

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

Cover Page

Principle Investigator (PI):	Brian Steffenson
Institution:	University of Minnesota
E-mail:	bsteffen@umn.edu
Phone:	612-325-4735
Fiscal Year:	2015
USDA-ARS Agreement ID:	59-0206-1-119
USDA-ARS Agreement Title:	Mapping Loci Conferring Resistance to FHB and DON Accumulation in Barley.
FY15 USDA-ARS Award Amount:	\$ 50,019
Recipient Organization:	Regents of the University of Minnesota Suite 450 Sponsored FIN RPT-P100100001 Minneapolis, MN 55455-2003
DUNS Number:	555917996
EIN:	41 -6007513
Recipient Identifying Number or Account Number:	CON000000031990
Project/Grant Reporting Period:	05/02/15-05/01/16
Reporting Period End Date:	05/01/16

USWBSI Individual Project(s)

USWBSI Research Category*	Project Title	ARS Award Amount
BAR-CP	Mapping Loci Conferring Resistance to FHB and DON Accumulation in Barley.	\$ 50,019
	FY15 Total ARS Award Amount	\$ 50,019



July 15, 2016

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: *Mapping Loci Conferring Resistance to FHB and DON Accumulation in Barley.*

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. The specific objective for this proposal is to determine the number, effect, and chromosomal position of FHB resistance loci in selected barley accessions using the advanced backcross-quantitative trait locus (AB-QTL) method. The AB-QTL method allows for the identification of resistance QTLs, while at the same time developing advanced lines that can feed into the breeding program. For this project, three of the most resistant accessions identified from extensive screening tests were used for developing biparental populations with the partially resistant cultivar Quest. These resistant accessions include Kutahya, a cultivated barley from the Netherlands; W-365, a wild barley from Iraq; and PI350725, a two-rowed accession from the Tirol in Austria.

2. What was accomplished under these goals?

1) major activities

We have completed quantitative trait locus (QTL) analysis of FHB resistance in two advanced backcross populations in the genetic background of the moderately resistant cultivar Quest. The Kutahya/Quest (N=361 lines) and W-365/Quest (N=378) populations were advanced to the BC₂F_{5:6} generation in 2013 and phenotyped for FHB severity and DON concentration at three or four locations (Nanjing, China; Crookston MN; St. Paul, MN; and Brandon, Canada (Kutahya/Quest population only)) over several succeeding years. Both populations were genotyped with the 9K single nucleotide polymorphism (SNP) chip (Illumina Infinium assay) and maps of 1,023 and 1,079 cM were constructed, respectively. Comprehensive QTL analyses were done with the software program QGene, which is capable of handling the special structure of AB populations. The third population of PI350725/Quest (N=158) was fast-tracked to homozygosity by double haploid production in spring 2016. It is being phenotyped for FHB resistance and DON accumulation in Crookston this summer.

2) specific objectives

The specific objective for this proposal was to determine the number, effect, and chromosomal position of FHB resistance loci in the Kutahya/Quest, W-365/Quest, and PI350725/Quest populations. The AB-QTL method allows for the identification of resistance QTLs, while at the same time developing advanced lines that can feed into the breeding program.

3) significant results

FHB QTL Mapping. QTL analysis in the Quest/W-365 population revealed a significant marker-trait association in the chromosome 2H bin 4 region, which was detected in three out of five environments where the trait was measured. SCRI_RS_207144 and BOPA2_12_30145 were each the most significant marker found in one of four environments, while SCRI_RS_207399 was significant in two of four environments. All three of these

markers are closely linked with each other and therefore may be detecting the same QTL. In this population, the chromosome 2H QTL (designated: FHB-qt1-2H-4) explained a minimum of 8% of the variation in the St. Paul 2013 environment and a maximum of 28% in the Crookston 2013 environment. The favorable allele was contributed by Quest in all environments. The results for the Quest/Kutahya population were different than the Quest/W-365 population. The most noticeable difference was the lack of a major effect QTL at or near FHB-qt1-2H-4 in the Quest/Kutahya population. Instead, only two small effect QTL were detected, each in a single environment. One QTL (FHB-qt1-1H-4) was identified in chromosome 1H bin 4 in Brandon 2013, explaining 9% of the variation. The second QTL (FHB-qt1-6H-10) was detected in bin 10 of chromosome 6H and explained 9% of the variation. Both QTL were contributed by Quest.

