USDA-ARS/
U.S. Wheat and Barley Scab Initiative
FY16 Final Performance Report
Due date: July 28, 2017

Cover Page

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Fiscal Year:	2016
USDA-ARS Agreement ID:	59-0206-4-032
USDA-ARS Agreement Title:	Mapping and Accelerated Introgression of FHB Resistance into Superior Wheat and Barley Varieties.
FY16 USDA-ARS Award Amount:	$ 159,044
Recipient Organization:	Virginia Polytechnic Institute and State University 1880 Pratt Drive, Suite 2006 Blacksburg, VA 24060
DUNS Number:	003137015
EIN:	54-6001805
Recipient Identifying Number or Account Number:	422419
Project/Grant Reporting Period:	6/17/16 - 6/16/17
Reporting Period End Date:	06/16/17

USWBSI Individual Project(s)

USWBSI Research Category*	Project Title	ARS Award Amount
BAR-CP	Variety Development and Mapping Resistance to FHB and DON in Winter Barley.	$ 48,544
VDHR-SWW	Improving FHB Resistance in SRWW via Breeding, MAS and Mapping in Native Sources.	$ 100,000
VDHR-SWW	Developing Double Haploids to Expedite Variety Development in SRWW.	$ 10,500
	FY16 Total ARS Award Amount	**$ 159,044**

Carl A. Griffey — 7/25/2017

Principal Investigator — Date

* MGMT – FHB Management
FST – Food Safety & Toxicology
GDER – Gene Discovery & Engineering Resistance
PBG – Pathogen Biology & Genetics
EC-HQ – Executive Committee-Headquarters
BAR-CP – Barley Coordinated Project
DUR-CP – Durum Coordinated Project
HWW-CP – Hard Winter Wheat Coordinated Project
VDHR – Variety Development & Uniform Nurseries – Sub categories are below:
SPR – Spring Wheat Region
NWW – Northern Soft Winter Wheat Region
SWW – Southern Soft Red Winter Wheat Region

Project 1: *Variety Development and Mapping Resistance to FHB and DON in Winter Barley.*

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

The primary goal of the project is to evaluate and enhance FHB resistance in commercially viable winter barley cultivars by identifying, mapping, and incorporating unique and/or complementary FHB resistance QTL from different sources using MAS and conventional breeding methods.

2. What was accomplished under these goals? *Address items 1-4) below for each goal or objective.*

1) Major activities

The program continues to develop and advance populations and pure lines derived from crosses between superior winter barley cultivars and lines with FHB resistant varieties from our program and spring barley lines. The program is conducting research to characterize and validate QTL and to identify diagnostic markers for FHB resistance in our barley cultivars Eve and Nomini. Current diagnostic markers for FHB resistance (ten SSR markers each for QTL on chromosomes 2H and 6H) from spring barley along with markers for other diseases (three SNP markers for leaf rust, three SNP markers for powdery mildew, eleven markers for net blotch, three SSR markers for spot blotch), yield (one SNP marker) and quality (one SNP marker) are being used to characterize parents and for MAS in the Virginia Tech barley program.

Breeding populations derived from crosses made with FHB resistance sources (Island, Gen129, AC Alberte, Atahulpa, and Fredrickson) are in advanced generations. This season (2016-17), we evaluated and selected pure lines from nearly 1,700 hulled and hulless FHB headrows at Warsaw, VA. We also evaluated 26 FHB resistant lines in an observation yield trial, and 114 populations were evaluated for FHB resistance in our scab nursery and advanced in the program.

2) Specific objectives

The specific objectives of this project are: 1) to evaluate and characterize FHB resistance in winter barley lines and commercial varieties; 2) to identify and validate FHB resistance QTL from native sources Eve and Nomini and; 3) to deploy MAS to incorporate and pyramid unique and complimentary FHB resistance QTL into adapted lines and varieties.

3) Significant results

A subset of 180 recombinant inbred lines (RIL) from an initial Eve/Doyce population (300 RIL) was phenotyped for FHB in scab nurseries in VA, KY, and NC in 2015 and 2016 (Tables 1 and 2). After harvest each year, fusarium damaged kernels (FDK) and deoxynivalenol (DON) content was assessed in samples from environments having desirable and uniform levels of FHB infection and that displayed significant differences in DON content between resistance and susceptible checks. Significant positive correlations were found between incidence, severity, and DON between the Kentucky and two Virginia locations during both growing seasons.

Parents and RIL of the Eve/Doyce population were genotyped with SNP and SSR markers during 2016 and 2017. Linkage analysis identified a gene region on chromosome 6H associated with

FHB resistance for lower FHB severity, FDK, and reduced DON accumulation (Figure 1). Genes associated with heading date and plant height were also located in the same gene region as those for FHB resistance. Further analysis was conducted to determine if the FHB resistance identified on chromosome 6H was unique to the moderately resistant cultivar Eve. Through this analysis, it was determined that the FHB resistance identified in Eve likely is similar to that previously reported on chromosome 6H.

