Report for FY22-BA-022: Genome-enabled Selection for FHB Resistance in Eastern Winter Malt and Feed Barley

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

Our ultimate goal is to develop agronomically viable varieties with suitable characteristics, including FHB resistance, that can meet grower needs. While we see value in the development of breeding lines with superior FHB resistance, these products are only valuable as germplasm for future breeding efforts if they cannot meet grower and industry needs. Thus, we strive to balance FHB resistance with other agronomic and quality characteristics that make new varieties viable in the marketplace, serving to increase profitability of small grain farmers in the United States.

1) Evaluate predictive ability of FHB traits, including visual scores, FDK and DON within the Virginia barley germplasm. Develop new barley varieties with improved resistance to fusarium head blight and excellent agronomic performance.
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.)*

Variety release – 'Fuller' two-row malting barley

A new two-row winter malting barley line, tested as VA22M-158, was released as a public variety in the fall of 2025 under the cultivar name 'Fuller'. Fuller has excellent agronomic characteristics, including high yield (comparable to the six-row feed varieties Thoroughbred and Secretariat), high test weight and acceptable malting characteristics based on four site-years of micro-malting at the CCRU in Madison, WI, and one year of pilot malting by AMBA. Across eight site-years in the Eastern Malt Barley Test evaluated in Virginia and North Carolina, Fuller ranked 5th, demonstrated 23% higher grain yield (122 bu/ac) than Avalon (99 bu/ac; $P < 0.05$), with similarly high test weight (47.6 vs. 47.7 lb/bu). Fuller also has excellent standability with the second best mean lodging score in the test of 0.9 on a 0 to 9 visual rating scale with 0 being no visible signs of lodging and 9 indicated the entire plot was completely lodged. Fuller is two days later than Avalon for heading date. The improved yield and standability, along with a different maturity, make Fuller ideal for eastern malt producers who need to diversify their production to avoid total failures due to late spring freeze and other climactic conditions. Fuller is moderately resistant to FHB, with resistance levels similar to Avalon, and was significantly below the trial mean for FDK and DON with ratings of 5% FDK (mean = 8%, maximum = 13%) and 7 ppm DON (mean = 9 ppm, maximum = 21 ppm). Two acres of breeder seed of Fuller were planted in the fall of 2025 at VCIA to produce 91 units in 2026. Yield was low due to extreme spring drought, but the crop fortunately avoided the late spring freeze that caused almost larger losses in earlier varieties under production.

Evaluation of cooperative nurseries

A total of 1,068 dual row plots representing 651 breeding lines across 7 trials were evaluated in the misted inoculated scab nursery in 2026. Trials evaluated in the misted inoculated FHB nursery included the Uniform Winter Barley Nursery (UBN), the North American Barley Scab Evaluation Nursery (NABSEN), the Winter Malt Barley Nursery (WMBT), Eastern Malt Barley Nursery (EMBT),

the Virginia state barley official variety trial (OVT), and internal year-2 (Hulled Preliminary) and year-1 trials (Hulled Observation). Particularly dry conditions along with a late spring freeze around flowering (April 23rd, 2026) lead to devastating losses due to freeze damage across the state, and low scab infection in barley. Wheat trials in the same inoculated misted nursery had high infection, with FDK rates up to 45%, demonstrating timing was the primary cause of low infection, and not poor inoculum or some other systematic experimental factor. Despite low visual symptoms, all plots were harvested and are currently being processed for FDK and DON. Relatively high heritability for FHB scores in some trials suggest it is likely we will still be able to differentiate highly susceptible breeding lines from those with some degree of resistance. Coupled with genomic prediction using previous years data should ensure effective selection for FHB traits.

Genomic prediction and genomic selection

Genomic information is now being used to estimate genetic values at all breeding stages, such that selection on predicted FHB traits is now conducted through multiple stages of advancement. Genomic prediction is routinely used for parental selection and prediction of mate-pair performance to guide crossing decisions. Predictive abilities of FHB traits are all within ranges useful for genomic selection. Genomic predictive abilities between unobserved and observed GBLUP estimates using 5-fold cross-validation were relatively high at 0.90 for FHB, 0.81 for FDK and 0.78 for DON.

In the Spring of 2026, 222 crosses were conducted with elite barley breeding materials at Virginia Tech using genomic prediction of mate pairs to design crosses. Segregating populations (F2-F4) totaling 290 families were evaluated at two locations in Blacksburg, VA, and Warsaw, VA. A total of 11,760 $F_{4:5}$ and $F_{5:6}$ lines, as well as 657 doubled haploid lines were evaluated in single rows split across Blacksburg, VA, and Warsaw, VA. Of those, 579 lines, including 35 doubled haploid lines, were advanced into year-1 trials for the 2027 harvest season. A total of 686 year-1 lines were evaluated across 2 locations in Virginia, including 56 lines known to not produce glycosidic nitrile (GN0), a carcinogen formed in the distillation process. A subset of 382 year-1 lines was included in the scab nursery and used along with all other lines phenotyped for FHB between 2021 and 2026 to predict FHB traits for the 302 unobserved year-1 lines.

