

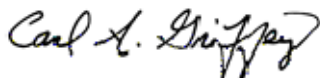
**USDA-ARS/  
U.S. Wheat and Barley Scab Initiative  
FY15 Final Performance Report  
Due date: July 15, 2016**

**Cover Page**

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<b>Fiscal Year:</b>	2015
<b>USDA-ARS Agreement ID:</b>	59-0206-4-032
<b>USDA-ARS Agreement Title:</b>	Mapping and Accelerated Introgression of FHB Resistance into Superior Wheat and Barley Varieties.
<b>FY15 USDA-ARS Award Amount:</b>	\$ 183,313
<b>Recipient Organization:</b>	Virginia Polytechnic Institute and State University 1880 Pratt Drive, Suite 2006 Blacksburg, VA 24060
<b>DUNS Number:</b>	003137015
<b>EIN:</b>	54-6001805
<b>Recipient Identifying Number or Account Number:</b>	422419
<b>Project/Grant Reporting Period:</b>	06/17/15-06/16/16
<b>Reporting Period End Date:</b>	06/16/16

**USWBSI Individual Project(s)**

<b>USWBSI Research Category*</b>	<b>Project Title</b>	<b>ARS Award Amount</b>
BAR-CP	Variety Development, Selection, and Characterization of Resistance to FHB and DON in Winter Barley.	\$ 57,337
VDHR-SWW	Improving FHB Resistance in SRW Wheat via Integrated Mapping, Phenotypic and MAS.	\$ 110,787
VDHR-SWW	Developing Doubled Haploids to Expedite Variety Development in SRWW.	\$ 15,189
	<b>FY15 Total ARS Award Amount</b>	<b>\$ 183,313</b>



Principal Investigator

7/12/16

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, Selection, and Characterization of 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 enhance the FHB resistance in commercially viable winter barley cultivars by incorporating unique and/or complementary FHB QTL from different resistance sources using MAS and conventional breeding methods.

**2. What was accomplished under these goals?**

1) major activities

Scab is a perpetual problem for barley growers and end users in Virginia, and epidemics such as that occurring in 2013 and prior years not only reduce yields and quality, but also reduce barley's marketability due to low test weights and DON toxin. As in the past several years, we have developed and advanced populations and pure lines derived from crosses between superior winter barley breeding lines and cultivars from our program with FHB resistant spring barley lines. However, the FHB resistant spring barley lines are not adapted to our environment and lack resistance to other prevalent diseases. Thus, the program has more recently initiated research to characterize and validate QTL and to identify diagnostic markers for FHB resistance in our native barley sources. 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 for MAS in the Virginia Tech barley program. The program is also characterizing FHB resistance in native cultivar Eve and Nomini.

Breeding populations derived from crosses made with FHB resistance sources (AC Alberte, Atahulpa, MN Brite, and Fredrickson) are in advanced generations. This season (2015-16), three elite FHB resistant barley lines were evaluated in Virginia's State Variety Trial, three advanced FHB resistant lines were evaluated in a preliminary yield test, 58 FHB resistant lines were tested in an observation yield trial, and 78 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 characterize FHB resistance in native (hulled and hullless) barley genotypes; 2) to utilize the native FHB resistance through selection and pyramiding such resistance into the adapted lines; 3) to validate and identify diagnostic markers for known unique FHB resistant QTL to be used in the MAS breeding; 4) to identify, validate, and deploy the FHB resistant QTL from native sources.

