

Virginia Small Grains Board Progress Report 2023

Breeding, mapping, and genome-enabled selection for scab resistance in barley and wheat

Nicholas Santantonio, Felipe Sabadin, Luciana Rosso and Joseph Oakes
216 Latham Hall, School of Plant and Environmental Sciences, Virginia Tech
Blacksburg VA 24061

PROGRESS REPORT

The specific objectives of this project are to: 1) Incorporate and combine resistance genes from newly improved scab resistant germplasm and/or scab-tolerant native wheat and barley lines to develop and release commercially viable cultivars; 2) Accelerate release of scab resistant cultivars and/or germplasm using marker assisted breeding (including marker assisted selection and genomic prediction), and doubled haploid methods and; 3) Characterize, map, and identify regions of the genome conferring scab resistance in our barley breeding materials through genome-wide association of markers with FHB traits.

Recent cultivars having moderately or higher levels of scab resistance developed and released by the Virginia Tech program include: VA15H-73 (2020; 'Greg') hulless barley, SB255 (VA11B-141 LA) hulled barley and wheat cultivars Jamestown (2007), USG 3555 (2007), USG 3315 (2009), 12V51 (2011), Yorktown (2012), Featherstone 73 (2013), Southern Harvest 3200 (2013), MCIA Venus (2013), SS8513 (2014), Hilliard (2015), L11550 (2016), Dyna-Gro 9811 and USG 3118 (2017), Laverne and Featherstone 125 (2019).

Four FHB resistant lines having *Fhb1* in the pedigree, 15VDH-FHB-MAS31-30, 15VDH-FHB-MAS25-15, 15VDH-FHB-MAS-33-13 and 15VDH-FHB-MAS38-01, have been developed from our marker-assisted breeding program and have been evaluated in the Virginia State Wheat since 2020. Of those four, 15VDH-FHB-MAS-33-13 and 15VDH-FHB-MAS38-01 were licensed to private companies in 2022, and 15VDH-FHB-MAS25-15 was released as a public variety in the spring of 2023.

Table 1: Table of SRW FHB breeding activities, with the number of Virginia Tech breeding lines at various stages of selection and testing.

Breeding Nursery	2018	2019	2020	2021	2022	2023
Populations	176	247	296	395	395	505
SRW, MAS, and DH Headrows	4400	2700	2500	4400	2122	9,905
Preliminary yield test	20	28	16	87	94	148
VA state yield test	18	21	11	19	30	30
Southern FHB uniform test	8	9	8	8	8	8
Northern FHB uniform test	5	5	5	5	5	5
Preliminary northern FHB test	5	5	6	5	6	6

One SRW line, 15VDH-FHB-MAS25-15, was selected for public release in 2023. Line 15VDH-FHB-MAS25-15 is a sister line to 15VDH-FHB-MAS33-13, which was released and privately licensed in 2022. Line 15VDH-FHB-MAS25-15 contains the *Fhb1* locus, known to limit the spread of scab within the grain head, and is resistant to scab and leaf rust, and is moderately resistant to powder mildew. Across three years in the Virginia Tech Official Variety Test, 15VDH-FHB-MAS25-15

ranked 17th in mean grain yield (86.7 bu/ac) across three years, 2020 to 2022, only significantly less than the two highest yielding line 'MAS #143' (90.3 bu/ac) and Dyna-Gro 9172 (90.1 bu/ac; data not shown). This line also exhibited average or above average yield performance in the 221 Gulf Atlantic Nursery in VA, SC, NC, AR and GA. Detailed release documents can be found at github.com/nsantantonio/releases2023.

The largest challenge we face is getting good environmental conditions for scab infection during flowering. The year 2021 had very little infection in the misted inoculated nursery, and almost no detectable natural infection throughout the Mid-Atlantic region. As such, our 2021 scab nursery was largely a failure that year. To help mitigate the issue of poor infection, we established brand new stocks of highly virulent FHB isolates from Dr. Schmale's lab. We also planted the nursery a few weeks later than usual to push flowering later in the spring when temperatures will be higher and more suited for FHB infection.

