.

Four backcross lines with the NDHRS13-0273 parent and four lines with the MN15005-4 parent showed less than half the disease pressure of the recurrent parent. The best backcross line with MT1621 as the recurrent parent displayed 40% reduction in disease.

Objective 2:

a) What were the major activities?

Vida was crossed to ND744, SD4343, and Lang and selfed to F₃ generation. Molecular mapping of *Fhb1* identified selections that will be expanded into populations fixed for the *Fhb1*, but segregating for the potential accessory genes.

b) What were the significant results?

Good seed set on the populations and segregation ratio was as expected.

c) List key outcomes or other achievements.

NA

Objective 3:

a) What were the major activities?

RNASeq data from the 2023 and 2024 greenhouse season was analyzed together (RNASeq #2/#3). One last greenhouse experiment was conducted in the Fall of 2025. This experiment consisted of eight HRSW lines (Sumai 3, ND2710, PI 277012, Alsen, Rollag, Glenn, Steele-ND, and Wheaton). Samples from these eight lines were taken at time points of 0, 3, 5, 7, 10 dpi. Non-sampled lines were also screened for disease scores. RNA samples were extracted, converted into cDNA and qPCR of candidate genes is underway currently.

b) What were the significant results?

Sumai 3, PI 277012, ND2710 and Alsen were consistently resistant. While Rollag, Glenn, and Steele-ND were moderately resistant, and quite variable in their response. Wheaton is consistently highly sensitive. Analysis of 284 spike samples with RNA-seq identified several groups of differentially-expressed genes (DEG) depending on the disease response. A small set of DEGs with biological significance were chosen for validation with qPCR in the 2025 greenhouse adding additional time points.

c) List key outcomes or other achievements.

The PFT and HRC genes that have been proposed to be *Fhb1* were not differentially expressed in our experiments.

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

The two students that are assisting in this project have learned several important skills Fhb nursery management, data science and bioinformatics in one-on-one training by the mentor.

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

Through personal conversations and poster presentations at the FHB Forum.

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

The Sumai 3 genome has been published and is available on Graingenes along with its annotations under the Toronto agreement. The Rollag and Glenn genome manuscript is written but waiting on ARS approval for submission. Vida crosses will be selfed to F₅ in the next two seasons and manuscripts of the transcription work will be submitted.