

## FY22 Performance Progress Report

Due date: July 26, 2023

### Cover Page

<b>USDA-ARS Agreement ID:</b>	59-0206-2-155
<b>USDA-ARS Agreement Title:</b>	Genome-enabled Selection for Host Fusarium Head Blight (FHB) Resistance
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<b>Institution:</b>	Virginia Polytechnic Institute and State University
<b>Institution UEI:</b>	QDE5UHE5XD16
<b>Fiscal Year:</b>	2022
<b>FY22 USDA-ARS Award Amount:</b>	\$178,940
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<b>Period of Performance:</b>	May 1, 2022 – April 30, 2026
<b>Reporting Period End Date:</b>	April 30, 2023

### USWBSI Individual Project(s)

USWBSI Research Category <sup>1‡</sup>	Project Title	ARS Award Amount
BAR-CP	Genome-enabled Selection for FHB Resistance in Eastern Winter Malt and Feed Barley	\$62,072
VDHR-SWW	A Double Haploid Initiative to Speed Development of FHB Resistant Soft Winter Wheat.	\$18,263
VDHR-SWW	Genome-enabled Selection for FHB Resistance in Winter Wheat	\$98,605
<b>FY22 Total ARS Award Amount</b>		<b>\$178,940</b>

I am submitting this report as an:  Annual Report

*I certify to the best of my knowledge and belief that this report is correct and complete for performance of activities for the purposes set forth in the award documents.*

Principal Investigator Signature



Date Report Submitted

7/26/2023

<sup>1‡</sup> BAR-CP – Barley Coordinated Project  
 DUR-CP – Durum Coordinated Project  
 EC-HQ – Executive Committee-Headquarters  
 FST-R – Food Safety & Toxicology (Research)  
 FST-S – Food Safety & Toxicology (Service)  
 GDER – Gene Discovery & Engineering Resistance  
 HWW-CP – Hard Winter Wheat Coordinated Project  
 MGMT – FHB Management  
 MGMT-IM – FHB Management – Integrated Management Coordinated Project  
 PBG – Pathogen Biology & Genetics  
 TSCI – Transformational Science  
 VDHR – Variety Development & Uniform Nurseries  
 NWW –Northern Soft Winter Wheat Region  
 SPR – Spring Wheat Region  
 SWW – Southern Soft Red Winter Wheat Region

**Project 1:** Genome-enabled Selection for FHB Resistance in Eastern Winter Malt and Feed Barley

**Dedication**

Mr. Wynse Brooks, the barley breeder at Virginia Tech retired March 31st, 2023. During his 30 year service in the Virginia Tech small grains breeding program, Wynse developed and released 13 barley varieties, including feed barleys 'Thoroughbred' (2003) and 'Secretariat' (2014), hullless, FHB resistant, barley 'Greg' (2020) and awnless barley 'VT Beahm' (2021). Wynse also spearheaded the development of our malt barley breeding program in 2010. From those efforts, Wynse developed and released 'Avalon' in 2020, the first two-row malt barley specifically bred for adaptation to the Eastern US. His expertise, charm and tireless dedication to the program and barley growers will never be forgotten.



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

- 1) Evaluate predictive ability of FHB traits, including visual scores, FDK and DON within the Virginia barley germplasm
- 2) Determine genetic relationships (i.e. genetic correlations) 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 and malting quality
- 3) Use genomic information to estimate breeding values for advancement and mating decisions to improve FHB resistance, agronomic performance and malting quality
- 4) Evaluate response to selection and impacts on malting quality.

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

**a) What were the major activities?**

**Scab nursery 2023**

Our scab nursery was intentionally late-planted this year on December 2<sup>nd</sup> to push flowering dates forward by a several days in an attempt to replicate excellent infection seen under late planting in 2022. Trials planted included the NABSEN (57 entries/2 replicates), Eastern Malt (47/2) and the Winter Malt (29/2). All Year 2 (Y2) lines, including 137 hulled and 34 hulless lines, have also been evaluated in the scab nursery in two replicates, as well as in yield trials in Blacksburg VA and Warsaw VA. We also including 258 year 1 (Y1) lines in the scab nursery that were randomly selected from each family of the 825 headrow selections from 2022 that will be evaluated in 2023, year 1 yield trials. We will use these 250 lines to predict the remaining 568 lines not included in the scab nursery for FHB scores, FDK, and DON.

