**Project FY22-SW-005**: Genome-enabled Selection for FHB Resistance in Winter Wheat

---

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

1. Evaluate available adapted wheat germplasm for FHB resistance and determine the predictive ability of FHB traits, including visual scores, FDK and DON within the Virginia germplasm. Develop new varieties on soft winter wheat with improved resistance to fusarium head blight and excellent agronomic performance.

2. Determine the linear (and potentially non-linear) genetic relationships (i.e. genetic correlation) between morphology (e.g. height), phenology (e.g. heading date, flowering time), and FHB traits (FHB index, FDK, DON), and their impact on agronomic performance

3. Use genomic information to estimate genetic and breeding values for advancement and mating decisions, respectively, to improve FHB resistance and agronomic performance. Redesign mate-pair decision making to include multiple traits and a selection index to maximize response to selection for both FHB traits and other agronomic and disease traits.

4. Evaluate response to selection and any unexpected consequences thereof.

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

### What were the major activities?

### Program status

In spring 2023, a new public soft red winter (SRW) wheat variety, developed primarily from support from the USWBSI VDHR, was released under the name ‘VT Pitman’. ‘VT Pitman’ performed well in state official variety trials, in 2024, ranking 20 out of 150 entries for grain yield across locations in Virginia, and placing 2nd across the state in North Carolina. Four SRW lines were released in the spring of 2024, 15VTK-1-101, 17VTK4-29, VA19FHB-36, and 16VDH-SRW02-023. Lines 17VTK4-29 and VA19FHB-36 were specifically developed for FHB resistance, with the first containing *Fhb1*, and the latter containing FHB QTL *Fhb1B-Jamestown*, and *Fhb1A-Neuse*. VA19FHB-36 was licensed to JoMar in the fall of 2024. Line 16VDH-SRW02-023 was liscensed to Williamsfield in 2024. Three SRW lines were released in the spring of 2025, VA20FHB-20, VA20FHB-18, and 18VTK10-23. The first two are high yielding and moderately resistant to FHB and were developed from explicitly from funding by the USWBSI. The 18VT10-23 won the Virginia state trial in 2025, has exceptionally high test weight and has an unknown native source of FHB resistance. It is predicted to be one of our most resistant breeding lines. VA20FHB-20 place 3rd in the 2025 Georgia state trial, 2nd in the 2025 South Carolina state trial and first in the 2025 North Carolina state trial.

Several high yielding lines with excellent FHB resistance are currently under evaluation in late stage regional trials. Genomic information is used to estimate genetic and breeding values at all breeding stages, such that selection on predicted FHB traits is now conducted at every generation. Genomic prediction of expected mate pair performance is being used to guide all crossing decisions.

### Genomic prediction of crosses using predicted family merit

In the spring of 2025, a genomic prediction model was trained using data from the VT breeding program across six years, 2019-2024. This dataset included 54,940 phenotypic records (i.e. plots, of which 39,936 are yield plots), representing 208,768 phenotypic data points for 6,150 breeding lines measured for 14 traits (unbalanced) across 228 trials. Included in the dataset were phenotypic records for 6,939 scab plots with 5,292 FHB scores, 5,702 FDK, and 4,908 DON measurements from 2,517 lines evaluated in the misted inoculated nurseries in Virginia from 2019 through 2024. All lines were genotyped with genotyping by sequencing markers, totaling 15,124 after variant calling, filtering and imputation. Genomic BLUPs were fit and marker effects estimated through backsolving.

Elite parents (41 inbred lines) were selected based on superior performance in advanced yield trials. Early generation parents (54 inbred lines) were selected based on predicted genomic merit of lines evaluated in first year yield trials (2024) in one plot in 1-3 locations using a sparse testing design across 5 locations in VA, IL, and SC. F1 seed (128 F1s) from the previous year of crossing (2023) was also selected based on the previous year's genomic estimated family merit. Inbred lines were planted in 9 to 12 pots, while F1s were limited to 3-4 pots each so that remaining seed could be planted earlier that fall. All selected parents were Virginia lines, or F1s between Virginia Lines to ensure high genetic connectivity for prediction.