Excellent infection was obtained for the 2022 misted inoculated scab nursery in Warsaw VA. It is unclear to what extent this was due to the use of new isolates or environmental conditions that benefited the pathogen at the timing of infection. Regardless, our breeding program will work to obtain fresh isolates every other year or so to avoid loss of virulence in culture.

Several new experimental SRW lines from our program were identified with excellent agronomic performance and good FHB resistance, including VA20FHB-20 (developed in this project), 18VDH-FHB-MAS07-173-03 (project 3), 16VDH-FHB-MAS60-7-03 (project 3) and 17VTK4-29. All four have been confirmed to have at least one *Fhb1* allele through genotyping, highlighting the importance of the locus.

For the 2023 crossing season, we worked to build a genomic prediction pipeline for agronomic and scab traits in SRW. This included agronomic data from 2019 through 2022 for 23,433 yield plots, and FHB data from 2,734 scab plots (with 2021 data omitted due to poor infection that year), representing 3,587 breeding lines. This phenotypic information was paired with genome-wide marker information (7,225 GBS markers) for these lines to train the genomic prediction model. Marker effects for FHB index, FDK and DON were predicted using a GBLUP framework and back-solving for marker effects. The only FHB traits considered for crossing were FDK and DON, as FHB indices have been shown to only be loosely correlated with these more important FHB traits. However, FHB index or score is still used to drop the very worst lines before they are advanced for further testing.

A genomic selection index was constructed by weighting, albeit somewhat arbitrarily, FHB traits and other agronomic and disease traits, including grain yield, test weight, heading date and plant height, as well as leaf rust and powdery mildew resistance (for which reliable data was readily available from multiple years). Estimates of family performance were predicted by averaging the parental genotype scores (i.e. obtaining the expected genotype of offspring), and multiplying by the marker effects for each trait and then the selection index to produce a single value of family merit. Currently, this method does not estimate family variance of each trait, but genetic covariance between parents is used to keep from selecting mate pairs between close relatives. We are continuing to work on how to properly weight each trait using an economic index to select mate pairs for profitability instead of specific traits on the family mean level, while also maximizing the probability of selecting superior lines by using estimates of family variation for each trait and incorporating information on population size (e.g. number of pure line selections possible).

With few exceptions, all crosses made in the SRW breeding program now incorporate FHB traits into those crossing decisions, via the selection index which includes genomic estimates of family performance for FDK and DON. A total of 457 SRW crosses were conducted in the spring of 2023. Genomic predictions of family expectations were used for almost all crossing decisions on a daily basis using the pipeline developed to provide the best crosses given a subset of possible females

and males. This included 106 topcrosses, and 3 double-crosses. Crosses sent for doubled haploid generation were chosen based on both the selection index and prior knowledge of the parents.

Less progress was made in barley, with efforts focused on the SRW. However, a pipeline for calling GBS variants was developed and resulted in 23,479 GBS markers called for 559 barley lines after filtering and LD pruning. Missing data were imputed with Beagle. Genomic prediction accuracy for FHB traits still needs to be 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.

Last summer, 751 hulled and 74 hulless barley lines were selected from 9,520 and 831 hulled and hulless headrows, respectively. Tissue from these 825 barley lines was sampled and sent for GBS library construction and sequencing. Sequence was received in May, but we have yet to process the new genotypic information. The pipeline will be rerun upon the completion of harvest and used to generate variant calls for all 1,384 sequenced lines.

Due to the larger number of first year observation lines in both SRW and barley, it is unrealistic to put all these lines in the scab nursery. A sparse testing approach was used in both SRW and barley observation (first year) lines where a subset of lines from each family was put into the scab nursery for FHB evaluation. The observed lines will be used to help train the prediction model for unobserved lines so that selection for FHB traits can occur at the full scale in first year lines.

Table 2: Performance of breeding lines in the 2022 State Wheat Variety Trial for fusarium head blight (FHB; scab) evaluated in a misted, inoculated nursery in Warsaw VA.

