

**USDA-ARS/
U.S. Wheat and Barley Scab Initiative
FY15 Final Performance Report
Due date: July 15, 2016**

Cover Page

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Phone:	919-513-0696
Fiscal Year:	2015
USDA-ARS Agreement ID:	N/A
USDA-ARS Agreement Title:	Genotyping Breeding Lines for FHB Resistance.
FY15 USDA-ARS Award Amount:	\$ 154,560

USWBSI Individual Project(s)

USWBSI Research Category*	Project Title	ARS Award Amount
EC-HQ	Genotyping Breeding Lines for FHB Resistance.	\$ 154,560
	FY15 Total ARS Award Amount	\$ 154,560

Principal Investigator

Date

* MGMT – FHB Management
 FST – Food Safety & Toxicology
 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
 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: Genotyping Breeding Lines for FHB Resistance.

1. What are the major goals and objectives of the project?

The Eastern Regional Small Grain Genotyping interacts with breeders in the Southern and Northern soft winter wheat growing region interested in using molecular markers to develop wheat cultivars with improved resistance to FHB. We proposed to continue to participate in coordinated regional effort to better characterize eastern soft wheat germplasm utilizing molecular markers and develop improved methods for genotyping. The specific objectives of this proposal were (1) to characterize entries in the Southern (SUWWSN) and Northern (NUWWSN and PNUWWSN) scab screening nurseries with markers linked to FHB QTL; (2) to characterize entries with diagnostic markers for genes having major effects on plant growth and development, as well as genes conferring resistance to other pests and for quality traits; (3) to investigate next generation sequencing (NGS) analysis as a means of genotyping SRWW to identify QTL associated with FHB resistance and performing genomic selection (GS). This project will provide genotypic data to breeders for use in selecting lines for advancement and identification of FHB resistant parents for crossing. This project will increase the capacity of the genotyping lab to process genotyping-by-sequencing (GBS) projects for wheat and result in the mapping of genomic regions involved in disease resistance

2. What was accomplished under these goals?

1) major activities

Entries in the eastern FHB screening nurseries were planted and DNA isolated from tissue was used for KSAP marker genotyping. In collaboration with University of Maryland and University of Illinois, analysis of DNA sequencing data was done for two mapping populations and an association mapping panel that had been evaluated for FHB resistance. Equipment was purchased for automated DNA isolation for improved genotyping throughput.

2) specific objectives

Entries in the Southern (SUWWSN) and Northern (NUWWSN and PNUWWSN) scab screening nurseries were evaluated with a total of 40 markers that were linked to FHB QTL or diagnostic markers for genes having major effects on plant growth and development, resistance to other pests and for quality traits. Data were provided to collaborators. DNA sequence data from two mapping populations and an association mapping panel data were aligned to the draft reference genome for wheat and thousands of SNP were identified that could be assigned to chromosome locations by alignment to the wheat chromosome arm survey sequence.

3) significant results

Genotyping reports are considered by breeders when selecting lines for advancement and as parents for crossing. Analysis done collaboratively with coordinator of the SUWWSN determined that *Fhb1*, along with new markers identified in eastern wheat cultivars, were significantly associated with FHB resistance in this nursery. As a result, new KASP assays were added to the screening panel for use in future years. Our analysis pipeline was used to identify a set of 19,992 SNPs that were used for genome wide association analysis for FHB resistance in a panel of lines evaluated by the University of Illinois

breeding program. Ten significant SNP-trait associations were detected on chromosomes 4A, 6A, 7A, 1D, 4D, 7D, and multiple SNPs were associated with *Fhb1* on chromosome 3B. Combinations of favorable alleles of these SNPs resulted in lower levels of severity (SEV), incidence (INC), and deoxynivalenol (DON) concentration; however, lines carrying multiple beneficial alleles were in very low frequency for most traits. The SNP dataset was also used in conjunction with the major KASP assays to develop and compare genomic selection (GS) models and marker-assisted selection (MAS) for FHB resistance. Intermediate to high values of prediction accuracy (0.4 – 0.9) were observed for most GS models, with lower values (< 0.3) found for MAS models. Treating QTL as fixed effects in GS models resulted in higher prediction accuracy when compared with a GS model with only random effects, but overestimated accuracies were obtained with *in house* QTL. For the same selection intensity, GS resulted in higher selection differentials than MAS for all traits. These results indicate that GS is a more appropriate strategy than MAS for FHB resistance.