A Thoroughbred/Nomini mapping population is currently being used to characterize FHB resistance in hulled barley cultivar Nomini. During 2016-17, a set of 180 RIL were planted in scab nurseries at three locations in VA, KY and NC. FHB data was collected in KY and VA (Table 3), but not in NC due to severe flooding in mid-April resulting in the loss of one entire rep and a portion of the second.

A cross was made between Nomini and the elite 2-row winter malt barley cultivar Violetta. The F_1 seed was sent to Dr. Pat Hayes' lab at Oregon State University to develop DH lines. These lines will be phenotyped for FHB during the 2017-18 field season. The population will be genotyped with a 50K SNP chip in collaboration with USDA ARS Genotyping Center at Fargo, ND.

4) Key outcomes or other achievements
Pure lines derived from crosses between known FHB resistant spring barley lines and adapted winter barley lines are being developed and evaluated for FHB resistance and agronomic performance. New SNP markers tightly linked to the FHB resistance QTL on 6H were identified and can be used to incorporate and pyramid FHB resistance genes into adapted cultivars via MAS breeding.

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

The project provided training to MS and BS students on wheat and barley genotyping using SSR and SNP primers. The project provided hands-on training to a graduate student on data analysis using SAS software. The project also gave hands-on training to a graduate student on SNP calling using Genome Studio software as well as analyzing data for QTL mapping using JoinMap, QTL cartographer, and ICIMapping software.

The project also provided professional development by allowing a graduate student to attend the annual USWBSI meeting and participate in poster presentation sessions.

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

Data on FHB incidence, FHB severity, FHB index, and DON accumulation along with standard agronomic traits obtained from Virginia's state hulled and hulless variety trials are reported online (http://www.pubs.ext.vt.edu/CSES/CSES-97/CSES-97.html) and in the extension bulletin CSES-97NP "Small Grains in 2016" to promote selection and production of FHB resistant cultivars. The results on FHB resistant QTL mapping were disseminated through USWBSI annual meetings.

Table 1. Mean FHB Severity, Fusarium damaged kernels (FDK), and Deoxynivalenol (DON) content in parent lines and Eve/Doyce population in KY, NC, and VA in the 2015 season.

Parent Variety	Severity (%)				Fusarium Damaged Kernels (%)			DON (ppm)		
	Kinston, NC	Lexington, KY	Mt. Holly, VA	**Over Locations**	Lexington, KY	Mt. Holly, VA	**Over Locations**	Mt. Holly, VA	Kinston, NC	**Over Locations**
Eve	14.5	18.3	26.6	**19.8**	70.0	78.0	**74.0**	22.1	4.3	**13.2**
Doyce	15.7	19.1	36.1	**23.6**	97.0	88.0	**92.5**	33.8	11.8	**22.8**
Population	16.2	17.4	36.8	**23.5**	92.0	84.0	**88.0**	97.8	9.1	**23.5**
Mean	15.5	18.3	33.2	**22.3**	86.3	83.3	**84.8**	91.2	8.4	**19.8**

Table 2. Mean FHB Severity, Fusarium damaged kernels (FDK), and Deoxynivalenol (DON) content in parent lines Eve and Doyce in KY, NC, and VA in the 2016 season.

Parent Variety	Severity (%)			Fusarium Damaged Kernels (FDK)			DON (ppm)		
	Blacksburg, VA	Lexington, KY	**Over Locations**	Blacksburg, VA	Lexington, KY	**Over Locations**	Blacksburg, VA	Lexington, KY	**Over Locations**
Eve	7.6	25.3	**16.5**	47.9	62.3	**55.1**	2.2	5.9	**4.1**
Doyce	10.2	31.2	**30.7**	61.4	74.4	**67.9**	6.6	16.9	**11.8**
Mean	8.9	28.3	**18.6**	54.7	68.4	**61.5**	4.4	11.4	**7.9**

Table 3. Mean FHB Incidence, Severity and Index values for Thoroughbred/Nomini population in VA and KY in 2017.