**Parent Selection for 2023 crossing**

FHB scores and FDK values from excellent scab infection in the 2022 nursery is being used to build the prediction model for FHB, agronomic and other disease traits for potential parental pairs to be used for crossing in the spring of 2023. Prediction accuracy of FHB traits is currently being evaluated using data from 2022 alone, given the excellent infection rates achieved that year. Addition of data from years 2019, 2020 may be included if prediction accuracy is shown to be increased. A total of 37 malt, 13 hulled, and 13 hulless inbred lines were selected as parents based on agronomic performance and FHB resistance. Of these, 34 have been genotyped with GBS by our program.

Our intention was to estimate and use marker effects to predict family mean performance for mate pair selection before crossing started in April of 2023. However, the retirement of our barley breeder, Wynse Brooks, produced a significant obstacle to completion of the pipeline. BLUPs were used to determine breeding values for genotyped lines, but predictions for mate pairs were delayed until crossing season of 2024. A postdoc in our lab, Felipe Sabadin, graciously stepped in to make crosses this season.

**b) What were the significant results?**

**Table 1:** Collaborative nursery means, broad-sense heritability, and error standard deviation for FHB scores (0-9) 2023 scab nursery.

Year: 2023	Winter Malt	Eastern Malt	NABSEN
Trait	FHB	FHB	FHB
Mean	2.67	2.32	2.39
Broad-sense heritability	0.78	0.72	0.74
Error standard deviation	0.57	0.71	0.69

**Genotyping**

We started on a new effort to genotype all new Virginia Tech barley lines that enter into yield trials and the scab nursery using Genotyping By Sequencing (GBS). Virginia breeding lines and varieties from our first year, second year, advanced and regional barley yield trails were planted in the greenhouse in the fall of 2021 for tissue sampling, totaling 565 barley lines. A second set of 855 first year lines (2023 Observation) was sent in Fall 2022. Preliminary results from our GBS pipeline produced 23,479 markers for 559 lines, with the 855 new lines to be added this summer. Missing data were imputed with Beagle, and we are beginning to work on LD pruning, and other marker filtering. Genomic prediction accuracy for FHB traits is being assessed this winter to determine how well the genotype phenotype information can be used for FHB trait selection. Preliminary results on genomic prediction of malting quality suggest that the markers are tracking familial relationships well, but capacity to delineate mendelian segregation is still unknown.

Acceptable infection and disease progression were observed for the 2023 harvest year, however, the unseasonably cool spring led to lower infection and disease rates than we observed in 2022. Processing of FDK and DON is ongoing.

For the 2022-2023 crossing season, 87 parental genotypes were selected. Parents were chosen considering their performance for important agronomic traits (yield, test weight, plant height, heading date, lodging, etc.), disease resistances (Fusarium head blight, leaf rust, powdery mildew, etc.), and quality malt traits (malt extract, diastatic power, wort viscosity, beta-glucan, alpha-amylase, etc), and crossing aimed to develop varieties for hulled malt, hullless, forage, and feed purposes.

In order to optimize crossing selection, data collected in the previous year were employed to fit best linear unbiased predictor (BLUP) for each genotype. Traits were jointly considered to select the best parental combination. A total of 167 crosses were obtained from the combination of 87 parents. Since disease resistance is essential for barley breeding, several crosses focused on

developing populations for those purposes. Thirty five crosses were made to explicitly FHB resistance (see Table 2).

**Table 2.** Proportion of parents and crosses made in the spring of 2023, considering breeding purpose.

Type / Purpose	Parents	Crosses*
Hulled	16	51
Hulless	6	106
Malt	65	11
Forage / Feeding		11
Fusarium Head Blight (FHB)		35
Leaf Rust		11
Powdery Mildew		50
Zero Glycosidic Nitriles		3

\* crosses can have more than one purpose.

Determination of genetic relationships between morphological/phenological traits and FHB traits is ongoing.