4) key outcomes or other achievements

The combined analysis of phenotypic data from the inoculated FHB nurseries with DNA markers linked to QTL and genome-wide SNPs is improving our understanding of the basis of FHB resistance in eastern wheat germplasm. As a result, new breeding strategies are being implemented that include genome wide analysis and selection.

3. What opportunities for training and professional development has the project provided?

Two graduate students and a post-doctoral scientist were trained in statistical analysis of phenotypic data, handling of large SNP marker datasets, association mapping analysis and development of genomic selection models. Extensive training in bioinformatics was provided to a post-doctoral scientist and an undergraduate student. Both have become proficient in use of the TASSEL GBS pipeline for identification of variants from DNA sequence data, as well as use of the Linux command line, and development of Perl and Python scripts for data analysis.

4. How have the results been disseminated to communities of interest?

Graduate student Martin Sarinelli provided a short training seminar on use of genomic selection to five eastern wheat breeders during a field visit to Raleigh, NC during June 2015.

Training of Next Generation Scientists

Instructions: Please answer the following questions as it pertains to the FY15 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 FY15 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 FY15 award period? YES**

If yes, how many? 1

- 3. Have any post docs who worked for you during the FY15 award period and were supported by funding from your USWBSI grant taken faculty positions with universities? NO**

If yes, how many?

- 4. Have any post docs who worked for you during the FY15 award period and were supported by funding from your USWBSI grant gone on to take positions with private ag-related companies or federal agencies? NO**

If yes, how many?

Release of Germplasm/Cultivars

Instructions: In the table below, list all germplasm and/or cultivars released with full or partial support through the USWBSI during the FY15 award period. All columns must be completed for each listed germplasm/cultivar. Use the key below the table for Grain Class abbreviations. *Leave blank if you have nothing to report or if your grant did NOT include any VDHR-related projects.*

Name of Germplasm/Cultivar	Grain Class	FHB Resistance (S, MS, MR, R, where R represents your most resistant check)	FHB Rating (0-9)	Year Released

Add rows if needed.

NOTE: List the associated release notice or publication under the appropriate sub-section in the ‘Publications’ section of the FPR.

Abbreviations for Grain Classes

- Barley - BAR
- Durum - DUR
- Hard Red Winter - HRW
- Hard White Winter - HWW
- Hard Red Spring - HRS
- Soft Red Winter - SRW
- Soft White Winter - SWW

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PI: Brown-Guedira, Gina

USDA-ARS Agreement #: N/A

Publications, Conference Papers, and Presentations

Refer to the FY15-FPR_Instructions for listing publications/presentations about your work that resulted from all of the projects included in the FY15 grant. If you did not have any publications or presentations, state 'Nothing to Report' directly above the Journal publications section.

Journal publications.

Arruda MP, Brown P, Brown-Guedira G, Krill AM, Thurber C, Merrill KR, Foresman BJ, Kolb FL. Genome-Wide Association Mapping of Fusarium Head Blight Resistance in Wheat using Genotyping-by-Sequencing. *The Plant Genome*. 2016 Mar 1;9(1).

Status: Article Published

Acknowledgement of Federal Support: YES

Arruda MP, Lipka AE, Brown PJ, Krill AM, Thurber C, Brown-Guedira G, Dong Y, Foresman BJ, Kolb FL. Comparing genomic selection and marker-assisted selection for Fusarium head blight resistance in wheat (*Triticum aestivum*). *Molecular Breeding*. 2016 Jul 1;36(7):1-1.

Status: Article Published

Acknowledgement of Federal Support: YES

Islam MS, Brown-Guedira G, Van Sanford D, Ohm H, Dong Y, McKendry AL. Novel QTL associated with the Fusarium head blight resistance in Truman soft red winter wheat. *Euphytica*. 2016 Feb 1;207(3):571-92.

Status: Article Published

Acknowledgement of Federal Support: YES

Clark AJ, Sarti-Dvorjak D, Brown-Guedira G, Dong Y, Baik BK, Van Sanford DA. Identifying Rare FHB-Resistant Segregants in Intransigent Backcross and F2 Winter Wheat Populations. *Frontiers in microbiology*. 2016;7.

Status: Article Published

Acknowledgement of Federal Support: YES

Books or other non-periodical, one-time publications.

Other publications, conference papers and presentations.