Line	FHBPlant Response 0-9	FDKFusarium DiseasedKernels %	DON ppm
MASSEY	4.0	30	7.8
HILLIARD	4.0	38	10.9
Liberty 5658	4.0	30	10.2
13VTK429-3	3.0	18	6.5
VA17W-75	4.0	25	6.9
15VDH-FHB-MAS38-01	2.5	12	4.5
15VDH-FHB-MAS25-15	3.0	40	9.6
15VDH-FHB-MAS33-13	3.0	15	7.0
MAS1407-056-6-3	3.5	30	12.4
14VDH-SRW14-150	4.5	66+	15.6
16VDH-SRW03-023	3.5	30	4.3
16VDH-SRW03-018	4.5	45	8.6
16VDH-SRW09-025	3.5	28	8.3
15VTK-1-101	4.0	15	11.4
VA19W-24	4.0	45	9.2
VA19W-29	5.0	32	9.9
VA19W-31	6.0+	52	10.4
17VDH-SRW03-143	4.0	45	6.6
17VDH-SRW05-169	5.0	50	9.3
VA19FHB-05	3.5	28	5.1
16VTK19-201	3.0	30	7.9
DH16-SRW120-064	5.5+	68+	13.0
VA19W-02	5.0	38	6.4
VA19W-43	4.0	65	14.0
17VDH-SRW01-077	4.5	48	8.4
VA19FHB-22	5.0	40	15.3
VA19FHB-36	3.5	30	5.2
VA20W-69	5.5+	35	5.9
VA20W-142	3.5	28	4.8
VA20W-171	4.0	25	11.0
17VTK6-61	4.5	28	7.9
17VTK19-15	3.5	32	11.9
DH17SRW136-066	3.0	55	6.6
mean	3.8	38	7.8
LSD	1.3	28	39.5
CV	17.1	38	28.2

continued ...

A plus or minus sign indicates a performance significantly above or below the test average.

The 0-9 ratings indicate a genotype's response to disease or lodging where 0 = highly resistant and 9 = highly susceptible.

Parentheses below column headings indicate the number of site-years in which data were collected.

Line	FHBPlant Response	FDKFusarium DiseasedKernels	DON
17VTK4-29	4.0	28	10.8
VA20FHB-20	3.5	45	8.0
18VDH-FHB-MAS06-152-03	4.0	48	7.9
18VDH-FHB-MAS07-164-01	7.0+	42	10.3
18VDH-FHB-MAS07-164-08	7.5+	50	12.9
VA19MAS7-519-1WS-R110	3.0	25	9.4
15VDH-FHB-MAS31-30	3.0	61	6.8
17VDH-SRW05-052	3.5	28	8.2
16VDH-FHB-MAS60-7-03	4.0	25	4.5
Dyna-Gro Shirley	5.5+	50	9.4
SH 7200	4.5	55	13.2
Vision 45	4.0	62	5.6
USG 3118	4.5	38	6.0
Progeny Berkeley	2.5	28	8.2
SY 007	5.5+	52	10.0
Pioneer 26R59	4.0	40	8.9
Pioneer 26R36	5.0	50	7.0
SY 547	4.0	45	11.0
SY Viper	6.5+	35	7.0
Progeny #Bullet	2.5	25	6.0
MAS #67	2.0-	30	2.1
Dyna-Gro Laverne	5.0	42	8.2
Featherstone 125	5.5+	38	9.4
Pioneer 26R45	3.0	20	5.4
MAS #316	2.5	10	7.2
SY 100	3.5	65	6.4
MAS #86	2.0-	28	4.1
MAS #106	3.0	15	2.5
Progeny #Buster	4.5	25	12.2
SY 576	2.0-	55	12.9
SY Richie	8.0+	50	12.1
LW2169	3.0	12	7.3
NC11546-14	3.0	25	5.9
AgriMAXX 502	4.0	45	7.8
AgriMAXX 503	3.0	10	3.1
AgriMAXX 505	3.5	55	7.7
Dyna-Gro 9172	3.5	12	5.8
mean	3.8	38	7.8
LSD	1.3	28	39.5
CV	17.1	38	28.2

continued ...

A plus or minus sign indicates a performance significantly above or below the test average.

The 0-9 ratings indicate a genotype's response to disease or lodging where 0 = highly resistant and 9 = highly susceptible.

Parentheses below column headings indicate the number of site-years in which data were collected.

