

**USDA-ARS/
U.S. Wheat and Barley Scab Initiative
FY13 Final Performance Report
July 15, 2014**

Cover Page

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Fiscal Year:	FY13
USDA-ARS Agreement ID:	59-0206-1-115
USDA-ARS Agreement Title:	Breeding and Genetics of Fusarium Head Blight Resistance in Barley.
FY13 USDA-ARS Award Amount:	\$ 15,704

USWBSI Individual Project(s)

USWBSI Research Category*	Project Title	ARS Award Amount
BAR-CP	Genomic Selection for FHB Resistance in Midwest Six-row Barley.	\$ 15,704
	FY13 Total ARS Award Amount	\$ 15,704



7/15/2014

Principal Investigator

Date

* MGMT – FHB Management
 FSTU – Food Safety, Toxicology, & Utilization of Mycotoxin-contaminated Grain
 GDER – Gene Discovery & Engineering Resistance
 PBG – Pathogen Biology & Genetics
 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: *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. We have also used traditional marker assisted selection (MAS) to manipulate two modest effect QTLs. However, there are currently no other MAS targets that have been consistently mapped with sufficient effects to warrant MAS. Thus, further progress must be made by exploiting genetic variation controlled by many genes with small effects. To complement phenotypic selection and MAS for targeted QTL, we 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 reduces our breeding cycle time from four years to one year and should accelerate development of new varieties. We have completed the 4th cycle of selection using 384 SNP markers on ~ 2,000 breeding lines this past year. 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 (1): I have assisted Co-PI Smith in directly comparing genomic selection to phenotypic selection in five sets of breeding lines developed over a five year period. The effectiveness of selection for both yield and DON levels was on average equal between genomic selection and phenotypic selection.

Impact: It appears the current approach to using genomic selection is equivalent to the standard method of phenotypic selection. However the cost of prediction with markers is about ¼ the cost of doing field evaluations and laboratory DON testing. In addition, genomic selection can be imposed one year after a cross is made as opposed to 3-4 years for phenotypic selection. Thus, we expect using genomic selection will reduce costs and speed up breeding progress.

Accomplishment (2): We have initiated a study to compare the base breeding population and three cycles of genomic selection for lower DON levels and increased yield. In 2013, we conducted FHB trials at 2 locations. In 2014, we planted 2 more trials for FHB and three locations for yield trials.

Impact: Initial results suggest we are making gains using genomic selection and will continue using this approach and collecting more data to document gain from selection.

Through reports and presentations of this work other breeding programs are considering using similar approaches in their breeding programs.

Accomplishment (3): Co-PI Lorenz has been studying the effect of degree of genetic relatedness on prediction accuracy. By sampling lines based on kinship, prediction accuracy can be improved by up to 25%. Lines with low kinship, and thus low levels of common linkage phases between markers and QTL, are poor predictors.

Impact: Sampling a genomic prediction training population intelligently can substantially improve prediction accuracy. We expect this improve genetic gain in the UMN barley breeding program, as well as other breeding programs targeting FHB.

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 FY13 grant. Please reference each item using an accepted journal format. If you need more space, continue the list on the next page.

Sallam, A., J. Endelman, J. Jannink, and K. P. Smith. 2013. Genomic Selection and Model Accuracy in Barley for Deoxynivalenol (DON). Plant & Animal Genome XXI Conference, January 12-16, 2013, Town & Country Convention Center, San Diego, CA.

Vikram, V., A. Lorenz, R. Horsely, J. Jannink, and K. P. Smith. 2013. Impact of Training Population Composition on Prediction Accuracy: Genomic Selection for Barley Scab Resistance in Upper Midwest. Plant & Animal Genome XXI Conference, January 12-16, 2013, Town & Country Convention Center, San Diego, CA.

Tiede, T., A. Sallam, E. Scheifelbein, K. Beaubian, G. Velasquez, S. Chao, A. Lorenz and K.P. Smith. 2013. Transitioning from Phenotypic Selection to Genomic Selection for Lower Deoxynivalenol in Barley. 2013 National Fusarium Head Blight Forum, December 3-5, 2013, Hyatt Regency Milwaukee, Milwaukee, WI USA P. 43

Lorenz, A.J. 2013. The effect of genetic relationships and other factors on genomic prediction accuracy in public plant breeding programs. Corn Breeding Research Meeting, Dec. 8-9. Chicago, IL.