### c) List key outcomes or other achievements.

- 1) The number of lines entering first year yield trials was greatly expanded to increase selection intensity. approximately 800 new lines were entered into first year yield trials in 2023, and approximately 650 were entered for 2024 first year yield trials.
- 2) A unique source of FHB resistance has been identified in a hulless Virginia Tech line, 'Greg' (tested as VA15H-73), and crosses are being done to determine if that resistance can be brought into a hulled line.
- 3) A cross made in 2022, Avalon x VA21HFHB-19DH0301, was sent to Oregon State University for DH production. Line VA21HFHB-19DH0301 has Greg as a parent and has demonstrated some FHB resistance in the field.

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

Felipe Sabadin, a postdoc in the small grains breeding program at Virginia Tech, took over crossing and headrow selection, with oversight from the PI and assistance from research technicians in the program. We are currently working to recruit him into the barley breeding position based on his exemplary performance at both the barley breeding activities, as well as other ongoing research projects.

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

Results from the 2023 FHB nurseries will be disseminated in the following weeks as FDK data becomes available. All results from these nurseries will be uploaded to T3 in the fall of 2023.

**Project 2:** A Double Haploid Initiative to Speed Development of FHB Resistant Soft Winter Wheat.

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

- 1) Develop DH lines that combine multiple effective FHB resistance genes/QTL.
- 2) Utilize marker assisted selection (MAS) to enrich topcross F<sub>1</sub> populations for those genes/QTL.
- 3) Share new DHs with all VDHR-SWW breeders after the initial culling such that each breeder evaluates about 475 new DHs each year.

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

**a) What were the major activities?**

This proposal expands the regional Double Haploid (DH) initiative to quickly develop and release high-yielding varieties that contain effective FHB resistance pyramids. Objectives are: 1) Develop DH lines that combine multiple effective FHB resistance genes/QTL in a high-yielding background; 2) Utilize molecular markers to track FHB genes/QTL and enrich F<sub>1</sub> DH populations; and 3) Share new DHs with all VDHR-SWW breeders after the initial culling such that each breeder evaluates about 475 new DHs each year.

The collaborative DH project has been very successful at rapidly developing pure lines with good FHB resistance. Three new varieties derived from DHs with good FHB resistance were released between 2022 and 2023 by Virginia Tech, 15VDH-FHB-MAS-38-02 (2022, private license), 15VDH-FHB-MAS33-13 (2022, private license), 15VDH-FHB-MAS25-15 (2023, public release; name pending).

In 2022, a single cross (18VDH-FHB-MAS07-173-03 / 16VDH-SRW03-018) segregating for 7 FHB QTL was chosen to produce a larger number of DH lines (350) for selection of lines with many QTL combinations. Fifty eight F<sub>1</sub> seeds from this cross were sent to Heartland in the summer of 2022 to produce the necessary 350 DH lines. These parents were chosen because they completely complementary FHB QTL (line 18VDH-FHB-MAS07-173-03 contains Fhb1 (3BS), FHB3B.Bess, FHB1A.Neusse, and FHB6A.Neusse, while line 16VDH-SRW03-018 contains FHB1B.Jtwn, FHB2B.Bess, FHB.3BL) yet have the same vernalization alleles, same photoperiod sensitivity alleles, and the same Rht alleles as determined by inhouse genotyping with SSR and KASP markers. Both parents were developed from this long running project, and have demonstrated strong agronomic performance, with 16VDH-SRW03-018 ranking first in the overall mean across the Uniform Southern Nursery in 2021, and 18VDH-FHB-MAS07-173-03 ranking first in the Mason Dixon trial at Warsaw, VA in 2022. We hope to select good lines with high scab resistance from this cross, but also intend to create a mapping population to investigate epistatic interactions between FHB QTL. In our proposal (FY22), we demonstrated that FHB QTL do not appear to act in an additive fashion, and it is unclear if all have non-zero effects in all genetic backgrounds. We hope that by standardizing the genes for photoperiod

sensitivity, vernalization and plant height, we can remove these confounding factors to dissect potential interactions at previously detected FHB QTL. DH lines are expected to be received this fall for This effort is in contrast to the selection of DH crosses based on GEBVs of DON, FDK and other agronomic traits in Project 2. Selection of crosses for DH production in 2023-2024 are still being determined, and will be sent in August 2023.