3) significant results

Mapping populations to characterize FHB resistance in the winter barley cultivar Eve were developed in our program. About 300 recombinant inbred lines (RIL) each for the populations Eve/Doyce and Eve/VA07H-35WS were phenotyped in 2015 for FHB in VA (two locations), KY (one location), NC (two locations), and in the scab nursery in Nanjing, China (one location) in 2015. The population size was reduced based on 2015 phenotypic data to 180 RIL for each population for FHB evaluation in 2016. The populations were planted in 2016 for evaluation of FHB in VA (two locations), KY (one location), and NC (one location). All 180 RIL from Eve/VA07H-35WS and 48 RIL (24 RIL from susceptible tail and 24 RIL from resistant tail) from Eve/Doyce were genotyped with 9K iSelect SNP at USDA ARS Genotyping Center at Fargo, ND in summer 2016. In Eve/VA07H-35WS mapping population, preliminary single marker analysis showed that markers on all barley chromosomes were significant ( $P < 0.01$ ) for FHB traits (phenotyping from 2015). Markers on barley chromosome 2H (bin 8) were highly significant ( $P < 0.001$ ) for FHB Severity at Kingston, NC. In Eve/Doyce mapping population, preliminary single marker analysis showed that markers on all barley chromosomes except 3H were significant ( $P < 0.01$ ) for 2015 FHB traits. A marker on chromosome 6H was highly significant ( $P < 0.001$ ) for DON content and FHB severity at Mt. Holly, VA as well as DON content and Fusarium damaged kernel percent at Kingston, NC. A comprehensive interval mapping analysis will be conducted in the populations to identify and validate FHB resistance QTL in native FHB resistant cultivar Eve. Diagnostic marker for FHB resistance QTL will be identified and utilized in MAS in Virginia Tech barley breeding program.

A RIL mapping population (Nomini/Thoroughbred) was developed to characterize FHB resistance in the winter barley cultivar Nomini at Virginia Tech. Due to low amount of seed for the population, RIL was only evaluated for FHB resistance in VA (one location). Seed of RILs in the population was increased in 2016. A DH mapping population from Nomini/Violetta is being developed in our program in collaboration with Oregon State University. Mapping populations will be phenotyped in 2016-2017 season. The population will be genotyped in house and with 50K SNP in collaboration with USDA ARS Genotyping Center at Fargo, ND.

#### 4) key outcomes or other achievements

We have continued to make progress improving resistance to FHB in the breeding program. Pure lines from populations derived from crosses between known FHB resistant spring barley lines and adapted winter barley lines are being evaluated for FHB resistance and agronomic performance. This season (2015-16), three elite FHB resistant barley lines were evaluated in Virginia's Official Variety Trial (OVT).

Preliminary single marker analysis showed that markers on barley chromosome 2H and 6H were significant ( $P < 0.001$ ) for FHB traits in Eve mapping populations. First year results will be validated with second year's phenotypic data and diagnostic marker associated with FHB resistant QTL will be identified to be utilized in MAS in VT barley breeding program.

**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 VT CSES graduate poster session.

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

Data on FHB incidence, FHB severity, FHB index, 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 2014" to promote selection and production of FHB resistant cultivars. The results on FHB resistant QTL mapping were disseminated through USWBSI annual meeting.

**Project 2: Improving FHB Resistance in SRW Wheat via Integrated Mapping, Phenotypic and MAS.**

**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 focuses on the identification, mapping, validation, and deployment of unique FHB 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?**

1) major activities

Development of competitive wheat cultivars having FHB resistance derived from exotic sources, such as *Fhb1* derived from Sumai 3, has been hindered by linkage drag. In addition, progress has been hindered by the lack of adequate characterization and validation of FHB resistance in adapted native sources and unavailability of diagnostic markers needed to implement marker assisted incorporation and pyramiding of diverse QTL for FHB resistance. 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 wheat cultivar Jamestown was mapped and validated using nested association mapping population and FHB resistance in the SRW wheat cultivar Tribute was also mapped in our program. Marker assisted selection (MAS) is being used to both enhance the level of scab resistance and to accelerate the development of superior scab resistant cultivars. Markers linked to scab resistance genes located on wheat chromosomes 3BS (*Fhb1*) 2D, and 5AS of Ning 7840 (Sumai 3 derivative), 2B, 3BSc, 4B and 5A of Ernie, 3BSc of Massey, 1B of Jamestown and 1A, 2A, 3BSc of Tribute are being used to screen, characterize and select parents and their progeny for scab resistance genes. Twelve top cross populations developed between 2008 and 2010 with either Ernie or Ning 7840 (or other Sumai3 derivatives) in their pedigrees were screened via MAS to enrich FHB resistance in these breeding populations. In 2016, FHB breeding materials evaluated in scab nursery and/or field tests included: 176 populations, 8000 headrows, and more than 800 pure lines.

