Project FY24-HW-005: Coordinating HWW Genomic Assisted Breeding to Develop FHB Resistant Varieties

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

The specific objectives of this collaboration among universities are to: 1) curate and leverage historical and newly generated genotypic (genome-wide marker data and haplotypes) for improvement of FHB and other important traits, 2) develop predictive model pipelines for genomic estimated breeding values (GEBVs) for FHB resistance traits and other agronomically relevant criteria for successful variety development; 3) execute exploratory analysis of existing and novel data for marker trait associations via mapping (genome wide association studies (GWAS) or QTL mapping), and 4) publish on findings to enhance knowledge of FHB resistant cultivar development techniques among cultivar development programs.

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

What were the major activities?

For objectives 1 and 2: For FY24, we initiated collaborations with the University of Nebraska and University of Illinois to screen 260 Colorado breeding lines (480 total rows with replication) for resistance to FHB. This included advanced breeding lines and doubled haploids and populations that contain FHB resistant parents, including sources of *FHB1*. Ideal infection was achieved at the UIUC site and the graduate student working on the project visited the site and collected ratings for disease incidence and severity. All rows were harvested for determination of FDK. Unfortunately visual ratings were not conducted at the UNL site due to late progression of symptoms. Some plots will be harvested for determination of FDK. We submitted an additional 15 entries to the Hard Winter Wheat Coordinated Nursery. We coordinated with five programs (TAMU, KSU, UNL, MSU, SDSU) in fall 2024 for a coordinated genotyping effort and received and processed 1,152 project samples for sequencing.

What were the significant results?

FHB data was collected on 260 CSU Breeding lines. The sequencing data was processed and genomic prediction was used to predict 20 traits and 7 genes across six programs.

List key outcomes or other achievements.

GEBVs and gene prediction results were provided to cooperators for use in making selections for the next season.

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

Emily Billow is a graduate student working on the program. Jessica Rutoski provided her hands on training for evaluated FHB incidence and severity in the field. She has also gained training in genomic prediction. Once samples are received for FDK, undergraduate students will gain training to assist in the process of these samples.

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

   Emily attended the USWBSI forum and gave a flash and dash talk and presented a poster. She also presented at the CSU Corteva Plant Breeding Symposium. The importance of scab and using the USWBSI risk tool was discussed at nine field days this summer with over 300 growers in attendance.

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

   We will update our genomic prediction models with data collected this season from the six participating programs. We will doing a second round of screening of CSU lines based on the results from this season.