**b) What were the significant results?**

Very poor DH seed was received back from Heartland Plant Innovations in the fall of 2022 from the FY21 project. This drastically limited the number of DH lines available for selection. Plant materials (67 F1 plants) were shipped to Heartland Plant Innovations Inc in the fall of 2021, but were damaged enroute. Heartland salvaged what they could but were only able to develop 38 DH lines instead of the expected 550. An additional 81 lines were sown in headrows from DH lines that were received the previous year (2021) with too few seeds (< 6), using seed grown in the greenhouse. For F1 lines submitted in 2022 and for the foreseeable future, only F1 seed will be sent. It is unclear to what degree the lack of DH lines produced and the poor quality of that seed had to do with damage during shipping.

Including lines with insufficient seed for field planting from the previous year, 48 lines were advanced from headrows to the 2024 SRW Observation nursery. DH lines selected from 2023 headrows will be distributed to all VDHR-SWW participants for fall planting in the coming weeks.

Selection intensity was greatly increased for traditional FHB breeding populations (non-DH). Heads were selected from additional FHB populations (56) and were planted in headrows for line purification to help make up for the loss of DH lines that would be under headrows selection in 2023. In the 2021-2022 field season, 1,520 FHB headrows from 11 FHB families were planted and selected from. For the 2022-2023 harvest season, this was greatly increased to 8,960 FHB headrows from 56 families. A total of 418 lines were selected out of these FHB headrows for entry into the SRW Observation nursery in 2024. This increased intensity should help make up for the loss in time.

**c) List key outcomes or other achievements.**

- 1) A new public variety was released in the spring of 2023, tested under the name 15VDH-FHB-MAS25-15. This variety is a sister line to 15VDH-FHB-MAS33-13 released the previous year, and has similar FHB resistance, and carries the *Fhb1* gene. In contrast to 15VDH-FHB-MAS33-13, 15VDH-FHB-MAS25-15 has demonstrated better powdery mildew resistance. Both lines have the *H13* allele for hessian fly resistance. A name for the public release is pending.
- 2) The number of FHB headrows was greatly expanded six-fold to increase selection intensity on FHB lines developed through standard inbreeding practices. This resulted in 418 new FHB lines being entered into first year trials in lieu of new DH lines (due to loss in shipping).

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

We have been working to recruit a postdoc to the position since the project started in summer 2022. Recently, a very qualified candidate applied and we are working to hire them in at the end of August, when their PhD degree is conferred (Cornell University).

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

DH lines were not shared last year due to relative lack of seed. Seed from 2023 harvest will be disseminated as yields were high, but several early lines may be lost due to preharvest sprouting.



**Project 3:** 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.)**

**a) What were the major activities?**

**Genomic prediction of crosses using predicted family merit**

A genomic prediction model was trained using data from the VT breeding program across four years, 2019-2022. This dataset included 29,700 phenotypic records (plots), representing 120,221 phenotypic data points for 3,587 breeding lines measured for 16 traits (unbalanced). Included in the dataset were phenotypic records for FHB, FDK, and DON from the misted inoculated nurseries in Virginia from 2019, 2020 and 2022. Data from 2021 was excluded due to very low FHB pressure. All lines were genotyped with genotyping by sequencing markers, totalling 7,225 after variant calling, filtering and imputation. Genomic BLUPs were fit and marker effects estimated through backsolving.

Elite parents (48 inbred lines) were selected based on superior performance in advanced yield trials. Early generation parents (50 inbred lines) were selected based on predicted genomic merit of lines evaluated in first year yield trials (2022) in one plot in 1 or 2 locations using a sparse testing design. F1 seed (48 F1) from the previous year of crossing (2021) 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 (10,585 predicted families) using 7,225 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 13 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 2022 were chosen based on both the selection index and prior knowledge of the parents. Selection of crosses for DH production in 2023-2024 are still being determined, and will be sent in August 2023.

