Project FY22-HW-009: Pyramiding and Deployment of Multiple FHB Resistance QTLs in Hard Winter Wheat

---

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

- Pyramid three major QTLs (*Fhb1, Fhb7* and *Fhb9*) in 15 locally adapted germplasm lines from HWW-CP breeding programs using marker-assisted backcrossing.
- Select breeding lines (Bc2F3/F4) with at least two major FHB resistance QTLs from each backcross population and send to HWW-CP breeding programs for further development of FHB resistant varieties
- Release germplasm lines with single Fhb7 and Fhb9 (2DL QTL) and combined three QTLs in US HWW backgrounds.
- Determine the combined e4ects of two or three genes on FHB resistance.

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

What were the major activities?

- Selected Bc2F1 and Bc2F2 plants with all three major genes (*Fhb1, Fhb7 and Fhb9)* a using diagnostic markers
- Crossed marker-selected Bc1F1 plants with all three major genes to three recurrent parents that did not get seeds in last cycle.
- Selected 120 Bc2F2 plants each from 6 populations using the three markers and identified 15 lines per group that carry single genes, two genes and three genes for FHB resistance in greenhouses.

What were the significant results?

- Backcrosses were completed for all 15 populations.
- Marker-selected at least 150 Bc2F2 plants per population for 12 crosses and BC2F1 seeds from 3 other crosses.
- confirmed that *Fhb7* we used in the gene pyramiding project is a major gene for FHB resistance and published the result in Phytopathology.

List key outcomes or other achievements.

- 'A Glutathione S-Transferase from Thinopyrum ponticum Confers Fhb7 Resistance to Fusarium Head Blight in Wheat' was published in Phytopathology. https://doi.org/10.1094/PHYTO-03-24-0106-SC
- One Fhb1 introgression line we developed using marker-assisted backcrossing funded by USWBSI has been released in OK as 'Scab Stryker'. The registration paper entitled "Development of Hard Red Winter Wheat 'Scab Stryker' for Adoption in Areas of Oklahoma Prone to Fusarium Head Blight" was submitted to Plant Reg. J. by Meriem Aoun, Jessica Rupp Noller, Guihua Bai, Amanda de Oliveira Silva, Katherine Brower, Robert M. Hunger, Brett F. Carver.
- One manuscript entitled "Characterization of quantitative trait loci for Fusarium head blight (FHB) resistance and agronomic traits in wheat cultivar 'Jagger' and its mutant 'JagR1097' by Yuzhou Xu, Na Liua, Yang Liu, Lanfei Zhao, Lirong Zhange, Guixiao La, Dongtao Liu, Zhenqi Su, Amy Bernardo, Paul St. Amand, Xiaomao Lin and Guihua Bai was submitted to Phytopathology after minor revision.

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

Two post-doc (Dr. Ruolin Bian) and a MS student (Ms. Jinan Park) have been trained on backcrossing, high-throughput marker genotyping, and FHB evaluation.

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

Development of breeding lines is in progressing and the selected lines carrying all three genes from BC2F3 will be released to breeders for further breeding process and cultivar development. Also, lines with each single gene (*Fhb1*, *Fhb7* or *Fhb9*) in elite HWW backgrounds will be selected, increased and deposited in USDA seed bank for global seed distribution.

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

1. 2024 fall: MAS to identify the Bc2F1 with all the three target genes (heterozygote) and advance the marker-selected Bc2F1s with all the three target genes; some crosses without su4icient seeds need to redo second backcrossing.
2. 2025 Spring: MAS to screen ~500 plants per cross for 13 crosses to identify the Bc2F2 with all the three target genes, either homozygote or heterozygote, for seed increase; two crosses that did not get enough seeds in last cycle need to select Bc2F1s with all the three target genes (heterozygotes) for generation advancement.
3. 2025 summer: screen the selected Bc2F2 plants with three homozygous genes using MRA-seq for background screening and release their Bc2F3 seeds to breeders.
4. 2025 fall: screen the selected Bc2F3 plants that were derived from heterozygous Bc2F2 plants to select plants homozygous for at least two target genes (plus one heterozygous gene) and the selected plants were also screened with MRAseq for background selection. Two crosses need to select Bc2F2s with all the three target genes for generation advancement.
5. 2026 spring: selected Bc2F4 plants will be increased, and seeds will be sent to breeding programs for other traits evaluation.