Expected family genotypes were calculated for all possible mate-pair combinations (24,976 predicted families) using 15,124 GBS markers and 47 loci of interest that were screened in house for inbred parents, and predicted for F1s from parental genotypes. Expected family merit for each of the 14 traits was calculated by the product of the expected GBS genotype values for each family and the predicted marker effects from the trained genomic selection model. A selection index was created by weighting the traits based on perceived importance within the program, with Yield, FDK, DON and test weight given the most weight. The initial intention for this project was to assign economic weights, but these are not trivial to estimate. Economic weights are highly influenced by the market (e.g. price of grain, dockage for DON, test weight, etc.) and regional importance of traits (e.g. disease pressure is not uniform across our target population of environments). Crosses with a high coefficient of coancestry were generally avoided to reduce population level inbreeding. Crosses sent for doubled haploid generation in 2024 were chosen based on both the selection index and prior knowledge of the parents.

A total of 348 single crosses and 106 top-crosses (F1 by elite) were made in the spring of 2025. Each day, a list of females and males that were ready for crossing was used to subset the list of potential crosses, and used to make high ranking crosses based on the selection index.

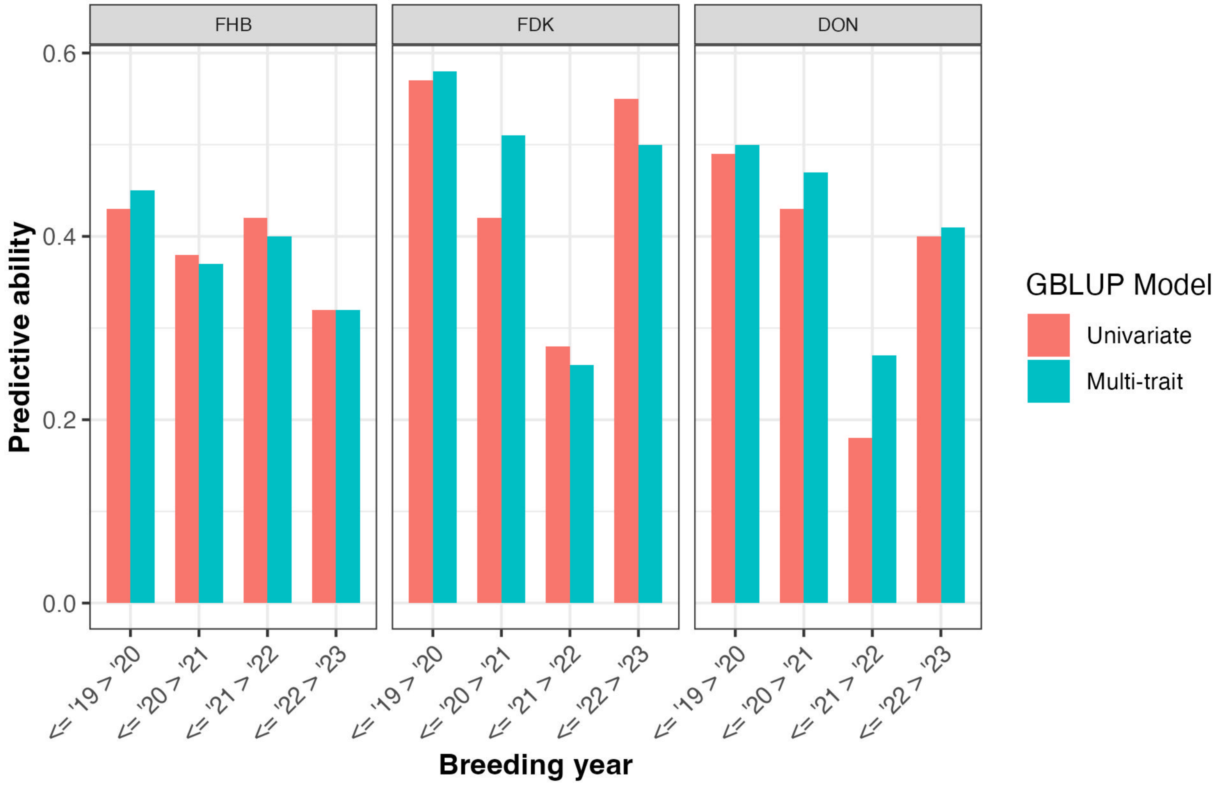

**Figure 1:** Predictive ability of univariate and multivariate (FHB scores, FDK and DON together) using previous years data to predict the performance of lines in a given year. Axis labels indicate using previous years to predict performance in the following year, for example "<= '22 > '23", the years 2019-2022 used to predict 2023.