Line	FHBPlant Response	FDKFusarium DiseasedKernels	DON
Dyna-Gro 9120	6.0+	32	6.8
Dyna-Gro 9151	3.5	22	4.6
Dyna-Gro 9002	4.0	28	4.9
MBX 127	3.0	15	4.6
MBX 176	3.5	30	6.9
MBX 223	3.0	22	5.4
Progeny 19-12	4.0	45	5.4
Progeny #Chad	4.0	48	8.8
MAS #143	3.0	18	2.4
MAS #133	3.5	38	6.6
AgriMAXX 513	2.5	35	3.4
AgriMAXX 514	3.5	32	6.4
AgriMAXX 516	3.0	20	6.6
CP8045	4.0	25	5.6
CPX91221	3.5	38	6.4
Dyna-Gro WX20738	4.5	40	8.8
Dyna-Gro WX21741	2.5	20	4.8
FS 891	3.0	20	5.3
FS 875	2.5	32	5.5
LW2148	2.0-	20	2.5
MAS #2	3.0	38	5.0
MAS #139	4.0	62	5.5
SH 9520	3.5	22	13.7
USG 3472	3.0	18	5.9
USG 3451	6.0+	68+	14.2
Hardy 2519	3.5	58	11.6
USG 3000	4.0	18	4.9
AgriMAXX EXP 2105	3.5	38	6.2
AgriMAXX EXP 2110	2.5	35	5.2
AgriMAXX EXP 2222	3.5	32	9.2
GP 381	3.5	42	4.8
GP 348	7.5+	68+	4.0
GP 463	3.0	48	1.6
CP8118	5.0	28	7.3
Dyna-Gro 9393	3.5	35	6.7
Dyna-Gro 9352	3.0	62	8.2
Dyna-Gro WX21793	3.5	30	10.1
mean	3.8	38	7.8
LSD	1.3	28	39.5
CV	17.1	38	28.2

continued ...

A plus or minus sign indicates a performance significantly above or below the test average.

The 0-9 ratings indicate a genotype's response to disease or lodging where 0 = highly resistant and 9 = highly susceptible.

Parentheses below column headings indicate the number of site-years in which data were collected.

Line	FHBPlant Response	FDKFusarium DiseasedKernels	DON
Dyna-Gro WX22741	2.0-	35	3.2
FS 745	3.0	12	4.8
FS 743	4.0	32	9.1
FS 597	3.5	40	7.0
KWS394	1.0-	50	7.0
KWS398	1.5-	28	3.6
KWS405	2.5	35	2.7
KWS414	3.5	52	12.0
KWS415	2.5	30	4.2
LW2266	3.5	42	5.8
LW2277	3.0	35	12.5
MBX 2261	3.5	40	11.0
MAS #155	4.0	40	8.2
MAS # 134	2.0-	35	4.4
MAS # 165	3.5	48	6.2
MAS # 166	2.0-	20	2.8
MAS # 170	4.0	52	8.7
MAS # 172	2.0-	30	10.0
NC15V25-20	2.0-	38	4.0
NC13211-9	3.0	32	11.7
NC13955-G125	2.5	50	8.3
NC18-16913	2.5	20	2.1
Progeny 20-2	5.5+	25	6.0
SH 7222	3.0	32	6.0
SH 4222	3.5	32	7.5
FL15105-LDH039	5.0	32	6.3
FL16009LDH-16	8.0+	58	15.8
FL16045LDH-25	4.0	30	6.2
GA 151313-LDH224-19E38	3.0	22	6.7
GA 111055-19LE12	7.0+	72+	17.9
GA 121012-19LE8	3.0	58	18.2
GA 11052-19LE15	3.5	32	6.0
USG 3783	3.5	42	6.5
USG 3352	3.0	45	7.0
USG 3563	3.0	30	6.9
USG 3463	2.5	62	4.4
USG 3661	4.5	60	15.9
mean	3.8	38	7.8
LSD	1.3	28	39.5
CV	17.1	38	28.2

continued ...

A plus or minus sign indicates a performance significantly above or below the test average.

The 0-9 ratings indicate a genotype's response to disease or lodging where 0 = highly resistant and 9 = highly susceptible.

Parentheses below column headings indicate the number of site-years in which data were collected.