Parent Variety	Incidence (%)			Severity (%)			FHB Index (0-100)		
	Mt. Holly, VA	Lexington, KY	**Over Locations**	Mt. Holly, VA	Lexington, KY	**Over Locations**	Mt. Holly, VA	Lexington, KY	**Over Locations**
Thoroughbred	77.5	95.0	**86.3**	16.7	10.0	**13.4**	1.9	9.7	**11.3**
Nomini	66.3	60.0	**63.1**	8.3	8.0	**8.2**	5.6	5.3	**5.5**
Population (N=180)	95.8	78.1	**82.0**	21.0	12.4	**16.7**	18.5	10.3	**14.4**
Mean	76.5	77.7	**77.1**	15.3	10.1	**12.7**	12.3	8.4	**10.4**

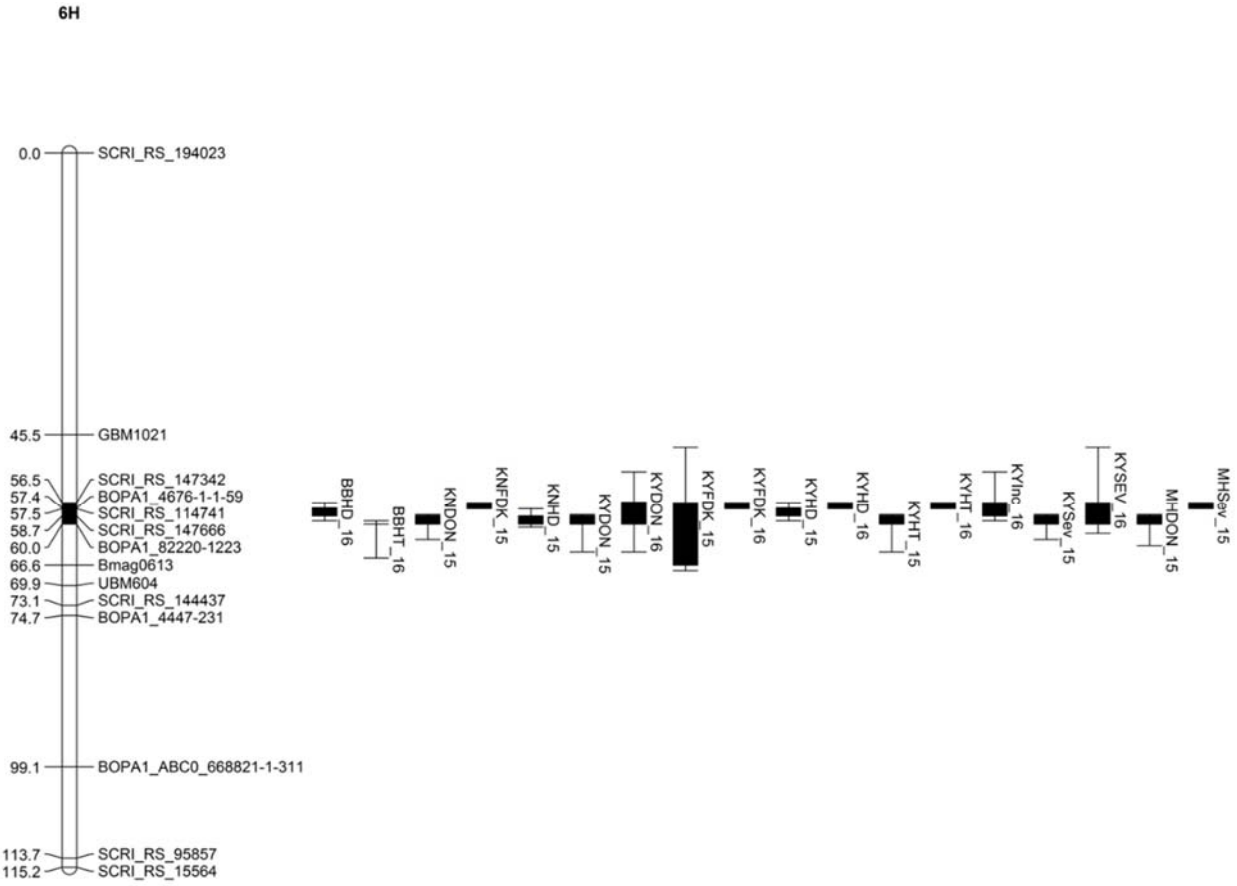

Figure 1. Chromosome map of 6H, derived from the moderately resistant parent Eve, identifying the gene region associated with FHB resistance.

Project 2: *Improving FHB Resistance in SRWW via Breeding, MAS and Mapping in Native Sources.*

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

The ultimate goal of the proposed research is to incorporate unique FHB resistance QTL from complementary types and sources of resistance into commercially viable cultivars using Marker Assisted Selection (MAS) and Doubled Haploid (DH) technologies in conjunction with conventional breeding methods. One objective focuses on the phenotypic and genotypic characterization and differentiation of FHB resistance derived from native germplasm and selection and pyramiding of such resistance into adapted lines. A second objective focused on the identification, mapping, validation, and deployment of unique FHB resistance QTL and diagnostic markers in MAS breeding that is critical for accelerating progress and improving selection efficiency in enhancing FHB resistance via gene pyramiding in wheat cultivars.

