USDA-ARS/
U.S. Wheat and Barley Scab Initiative
FY14 Final Performance Report
July 15, 2015

Cover Page

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Fiscal Year:	FY14
USDA-ARS Agreement ID:	59-0206-1-119
USDA-ARS Agreement Title:	Mapping Loci Conferring Resistance to FHB and DON Accumulation in Barley.
FY14 USDA-ARS Award Amount:	$ 44,061

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.	$ 44,061
	FY14 Total ARS Award Amount	**$ 44,061**

Brian J Steffenson

July 15, 2015

Principal Investigator Date

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[*] MGMT – FHB Management
FSTU – Food Safety, Toxicology, & Utilization of Mycotoxin-contaminated Grain
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
WES-CP – Western 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 major problem or issue is being resolved relevant to Fusarium head blight (scab) and how are you resolving it?**

   Our primary and long-term goal is to reduce the economic losses caused by 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. We identified about 20 promising accessions with partial FHB resistance through multiple years of field screening. Three of these accessions (Kutahya, a two-rowed cultivar from the Netherlands; W-365, a wild barley accession from Iraq; and PI 350725, a two-rowed landrace from Tirol, Austria) were backcrossed to the partially resistant six-rowed cultivar 'Quest' to develop BC_2F_5 populations for mapping and characterizing quantitative trait loci (QTL) conferring FHB resistance and low DON accumulation. The specific objective for this proposal is to determine the number, effect, and chromosomal position of FHB resistance loci in these select barley accessions using the advanced backcross-QTL method. The information and germplasm generated from this study will lead to the development of malting barley cultivars with FHB resistance and low DON accumulation, thereby minimizing this disease threat for producers, processors, and consumers.

2. **List the most important accomplishments and their impact (i.e. how are they being used) to minimize the threat of Fusarium Head Blight or to reduce mycotoxins. Complete both sections; repeat sections for each major accomplishment:**

   <u>Accomplishment:</u>

   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 (361 lines) and W-365/Quest (378) populations were advanced to the $BC_2F_{5:6}$ 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 two years. Both populations were genotyped with the 9K (single nucleotide polymorphism (SNP) chip (Illumina Infinium assay) and maps of 1,137 and 1,079 cM were constructed, respectively. QTL analyses revealed a strong effect in bin 4 of chromosome 2H at or near the photoperiod response gene *Ppd-H1*. In the W-365/Quest population, this QTL was identified in 4 out of 5 environments for FHB severity and all 4 tested environments for DON accumulation. This QTL explained from 4.9 to 27.6% of the variation for FHB and 4.7 to 62% of the variation for DON. In the Kutahya/Quest population, a QTL for DON accumulation was identified in bin 4 of chromosome 2H only in the 2013 Brandon nursery and explained 6.8% of the variation. The beneficial allele in both populations and all but one environment was contributed by Quest, the recurrent parent. In the 2014 Crookston nursery, the allele for DON concentration in bin 4 of chromosome 2H was contributed by W-365, explaining 5.5% of the variation. Other than the 2H bin 4 QTL, only two other QTL were identified in the W-365/Quest population. A QTL for FHB severity was identified on chromosome 2H bin 3 (2013 Saint Paul) explaining 7.9% of the variation and another one on chromosome 4H bin 4 (2013 Nanjing) explaining 8.2% of the variation. The beneficial allele for both QTL was contributed by Quest, and both QTL are coincident with QTL for plant height and/or heading date. In the Kutahya/Quest population, another QTL for FHB severity was detected in 3 out of 7 environments. It was identified on chromosome 1H bins 4-7, explaining from 4.3 to 9.0% of the variation. Quest contributed the beneficial allele in 2 out of the 3 environments with Kutahya contributing the beneficial allele in the 2013 Nanjing nursery.

An additional population is being developed from the partially resistant accession PI 350725. These populations are currently at the BC_2 generation and will be available for phenotyping during the 2016 field season.

Impact:

We have developed and advanced two backcross populations (Kutahya/Quest and W-365/Quest) in the genetic background of Quest--the first cultivar released from the Midwest that possesses moderate resistance to FHB. QTL analyses revealed the number, effect, and chromosomal position of FHB resistance and DON accumulation loci in these select barley accessions using the advanced backcross-QTL method. Additionally, we identified several agronomically advanced two- and six-rowed progeny that may possess transgressive resistance. These progeny lines will be given to breeders for use as parents in their FHB-resistance breeding programs. The pyramiding of new FHB resistance loci in malting barley cultivars will minimize this disease threat for producers, processors, and consumers. Moreover, molecular markers linked with the resistance loci can be used for marker assisted and genomic selection in breeding programs.

Training of Next Generation Scientists

Instructions: Please answer the following questions as it pertains to the FY14 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 FY14 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 FY14 award period?** No, but one (Matthew Haas) will finish his doctorate in 2016.

   If yes, how many?

3. **Have any post docs who worked for you during the FY14 award period and were supported by funding from your USWBSI grant taken faculty positions with universities?** None

   If yes, how many?

4. **Have any post docs who worked for you during the FY14 award period and were supported by funding from your USWBSI grant gone on to take positions with private ag-related companies or federal agencies?** None

   If yes, how many?

Include below a list of all germplasm or cultivars released with full or partial support of the USWBSI during the FY14 award period. List the release notice or publication. Briefly describe the level of FHB resistance. *If not applicable because your grant did NOT include any VDHR-related projects, enter N/A below.*

No. However, please note we hope to release breeding lines that appear to possess transgressive resistance from the Kutahya/Quest and W-365/Quest populations in 2016.

Include below a list of the publications, presentations, peer-reviewed articles, and non-peer reviewed articles written about your work that resulted from all of the projects included in the FY14 grant. Please reference each item using an accepted journal format. If you need more space, continue the list on the next page.

Haas, M., Laskowski, M., Chao, S., Dong, Y., Szinyei, T., and Steffenson, B. 2014. Genetic mapping of quantitative trait loci for Fusarium head blight resistance in spring barley 'Kutahya' and wild barley 'W-365.' In: Proceedings of the 2014 National Fusarium Head Blight Forum. S. Canty, A. Clark, N. Turcott, and D. Van Sanford, Eds. December 7-9. 2014, St. Louis, MO. Publisher: East Lansing MI/Lexington, KY. US Wheat and Barley Scab Initiative.