Line	FHBPlant Response	FDKFusarium DiseasedKernels	DON
HR 5210	7.0+	85+	16.0
15VDH-HRW15-062	4.5	80+	19.1
VA18HRW-57	4.0	60	5.6
VA18HRW-58	4.0	55	6.7
VA18HRW-96	3.5	55	12.6
mean	3.8	38	7.8
LSD	1.3	28	39.5
CV	17.1	38	28.2

A plus or minus sign indicates a performance significantly above or below the test average.

The 0-9 ratings indicate a genotype's response to disease or lodging where 0 = highly resistant and 9 = highly susceptible.

Parentheses below column headings indicate the number of site-years in which data were collected.

Table 3: Performance of breeding lines in the 2022 SRW Preliminary for fusarium head blight (FHB; scab) evaluated in a misted, inoculated nursery in Warsaw VA.

Line	FHBPlant Response 0-9	FDKFusarium DiseasedKernels %	DON ppm
17VDH-SRW02-125	2.0	18	5.0
VA20FHB-18	3.5	20	5.2
18VTK10-77	3.0	20	4.3
SY-VIPER	5.0	35	2.1
18VTK5-95	3.5	30	2.7
18VTK6-3	2.5	22	5.8
VA19W-87	3.5	35	7.2
VA17W-74	2.2	26	2.7
VA21W-59	5.0	62+	11.9+
AGRIMAXX502	3.5	18	4.3
17VDH-SRW03-204	4.0	38	4.8
18VTK15-27	5.0	30	2.7
DH13SRW022-216	2.5	20	2.9
MAS#143	3.0	15	3.2
VA20FHB-21	3.5	25	4.3
L11541	2.5	18	3.0
18VTK10-188	2.5	18	3.1
HILLIARD	3.5	20	4.4
VA21W-170	4.0	52	7.6
18VTK10-23	3.0	15	2.5
VA21W-76	5.0	60	19.5+
PIONEER26R59	4.5	38	6.7
18VTK10-110	2.5	22	3.1
18VTK12-111	2.5	20	5.3
18VTK12-60	3.5	22	1.5
VA21W-75	3.5	28	7.1
17VTK18-13	5.0	50	11.5+
VA21W-39	3.5	28	4.3
18VTK10-5	3.0	25	5.6
VA21W-113	4.0	22	9.2+
VA21W-165	3.5	32	5.4
18VTK10-147	2.5	20	4.6
VA21W-112	3.0	25	8.4
mean	3.5	30	5.0
LSD	1.5	31	3.8
CV	22.1	52	38.4

continued ...

A plus or minus sign indicates a performance significantly above or below the test average.

The 0-9 ratings indicate a genotype's response to disease or lodging where 0 = highly resistant and 9 = highly susceptible.

Parentheses below column headings indicate the number of site-years in which data were collected.

Line	FHBPlant	FDKFusarium	DON
	Response	DiseasedKernels	
17VDH-SRW05-170	3.0	38	4.4
VA19W-79	3.5	40	2.8
SHIRLEY	5.0	28	8.4
VA20W-5	4.0	40	6.7
18VTK10-40	2.5	25	6.0
18VDH-FHB-MAS15-367-12	2.5	40	6.4
18VTK9-6	3.0	22	3.3
13VTK59-55	4.0	12	6.6
VA21W-57	3.5	48	4.1
VA21W-164	3.0	30	7.3
18VTK12-25	3.5	15	3.9
18VTK9-68	3.5	15	2.5
18VTK10-133	3.0	15	4.2
VA21W-18	4.5	22	4.5
18VTK18-112	3.0	25	3.1
VA21W-53	5.5+	32	6.8
VA21W-52	2.5	15	5.0
18VTK5-149	2.5	12	1.8
VA21W-124	3.5	28	5.0
VA21FHB-24	4.5	30	1.8
18VTK15-79	3.5	52	3.0
VA20W-191	4.5	38	9.6+
19VT1FHB_DH-147	3.5	72+	11.3+
VA21W-111	3.0	22	7.3
DH15SRW65-53	4.0	20	6.2
VA21W-126	3.0	12	3.8
VA21W-188	2.5	18	4.0
VA21W-178	4.0	25	1.9
VA21W-77	4.0	28	6.0
18VTK12-90	2.0	18	4.1
18VTK17-33	2.0	62+	4.4
VA19W-89	2.5	20	5.1
18VTK17-15	4.0	62+	8.3
VA21W-14	4.5	30	3.8
18VTK18-79	2.0	38	6.3
17VDH-SRW05-223	3.0	25	7.1
VA19W-46	4.0	40	5.5
mean	3.5	30	5.0
LSD	1.5	31	3.8
CV	22.1	52	38.4

continued ...