### **Evaluation of line performance in Misted Inoculated nursery**

Regional trials and early generation trials (first and second year) were evaluated in a misted inoculated nursery. The scab nursery was intentionally planted late to increase the likelihood of warmer temperatures during flowering. This strategy was started for the harvest year 2022, and was continued for the 2023 harvest due to excellent infection and high disease pressure. While disease pressure was slightly less in 2023, infection was still very good and FDK values of up to 90% were observed. Susceptible scab spreader rows demonstrated almost 100% infection with FDK > 99%. New isolates obtained in the fall of 2021 appear to be highly virulent.

A total of 1,860 soft winter wheat plots were evaluated in the misted inoculated nursery for the 2023 harvest season, representing 983 breeding lines and check varieties. Regional nurseries included the Northern Uniform Scab (49 entries), Preliminary Northern Uniform Scab (36 entries), Southern Uniform Scab (63 entries), Uniform Eastern (28 entries), Uniform Southern (37 entries), Gulf Atlantic (59 entries), and Mason Dixon (67 entries) nurseries. Local nurseries evaluated included the second year SRW Preliminary (280 entries) and first year SRW Observation (247 entries). While the other scab trials have a complete entry list, the SRW Observation was subset to reduce the total amount of lines under FHB evaluation as part of the sparse testing design. All families were sampled to maximize the prediction accuracy of FHB traits in unobserved lines.

**Table 2:** Crosses sent for DH production in 2022 through genome-enabled selection or parents with complementary QTL. Lines in italics were developed through this double haploid project (3) while lines in bold were developed by project 3.

Pedigree	Year	No. DH	Fhb1 <sup>a</sup>	FDK <sup>b</sup>	DON <sup>c</sup>	Yield <sup>d</sup>	Selection Index <sup>e</sup>
17VTK4-29 / <b>15VDH-FHB-MAS38-01</b>	2022	50	fixed	-2.22	-1.81	3.05	5.58
18VTK12-60 / <b>15VDH-FHB-MAS38-01</b>	2022	50	seg	-2.22	-2.00	2.73	5.32
<b>15VDH-FHB-MAS38-01</b> // 17VTK4-29 / <b>15VDH-FHB-MAS33-13</b>	2022	60	fixed	-2.80	-1.99	2.30	5.21
<b>15VDH-FHB-MAS38-01</b> / <b>19VT1FHB_DH-170</b>	2022	50	seg	-2.65	-1.64	2.04	4.94
<b>15VDH-FHB-MAS38-01</b> / 15VTK-1-101 // 18VTK12-60	2022	60	seg	-1.70	-1.57	2.41	4.86
<b>15VDH-FHB-MAS33-13</b> / <b>15VDH-FHB-MAS38-01</b>	2022	50	fixed	-3.37	-2.16	1.56	4.84
17VTK4-29 / <b>15VDH-FHB-MAS33-13</b> // 18VTK13-4	2022	60	seg	-1.84	-1.22	2.38	4.77
17VTK4-29 / <b>18VDH-FHB-MAS07-164-01</b>	2022	80	seg	-0.03	-1.21	2.91	4.50
<b>15VDH-FHB-MAS33-13</b> / 17VTK4-29	2022	60	fixed	-2.09	-1.89	1.77	4.37

<sup>a</sup>status of *Fhb1* in the cross. “Fixed” means both parents are homozygous for the *Fhb1* allele, wheels seg indicates that only one parent contains the allele, and a dash indicates neither parent has *Fhb1*. Crosses were not designed with *Fhb1* explicitly, but were clearly favored due to low FDK and DON.

<sup>b</sup>Genomic prediction of FDK in standard units from the population mean (i.e. z-scores of GBLUP).

<sup>c</sup>Genomic prediction of DON in standard units from the population mean (i.e. z-scores of GBLUP).

<sup>d</sup>Genomic prediction of Grain Yield in standard units from the population mean (i.e. z-scores of GBLUP).

<sup>e</sup>Selection index included genomic predictions for FDK, DON, grain yield (shown in b-d), test weight, heading date, powdery mildew and leaf rust (not shown).

## b) What were the significant results?

### Crosses

A total of 348 single crosses and 106 top-crosses (F1 by elite) were made, as well as 3 double crosses (F1 by F1) of specific interest in spring of 2023. 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. A training dataset consisting of data from 2019 to 2022 was used to train the genomic prediction model. A set of 99 crosses were also made to introgress a dominant male sterility gene from New York germplasm into a Virginia germplasm background for the second cycle of backcrossing to elite virginia materials. The dominant male sterile gene is intended to facilitate crossing in a future rapid cycling breeding scheme.