2. What was accomplished under these goals? *Address items 1-4) below for each goal or objective.*

1) Major activities

FHB resistance in the SRW wheat cultivar Massey was mapped and resistance in Ernie was validated and fine mapped previously in our program. FHB resistance in the SRW Jamestown was mapped to chromosomes 1B and 6A and validated using nested association mapping population, and FHB resistance in the SRW Tribute was mapped to chromosomes 1A and 2A. Molecular markers linked to 15 scab resistance genes located on wheat chromosomes 2D, 3B (Fhb1), and 5A of Ning 7840, 1B and 6A of Jamestown, 1A and 2A of Tribute, 3B and 4B of Ernie, 2B and 3B of Bess, 3B of Massey, and 1A, 4A, and 6A of Neuse are being used to screen parental lines of crosses and in marker-assisted selection to pyramid different FHB resistance genes. MAS enrichment was applied in 13 SRW-FHB populations in 2015 (Table 4) and 13 SRW-FHB populations in 2016 (Table 5). During 2016-17, FHB breeding materials evaluated in scab nursery and/or field tests included: 140 populations, 3,400 headrows, and more than 800 pure lines.

2) Specific objectives

The specific objectives were: 1) to screen, characterize, and identify adapted wheat varieties having resistance to FHB and other prevalent diseases; 2) to identify, map, validate, and deploy unique FHB QTL and diagnostic markers in MAS and DH breeding that is critical for accelerating progress and improving selection efficiency in enhancing FHB resistance via gene pyramiding in wheat cultivars.

3) Significant results

Two QTL on chromosomes 1B and 6A of Jamestown identified in our program are currently being used routinely by the USDA-ARS Genotyping Lab and in other breeding programs. The SRW wheat cultivars Hilliard and L11550 having the FHB resistance QTL on 1B were released in 2015 and 2016, respectively.

Three QTL conferring resistance to FHB in Tribute were mapped to chromosomes 1A, 2A, and 3BSc. Diagnostic markers (1A: IWB62117, IWB65763; 2A: IWB39170; 3BSc: IWB7909, IWB29048) are being used in MAS breeding in the Virginia Tech wheat breeding program.

4) Key outcomes or other achievements
Data on FHB and DON is collected each year on all wheat cultivars and experimental lines included in Virginia's Official Variety Trial and provided to growers and stakeholders in the annual Small Grains bulletin and online. The SRW wheat cultivars Hilliard and L11550, having the FHB resistance QTL on 1B, provide growers with widely adapted and high yielding varieties that also have resistance to other prevalent diseases in the eastern U.S. Identification and validation of QTL in native sources such as Jamestown (1B and 6A), and Tribute (1A, 2A, and 3BSc) has potential to enhance both breeding effectiveness and level of FHB resistance in SRW wheat. These QTL are being used for MAS to enhance scab resistance in wheat breeding programs.

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

The project also provided professional development by allowing a research scientist and post doc to attend and present research results at annual USWBSI meetings.

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

Data on FHB incidence, severity, and index obtained from the Virginia's state wheat variety trial are reported online (http://www.pubs.ext.vt.edu/CSES/CSES-97/CSES-97.html) and in the extension bulletin CSES-97NP "Small Grains in 2016" to promote selection and production of FHB resistant cultivars. Data on seedling resistance to leaf rust, resistance to FHB and other prevalent diseases as well as agronomic traits (e.g. heading date, height, lodging tolerance, yield, and test weight) and quality (samples provided to Soft Wheat Quality Lab) are collected and provided to cooperators in three uniform scab nurseries (SUWWSN, NUWWSN, and PNUWWSN). The results on QTL for FHB resistance mapped in Jamestown and Tribute were disseminated through USWBSI annual meetings and directly implemented by the Genotyping Center.

Table 4. SRW wheat scab top cross populations enriched via MAS in 2015 for DH line development or pedigree advancement in F_2 headrows (2016) and F_3 headrows (2017) at Warsaw, VA