A plus or minus sign indicates a performance significantly above or below the test average.

The 0-9 ratings indicate a genotype's response to disease or lodging where 0 = highly resistant and 9 = highly susceptible.

Parentheses below column headings indicate the number of site-years in which data were collected.

Line	FHBPlant Response	FDKFusarium DiseasedKernels	DON
DH17SRW136-026	4.0	22	5.5
VA21W-60	1.5-	28	2.7
18VTK7-14	3.0	40	6.7
19VT1FHB_DH-77	3.5	15	3.4
18VDH-FHB-MAS06-141-27	3.5	32	2.5
18VTK18-114	4.0	22	6.2
DH16-SRW123-029	4.5	38	5.9
18VTK13-112	3.5	38	4.3
18VDH-FHB-MAS15-367-09	4.0	28	4.2
VA21W-177	3.5	48	4.0
19VT1FHB_DH-210	3.5	22	3.2
19VT1FHB_DH-241	2.5	6	1.1-
18VTK17-106	4.5	45	6.5
16VDH-FHB-MAS60-7-03	2.5	22	3.1
18VTK17-123	3.0	28	3.7
19VT1FHB_DH-74	2.0	25	4.8
18VTK18-49	3.0	38	4.6
18VTK18-159	4.0	58	4.4
VA20W-193	4.5	65+	12.0+
VA21W-84	4.0	35	5.7
18VTK5-147	4.5	40	4.5
VA21W-182	4.0	30	3.5
VA21W-116	3.5	18	5.1
VA21W-56	4.5	48	5.9
18VTK12-91	2.5	15	4.4
VA21W-15	5.0	45	10.0+
19VT3FHB_DH-25	3.0	38	5.1
USG3316	3.5	40	10.1+
19VT1FHB_DH-21	2.5	18	3.7
19VT1FHB_DH-170	4.0	8	2.6
USG3118	4.5	25	3.4
VA21W-194	2.5	25	4.7
VA21FHB-8	1.5-	15	2.4
18VDH-FHB-MAS06-141-31	3.0	25	4.0
18VTK16-192	3.5	65+	6.1
VA21W-28	2.0	8	0.8-
18VTK18-81	6.0+	78+	10.1+
mean	3.5	30	5.0
LSD	1.5	31	3.8
CV	22.1	52	38.4

continued ...

A plus or minus sign indicates a performance significantly above or below the test average.

The 0-9 ratings indicate a genotype's response to disease or lodging where 0 = highly resistant and 9 = highly susceptible.

Parentheses below column headings indicate the number of site-years in which data were collected.

Line	FHBPlant Response	FDKFusarium DiseasedKernels	DON
17VTK20-2	3.0	40	8.9+
VA21W-181	3.0	25	3.5
VA21W-176	2.0	28	3.0
19VT1FHB_DH-139	2.5	18	4.2
19VT1FHB_DH-163	4.0	8	1.7
16VT07-5-4-3	1.0-	20	1.3
18VTK18-65	4.0	48	3.7
VA21FHB-25	2.5	16	2.6
VA21W-48	5.0	52	8.4
VA21W-17	4.5	38	6.3
VA21W-12	2.5	28	7.7
VA21W-196	3.5	20	2.7
VA21FHB-11	3.0	10	3.4
17VDH-SRW03-266	2.5	32	5.2
VA21W-47	3.5	62+	9.4+
COKER9835	8.0+	60	14.0+
17VTK18-18	3.0	24	3.8
17VTK4-92	3.0	25	1.1-
17VTK6-54	3.5	10	2.1
VA21FHB-12	2.5	22	2.3
18VTK5-186	2.5	25	7.6
VA21FHB-13	5.0	20	5.9
17VTK2-25	3.5	25	6.6
16YR0106-5-2	6.0+	45	5.2
18VTK13-52	3.5	38	4.7
16VT51-4-7-2	3.5	40	2.3
VA21FHB-22	3.0	30	1.5
VA21W-51	5.0	48	5.5
17VDH-SRW01-112	2.5	18	4.6
PIONEER26R46	7.0+	38	17.2+
VA21W-71	6.5+	20	1.5
VA21W-69	5.5+	48	3.1
VA21W-175	3.0	22	3.6
VA21W-174	3.0	18	3.8
18VTK16-57	3.0	62+	8.3
18VTK17-163	3.0	28	3.5
VA21W-16	6.0+	30	4.1
mean	3.5	30	5.0
LSD	1.5	31	3.8
CV	22.1	52	38.4

