

**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:	59-0206-1-115
USDA-ARS Agreement Title:	Breeding and Genetics of Fusarium Head Blight Resistance in Barley.
FY14 USDA-ARS Award Amount:	\$ 15,689

USWBSI Individual Project(s)

USWBSI Research Category*	Project Title	ARS Award Amount
BAR-CP	Genomic Selection for FHB Resistance in Midwest Six-row Barley.	\$ 15,689
	FY14 Total ARS Award Amount	\$ 15,689

7/15/15

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: *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, slow progress for FHB resistance in barley has been made. To complement phenotypic selection and MAS for targeted QTL, PI Smith initiated a genomic selection (GS) approach using large marker and trait data sets to predict breeding values for FHB resistance in early generation breeding lines that have not been phenotyped. This approach dramatically reduced breeding cycle time from four years to one year and should accelerate development of new varieties. PI Smith is 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:

I assisted PI Smith with the analysis of a series of experiments evaluating 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. A paper was published in Crop Science describing the effect of training populations-selection candidate relationships on prediction accuracy. We believe this is an important contribution of information for barley breeders desiring to implement GS.

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?**

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.*

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

Lorenz, A.J., K.P. Smith, and J-L. Jannink. 2012. Potential and optimization of genomic selection for Fusarium head blight resistance in six-row barley. *Crop Sci.* 52:1609-1621.

Presentations

Lorenz, A.J., K.P. Smith, D. Jarquin. 2014. Effect of relationships on genomic prediction accuracy in plant breeding. Dow AgroSciences, Oct 28. Indianapolis, IN.

Lorenz, A.J., K.P. Smith, D. Jarquin. 2014. Effect of relationships on genomic prediction accuracy in plant breeding. Plant Genomics Congress, Sept 11-12. St. Louis, MO.

Lorenz, A.J., K.P. Smith, P.S. Baenziger, G.G. Graef. 2014. Optimizing genomic prediction for public plant breeding programs. ICRISAT 4th International Workshop on Next Generation Genomics and Integrated Breeding for Crop Improvement, Feb 19-21. Hyderabad, AP, India.

Tiede, T., A. Sallam, K. Beaubian, S. Chao, **A. Lorenz**, K. Smith. 2015. Allele frequency changes over five cycles of genomic selection in a barley breeding population. Plant and Animal Genome Conference, January 10-14. San Diego, CA.