Pop no.	Short Pedigree	Traits for MAS	F_3 Rows Tested in 2017
1	MD08-26-H2-7-12-9 / USG 3555 // VA12W-150	Scab (Fhb1, FHB-2DL, FHB-3BL, FHB-5AS), Leaf rust (Lr24, Lr26, Lr37), Stripe Rust (Yr9, Yr17, Qyr-2AS, Qyr-4BL), Stem rust (Sr24, Sr31, Sr36, Sr38), Mildew (Pm8, APR-PM2B), Quality (2B_QTL)	56
2	MD08-26-H2-7-12-9 / Jamestown // Featherstone 73	Scab (Fhb1, FHB-1B, FHB-2DL, FHB-5AS), Leaf rust (Lr18, Lr24, Lr37), Stripe Rust (Yr17, Qyr-2AS), Stem rust (Sr24, Sr38), Short Vernalization	80
3	MD08-26-H2-7-12-9 / Jamestown // VA12W-54	Scab (Fhb1, FHB-1B, FHB-2DL, FHB-5AS), Leaf rust (Lr18, Lr24, Lr37), Stripe Rust (Yr17, Qyr-2AS), Stem rust (Sr24, Sr38), Short Vernalization	16
4	MD08-26-H2-7-12-9 / 12V51 // VA11W-95	Scab (Fhb1, FHB-2DL, FHB-3BL, FHB-5AS), Leaf rust (Lr9, Lr24, Lr37), Stripe Rust (Yr17, Qyr-2AS, Qyr-4BL), Stem rust (Sr24, Sr38), Short Vernalization	88
5	MD08-26-H2-7-12-9 / 12V51 // VA12W-150	Scab (Fhb1, FHB-2DL, FHB-3BL, FHB-5AS), Leaf rust (Lr9, Lr24, Lr37), Stripe Rust (Yr17, Qyr-2AS, Qyr-4BL), Stem rust (Sr24, Sr38), Short Vernalization	72
6	MD08-26-H2-7-12-9 / Featherstone73 // Hilliard	Scab (Fhb1, FHB-1B, FHB-2DL, FHB-5AS), Leaf rust (Lr9, Lr24, Lr37), Stripe Rust (Yr17, Qyr-2AS, Qyr-4BL), Stem rust (Sr24, Sr38)	40
7	MD08-26-H2-7-12-9 / Featherstone73 // VA12W-54	Scab (Fhb1, FHB-1B, FHB-2DL, FHB-5AS), Leaf rust (Lr9, Lr24, Lr37), Stripe Rust (Yr17, Qyr-2AS, Qyr-4BL), Stem rust (Sr24, Sr38)	0
8	MD08-26-H2-7-12-9 / Featherstone73 // VA12W-150	Scab (Fhb1, FHB-1B, FHB-2DL, FHB-5AS), Leaf rust (Lr9, Lr24, Lr37), Stripe Rust (Yr17, Qyr-2AS, Qyr-4BL), Stem rust (Sr24, Sr38)	16
9	MD08-26-H2-7-12-9 / VA11W-278 // Hilliard	Scab (Fhb1, FHB-2DL, FHB-3BL, FHB-5AS), Leaf rust (Lr9, Lr24, Lr37), Stripe Rust (Yr17, Qyr-2AS, Qyr-4BL, Qyr-6BL), Stem rust (Sr24, Sr38), Mildew (APR-PM2A), Hessian fly (H13)	48
10	MD08-26-H2-7-12-9 / VA11W-278 // VA12W-150	Scab (Fhb1, FHB-2DL, FHB-3BL, FHB-5AS), Leaf rust (Lr9, Lr24, Lr37), Stripe Rust (Yr17, Qyr-2AS, Qyr-4BL, Qyr-6BL), Stem rust (Sr24, Sr38), Mildew (APR-PM2A), Hessian fly (H13)	72
11	MDC07027-12-24 / Hilliard // Featherstone 73	Scab (Fhb1, FHB-1B, FHB-2DL, FHB-5AS), Leaf rust (Lr9, Lr18, Lr24, Lr37), Stripe Rust (Yr17, Qyr-2AS, Qyr-4BL), Stem rust (Sr24, Sr38), Hessian fly (H5)	88
12	MDC07027-12-24 / Hilliard // SS8412	Scab (Fhb1, FHB-1B, FHB-2DL, FHB-5AS), Leaf rust (Lr9, Lr18, Lr24, Lr37), Stripe Rust (Yr17, Qyr-2AS, Qyr-4BL), Stem rust (Sr24, Sr38), Hessian fly (H5)	128
13	MDC07027-12-24 / Hilliard // VA11W-278	Scab (Fhb1, FHB-1B, FHB-2DL, FHB-5AS), Leaf rust (Lr9, Lr18, Lr24, Lr37), Stripe Rust (Yr17, Qyr-2AS, Qyr-4BL), Stem rust (Sr24, Sr38), Hessian fly (H5)	24

Table 5. SRW wheat scab top cross populations enriched via MAS in 2016 for DH line development or pedigree advancement in 2017 (greenhouse) and F_2 headrows in 2018 at Warsaw, VA

