USDA-ARS/
U.S. Wheat and Barley Scab Initiative
FY11 Final Performance Report
July 13, 2012

Cover Page

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Fiscal Year:	FY11
USDA-ARS Agreement ID:	59-0206-9-072
USDA-ARS Agreement Title:	Breeding and Genetics of Fusarium Head Blight Resistance in Barley.
FY11 USDA-ARS Award Amount:	$ 134,969

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.	$ 85,209
BAR-CP	Genomic Selection for FHB Resistance in Midwest Six-row Barley.	$ 49,760
	Total ARS Award Amount	**$ 134,969**

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
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: *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?**

   Currently, the most popular six-rowed barley varieties in the Midwest have insufficient resistance to Fusarium head blight to consistently produce grain with acceptable levels of deoxynivalenol. Our latest release, Quest, has a level of resistance that reduces toxin levels by 40% compared to other popular varieties. Growers continue to need new varieties with greater levels of resistance, higher yield, and acceptable malting quality to create a profitable farm economy and maintain barley production in the Midwest to serve the malting and brewing industries. We are conducting a comprehensive field-based breeding effort and implementing marker assisted selection (MAS) to develop new barley varieties to meet this need. We use genetic markers to select for resistance in early generations followed by extensive field evaluation for FHB resistance in inoculated and mist-irrigated nurseries in two locations in Minnesota. Promising breeding lines that combine improved FHB resistance with superior agronomic and end-use performance are advanced to industry malting and brewing tests and then considered for release as new varieties. We also recently initiated a winter barley breeding program for the Midwest that may provide another way to increase barley production and manage disease through earlier harvest. Early generation material in our winter program is being evaluated in field disease nurseries and advanced to multi-location yield testing.

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):**

   Accomplishment:
   The variety Quest was released in 2010. The malting and brewing industries were contracting Quest for the 2012 growing season and all available certified seed was sold. Quest continues to be equal in yield to Tradition, currently the most popular variety in the Midwest, while providing improved FHB resistance and lower DON.

   Impact: Variety acreage reports for 2012 should be available soon and will allow us to track the adoption of Quest in Minnesota and North Dakota.

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. 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 multiple genes with small effects. To complement phenotypic selection and MAS for targeted QTL, we initiated a genomic a 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 accelerating development of new varieties. We have completed the second cycle of selection using 384 SNP markers on ~ 2,000 breeding lines this past year. We published a study measuring the accuracy of GS by cross-validation using a large data set generated as part of the Barley CAP (Lorenz et al., 2012). We are conducting experiments to directly measure the accuracy of GS in our selection program as well as gain from selection. This study will include data from trials conducted in 2011 and 2012 and will be completed by the end of 2012. The results of this study will provide guidance on the implementation of GS in our spring and winter breeding programs as well as for other wheat and barley programs in the imitative.

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:</u> We have successfully conducted two cycles of GS using 384 SNP markers (2,000 lines per cycle). Random and selected sets of lines are being evaluated in field trials to measure the accuracy of GS and the gain from selection. Our cross-validation study indicated that this approach should provide an accuracy of ~0.6 for DON and FHB severity. Preliminary results from our breeding selection study indicate accuracies that are near that level.

   <u>Impact:</u> While it is not possible to measure the impact of our GS project at this time, a four-fold reduction in breeding cycle time with an GS accuracy of 0.5 would double the rate of gain in breeding. This is a substantial improvement. In addition, it is difficult to collect high quality disease data consistently each year, therefore using GS will allow us to make selections in years where phenotypic evaluations are not possible or are of poor quality due to unfavorable field conditions.

Include below a list of all germplasm or cultivars released with full or partial support of the USWBSI. List the release notice or publication. Briefly describe the level of FHB resistance.

Smith, K.P., A. Budde, R. Dill-Macky, D.C. Rasmusson, E. Schiefelbein, J.J. Wiersma, J.V. Wiersma, B.J. Steffenson. 2012. Registration of 'Quest' Spring Malting Barley with Improved Resistance to Fusarium Head Blight. J. Plant Reg. (accepted with revision).

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.

<u>Peer-reviewed Publications</u>

Lorenz, A. J., Chao, S., Asoro, F.G, Heffner, E.L., Hayashi, T., Iwata, H., Smith, K.P., Sorrells, M.E. and Jannink, J.L. 2011. Genomic Selection in Plant Breeding: Knowledge and Prospects. Advances in Agronomy 110:77-123.

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

<u>Oral Presentations</u>

Smith, K.P. Genomic Selection for Fusarium Head Blight Resistance in Barley. 2011. 2011 National Fusarium Head Blight Forum, December 4-6, 2011, Hyatt Regency St. Louis at the Arch, St. Louis, Missouri.

Smith, K. P. 2012. The Breeders' Eye: Can More Data Improve Our Vision. 2012 University of Minnesota Plant Breeding Symposium "Riding the Data Wave: Utilization of Large Datasets in Plant Breeding" . March 9th, 2012. St Paul, MN

Smith, K. P. 2012. Implementing and Evaluating Genomic Selection in Barley. Plant Breeding & Genetics Spring 2012 Seminar Series. Cornell University, March 27, 2012.

Smith, K. P. 2012. Application of Genomic Selection in Barley Improvement. 11th International Barley Genetics Symposium, Hangzhou, China, April 15-20, 2012.

<u>Posters and other publications</u>

Smith, K.P., Sallam, A., J. Jannink, and C. Sneller, 2012. Evaluating Genomic Selection for Applied Plant Breeding. Annual AFRI Project Director Meeting, Town & Country Convention Center, San Diego, CA. January 13, 2012.

Smith, K.P. Winter Malting Barley Variety Development
Progress and Challenges. Next Generation Barley Varieties III, Jan 16, 2012, Hacienda Hotel, San Diego, CA.

Vikram, V., R. D. Horsely, and K. P. Smith. 2012. Association-mapping with elite breeding lines from two North American barley improvement programs. Plant & Animal Genomes XVIII Conference, January 14-18, 2012, Town & Country Convention Center, San Diego, CA.

Smith, K. P., J. Wiersma, R. Dill-Macky, J. Wiersma, B. Steffenson, and E. Schiefelbein 2011 Barley Variety Performance in Minnesota. Prairie Grains Issue 116.