# **Project FY24-SW-001:** Fusarium Head Blight Breeding Research at North Carolina State University

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

1. Collaboration and nursery coordination to identify and incorporate new genes/traits/germplasm.
2. Improving breeding efficiency and better placement of new cultivars with genomic selection
3. Develop and release new cultivars and germplasm of small grains with high levels of FHB resistance.
4. Data integration and provide bioinformatics support for genomic selection in the Southern soft wheat region

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

### 1. Collaboration and Nursery Coordination to Identify and Incorporate New Genes/Traits/Germplasm

a. Phenotypic data from the 2024 Uniform Southern Scab Nursery, collected across nine locations, was analyzed for Fusarium head blight (FHB) severity, FHB rating, Fusarium-damaged kernels (FDK), deoxynivalenol (DON), and additional agronomic traits. This data was combined with genomic estimated breeding values (GEBVs) and compiled into the 2024 Uniform Southern Winter Wheat Scab Nursery Report. The initial report was distributed to collaborators in November 2024, with a final update including complete DON data released in December 2024. Findings were also presented at the 2024 FHB Forum in Austin, TX.

b. The 2025 Uniform Southern Scab Nursery includes 54 entries submitted by eight breeding programs. Seed was packed and distributed to 13 collaborators in September 2024. The nursery will be grown at 12 locations across AR, GA, IL, KY, LA, MD, NC, SC, TX, and VA.

c. To facilitate consistent and efficient data collection, customized templates were developed and implemented across participating sites. These templates ensure standardized data submission, improving the accuracy and comparability of results.

### 2. Improving Breeding Efficiency and Placement of New Cultivars Using Genomic Selection

a. GEBVs for southern breeding materials and the 2024 Uniform Southern Scab Nursery were distributed in Spring and Summer 2024. Predictive accuracy between observed and predicted values in the nursery was moderate to strong: 0.68 for FHB severity, 0.69 for FDK, and 0.21 for DON. A total of 121 trait–training population–effect combinations were evaluated, encompassing FHB resistance, additional disease and insect resistance traits, grain quality parameters, yield, test weight, heading date, and plant height.

b. Predicted quantitative trait loci (QTL) were reported for 33 major genes, including FHB resistance loci from NC-Neuse, Bess, Massey, and Jamestown. This information was made available for all lines submitted to the genomic selection pipeline. Reporting QTL in early-generation materials allows breeders to incorporate this data into selection decisions with no additional burden on genotyping laboratories. Forward validation accuracy for FHB resistance QTL was high, apart from Bess-2B where QTL frequency is low. When calls for predicted FHB QTL were compared with genotyping results from the Eastern Regional Small Grains Genotyping Lab, accuracy ranged from 0.93-1.0.

### 3. Development and Release of New Cultivars and Germplasm with High Levels of FHB Resistance

a. The Southern Region SNP discovery database was updated in January 2025 to include new germplasm and enhance coverage of key SNPs, particularly those related to FHB traits. The updated database contained 27897 genotypes representative of the eastern region. SNPs linked to Fhb1 were identified via GWAS and incorporated into genomic selection models for improved prediction of FHB severity, rating, and FDK. Inclusion of Fhb1 SNPs slightly increased model accuracy and improved QTL prediction performance for Fhb1 using machine learning, with predictive accuracy increasing from 0.78 to 0.85 over two years.

b. In Spring 2025, genomic selection was be used to predict FHB traits (severity, rating, FDK, and DON) in approximately 4,000 new SunGrains selection candidates and 500 from the University of Kentucky. Predictions were also generated for additional agronomic traits. The presence or absence of eight FHB resistance QTL were assessed using machine learning. Results were distributed to collaborators in March 2025 to inform selection decisions.

### 4. Data Integration and Bioinformatics Support for Genomic Selection in the Southern Soft Wheat Region

a. In 2024, over 7,300 SunGrains and 8,700 University of Kentucky samples were processed through the genomic selection pipeline. These included selection candidates, regional nurseries, and training populations. Genomic predictions were generated for 28 traits using regional, state-specific, and trait-specific training populations. Thirty-three QTL were predicted via machine learning, replacing the need for approximately 62 individual assays—saving an estimated $18,500 in consumables and 70 days of labor.

b. For 2025, the pipeline is handling over 8,300 SunGrains samples and over 8,500 from the University of Kentucky. These samples include selection candidates, training sets, and program-specific study materials. Bioinformatics support includes data curation, multi-location analysis, training population design, and GWAS. In 2024, reporting protocols were revised to include breeder-requested summary statistics, which will be included in 2025 reports.

c. Parental crosses will be predicted using the R package PopVar for two consecutive years (2024 and 2025), covering all parents in the GAWN, Sunwheat, SunPre, Uniform Southern Scab, and Mason-Dixon regional nurseries. Predictions will focus on yield, FDK, and DON and will be provided to breeders in Summer 2025. Enhanced reporting will include trait-specific summary statistics to help breeders quickly identify optimal parental combinations with high yield and low DON. A sample coding project to demonstrate PopVar-based crossing simulations and custom reporting is now available for training and research purposes at https://github.com/jhlyerly/KY_PopVar_example.git.

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

We provided training to two students in the identification and assessment of plant disease symptoms, with a particular focus on evaluating scab incidence and severity in nursery trials.

We provided a semester internship opportunity in data science for one undergraduate student. During the internship the student gained experience in gathering, formatting, and cleaning data for multiple location-years and generating a useable data set for breeders in the southern region.

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

The PI gave presentations at Field Days hosted by NCSU Research Extension Centers and NC Small Grains Growers Associations. (May include some month/year dates here). Results for the 2024 Uniform Southern Scab Nursery were presented at the FHB Forum in December 2024 in Austin, TX and the annual report is published on the USWBSI website.

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

Data from the 2025 scab nursery will be compiled and analyzed to assess disease resistance across a range of breeding materials. A final report summarizing the findings will be distributed to all collaborators in Fall 2025.

In addition, new crosses and breeding lines will be introduced into the nursery for preliminary assessment of scab resistance, supporting the continuous advancement of breeding efforts.