Pop No.	Cross Pedigree	Max# FHB QTLs	Marker Traits	No. F_2 Plants
1	NC8248-14 / Jamestown // MDC07026-F2-19-13-1	**6**	**Fhb1, FHB1B_Jtw, FHB3B_Bes, FHB1A_Nse, FHB4A_Nse, FHB6A_Nse, Sbm1, Lr37, Lr/Sr24, Sr36**	105
2	NC8248-14 / Featherstone 73 // MDC07026-F2-19-13-1	**5**	**Fhb1, FHB1B_Jtw, FHB3B_Bes, FHB4A_Nse, FHB6A_Nse, Sbm1, Lr37, Lr9, Lr/Sr24, Sr36**	52
3	NC8248-14 / Hilliard // MDC07026-F2-19-13-1	**5**	**Fhb1, FHB1B_Jtw, FHB3B_Bes, FHB1A_Nse, FHB6A_Nse, Sbm1, Lr37, Lr/Sr24, Sr36**	106
4	NC8248-14 / GA03564-12E6 // MDC07026-F2-19-13-4	**5**	**Fhb1, FHB1B_Jtw, FHB3B_Bes, FHB4A_Nse, FHB6A_Nse, Sbm1, Lr37, Lr/Sr24, Sr36, 1A.1R**	77
5	NC8248-14 / VA12W-54 // MDC07026-F2-19-13-1	**5**	**Fhb1, FHB1B_Jtw, FHB3B_Bes, FHB4A_Nse, FHB6A_Nse, Sbm1, Lr37, Lr/Sr24, Sr36, Lr46, H13**	89
6	NC8248-14 / VA12W-72 // MDC07026-F2-19-13-4	**6**	**Fhb1, FHB1B_Jtw, FHB3B_Bes, FHB3B_Msy, FHB4A_Nse, FHB6A_Nse, Sbm1, Lr37, Lr/Sr24, Sr36**	72
7	NC8248-14 / MDC07026-F2-19-13-4 // VA11W-108PA	**5**	**Fhb1, FHB1B_Jtw, FHB3B_Bes, FHB4A_Nse, FHB6A_Nse, Sbm1, Lr37, Lr/Sr24, Sr36**	20
8	NC8248-14 / MDC07026-F2-19-13-4 // VA11W-279	**6**	**Fhb1, FHB1B_Jtw, FHB3B_Msy, FHB4A_Nse, FHB1A_Nse, FHB6A_Nse, Sbm1, Lr37, Lr/Sr24, Sr36, H13**	21
9	NC8248-14 / MDC07026-F2-19-13-4 // VA12W-72	**5**	**Fhb1 or FHB3B_Bes, FHB1B_Jtw, FHB3B_Msy, FHB4A_Nse, FHB6A_Nse, Sbm1, Lr37, Lr/Sr24, Sr36, Lr46, H13**	20
10	NC8248-14 / MDC07026-F2-19-13-4 // TXGA06343-17-3-5-EL2	**4**	**Fhb1, FHB1B_Jtw, FHB3B_Bes, FHB4A_Nse, FHB6A_Nse, Sbm1, Lr37, Lr/Sr24, Sr36**	15
11	NC8248-14 / MDC07026-F2-19-13-4 // VA14FHB-28	**5**	**Fhb1, FHB1B_Jtw, FHB3B_Bes, FHB4A_Nse, FHB6A_Nse, Sbm1_het, Lr37, Lr/Sr24, Sr36**	14
12	NC8248-14 / MDC07026-F2-19-13-4 // VA07MAS3-7304-3-2-4-3	**5**	**Fhb1, FHB1B_Jtw, FHB3B_Bes, FHB4A_Nse, FHB6A_Nse, Sbm1_het, Lr37, Lr/Sr24, Sr36**	16
13	NC8248-14 / MDC07026-F2-19-13-4 // VA09MAS6-122-7-1	**4**	**Fhb1, FHB1B_Jtw, FHB3B_Bes, FHB4A_Nse, FHB6A_Nse, Sbm1_het, Lr37, Lr/Sr24, Sr36**	11

Project 3: *Developing Double Haploids to Expedite Variety Development in SRWW.*

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

One of the main objectives of the VDHR research area is to increase the efficiency of coordinated project breeding programs in developing and releasing FHB-resistant varieties. Doubled haploids (DH) shorten variety development time in fall-sown small grains by approximately three years.

2. What was accomplished under these goals? *Address items 1-4) below for each goal or objective.*

1) Major activities

Research is focused on shortening breeding cycles through the development of doubled haploid populations and enhancing FHB resistance via MAS breeding efforts in selection of parents, designing crosses, gene introgression and pyramiding, population enrichment, and selection of pure lines. Marker haplotypes of parents for validated FHB resistance QTL and other traits of importance such as dwarfing genes, disease and insect resistance, rye translocations, and quality are being assessed and utilized to enhance breeding efficiency. Molecular markers linked to 15 scab resistance genes located on wheat chromosomes 2D, 3B (Fhb1), and 5A of Ning 7840, 1B and 6A of Jamestown, 1A and 2A of Tribute, 3B and 4B of Ernie, 2B and 3B of Bess, 3B of Massey, and 1A, 4A, and 6A of Neuse are being used to screen parental lines of crosses and in marker-assisted selection to pyramid different FHB resistance genes. Marker assisted selection (MAS) was applied in 13 SRW-FHB top cross populations in 2015 and 2016 (See Tables 4 and 5 above). Individual plants having multiple FHB resistance QTL and other traits of interest were delivered to Heartland Plant Innovations for development of DH lines. Other MAS plants were grown out in the greenhouse and are being advance in our breeding program using the Pedigree method. Lines selected from DH populations will be shared with and evaluated in breeding programs in AR, GA, KY, LA, NC, and VA.

