

**USDA-ARS/
U.S. Wheat and Barley Scab Initiative
FY16 Final Performance Report
Due date: July 28, 2017**

Cover Page

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Phone:	919-513-0696
Fiscal Year:	2016
USDA-ARS Agreement ID:	N/A
USDA-ARS Agreement Title:	Genotyping Breeding Lines for FHB Resistance.
FY16 USDA-ARS Award Amount:	\$ 33,695

USWBSI Individual Project(s)

USWBSI Research Category*	Project Title	ARS Award Amount
VDHR-NWW	Genotyping Lines for FHB Resistance - Northern.	\$ 18,300
VDHR-SWW	Genotyping Lines for FHB Resistance - Southern.	\$ 15,395
	FY16 Total ARS Award Amount	\$ 33,695

GINA BROWN GUEDIRA

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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 Lines for FHB Resistance - Northern.*

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

The specific objectives of this proposal are (1) to characterize entries in the 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 use next generation sequencing (NGS) analysis to genotype SRWW to identify QTL associated with FHB resistance and perform genomic selection (GS). This project will provide breeders with genotypic data for loci linked to FHB resistance as well as genomic estimated breeding values for selecting lines for advancement and identification of FHB resistant parents for crossing. This project utilizes the capacity of the genotyping lab to work cooperatively with breeding programs to identify genomic regions involved in disease resistance and develop GS models.

2. What was accomplished under these goals? *Address items 1-4) below for each goal or objective.*

- 1) Major activities – Genomic DNA was isolated from entries in the 2016 NUWWSN and PNUWWSN. KASP assays developed for markers linked to FHB resistance QTL including QTL from Asian sources (Fhb1, QTL on chromosome 5A and 2D) as well as QTL more recently identified from SRWW sources including the cultivars Bess, NC-Neuse and Jamestown.
- 2) Specific objective: Characterize entries in the Northern (NUWWSN and PNUWWSN) scab screening nurseries with markers linked to FHB QTL.
- 3) Significant results: Analyses indicate that the new QTL from SRWW sources contribute significantly to reducing FHB levels.
- 4) Key outcomes or other achievements: These new markers linked to FHB resistance QTL are now evaluated on all entries in the eastern uniform and collaborative nurseries as well as three-way cross F1s and other materials submitted by breeders. Data are used for selection of parents for targeted crossing to improve FHB resistance and selection of doubled haploid mother plants segregating for multiple FHB resistance genes.

- 1) Major activities – Genomic DNA was isolated from entries in the 2016 NUWWSN and PNUWWSN. KASP assays developed for markers linked to genes for plant growth and development, disease resistance genes, and quality traits were evaluated on all entries.
- 2) Specific objective: 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) Significant results: Nurseries were evaluated with markers linked to 45 loci and reports were shared with contributors. Data were also provided to the T3 database.
- 4) Key outcomes or other achievements: Data are used for selection of parents for crossing. Genotypes of major genes can also be utilized as co-variates to improve efficiency of genomic selection models.

- 1) Major activities – Genomic DNA was isolated from entries in the 2014, 2015 and 2016 NUWWSN and PNUWWSN. Next generation sequencing was done to identify genome-wide SNP markers.
- 2) Specific objective: To use next generation sequencing (NGS) analysis to genotype SRWW to identify QTL associated with FHB resistance and perform genomic selection (GS).
- 3) Significant results: Genotyping of all entries in the 2014, 2015 and 2016 NUWWSN and PNUWWSN identified more than 30,000 polymorphic SNP markers.
- 4) Key outcomes or other achievements: SNP marker data is being combined with phenotypic data collected by breeders to develop genomic selection models for FHB resistance traits, in addition to other traits such as grain yield.

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

The efforts of a PhD student and a post-doctoral scientist have been directed towards this project. The student and post-docs each contributed to development of a workshop on genomic selection in wheat held at Raleigh, NC during Sept. 2016 that received additional support from the USWBSI. The workshop was attended by more than 30 wheat breeders, graduate students and support scientists from NCSU, UGA, LSU, UA, MSU, UI, OSU, Purdue, VA Tech, and UK.

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

Genotypic data was provided to public and private wheat breeders via email in the form of marker reports on the nurseries. Marker data for major genes/QTL was uploaded to the T3 database.

Project 2: *Genotyping Lines for FHB Resistance - Southern.*

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

The specific objectives of this proposal are (1) to characterize entries in the Southern scab screening nursery 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 use next generation sequencing (NGS) analysis to genotype SRWW to identify QTL associated with FHB resistance and perform genomic selection (GS). This project will provide breeders with genotypic data for loci linked to FHB resistance as well as genomic estimated breeding values for selecting lines for advancement and identification of FHB resistant parents for crossing. This project utilizes the capacity of the genotyping lab to work cooperatively with breeding programs to identify genomic regions involved in disease resistance and develop GS models.

2. What was accomplished under these goals? *Address items 1-4) below for each goal or objective.*

1) Major activities – Genomic DNA was isolated from entries in the 2016 Uniform Southern Soft Red Winter Wheat Scab Nursery. KASP assays developed for markers linked to FHB resistance QTL including QTL from Asian sources (Fhb1, QTL on chromosome 5A and 2D) as well as QTL more recently identified from SRWW sources including the cultivars Bess, NC-Neuse and Jamestown.

2) Specific objective: Characterize entries in the Southern scab screening nurseries with markers linked to FHB QTL.

3) Significant results: Analyses indicate that the new QTL from SRWW sources contribute significantly to reducing FHB levels.

4) Key outcomes or other achievements: These new markers linked to FHB resistance QTL are now evaluated on all entries in the eastern uniform and collaborative nurseries as well as three-way cross F1s and other materials submitted by breeders. Data are used for selection of parents for targeted crossing to improve FHB resistance and selection of doubled haploid mother plants segregating for multiple FHB resistance genes.