DON QTL mapping. In the Quest/W-365 population, a QTL (DON-qt1-2H-4) coincident with the one identified for resistance (FHB-qt1-2H-4) was detected in all four environments where the trait was measured, explaining a minimum of 6% of the variation in the Crookston 2013 environment and a maximum of 62% in the St. Paul 2014 environment. The allelic effect was inconsistent with the favorable allele coming from Quest in three out of four environments, while W-365 provided the favorable allele in Crookston 2014. In the Kutahya/Quest population, a single QTL (DON-qt1-2H-4) for reduced DON accumulation was identified in the Brandon 2013 nursery, explaining 7% of the variation with the beneficial allele contributed by Quest.

The results we found were somewhat disappointing because the major resistance alleles found were mostly from the partially resistant recurrent parent of Quest. While this provides important validation data, we had hoped to identify new alleles for FHB resistance from the sources of Kutahya and W-365.

4) key outcomes or other achievements

The most frequently detected QTL for reduced FHB severity (FHB-qt1-2H) that also explained the greatest amount of variation for DON accumulation (DON-qt1-2H) was found in the bin 4 region of chromosome 2H (broadly, FHB-qt1-2H-4 and DON-qt1-2H-4). Both FHB-qt1-2H-4 and DON-qt1-2H-4 were coincident with each other having the same significant SNP marker association (SCRI_RS_182408). Moreover, major effect QTL for heading date and plant height were also identified at this same coincident locus, suggesting that the reduced disease and mycotoxin levels may be a pleiotropic effect of increased plant height and delayed heading date. This phenomenon has been reported by a number of other researchers. From this research, we have identified several progeny lines with putative transgressive resistance to FHB. These lines have been given to breeders for use in their FHB resistance program.

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

Our USWBSI-funded research has provided an excellent training module for many scientists. The current research comprised a portion of the Ph.D. dissertation of Dr. Matthew Haas. Other participants in this research included post-doctoral research associate Ahmad Sallam;

Junior Scientists Tamas Szinyei, Matthew Martin, and Ryan Johnson; and graduate students Austin Case, Shuyi Huang, and Fazal Manan. There were also many undergraduate students who assisted on this project in various capacities. 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?

This research was published in the Ph.D. dissertation of Dr. Matthew Haas entitled: Genetics of Resistance To Fusarium Head Blight and Spot Blotch in *Hordeum*, University of Minnesota, June 2016. In addition, Matthew has presented preliminary results of this work at the past two USWBSI forums and also to a group of Wisconsin barley growers via SKYPE.

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? No.**

If yes, how many?

- 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? No.**

If yes, how many?

- 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

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

FY15 Final Performance Report
PI: Steffenson, Brian
USDA-ARS Agreement #: 59-0206-1-119

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.

Mamo, B.E. and Steffenson, B.J. 2015. Genome-wide association mapping of Fusarium head blight resistance and agromorphological traits in barley landraces from Ethiopia and Eritrea. *Crop Science*. 55:1494-1512.

Status: Published

Acknowledgement of Federal Support: Yes

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

Nothing to report

Other publications, conference papers and presentations.

Huang, Y., Heinen, S., Steffenson, B., Smith, K. P., and Muehlbauer, G. J. 2015. Coarse and fine mapping of quantitative trait loci for FHB in barley. In: S. Canty, A. Clark, S. Vukasovich and D. Van Sanford (Eds.), *Proceedings of the 2015 National Fusarium Head Blight Forum* (p. 47). East Lansing, MI/Lexington, KY: U.S. Wheat & Barley Scab Initiative.

Status: Abstract Published and Poster Presented

Acknowledgement of Federal Support: Abstract: No; Poster: yes

Haas M., and Steffenson B.J. 2015. Genetics of Fusarium head blight resistance in barley: The way forward. In: S. Canty, A. Clark, S. Vukasovich and D. Van Sanford (Eds.), *Proceedings of the 2015 National Fusarium Head Blight Forum* (p. 88). East Lansing, MI/Lexington, KY: U.S. Wheat & Barley Scab Initiative.

Status: Abstract Published and Poster Presented

Acknowledgement of Federal Support: Yes