### Evaluation of across season genomic predictive ability

Multivariate prediction of FHB traits is predictive across years, with previous years data able to predict unobserved lines in the following year, and is generally marginally better than single trait prediction across years (Figure 1). Loss of prediction accuracy in 2022 is likely due to the use of new races, suggesting there may be race specific tolerance in wheat. Investigation into the degree of race specificity and tolerance / susceptibility needs further work to determine to what degree this is a problem. Year to year variability in response to infection may be due to, among timing of infection, which races are most prevalent at a given site. If so, understanding what leads to race specific tolerance / susceptibility would allow breeders to develop lines more stable to year to year (i.e. race to race) variation.

### Evaluation of line performance in Misted Inoculated nursery

Disease pressure appeared visually less in 2025 compared to previous years, and FDK values were observed lower than previous years. entries), Southern Uniform Scab (54 entries), Uniform Eastern (35 entries), Uniform Southern (39 entries), Gulf Atlantic (61 entries), and Mason Dixon (77 entries) nurseries. Local nurseries evaluated included the second year SRW Preliminary (224 entries) and a portion of the first year SRW Observation (245 entries out of 1,189). While the other scab trials have a complete entry list, the SRW Observation was subset to reduce the total number of lines under FHB evaluation as part of the sparse testing design. All families were

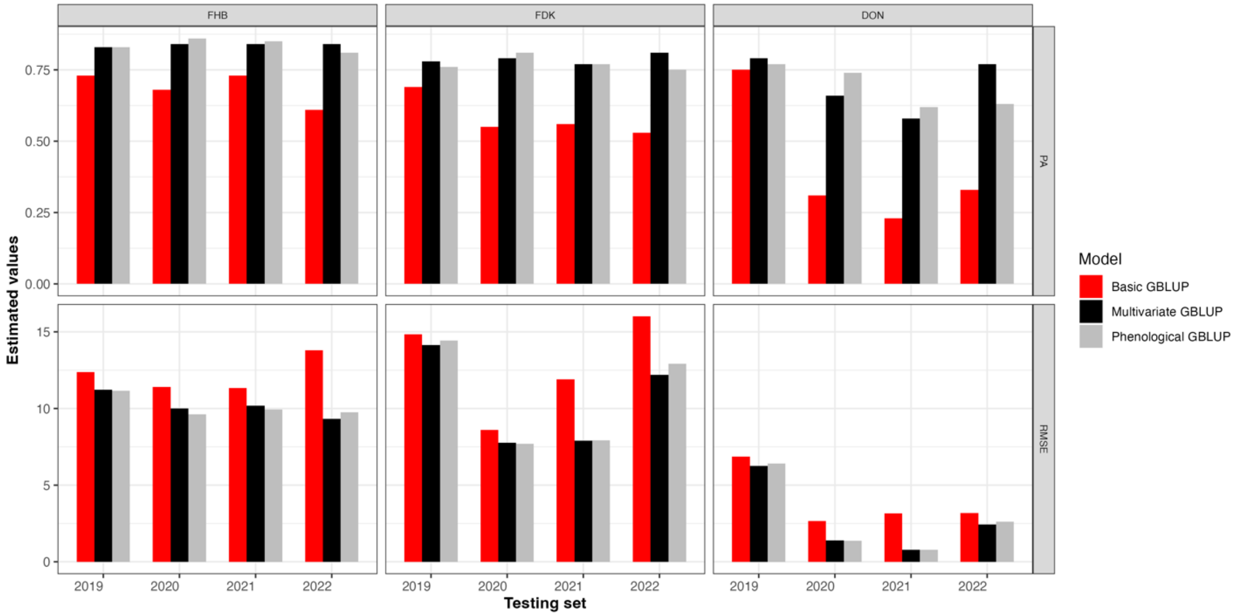

**Figure 2:** Predictive ability and root of mean square error of the RKHS with linear kernel as Bayesian genomic prediction models on FHB, FDK and DON traits for each environment used as testing set.

sampled to maximize the prediction accuracy of FHB traits in unobserved lines. Entries from all regional trials will be prepped for planting in Fall 2025.

