USDA-ARS
U.S. Wheat and Barley Scab Initiative
FY18 Performance Report
Due date: July 12, 2019

Cover Page

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Fiscal Year:	2018
USDA-ARS Agreement ID:	59-0206-6-006
USDA-ARS Agreement Title:	Mapping Loci Conferring Resistance to FHB and DON Accumulation in Barley.
FY18 USDA-ARS Award Amount:	$ 61,501
Recipient Organization:	Regents of the University of Minnesota Suite 450 Sponsored FIN RPT-P100100001 Minneapolis, MN 55455-2003
DUNS Number:	555917996
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Recipient Identifying Number or Account Number:	CON000000060625
Project/Grant Reporting Period:	5/2/18 - 5/1/19
Reporting Period End Date:	05/01/19

USWBSI Individual Project(s)

USWBSI Research Category[*]	Project Title	ARS Award Amount
BAR-CP	Evaluation and Genetic Characterization of Barley Germplasm for FHB Resistance.	$ 61,501
	FY18 Total ARS Award Amount	$ 61,501

Brian J. Steffenson

July 12, 2019

Principal Investigator Date

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[*] 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

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Project 1: *Evaluation and Genetic Characterization of Barley Germplasm for FHB Resistance.*

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

Our major goal is to reduce the economic losses caused by Fusarium head blight (FHB) in barley, including quality discounts due to deoxynivalenol (DON) contamination. This can be best achieved by developing barley cultivars with the highest level of resistance possible, in conjunction with various cultural and chemical control methods. Through extensive germplasm evaluations funded by the USWBSI over the past 16 years, we have identified 78 accessions that possess a level of resistance comparable to the six-rowed and two-rowed controls of Chevron and CIho 4196, respectively. One of the most resistant accessions identified in this group is PI 350725, a two-rowed accession from the Tirol in Austria. Six-rowed barleys have been the preferred type for malting in the Midwest region for more than 80 years. A resistant two-rowed barley was selected for this investigation because this is now the industry-preferred row type for Midwestern malting barley cultivars. Our specific objectives for this proposal are to: 1) determine the number, effect, and chromosomal position of FHB resistance loci in barley accession PI 350725 using the advanced backcross QTL method and 2) provide adapted FHB-resistant parental materials to barley improvement programs. This research addresses Barley-CP VDHR objective #2 (Mapping novel QTL for resistance to FHB in barley), but is also an important step in advancing objective #4 (Develop new barley varieties with enhanced resistance to FHB and lower DON). The outputs from this work will be advanced breeding lines with novel genes for FHB resistance. Use of this germplasm in breeding will help fulfill the USWBSI primary goal to develop as quickly as possible effective control measures that minimize the threat of FHB, including the reduction of mycotoxins, to the producers, processors, and consumers of barley.

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

1) Major activities

Objective 1: PI 350725 was crossed with ‘Quest,’ the first Midwestern six-rowed cultivar with partial FHB resistance. About 50 F_1 progeny were then backcrossed with ‘Quest’ to obtain the BC_1 generation. At least 5 crossed seeds were obtained per backcross. Then, about 90 BC_1 plants were backcrossed to ‘Quest’ to obtain the BC_2 generation. Through timely supplemental support from the USWBSI, the BC_2 generation was made into doubled haploids (DHs) by Patrick Hayes’ group at Oregon State University. This critical DH step shortened the time needed to obtain homozygous lines, allowing for earlier phenotyping in the field. From each BC_2 plant, 5 seeds were used for DH production. Due to the recalcitrant nature of this cross, only 170 doubled haploid progeny were obtained from Oregon State University. These DH progenies were increased in the fall/winter greenhouse season of 2015-2016 and were phenotyped at our late-planted FHB nursery in Crookston in 2016. Due to the lower than expected number of DH progeny, we also advanced remnant BC_2 seed by single seed descent, which will serve to expand the population for QTL mapping and validate the results found in the DH population. The number of BC_2 Recombinant Inbred Lines (RILs) generated was 328. The DH and RIL populations were phenotyped for FHB severity and DON concentration at St. Paul in 2017 and in St. Paul and Crookston in 2018. The same populations are now being evaluated in Crookston in 2019. From these five environments, we hope to obtain a robust phenotyping dataset for mapping quantitative trait loci (QTL) for resistance to the disease and accumulation of the mycotoxin. The 50K iSelect single nucleotide polymorphism (SNP) array was used to genotype 161 DH lines and 317 RIL lines. SNP calls were manually edited to reduce missing data using GenomeStudio v2.0 and were filtered to remove markers with >10% missing data and >2% heterozygosity. Single marker analysis was performed using general linear model in Tassel v5.0 as a preliminary investigation of potentially significant QTL for FHB severity across all environments. After collection of 2019 data for these populations, composite interval mapping will be performed for more robust QTL analysis.

Objective 2: Data from the first two years of phenotyping have identified agronomically advanced progeny lines with low FHB severity and DON accumulation. When all of the data for the three years of phenotyping are compiled, we will select the top three most resistant two-rowed progeny for distribution to barley breeders.

2) Specific objectives

Objective 1: determine the number, effect, and chromosomal position of FHB resistance loci in barley accession PI 350725 using the advanced backcross QTL method

Objective 2: provide adapted FHB-resistant parental materials to barley improvement programs.

