

**Project FY22-SP-010:** Development of Elite Spring Wheat Germplasm with Fusarium Head Blight Resistance

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

The major goal and objective of this project is to develop adapted hard red spring wheat (HRSW) germplasm by transferring FHB resistance from unadapted sources into the HRSW cultivars.

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

- Established a modified NAM (nested association mapping) population of 288 spring wheat genotypes, including 276 synthetic hexaploid wheat (SHW) derived hard red spring wheat (HRSW) lines and their 12 parents and checks. These lines were previously selected based on their reactions to FHB and bacteria leaf streak (BLS, caused by *Xanthomonas translucens*) from approximately 900 BC<sub>1</sub>F<sub>5</sub> lines derived from 18 BC<sub>1</sub>F<sub>1</sub> populations from backcrossing the synthetic hexaploid wheat (SHW) lines SW91, SW93, SW183, and SW187 to hard red spring wheat (HRSW) varieties 'Glenn', 'Barlow', 'Vitpro', 'Grandin', 'Linert' and 'Bolles' and breeding lines ND828, NDHRS16-1436, and NDHRS16-13-89 in the FHB nurseries. The population were evaluated for FHB resistance using the randomized complete block design (RCBD) with three replications in greenhouse for two seasons in the fall 2023 and spring 2024 and in mist-irrigated FHB nurseries in two locations (Prosper and Frago, ND) during the summer season (May – August) in 2023.
- Performed preliminary genome-wide association studies (GWAS) using the modified NAM population above, FHB disease data collected from greenhouse and field nurseries so far, and the 90K SNP marker genotypic data set.
- Developed and evaluated approximately 170 elite hard red spring wheat lines that are homozygous for 5AL QTL and *Fhb1*, including six doubled haploid (DH) lines and 164 BC<sub>1</sub>F<sub>5</sub> lines. These lines were previously selected by genotyping 700 BC<sub>1</sub>F<sub>2</sub> plants (15FAR1157-1/2\*ND Frohberg) and 15 DH lines (15FAR1157-1/ND Frohberg) using the STARP markers for PI 277012 derived 5AL QTL and *Fhb1*. A sub-set of 92 lines with adequate seeds were evaluated in the FHB nurseries in Fargo and Prosper, ND during the summer season in 2023. All 170 lines and their parents have been grown to BC<sub>1</sub>F<sub>5</sub> generations in greenhouse and they have been planted in the FHB nurseries in two locations (Prosper and Frago, ND). A sub-set of 141 lines and their parents were planted for seed increase and observation in the single-row plots in Prosper, ND.
- Developed BC<sub>4</sub>F<sub>1</sub> populations by backcrossing a wheat-*Thinopyrum ponticum* 7D/7eI2 introgression line RWG52 (591) with HRSW variety 'Alsen' and Alsen-*ph1b* line to eliminate yellow pigment gene Y tightly linked to *Fhb7* on chromosome 7D. Approximately 2,300 BC<sub>2</sub>F<sub>1</sub> seeds have been genotyped and 10 new tentative homoeologous recombinants without the yellow pigment gene Y have been developed.

- Produced BC<sub>4</sub>F<sub>1</sub> hybrid seeds by backcrossing a wheat-*Th. elongatum* 7B/7E introgression line XWC14-255-13-1 (WGC002) carrying new Fhb7 allele Fhb7<sup>The2</sup> to ND Frohberg.
- Developed BC<sub>3</sub>F<sub>1</sub> seeds from backcrossing Wangshuibai lines with ND Frohberg to simultaneously transfer major FHB resistance QTL *Fhb1*, *Fhb2*, *Fhb4*, and *Fhb5*.

### What were the significant results?

- A total of 39 SHW derived lines showed promising FHB resistance and approximately 47 lines also showed excellent BLS resistance.
- Several FHB resistance QTL on chromosomes 4A, 6A, 2B, 3B, 1D and 4D have been identified from the modified NAM population.
- Performed preliminary genome-wide association studies (GWAS) using the modified NAM population
- Preliminary analysis showed that approximately 27 elite hard red spring wheat lines (DH and BC<sub>1</sub>F<sub>5</sub> lines) that are homozygous for 5AL QTL and *Fhb1* showed higher levels of FHB resistance than ND Frohberg. These lines also showed the same or similar agronomic traits and performance as the HRSW varieties used as the checks.

### List key outcomes or other achievements.

- The elite hard red spring wheat lines that are homozygous for 5AL QTL and *Fhb1* with high levels of FHB resistance, including DH (15FAR1157-1/ND Frohberg) and BC<sub>1</sub>F<sub>5</sub> lines (15FAR1157-1/2\*ND Frohberg) will be useful germplasm for developing adapted HRSW germplasm and varieties for resistance to FHB and other diseases. A set of 141 lines are currently grown in the NDSU spring wheat breeding program for seed increase and observation in the single-row plots in Prosper, ND. The promising lines will be included in breeding trials in 2025.
- A modified NAM population consisting of 276 SHW derived HRSW lines and their 12 parents and checks and their genotypic (90k SNP marker) data set is available for identifying and mapping the genes and QTL for resistance to FHB and other major wheat diseases. Several FHB resistance QTL on chromosomes 4A, 6A, 2B, 3B, 1D and 4D have been identified from the modified NAM population.
- The SHW derived lines showing FHB and BLS resistance will be useful germplasm for developing adapted HRSW germplasm and varieties for resistance to FHB, BLS, and other diseases.

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

Nothing to Report.

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

The results have been disseminated through publications and presentations at various workshops and seminars and communications with breeders and collaborators.

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

- Conduct yield trials to evaluate ~40 elite HRSW lines (15FAR1157-1/2\*ND Frohberg) and DH lines (15FAR1157-1/ND Frohberg) that are homozygous for *Fhb1* and 5AS/5AL QTL.
- Perform final GWAS analysis using the modified NAM population above, FHB disease data collected from greenhouse and field nurseries so far, and the 90K SNP marker genotypic data set. Validate the QTL and their linked markers.
- Transfer the novel QTL identified from the modified NAM population by crossing and backcrossing two SHW-derived lines with ND Frohberg and ND Harvest.
- Develop BC<sub>5</sub>F<sub>1</sub> seeds from backcrossing Wangshuibai and *Fhb7* introgression lines with ND Frohberg and newer variety or breeding lines carrying two PI277012-derived 5A QTL.