### Scab nursery

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, were scored for FDK after harvest (See Table 1). Other nurseries are in progress for FDK and DON sample processing.

### FHB Headrows

As DH seed received as part of project 2 was very poor, selection intensity was greatly increased for traditional FHB breeding populations (non-DH). Heads were selected from additional FHB populations (56) and were planted in headrows for line purification to help make up for the loss of DH lines that would be under headrows selection in 2023. In the 2021-2022 field season, 1,520 FHB headrows from 11 FHB families were planted and selected from. For the 2022-2023 harvest season, this was greatly increased to 8,960 FHB headrows from 56 families. A total of 418 lines were selected out of these FHB headrows for entry into the SRW Observation nursery in 2024. This increased intensity should help make up for the loss in time.

**Table 1:** Preliminary results from collaborative nurseries. Means, broad-sense heritability, and error standard deviation for FHB scores (0-9) and FDK (%) for the 2023 scab nursery are shown.

Year: 2023	NUWWSN		PNUWWSN		SUWWSN		Gulf Atlantic	Mason Dixon	UEN	USN
Trait	FHB	FDK	FHB	FDK	FHB	FDK	FHB	FHB	FHB	FHB
Mean	3.0	12.7	3.9	26.9	4.6	27.0	3.6	3.6	3.7	4.04
Broad-sense heritability	0.63	0.64	0.4	0.57	0.45	0.73	0.78	0.36	0.64	0.22
Error standard deviation	0.79	5.9	1.02	12.7	1.02	11.5	0.86	0.96	0.8	1.05

**c) List key outcomes or other achievements.**

- 1) A pipeline for genomic prediction of mate pairs for multiple traits and single genes, including FHB traits, has been fully implemented and
- 2) All regional nurseries we participate in (7) are currently also being screened in our misted inoculated nursery for FHB scores, FDK and DON.
- 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.

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

Sunilda Frias, a WheatCAP student, is involved in the scoring of FHB traits, processing samples, crossing and making selections. She is particularly invested in the sparse testing design for year 1 materials (SRW Observation), working to coordinate splitting families and allocating seed.

We are currently working to hire a new Postdoctoral Associate position. with the current applicant expected to start in August. That person received their PhD from Cornell University this summer (2023) has a strong background in quantitative genetics. We fully expect that position will allow for accelerated progress of this project, and publication in peer-reviewed journals.

**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 2023 harvest data will be uploaded to T3 as data becomes available for access by other breeders and interested parties.

## Publications, Conference Papers, and Presentations

Please include a listing of all your publications/presentations about your FHB work that were a result of funding from your FY22 grant award. Only citations for publications published (submitted or accepted) or presentations presented during the **award period** should be included.

**Did you publish/submit or present anything during this award period May 1, 2022 – April 30, 2023?**

- Yes, I've included the citation reference in listing(s) below.  
 No, I have nothing to report.

### Journal publications as a result of FY22 award

*List peer-reviewed articles or papers appearing in scientific, technical, or professional journals. Include any peer-reviewed publication in the periodically published proceedings of a scientific society, a conference, or the like.*

Identify for each publication: Author(s); title; journal; volume: year; page numbers; status of publication (published [include DOI#]; accepted, awaiting publication; submitted, under review; other); acknowledgement of federal support (yes/no).

### Books or other non-periodical, one-time publications as a result of FY22 award

*Report any book, monograph, dissertation, abstract, or the like published as or in a separate publication, rather than a periodical or series. Include any significant publication in the proceedings of a one-time conference or in the report of a one-time study, commission, or the like.*

Identify for each one-time publication: Author(s); title; editor; title of collection, if applicable; bibliographic information; year; type of publication (book, thesis, or dissertation, other); status of publication (published; accepted, awaiting publication; submitted, under review; other); acknowledgement of federal support (yes/no).

### Other publications, conference papers and presentations as a result of FY22 award

Identify any other publications, conference papers and/or presentations not reported above. Specify the status of the publication.