2) specific objectives

The specific objectives are: 1) to characterize and differentiate FHB resistance derived from native germplasm and selection and pyramiding of such resistance into adapted lines; 2) to identify, map, validate, and deploy unique FHB 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.

3) significant results

A QTL for FHB resistance on chromosome 1B in a Pioneer 25R47/Jamestown (P47/JT) mapping population was validated in FG95195/Jamestown (FG/JT) and Jamestown/LA97UC113-124 (JT/LA) populations. Markers Xwmc500 (SSR marker) and Kukri\_c31554\_437 (SNP marker) are diagnostic markers for the QTL on chromosome 1B. Other minor QTL on 2B and 6A act synergistically to produce a major effect. The diagnostic markers Wmc500 and Kukri\_c31554\_437 for QTL on chromosome 1B are being used in MAS in the Virginia Tech wheat breeding program and USDA-ARS genotyping center at Raleigh, NC. The SRW wheat cultivar Hilliard having the FHB resistance QTL on 1B was released in 2015.

During 2012-2013 and 2013-2014, phenotypic data was collected in a Pioneer26R46/Tribute double haploid (DH) population in AR (Milus), KY (Van Sanford), NC (Murphy), MD (Costa), and VA (Griffey). Three consistent QTL were observed on chromosome 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 cultivar Hilliard, having the FHB resistance QTL on 1B, provides growers with a widely adapted and high yielding variety that also has resistance to other prevalent diseases in the eastern U.S. Identification and validation of consistent QTL in native sources such as Ernie (on chromosomes 2B, 3BSc, 4B, and 5A), Massey (3BSc), Jamestown (1B), 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 to attend annual USWBSI meeting.

**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 2014" to promote selection and production of FHB resistant cultivars. The results on FHB resistant QTL mapping were disseminated through USWBSI annual meeting.

**Project 3:** *Developing Doubled 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?**

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. Markers linked to scab resistance genes located on wheat chromosomes 1B of Jamestown, 2DL, 3BS (*Fhb1*) and 5AS of Ning 7840 (Sumai 3 derivative), 2B, 3BSc, 4B and 5A of Ernie are being used to screen, characterize and select parents and their progeny for scab resistance genes. Seven crosses were made to pyramid *Fhb1*, and QTL on chromosomes 5AS, 2DL, and 3BSc (Ernie) in spring 2014. Doubled haploid populations were developed at Heartland Plant Innovations and are being evaluated in yield trials and the scab nursery. 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 in fall-sown small grains by approximately four years.

3) significant results

**Accomplishment:**

A top cross (MD03W61-09-7 (*Fhb1*) / Jamestown (QTL on 1B) // GA04570-10E46) was made in spring 2013. The doubled haploid (DH) population consisting of 250 lines was developed at Heartland Plant Innovations in Manhattan, KS in 2013. The DH lines were genotyped for the 1B QTL of Jamestown, *Fhb1*, *Lr9*, *Sbm1*, and 1B.1R in our lab and evaluated in headrows at Warsaw in 2014. Selected DH lines were shared with other cooperators. The DH lines from a single cross MDC07027-12-24 (QTL on 2DL, 3BS (*Fhb1*) and 5AS from Ning 7840) / Hilliard (QTL on 1B) were developed by Heartland in 2015 and were evaluated in headrows at Warsaw, VA in 2016. Selected lines will be genotyped and subsequently shared with cooperators.