continued ...

A plus or minus sign indicates a performance significantly above or below the test average.

The 0-9 ratings indicate a genotype's response to disease or lodging where 0 = highly resistant and 9 = highly susceptible.

Parentheses below column headings indicate the number of site-years in which data were collected.

Line	FHBPlant Response	FDKFusarium DiseasedKernels	DON
VA21W-49	5.0	30	5.1
DH17SRW136-025	6.5+	25	5.8
19VT1FHB_DH-62	1.5-	18	0.8-
19VT1FHB_DH-80	2.5	15	2.0
JAMESTOWN	3.0	25	3.4
18VTK5-133	4.0	45	8.8
VA20W-172	5.0	22	4.2
18VTK13-4	2.5	35	2.7
DH16-SRW120-019	5.5+	58	9.2+
VA21W-61	4.0	32	3.6
19VT1FHB_DH-76	2.0	8	3.5
18VTK18-123	3.5	30	2.0
VA21W-198	3.0	18	3.4
VA21W-50	2.0	28	7.2
VA21W-121	5.0	35	4.1
VA21W-123	3.5	45	3.5
18VTK13-26	4.5	28	4.1
mean	3.5	30	5.0
LSD	1.5	31	3.8
CV	22.1	52	38.4

A plus or minus sign indicates a performance significantly above or below the test average.

The 0-9 ratings indicate a genotype's response to disease or lodging where 0 = highly resistant and 9 = highly susceptible.

Parentheses below column headings indicate the number of site-years in which data were collected.

Table 4: Performance of varieties and breeding lines in the 2022 State Barley Variety Trial for fusarium head blight (FHB; scab) evaluated in a misted, inoculated nursery in Warsaw VA.

Line	FHBPlant Response 0-9	FDKFusarium DiseasedKernels %	DON ppm
VA20BFHB-18DH442 SA	9.0+	45	19.4
Marouetta	6.0	45	26.7
Secretariat	6.0	40	17.2
Hirondella	7.0	35	57.8
VA18B-34	6.5	40	14.0
VA20B-35 LA	8.0	45	25.0
VA20B-37 LA	7.5	70+	26.8
VA19B-20 LA	9.0+	65	32.7
VA20B-40 LA	6.5	40	28.7
VA18B-39	7.5	30	17.5
VA17B-166 LA	4.5	35	26.1
Thoroughbred	7.0	40	18.3
Atlantic	9.0+	50	27.6
VA18B-23 LA	7.5	55	26.9
VA18B-43 LA	7.5	40	16.0
VA18B-52 LA	7.5	70+	17.1
VA18BFHB-80 LA	8.0	45	21.6
VA18B-33 LA	7.5	45	36.4
VA17B-163 LA	7.5	35	20.6
SB255	7.0	15-	16.3
Barsoy	5.5	35	23.2
BC Fay	4.0	35	33.0
LCS Calypso	4.5	55	18.0
DH142010	3.5-	55	26.2
VA16BFHB-266 NA-19	3.5-	45	13.1
LCS Violetta	5.5	35	32.7
VA16FHB-268NA	3.5-	30	10.5
Avalon	5.5	25	21.3
DH150115	5.5	25	38.3
Flavia	5.0	20	18.9
Nomini	4.0	65	16.7
VA92-42-46	4.5	40	12.8
BC Clementine	6.0	45	22.9
mean	5.9	42	23.1
LSD	2.4	27	
CV	20.3	31	

continued ...

A plus or minus sign indicates a performance significantly above or below the test average.

