USDA-ARS/
U.S. Wheat and Barley Scab Initiative
FY12 Final Performance Report
July 16, 2013

Cover Page

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Fiscal Year:	FY12
USDA-ARS Agreement ID:	59-0206-1-115
USDA-ARS Agreement Title:	Breeding and Genetics of Fusarium Head Blight Resistance in Barley.
FY12 USDA-ARS Award Amount:	$ 15,719[*]

USWBSI Individual Project(s)

USWBSI Research Category[**]	**Project Title**	**ARS Award Amount**
BAR-CP	Genomic Selection for FHB Resistance in Midwest Six-row Barley.	$ 15,719
	Total ARS Award Amount	**$ 15,719**

Principal Investigator Date

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[*] Partial funding for this research is under ARS agreement # 59-0206-9-055

[**] 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?**

   Breeding new barley cultivars with resistance to FHB infection is expensive and laborious. It would be desirable to use molecular markers to predict the level of resistance of breeding progenies without the need for disease nurseries and visual screening. Unfortunately it appears that resistance to this disease is genetically complex, being controlled by many genes of small effect. Advances in marker technologies have made markers less expensive and more abundant, allowing breeders to saturate the genome with markers for less cost than screening an individual line. Also, better uses of statistical modeling have produced far more accurate predictions. This form of marker-based selection is referred to as genomic selection. We are in the process of actually carrying out genomic selection for FHB resistance in a breeding program. Many questions regarding its optimal implementation remain, and we believe this case study will produce a rich source of information. Besides potentially directly resulting in new barley cultivars with greater levels of resistant, this project will help future barley breeding programs more effectively incorporate next-generation marker and DNA sequencing technologies so that more productive and resistant varieties are developed.

2. **List the most important accomplishment and its impact (i.e. how is it 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 (1):</u>

   We carried out three cycles of genomic selection for FHB resistance. Along the way, predictions based on a model developed using C0 data was validated using progenies after one cycle of selection and recombination. Results suggest while prediction accuracy decreases, it is sufficient to make progress economically. This will allow faster genetic gain for FHB resistance.

   <u>Impact:</u>

   1) A population of barley progenies with a greater average resistance to FHB than the starting population. We validated this by comparing the original population to the new population.
   2) Generation of new knowledge on how to handle the logistics of a genomic selection program. This has not been performed in wheat and barley before.
   3) A valuable dataset that will allow us and future researchers to learn how to build the best genomic selection model. For example, to what extent does the inclusion of breeding progenies from different populations benefit accuracies of prediction of genetic value for different, but related, populations? Answers to such questions will maximize the likelihood superior barley cultivars resistant to FHB will be released in the future.

Accomplishment (2):

We have determined that genomic prediction accuracy can be substantially boosted by selecting a subset of the training population based on kinship.

Impact:

This is informative for breeders wanting to practice genomic selection, showing them how to design their training population to maximize accuracy.

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

Smith, K. V. Vikram, **A. Lorenz,** J-L. Jannink, S. Chao, and R. Horsley. 2012. Evaluating genomic selection for DON in a collaborative breeding effort. National Fusarium Head Blight Forum, Dec 4. Orlando, FL.

Lorenz, A.J. 2012. Resource allocation for genomic selection. ICRISAT 3rd International Workshop on Next Generation Sequencing Data Analysis and Modern Breeding Approaches, Aug 29-31. Hyderabad, AP, India.

Lorenz, A.J. 2012. Optimizing genomic selection for plant breeding. Pioneer Hi-Bred, Aug 7. Johnston, IA.

Jia, Y., **A.J. Lorenz**, K.P. Smith, M. Sorrells, J-L. Jannink. 2012. Multiple trait genomic selection (MT-GS) in plant breeding via multivariate Bayesian modeling. Jan 15. San Diego, CA.

Vikram, V., K.P. Smith, **A.J. Lorenz**, and R. Horsley. 2012. Impact of training population composition on prediction accuracy: genomic selection for barley scab resistance in Upper Midwest. Plant and Animal Genome Conference, Jan. 14. San Diego, CA.

Vikram, V., K.P. Smith, **A.J. Lorenz**, R. Horsley, S. Chao, and J-L. Jannink. Impact of training population composition on progeny prediction accuracy: genomic selection using breeding lines from two North American barley improvement programs. (*In preparation).*

Lorenz, A.J., V. Vikram, and K.P. Smith. The effect of kinship on genomic prediction accuracy in barley. (*In preparation*)