3) Significant results

Objective 1: At St. Paul (2017-18), the six-rowed resistant (Chevron), six-rowed susceptible (PI 383933), two-rowed resistant (CIho 4196), and two-rowed susceptible (ICB111809) accessions exhibited an average FHB severity and DON concentration of 11.1% and 1.9ppm; 55.5% and 14.0ppm; 10.6% and 2.4ppm, and 20.2% and 3.6ppm, respectively. At Crookston (2018), Chevron, PI 383933, CIho 4196, and ICB11180, exhibited a FHB severity and DON concentration of 2.8% and 3.3ppm; 92.1% and 13.3ppm; 2.1% and 2.3ppm, and 16.8% and 8.3ppm, respectively. With the mapping populations, two-rowed progeny ranged in FHB severity and DON concentration from 0.8 to 33.7% and from 0.11 to 15.0ppm in St. Paul and from 0.7 to 27.1% and from 0.6 to 28.1ppm in Crookston, respectively. These data indicate that DH and RIL progeny with low FHB severity and DON accumulation can be recovered from the PI 350725/Quest population. QTL analyses will be completed when data from the last trial in Crookston are collected and compiled. Agro-morphological traits such as heading date, height, and spike density can have a pronounced effect on FHB severity. Thus, these traits will also be scored to determine if they co-locate with QTLs for FHB reaction.

Objective 2: When all of the data for the three years of phenotyping are compiled, we will select the top three most resistant two-rowed progeny for distribution to barley breeders.

4) Key outcomes or other achievements

None at this time. We hope to identify novel resistance alleles in the PI350725/Quest population once the data are analyzed. Additionally, we expect to identify progeny with relatively high levels of resistance that can be distributed to breeders for their resistance programs.

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

Our USWBSI-funded research has provided an excellent training opportunity for many scientists. The immediate past research comprised a portion of the Ph.D. dissertation of Dr. Matthew Haas, and the current research project is part of the M.S. thesis of my new graduate student Rae Page. Other participants in this research included post-doctoral research associates Ahmad Sallam, Oadi Matny, and Ali Mehrabi and Researcher 2 scientists Tamas Szinyei, Matthew Martin, and Ryan Johnson. There were also many undergraduate students who assisted on this project in various capacities, the two current ones being Michelle Jugovich and Michael Miller. All of these individuals were trained in the methodology for working with FHB, including production and storage of inoculum; inoculation techniques; disease severity scoring; and DON analyses. Moreover, several members of my senior research team gained valuable experience in SNP genotyping, molecular map construction and QTL analysis.

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

The current research project is part of Rae Page's M.S. thesis. Her aim is to present her research at the 2019 USWBSI forum and then publish it in a refereed journal.

Training of Next Generation Scientists

Instructions: Please answer the following questions as it pertains to the FY18 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 FY18 award period?**

   Yes

   If yes, how many? One: Matthew Martin

2. **Did any graduate students in your research program supported by funding from your USWBSI grant earn their Ph.D. degree during the FY18 award period?**

   No

   If yes, how many?

3. **Have any post docs who worked for you during the FY18 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 FY18 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 FY18 award period. All columns must be completed for each listed germplasm/cultivar. Use the key below the table for Grain Class abbreviations.

NOTE: 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**

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

Instructions: Refer to the FY18-FPR_Instructions for detailed instructions for listing publications/presentations about your work that resulted from all of the projects included in the FY18 grant. Only include citations for publications submitted or presentations given during your award period (5/2/18 - 5/1/19). If you did not have any publications or presentations, state 'Nothing to Report' directly above the Journal publications section.

NOTE: Directly below each reference/citation, you must indicate the Status (i.e. published, submitted, etc.) and whether acknowledgement of Federal support was indicated in publication/ presentation. See example below for a poster presentation with an abstract:

> Conley, E.J., and J.A. Anderson. 2018. Accuracy of Genome-Wide Prediction for Fusarium Head Blight Associated Traits in a Spring Wheat Breeding Program. In: Proceedings of the XXIV International Plant & Animal Genome Conference, San Diego, CA.
> Status: Abstract Published and Poster Presented
> Acknowledgement of Federal Support: YES (poster), NO (abstract)

Journal publications.

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

Other publications, conference papers and presentations.

Qiu, R., Yang, C., Moghimi, A., Anderson, J., Steffenson, B., and Marchetto, P. 2018. Detection of Fusarium head blight in small grains using hyperspectral imaging.
Pages 32-36 of Proceedings of the 2018 National Fusarium Head Blight Forum, St. Louis, MO. December 2-4, 2018.
Status: Abstract Published and Poster Presented
Acknowledgement of Federal Support: YES (poster), NO (abstract)

Huang, Y., Heinen, S., Steffenson, B., Smith, K. P., and Muehlbauer, G. J. 2018. Fine mapping of FHB quantitative trait loci on chromosomes 6H and 2H in barley. Page 71 of Proceedings of the 2018 National Fusarium Head Blight Forum, St. Louis, MO. December 2-4, 2018.
Status: Abstract Published and Poster Presented
Acknowledgement of Federal Support: YES (poster), NO (abstract)