

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

Cover Page

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USDA-ARS Agreement Title:	Mapping Loci Conferring Resistance to FHB and DON Accumulation in Barley.
FY16 USDA-ARS Award Amount:	\$ 53,684
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Project/Grant Reporting Period:	5/2/16 - 5/1/17
Reporting Period End Date:	05/01/17

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.	\$ 53,684
	FY16 Total ARS Award Amount	\$ 53,684


 Principal Investigator

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 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? *Address items 1-4) below for each goal or objective.*

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 was being phenotyped for FHB resistance and DON accumulation in Crookston in 2016 and 2017 and in St. Paul in 2017.

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. FHB phenotyping of the PI350725/Quest is in progress at two locations in Minnesota. Variation for FHB severity was observed in the population.

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. Analysis of the DON accumulation data for PI350725/Quest population from Crookston 2016 is in progress. Two additional DON datasets will be obtained from St. Paul and Crookston in 2017.

The results we found for the Quest/Kutahya and Quest/W-365 populations 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. We hope we will identify novel resistance alleles in the PI350725/Quest population once the data are analyzed.

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 and is being summarized in a meta-analysis review paper of FHB resistance in barley. From this research, we have identified several progeny lines

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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; graduate students Austin Case, Shuyi Huang, Fazal Manan, Grete Slaugh and Abdul Wajid. 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. Additionally, I gave an address at the 2016 National Fusarium Head Blight Forum on A meta-analysis of the genetics of Fusarium Head Blight resistance in barley.

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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?

Two: Shuyi Huang and Fazal Manan

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? Yes.**

If yes, how many?

Two: Matthew Haas and Austin Case.

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?

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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 (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 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 (5/2/16 - 5/1/17). If you did not have any publications or presentations, state 'Nothing to Report' directly above the Journal publications section.

Journal publications.

Steffenson, B. J., Haas, M., and Sallam, A., 2016. A meta-analysis of the genetics of Fusarium Head Blight resistance in barley. In: Page 94 in Proceedings of the 2016 National Fusarium Head Blight Forum, St. Louis, MO. December 4-6, 2016.

Status: Abstract published and oral presentation given.

Acknowledgement of Federal Support: YES (oral presentation), NO (abstract)

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

Haas, M. 2016. Genetics of Resistance To Fusarium Head Blight and Spot Blotch in *Hordeum*. Ph.D. dissertation, University of Minnesota, St. Paul.

Status: Thesis published.

Acknowledgement of Federal Support: YES (thesis), NO (abstract)

Other publications, conference papers and presentations.