

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

Cover Page

PI:	Kevin Smith
Institution:	University of Minnesota
Address:	Department of Agronomy and Plant Genetics 411 Borlaug Hall 1991 Upper Buford Circle St. Paul, MN 55108
E-mail:	smith376@umn.edu
Phone:	612-625-1211
Fax:	612-625-1268
Fiscal Year:	FY14
USDA-ARS Agreement ID:	59-0206-4-020
USDA-ARS Agreement Title:	Breeding and Genetics of Fusarium Head Blight Resistance in Barley.
FY14 USDA-ARS Award Amount:	\$ 151,569

USWBSI Individual Project(s)

USWBSI Research Category*	Project Title	ARS Award Amount
BAR-CP	Developing Six-rowed Malting Barley Varieties with FHB Resistance and Low DON.	\$ 89,310
BAR-CP	Genomic Selection for FHB Resistance in Midwest Six-row Barley.	\$ 62,259
	FY14 Total ARS Award Amount	\$ 151,569

Principal Investigator

Date

* 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: *Developing Six-rowed Malting Barley Varieties with FHB Resistance and Low DON.*

1. What major problem or issue is being resolved relevant to Fusarium head blight (scab) and how are you resolving it?

New barley cultivars with improved FHB resistance, lower DON, high yield, and acceptable malting quality are needed to sustain barley production in the Midwest. Currently available varieties lack sufficient resistance to mitigate the risk of DON contamination in years when the disease is severe. We released the cultivar Quest with a moderate level of resistance that is sufficient in years of low levels of disease. Thus, we are continuing our breeding effort to further increase the level of resistance while maintaining and/or improving agronomic performance and malting quality. We are implementing a comprehensive breeding program that utilizes diverse sources of resistance, implements selection using genomic prediction and field trial performance data, and evaluates cultivar candidates in multi-location trials across the region.

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:

Accomplishment:

We collect a wide range of performance data on current cultivars available in the region. Data from Quest shows that it has approximately half the level of DON compared to current popular cultivars and similar yield levels in Minnesota. This information is made available to growers and to the malting and brewing industry.

Impact:

The cultivar Quest went from 0.2% of the acres in Minnesota in 2013 to 12.4% in 2014. Producers growing Quest have reduced exposure to the risk of FHB and will produce grain with lower levels of DON compared to other six-row cultivars.

Accomplishment:

One of our five submissions to industry pilot malt evaluations was rated as satisfactory, M160 (M139/FEG160-03). This line has similar resistance to FHB compared to Quest, slightly better yield, and a better malt profile.

Impact:

If M160 performs well in 2015, it could be moved to plant-scale testing and increased for release.

Project 2: *Genomic Selection for FHB Resistance in Midwest Six-row Barley.*

1. What major problem or issue is being resolved relevant to Fusarium head blight (scab) and how are you resolving it?

Selecting for FHB resistance in the field is laborious, expensive, and inherently imprecise. Despite these challenges, we have made slow progress enhancing FHB resistance in barley. To complement phenotypic selection for FHB resistance, we initiated a genomic selection (GS) approach using large marker and trait data sets to predict breeding values for DON concentration and yield in early generation breeding lines that have not been phenotyped. This approach dramatically reduces our breeding cycle time from four years to one year and should accelerate development of new cultivars. In the fall of 2014 we completed the 5th cycle of selection using 384 SNP markers on ~ 2,000 breeding lines this past year. We published a study investigating the accuracy of GS using data from our breeding program (Sallam et al., 2015). We are conducting experiments to directly measure the accuracy of GS in our selection program as well as gain from selection. We are using information from these studies to fine tune our GS methodology.

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:

Accomplishment:

We have conducted a series of experiments that evaluate the use of genomic selection. We have examined the impact of various parameters of GS on prediction accuracy including training population size and composition as well as marker panel size and composition.

Impact:

We have provided useful information to others that have expressed interest in using GS. We have replaced phenotypic selection of early generation breeding lines with predictions. This has resulted in a 50% reduction of the size of our FHB nursery for spring six-row barley freeing up resources for winter and two-rowed 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?**

Yes

If yes, how many? 1

- 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?**

Yes

If yes, how many? 1

- 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.*

None

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.

Peer-reviewed articles

Sallam, A., Endleman, J., Jannink, J.L., and K. P. Smith. 2014. Assessing genomic selection prediction accuracy in a dynamic barley breeding population. *The Plant Genome* (online Sept, 2014). doi: 10.3835/plantgenome2014.05.0020.

Mohammadi, M., T. Tiede, K.P. Smith. 2015. PopVar: A Genome-Wide Procedure for Predicting Genetic Variance and Correlated Response in Biparental Breeding Populations *Crop Sci.* (online June, 2015). doi:10.2135/cropsci2015.01.0030.

Presentations

Tiede, T., A. Sallam, E. Scheifelbein, K. Beaubian, G. Velasquez, Yadong Huang, S. Chao, A. Lorenz and K.P. Smith. 2014. Changes in Fusarium Head Blight and Grain Yield Traits Over Three Cycles of Genomic Selection in a Barley Breeding Population. 2014 National Fusarium Head Blight Forum, Hyatt Regency St. Louis at the Arch, St. Louis, MO December 7-9, 2014..

Mohammadi, M., T. Tiede and K.P. Smith. 2014. A Breeding Tool for Estimating Genetic Variance and Correlated Response in Bi-Parental Crosses: Targeting High-Yield and Low-Deoxynivalenol (DON). 2014 National Fusarium Head Blight Forum, Hyatt Regency St. Louis at the Arch, St. Louis, MO December 7-9, 2014.

Sallam A. and K.P. Smith. 2014. Equal Genomic and Phenotypic Selection Gain for FHB Resistance and DON Accumulation in Barley. 2014 National Fusarium Head Blight Forum, Hyatt Regency St. Louis at the Arch, St. Louis, MO December 7-9, 2014.

Sallam A. and K.P. Smith. 2014. Comparing the Gain from Genomic vs. Phenotypic Selection in Barley. *Plant and Animal Genome XXII Conference*, San Diego, CA, Jan 11-15, 2014.

Sallam A. and K.P. Smith. 2014. Comparing Phenotypic Selection and Genomic Selection. *North American Barye Researchers Workshop*. Minneapolis, MN June 31, 2014- July 2, 2014