## New phenological model

We have developed a new phenological model of FHB infection to determine resistance loci that are sensitive to environmental conditions around the time of infection. Infection occurs during anthesis and is known to be influenced by weather conditions. Timing of flowering relative to weather conditions causes inherent genotype by environment interactions, making it difficult to select for resistant varieties. Understanding which loci contribute toward stable resistance across environmental conditions versus those that are sensitive to weather is critical for improvement of quantitative resistance to FHB. A data set of 879 genotyped lines evaluated in misted FHB-inoculated nurseries in Warsaw, VA over four cropping seasons (2019-2022) was used to investigate as an initial investigation. We developed a phenological model of host response to disease infection and progression under variable weather conditions relative to flowering. Weather covariates including temperature, precipitation and humidity were adjusted by the flowering date of each plot, such that weather variables were indicative of conditions at flowering and at one day intervals 7 days before and after flowering. Main genetic effects of markers, phenologically adjusted weather variables, and their interactions were included in a Bayesian mixed model to separate the effects into three categories, 1) stable genetic marker effects across environmental conditions, 2) effects of weather on infection and disease progression per se, and 3) unstable genetic effects sensitive to weather conditions, respectively. The deviance information criterion statistic found the phenological model that included all three terms the best for three FHB traits, indicating marker-by-weather interactions were significant. High temperatures at post-anthesis have the greatest effect, reducing the rate and severity of FHB infection and deoxynivalenol (DON), accumulation. Total precipitation had little effect on

FHB infection in the misted nursery. but is likely to have an effect under standard growing conditions. We recommend breeders focus on stable genetic effects on host resistance and explicitly ignore or select against those with unstable effects. A draft of this manuscript has been prepared and is expected to be submitted by the end of July 2025.

**Scab nursery 2025**

All trials were given a visual score for FHB approximately 2 weeks after flowering, after scab infection was allowed to progress and was very apparent, but before dry down. The Uniform Scab nurseries, Northern, Preliminary Northern and Southern, as well as the Mason Dixon and Gulf Atlantic are currently being scored for FDK after harvest, and will be processed for DON accumulation (Tables 2 and 3). FHB infection was poor in part due to mechanical failure of the pump that runs the mist irrigation system. A new pump was purchased and delivered to the scab nursery the new pump had standard 3" input and output diameters, while the old pump had non-standard 2.5" input/output diameters meaning the pickup and pipe to the irrigation lines would not fit the new pump. Couplers were sought and were installed making the pump operational but further delayed the start of misting by a couple days. Barley was impacted more than wheat, displaying almost no signs of FHB, while wheat had poor but scorable infection, with heritabilities of FHB scores ranging between 0.3 and 0.9. Importantly, *all* the lines in FHB nursery in 2025 were genotyped. This has allowed us to select on FHB resistance despite having poor infection and no phenotypes for the new Y1 lines.

**Key outcomes**

1) A pipeline for genomic prediction of mate pairs for multiple traits and single genes, including FHB traits, has been fully implemented
2) All regional nurseries we participate in (7) were screened in our misted inoculated nursery for FHB scores. FDK and DON traits are currently being collected.
3) Lines with improved resistance and agronomic traits have been advanced to regional nurseries. One DH line with improved FHB resistance (including *Fhb1*), 15VDH-FHB-MAS25-15 was released as a public variety in the spring of 2023, under the name 'VT Pitman'.
4) Four SRW lines were released in the spring of 2024, 15VTK-1-101, 17VTK4-29, VA19FHB-36, and 16VDH-SRW02-023. Lines 17VTK4-29 and VA19FHB-36 were specifically developed for FHB resistance, with the first containing *Fhb1*, and the latter containing FHB QTL *Fhb1B-Jamestown*, and *Fhb1A-Neuse*.
5) Three SRW lines were released in 2025, VA20FHB-18, VA20FHB-20 and 18VTK10-23. The first two were developed with explicit support from USWBSI.

**Table 1:** Results from Uniform Scab nurseries in 2024. Means, broad-sense heritability, and error standard deviation for FHB scores (0-9), FDK (%) and DON (ppm) for the 2023 scab nursery are shown.

| Year: 2024 | NUWWSN | | | PNUWWSN | | | SUWWSN | | |
|---|---|---|---|---|---|---|---|---|---|
| Trait | FHB (0-9) | FDK % | DON ppm | FHB (0-9) | FDK % | DON ppm | FHB (0-9) | FDK % | DON ppm |
| Mean | 3.0 | 11.9 | 4.5 | 6.0 | 9.5 | 5.2 | 4.8 | 20.9 | 9.6 |
| Broad-sense heritability | 0.29 | 0.66 | 0.84 | 0.3 | 0.71 | 0.75 | 0.02 | 0.80 | 0.81 |
| Error standard deviation | 1.52 | 6.1 | 1.6 | 1.04 | 3.4 | 1.9 | 1.02 | 11.5 | 4.48 |