The 0-9 ratings indicate a genotype's response to disease or lodging where 0 = highly resistant and 9 = highly susceptible.

Parentheses below column headings indicate the number of site-years in which data were collected.

Line	FHBPlant Response	FDKFusarium DiseasedKernels	DON
VA16BFHB-268 NA	5.0	50	20.8
Wysor	4.5	75+	24.9
DH141969	3.5-	25	14.5
Amaze 10	8.0	75+	40.8
DH141515	4.5	40	29.8
VA16BFHB-266 NA-16	4.5	30	14.4
VA16M-84	4.0	30	13.1
VA15H-73	3.0-	20	9.3
mean	5.9	42	23.1
LSD	2.4	27	
CV	20.3	31	

A plus or minus sign indicates a performance significantly above or below the test average.

The 0-9 ratings indicate a genotype's response to disease or lodging where 0 = highly resistant and 9 = highly susceptible.

Parentheses below column headings indicate the number of site-years in which data were collected.

Table 5: Performance of varieties and breeding lines in the 2022 Eastern Malt Barley Trail for fusarium head blight (FHB; scab) evaluated in a misted, inoculated nursery in Warsaw VA.

Line	FHBPlant Response 0-9	FDKFusarium DiseasedKernels %	DON ppm
VA19M-16DH2222 LX	4.5	40	11.4
VA19M-DH161187 LX	5.0	25	7.8
Thoroughbred	5.5	60	18.9
VA18M-DH170740 LX	5.5	70+	24.0
VA19M-17DH0102 LX	7.0+	65	33.7
Hirondella	5.0	55	51.7+
ARS20B55	3.0	30	9.2
ARS20B48	2.5-	30	8.2
VA20MFHB-18DH533	2.5-	20	45.4
VA17M-13DH1720 LX	7.0+	50	36.9
VA20MFHB-18DH548 LX	6.5	35	19.9
ARS20B50	4.5	45	12.1
VA20MFHB-18DH524 LX	6.5	60	41.4
VA19M-16DH2261	6.5	65	17.0
VA19M-DH170735 LA	7.5+	85+	40.9
VA19M-DH170073 LA	8.0+	70+	29.7
VA19M-DH170760 LA	7.0+	45	20.3
VA19M-DH170615 LX	5.0	30	11.1
VA19M-17DH0091 LX	7.0+	50	27.0
VA20MFHB-18DH535	3.0	20	11.3
Calypso	3.5	20	8.3
12W587-n-28	3.0	30	19.4
ARS20B09	3.5	20	22.0
Avalon	3.5	35	14.8
VA20MFHB-18DH349	4.5	55	26.2
ARS15B12	3.5	15	17.3
12W587-n-23	3.5	20	15.3
VA20MFHB-18DH350	5.5	30	22.4
Flavia	6.0	45	26.5
VA20MFHB-18DH541	5.0	55	22.3
VA20MFHB-18DH532	4.0	25	13.6
ARS20B18	4.0	30	11.9
ARS20B45	4.5	35	23.0
mean	4.8	40	21.3
LSD	2.2	26	24.4
CV	22.8	32	56.8

continued . . .

A plus or minus sign indicates a performance significantly above or below the test average.

The 0-9 ratings indicate a genotype's response to disease or lodging where 0 = highly resistant and 9 = highly susceptible.

Parentheses below column headings indicate the number of site-years in which data were collected.

Line	FHBPlant Response	FDKFusarium DiseasedKernels	DON
ARS20B38	4.5	50	31.5
Wintmalt	3.0	25	14.1
Violetta	3.5	25	20.4
ARS20B60	5.0	20	21.8
ARS20B34	4.5	55	16.9
VA18M-DH162217	3.5	45	13.8
VA16M-84	3.0	20	7.2
ARS18B107	6.0	35	29.2
ARS20B15	4.0	40	18.0
mean	4.8	40	21.3
LSD	2.2	26	24.4
CV	22.8	32	56.8

A plus or minus sign indicates a performance significantly above or below the test average.

The 0-9 ratings indicate a genotype's response to disease or lodging where 0 = highly resistant and 9 = highly susceptible.

Parentheses below column headings indicate the number of site-years in which data were collected.