2) Specific objectives

The specific objective is to shorten variety development time and enhance FHB resistance and other critical traits in SRW wheat cultivars by deploying a combination of MAS and DH breeding methods.

3) Significant results

<u>Accomplishment:</u>

Virginia Tech FHB-DH lines developed as part of USWBSI include 3 DH lines in Virginia's 2017 Advance test, 5 lines in the Preliminary test, and 317 lines in an Observation test.

Twenty five superior DH lines derived from crosses having *Fhb1* and other QTL (Jamestown FHB-1B) were selected among headrows of three populations (MD03W61-09-7/Jamestown// GA04570-10E46, MD03-69-15/Yorktown, and Pioneer 25R32/ GA001138-8E36//VA09W-73) evaluated in the field at Warsaw, VA in 2014. These lines were evaluated in observation yield tests at two locations in Virginia in 2015. Seed of superior lines were provided to other cooperating breeding programs in 2016.

New DH lines being developed will have diverse pyramids of FHB resistance genes including *Fhb1* and QTL on chromosomes 2DL, 5AS (Ning 7840), 1B (Jamestown) 1A and 2A of Tribute, 3B and 4B of Ernie, 2B and 3B of Bess, 3B of Massey, and 1A, 4A, and 6A of Neuse combined with other favorable traits. Approximately 921 plants from 13 populations (see Table 6 below) were sent to the USDA-ARS Genotyping Lab in Raleigh, NC where MAS was applied for multiple FHB resistance genes/QTL and other traits of interest (see Table 4 above). The DH lines were grown and evaluated during 2015-16 at Griffin, GA. In fall 2016, we distributed seed of 750 of these FHB-MAS derived DH lines to breeders at University of Arkansas, University of Kentucky, Ohio State University, NCSU, and LSU. We also sent vernalized plants from FHB-MAS populations (see Table 5 above) to Heartland Plant Innovations to develop DH lines for VA (34 plants), LSU (15 plants), University of Arkansas (10 plants), University of Georgia (16 plants), NCSU (13 plants), and University of Kentucky (17 plants).

Table 6. Number of FHB-MAS double haploids generated from wheat crosses in 2015

Cross	No. Doubled Haploids
MD08-26-H2-7-12-9/USG 3555//VA12W-150	131
MD08-26-H2-7-12-9/Jamestown//VA09W-73	81
MD08-26-H2-7-12-9/12V51//VA11W-95	34
VA11W-95//MD08-26-H2-7-12-9/12V51	103
MD08-26-H2-7-12-9/12V51//VA12W-150	125
MD08-26-H2-7-12-9/VA09W-73//VA12W-54	43
MD08-26-H2-7-12-9/VA09W-73//VA12W-150	44
MD08-26-H2-7-12-9/VA11W-278//VA11W-108	164
VA11W-108//MD08-26-H2-7-12-9/VA11W-278	70
VA12W-150//MD08-26-H2-7-12-9/VA11W-278	18
MD08-26-H2-7-12-9/VA11W-278//VA12W-150	58
MDC07027-12-24/VA11W-108//VA11W-278	50
Total Number of Doubled Haploid Lines	**921**

4) Key outcomes or other achievements
Elite FHB-MAS derived doubled haploid lines are currently being evaluated in replicated yield trials. A set of 750 FHB-MAS derived DH lines was distributed to cooperators in 2016 and were evaluated in 7 breeding programs in 2017. A set of 105 vernalized plants selected on the basis of MAS for multiple FHB resistance gene/QTL and other critical traits where delivered to Heartland Plant Innovations in 2016 to develop DH lines for 6 breeding programs to evaluate in 2017-18.

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

This research project has provided training and hands on experience to several program personnel including a post doc, several research scientists and specialists, and several graduate and undergraduate students.

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

The FHB-MAS method used by our program to develop and select plants from large top-cross populations for development of DH lines or pure lines advanced using a pedigree method was endorsed by other cooperating breeding programs. To date, our program has provided more than 800 FHB-MAS selected plants and DH lines to cooperating programs.

Training of Next Generation Scientists

Instructions: Please answer the following questions as it pertains to the FY16 award period. The term "support" below includes any level of benefit to the student, ranging from full stipend plus tuition to the situation where the student's stipend was paid from other funds, but who learned how to rate scab in a misted nursery paid for by the USWBSI, and anything in between.