Approximately 921 plants were developed for 12 populations in which USDA ARS Genotyping Lab, Raleigh, NC made marker assisted selection on multiple FHB resistance genes/QTL and other traits of interest (Table 1). DH lines derived from these populations were grown and harvested by Jerry Johnson at Griffin, GA in 2016, and seed will be shared with cooperators this fall.

**Table 1.** List of number of double haploids generated from wheat crosses.

<b>Cross</b>	<b>No. Doubled Haploids</b>
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
<b>Total Number of Doubled Haploid Lines</b>	<b>921</b>

4) key outcomes or other achievements

A total of 200 DH lines from the cross MDC07027-12-24/Hilliard(VA11W-108) were evaluated at Warsaw, VA in 2016. Selected lines from the cross will be genotyped and subsequently shared with cooperators.

A total of 921 DH lines from 12 crosses were grown for seed increases. The DH lines will be shared with cooperators for evaluation in 2017.



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

The project has facilitated exchange of knowledge and FHB resistant germplasm among cooperating breeding programs and the genotyping center as well as strategies most likely to accelerate development of FHB resistant varieties.

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

Information on FHB resistance and DH lines developed through this program have been shared with cooperators. Seven DH lines developed and selected at Virginia Tech from the cross MD03W61-09-7 / Jamestown // GA04570-10E46, having Fhb1 or the Jamestown FHB resistance QTL on 1B, were shared with cooperators in fall 2015.

### **Training of Next Generation Scientists**

**Instructions:** Please answer the following questions as it pertains to the FY15 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 FY15 award period?**  
Yes.  
**If yes, how many?**  
One.
  
- 2. Did any graduate students in your research program supported by funding from your USWBSI grant earn their Ph.D. degree during the FY15 award period?**  
No.  
**If yes, how many?**
  
- 3. Have any post docs who worked for you during the FY15 award period and were supported by funding from your USWBSI grant taken faculty positions with universities?**  
Yes.  
**If yes, how many?**  
One.
  
- 4. Have any post docs who worked for you during the FY15 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 FY15 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 (0-9)	Year Released
Hilliard	SRW	MR	3	2015
VA10W-96	SRW	MR	3	2016
VA10W-119	SRW	MR	4	2016
VA11W-106	SRW	MR	4	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

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## **Publications, Conference Papers, and Presentations**

Refer to the FY15-FPR\_Instructions for listing publications/presentations about your work that resulted from all of the projects included in the FY15 grant. If you did not have any publications or presentations, state 'Nothing to Report' directly above the Journal publications section.

### **Journal publications.**

Nothing to Report

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

Nothing to Report

### **Other publications, conference papers and presentations.**

Malla, S., C. Griffey, J.P. Murphy, E. Milus, A. Clark, D. Van Sanford, J. Costa, N. McMaster, D. Schmale III, S. Chao, and G. Brown-Guedira. 2015. Characterization of FHB resistance QTL in SRW Wheat Cultivar Tribute. In: S. Canty, Clark, S. Vukasovich and D. Van Sanford (Eds.), *Proceedings of the 2015 National Fusarium Head Blight Forum*. East Lansing, MI/Lexington, KY: U.S. Wheat & Barley Scab Initiative. p. 94.

Status: Abstract Published and Poster Presented

Acknowledgement of Federal Support: Abstract-NO, Poster-YES

Ullrich, J., S. Malla, C. Griffey, W. Brooks, D. Schmale III, N. McMaster, D. Van Sanford, A. Clark, C. Cowger, S. Chao, G. Brown-Guedira, P. Murphy, and R. Brueggeman. 2015. Identification of Quantitative Trait Loci for Resistance to Fusarium Head Blight in Winter Barley Cultivar Eve. In: S. Canty, Clark, S. Vukasovich and D. Van Sanford (Eds.), *Proceedings of the 2015 National Fusarium Head Blight Forum*. East Lansing, MI/Lexington, KY: U.S. Wheat & Barley Scab Initiative. p. 113.

Status: Abstract Published and Poster Presented

Acknowledgement of Federal Support: Abstract-NO, Poster-YES