Summer 2026 harvest data was compiled to update the multi-environment, multi-trait genomic prediction models for advancement of lines evaluated in 2026 for fall 2027 planting. As of July 2026, our genomic prediction training model for barley contains 27,924 plots (17,936 of which are yield plots) from 207 trials evaluated across 6 years, representing 3,809 breeding lines. This training model includes 4,175 plots from our scab nursery representing 1,699 genotyped lines across 32 FHB trials spanning 6 years, 2021-2026. Genomic estimated breeding values were calculated for agronomic, FHB and malt quality traits and used for advancement decisions.

Genetic correlation of agronomic and malting quality traits to FHB traits

Initially, effects of indirect selection on agronomic and malting quality traits were intended to be tracked as selection occurred. Because a genomic selection index incorporating all FHB, agronomic and malting traits was used for advancement decisions, especially in year-1 trials, indirect selection on agronomic or malting traits did not occur. Thus, we are relying on genetic correlations from a bivariate GBLUP model to infer expected consequences to selection under more naïve selection conditions. Data used to calculate genetic correlations included data from 4,175 scab nursery plots, 21,150 yield plots and 994 micro-malt quality samples across 2022-2026. Most genetic correlations were moderate to low, with the highest magnitude of 0.43 showing a positive genetic correlation between heading date and DON accumulation (Table 1). The lack of a strong genetic correlation structure between most traits indicates that improvement of FHB should be possible without drastic indirect impact to other key agronomic or malting traits. We suspect the relationship between DON and heading is largely an escape mechanism, where earlier materials are more likely to escape weather conditions that promote disease progression.

Table 1: Genetic correlations between FHB traits, malting quality and agronomic traits estimated in a bivariate GBLUP model from data collected between 2022 and 2026.

	FHB	FDK	DON
FHB		0.41	0.58
FDK			0.46
Grain Yield	**0.34**	-0.03	**0.25**
Test Weight	-0.19	-0.14	-0.22
Plant Height	-0.02	-0.01	-0.01
Heading Date	-0.17	-0.15	**0.43**
Malt Extract	-0.23	-0.33	-0.05
Barley Protein	-0.31	0.32	-0.23
Wort Protein	-0.25	0.04	-0.16
S/T	0.15	-0.28	0.15
Diastatic Power	-0.08	-0.29	0.01
Alpha Amylase	0.00	-0.22	-0.06
Beta Glucan	0.25	0.29	0.11
Free Amino Nitrogen	-0.05	0.04	-0.07

List key outcomes or other achievements.

1) Release of 'Fuller' two-row malting barley with moderate resistance to FHB.
2) Robust genomic prediction framework has been implemented allowing genomic selection of parents, mate-pairs and advancement of elite materials for FHB traits.
3) Lexi Perry M.S. was hired as the barley breeder in the fall of 2025. She is excellent.

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

Postdoctoral associate, Dr. Moshood Bakare, completed a three-year postdoc managing this USWBSI project in the Summer of 2026. He has completed a manuscript on which he was invited to present at the December 2025 USWBSI forum. The manuscript is ready for submission but has been delayed due to the PI's available time.

Bakare, M.A, Sabadin, F., Loeb, A., Perry, L., Frias, S., Liu, L., Brooks, W.S., Dewitt, N., Brown-Guidera, G. and Santantonio, N. (2025) *The effect of weather conditions on flowering and the selection for loci that contribute to durable resistance.* U.S. Wheat and Barley Scab Initiative – 2025 National FHB Forum. Denver CO. *Invited*.

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

Summaries of regional nurseries in the FHB nursery have been sent to nursery collaborators, and will continue to be updated as grain samples are processed for FDK and DON. State official variety trial data is now posted with FHB traits for multi-year analyses at https://cropgenetics.spes.vt.edu/small-grains-breeding/variety-data.html. We have done a poor job getting the barley data uploaded to T3 (but a good job with the wheat data). Special attention will be put towards this effort.

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

After planting the 2027 field trials and scab nursery, the following manuscript should be submitted to Crop Science. Internal revisions have taken longer than expected due to other PI commitments.

Bakare, M.A., Sabadin, F., Loeb, A., Perry, A., Frias, S., Liu, L., Brooks, W.S., Schmale, D., McMaster, N., Dewitt, N., Brown-Guidera, G., Oakes, J. and Santantonio, N. (2026) *A phenological model to evaluate host sensitivity to weather conditions for infection and disease progression of Fusarium head blight.* Expected submission to Crop Science Fall 2026.