1. **Did any graduate students in your research program supported by funding from your USWBSI grant earn their MS degree during the FY16 award period?** Yes

   If yes, how many? 1

2. **Did any graduate students in your research program supported by funding from your USWBSI grant earn their Ph.D. degree during the FY16 award period?** No

   If yes, how many?

3. **Have any post docs who worked for you during the FY16 award period and were supported by funding from your USWBSI grant taken faculty positions with universities?** No

   If yes, how many?

4. **Have any post docs who worked for you during the FY16 award period and were supported by funding from your USWBSI grant gone on to take positions with private ag-related companies or federal agencies?** No

   If yes, how many?

Release of Germplasm/Cultivars

Instructions: In the table below, list all germplasm and/or cultivars released with full or partial support through the USWBSI during the FY16 award period. All columns must be completed for each listed germplasm/cultivar. Use the key below the table for Grain Class abbreviations.
Leave blank if you have nothing to report or if your grant did NOT include any VDHR-related projects.

Name of Germplasm/Cultivar	Grain Class	FHB Resistance (S, MS, MR, R, where R represents your most resistant check)	FHB Rating: VA-OVT (0-9)	Year Released
L11550 (VA11W-106)	SRW	MR	2	2016
VA11W-279	SRW	MR	2	2016
VA12W-72	SRW	MR	1	2016
Vision 50 (VA09HRW-64)	HRW	MR	1	2016

Add rows if needed.

NOTE: List the associated release notice or publication under the appropriate sub-section in the 'Publications' section of the FPR.

Abbreviations for Grain Classes

Barley - BAR
Durum - DUR
Hard Red Winter - HRW
Hard White Winter - HWW
Hard Red Spring - HRS
Soft Red Winter - SRW
Soft White Winter - SWW

Publications, Conference Papers, and Presentations

Instructions: Refer to the FY16-FPR_Instructions for detailed instructions for listing publications/presentations about your work that resulted from all of the projects included in the FY16 grant. Only include citations for publications submitted or presentations given during your award period (6/17/16 - 6/16/17). If you did not have any publications or presentations, state 'Nothing to Report' directly above the Journal publications section.

Journal publications.

Brooks, W. S., M. E. Vaughn, G. L. Berger, C. A. Griffey, W. E. Thomason, R. M. Pitman, S. Malla, J. E. Seago, D. W. Dunaway, E. G. Rucker, H. D. Behl, B. R. Beahm, P. W. Browning, Jr., D. G. Schmale III, N. McMaster, T. Hardiman, J. T. Custis, D. E. Starner, S. A. Gulick, S. R. Ashburn, E. H. Jones Jr., D. S. Marshall, M. O. Fountain, T. D. Tuong, M. J. Kurantz, R. A. Moreau, and K. B. Hicks. 2016. Registration of 'Secretariat' Winter Barley. J. of Plant Registrations 10:217-222. doi:10.3198/jpr2016.03.0017crc.
Status: Paper Published
Acknowledgement of Federal Support: YES (paper)

Books or other non-periodical, one-time publications.

Ullrich, J. 2016. Quantitative Trait Loci for Resistance to Fusarium Head Blight in the Hulless Winter Barley Cultivar Eve. M.S. Thesis. Virginia Tech, Dec. 2016.

Other publications, conference papers and presentations.

Ullrich, J. and N. Carpenter. 2016. Characterization and Mapping Native Scab Resistance in Barley Varieties. Annual Meeting of Virginia Small Grains Board. Richmond, VA, July 2016.
Status: Oral Presentation delivered
Acknowledgement of Federal Support: YES (presentation)

Ullrich, J., S. Malla, C. Griffey, W. Brooks, D. Van Sanford, A. Clark, P. Murphy, R. Brueggeman, C. Cowger, G. Brown-Guedira, N. McMaster, D. Schmale III, and S. Chao. 2016. Evaluation of two winter barley mapping populations for resistance to Fusarium Head Blight. NAPB Conference. Raleigh, NC, August 15-18, 2016.
Status: Abstract Published and Poster Presented
Acknowledgement of Federal Support: YES (poster), NO (abstract)

Ullrich, J, S. Malla, C. Griffey, N. Carpenter*, W. Brooks, D. Van Sanford, A. Clark, J.P. Murphy, R. Brueggeman, C. Cowger, N. McMaster, D. Schmale III, S. Chao, and G. Brown-Guedira. 2016. "Evaluation of the Winter Barley Cultivar Eve for Quantitative Resistance to Fusarium Head Blight. "In: S. Canty, A. Clark, K. Wolfe, and D. Van Sanford (Eds.), *Proceedings of the 2016 National Fusarium Head Blight Forum* (p. 101). East Lansing, MI / Lexington, KY: U.S. Wheat and Barley Scab Initiative.
Status: Abstract Published and Poster Presented
Acknowledgement of Federal Support: YES (poster), YES (abstract)