**Table 2:** Results from collaborative nurseries in 2024. Means, broad-sense heritability, and error standard deviation for DON (ppm) and FDK (%) for the 2023 scab nursery are shown. Statistics on FHB scores are omitted for brevity. FDK and DON for the Uniform Eastern and Uniform Southern were not determined.

| Year: 2024 | Gulf Atlantic | | Mason Dixon | | Uniform Eastern | | Uniform Southern | |
|---|---|---|---|---|---|---|---|---|
| Trait | DON ppm | FDK % | DON ppm | FDK % | DON ppm | FDK % | DON ppm | FDK % |
| Mean | 9.6 | 23.9 | 9.17 | 15.8 | - | - | - | - |
| Broad-sense heritability | 0.45 | 0.63 | 0.85 | 0.68 | - | - | - | - |
| Error standard deviation | 4.53 | 8.4 | 2.29 | 8.0 | - | - | - | - |

**Table 3:** Results from Uniform Scab nurseries in 2025. Means, broad-sense heritability, and error standard deviation for FHB scores (0-9), FDK (%) and DON (ppm) for the 2023 scab nursery are shown.

| Year: 2024 | NUWWSN | | | PNUWWSN | | | SUWWSN | | |
|---|---|---|---|---|---|---|---|---|---|
| Trait | FHB (0-9) | FDK % | DON ppm | FHB (0-9) | FDK % | DON ppm | FHB (0-9) | FDK % | DON ppm |
| Mean | 1.48 | TBD | TBD | 1.31 | TBD | TBD | 1.67 | TBD | TBD |
| Broad-sense heritability | 0.32 | TBD | TBD | 0.75 | TBD | TBD | 0.48 | TBD | TBD |
| Error standard deviation | 0.59 | TBD | TBD | 0.3 | TBD | TBD | 0.57 | TBD | TBD |

* Reasoning for low heritability for FHB scores in the Southern Uniform is unknown.

**Table 4:** Preliminary results from collaborative nurseries in 2024. Means, broad-sense heritability, and error standard deviation for FHB scores (0-9) and FDK (%) for the 2023 scab nursery are shown.

| Year: 2024 | Gulf Atlantic | | Mason Dixon | | Uniform Eastern | | Uniform Southern | |
|---|---|---|---|---|---|---|---|---|
| Trait | FHB (0-9) | FDK % | FHB (0-9) | FDK % | FHB (0-9) | FDK % | FHB (0-9) | FDK % |
| Mean | 2.25 | TBD | 1.92 | TBD | 1.61 | TBD | 1.96 | TBD |
| Broad-sense heritability | 0.46 | TBD | 0.34 | TBD | 0.33 | TBD | 0.84 | TBD |
| Error standard deviation | 0.75 | TBD | 0.65 | TBD | 0.64 | TBD | 0.46 | TBD |

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

Postdoctoral associate, Dr. Moshood Bakare, learned to access weather data from online sources to be used in genomic prediction models that take environmental variables into account. Dr. Bakare has completed a draft of a manuscript that uses weather variables to separate genomic regions of resistance that are sensitive to environmental conditions at and around flowering from those that are more stable across environmental conditions.

Graduate students Lexi Perry and Sunilda Frias assisted Moshood Bakare in scoring FHB traits in the field, and thus gained experience recognizing and quantifying FHB. Several undergraduate students assisted with FHB inoculum in the winter of 2024/2025 gaining experience in sterile technique and the cultivation of fusarium on media.

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

Results from the regional nurseries have been supplied to the lead PI's on those efforts, and we will continue to provide FDK and DON data as it becomes available. All 2025 harvest data will be uploaded to T3 as data becomes available for access by other breeders and interested parties.

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

We have now a draft of a manuscript that uses weather variables to separate genomic regions of resistance that are sensitive to environmental conditions at and around flowering from those that are more stable across environmental conditions.

Bakare, M. et al. *A phenological model to evaluate host sensitivity to weather conditions for infection and disease progression of fusarium head blight.* Expected submission to Crop Science in July 2025

Additionally we will evaluate the efficacy of genomic prediction through validation of families in the 2026 scab nursery.

Approximately 2,000 wheat plots will be evaluated in our misted inoculated FHB nursery, including Y1, Y2 and elite lines from our program and lines from other programs entered into regional nurseries.