1) Major activities – Genomic DNA was isolated from entries in the 2016 Uniform Southern Soft Red Winter Wheat Scab Nursery. KASP assays developed for markers linked to genes for plant growth and development, disease resistance genes, and quality traits were evaluated on all entries.

2) Specific objective: 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) Significant results: Nurseries were evaluated with markers linked to 45 loci and reports were shared with contributors. Data were also provided to the T3 database.

4) Key outcomes or other achievements: Data are used for selection of parents for crossing. Genotypes of major genes can also be utilized as co-variates to improve efficiency of genomic selection models.

- 1) Major activities – Genomic DNA was isolated from entries in the 2011 to 2016 Uniform Southern Soft Red Winter Wheat Scab Nursery. Next generation sequencing was done to identify genome-wide SNP markers.
- 2) Specific objective: To use next generation sequencing (NGS) analysis to genotype SRWW to identify QTL associated with FHB resistance and perform genomic selection (GS).
- 3) Significant results: Genotyping of all 287 entries in the 2011-2016 USSRWWSN identified more than 15,000 polymorphic SNP markers. Association mapping did not identify highly significant markers associated with FHB resistance. However, accuracies from cross validation for FHB traits were high. The mean observed accuracies (r) from 100 cycles of five-fold cross validation were 0.46 for incidence, 0.66 for severity, 0.61 for Index, 0.59 for FDK, 0.59 for ISK and 0.53 for DON. Addition of markers for the *Rht1* and *Fhb1* loci as fixed effects in the model resulted in small increases in prediction accuracy. In particular, incidence accuracies increased with the addition of the *Rht-D1* marker ($r = 0.50$). DON accuracies were slightly increased with the addition of the *Fhb1* marker ($r = 0.57$). Based on GS models using the 2011-2015 nurseries as a training population, GEBVs were determined and reported for entries in the 2016 Uniform Southern Soft Red Winter Wheat Scab Nursery report. Comparison of predicted values and phenotypes of the 2016 Uniform Southern Soft Red Winter Wheat Scab Nursery indicate using a selection intensity of 40% based on genomic predictions resulted in selection 10 of the 11 most FHB resistant lines for DON content of grain and 9 of the top 11 lines based ratings of Fusarium Damaged Kernels (FDK).
- 4) Key outcomes or other achievements: Overall, our results suggest that GS for FHB resistance can be utilized to streamline variety selection and evaluation. This work is continuing to expand as the models developed are being used to predict FHB resistance in earlier generation breeding lines provided by breeders.

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

The efforts of a post-doctoral scientist and two PhD students (one supported by the NC Small Grains Growers Association) have been directed towards this project. The students and post-doc each attended and contributed to development of a workshop on genomic selection in wheat held at Raleigh, NC during Sept. 2016 that received additional support from the USWBSI. The workshop was attended by more than 30 wheat breeders, graduate students and support scientists from NCSU, UGA, LSU, UA, MSU, UI, OSU, Purdue, VA Tech, and UK.

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

Genotypic data was provided to public and private wheat breeders via email in the form of marker reports on the nurseries. Marker data for major genes/QTL is also uploaded to the T3 database. Genomic predications for FHB traits were included in the 2016 Uniform Southern Soft Red Winter Wheat Scab Nursery report.

Training of Next Generation Scientists

Instructions: Please answer the following questions as it pertains to the FY16 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 FY16 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 FY16 award period? Yes**

If yes, how many? One

- 3. Have any post docs who worked for you during the FY16 award period and were supported by funding from your USWBSI grant taken faculty positions with universities? Yes**

If yes, how many? One

- 4. Have any post docs who worked for you during the FY16 award period and were supported by funding from your USWBSI grant gone on to take positions with private ag-related companies or federal agencies?**

If yes, how many? Yes. One.

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 FY16 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

Publications, Conference Papers, and Presentations

Instructions: Refer to the FY16-FPR_Instructions for detailed instructions for listing publications/presentations about your work that resulted from all of the projects included in the FY16 grant. Only include citations for publications submitted or presentations given during your award period. If you did not have any publications or presentations, state ‘Nothing to Report’ directly above the Journal publications section.

Journal publications.

Petersen, S., Lyerly, J.H., Maloney, P.V., Brown-Guedira, G., Cowger, C., Costa, J.M., Dong, Y. and Murphy, J.P., 2016. Mapping of Head Blight Resistance Quantitative Trait Loci in Winter Wheat Cultivar NC-Neuse. *Crop Sci.* 56:1473-1483.

Status: Manuscript Published

Acknowledgement of Federal Support: YES

Arruda, M.P., Lipka, A.E., Brown, P.J., Krill, A.M., Thurber, C., Brown-Guedira, G., Dong, Y., Foresman, B.J. and Kolb, F.L., 2016. Comparing genomic selection and marker-assisted selection for Fusarium head blight resistance in wheat (*Triticum aestivum*). *Mol Breeding*, 36:1-11.

Status: Manuscript Published

Acknowledgement of Federal Support: YES

Islam, M.S., Brown-Guedira, G., Van Sanford, D., Ohm, H., Dong, Y. and McKendry, A.L., 2016. Novel QTL associated with the Fusarium head blight resistance in Truman soft red winter wheat. *Euphytica*, 207:571-592.

Status: Manuscript Published

Acknowledgement of Federal Support: YES

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

Other publications, conference papers and presentations.

Brown-Guedira G., J. M. Sarinelli, P. Tyagi, J. Lyerly, R. Acharya and P. Murphy. Genomic Selection for FHB Resistance Using the Uniform Scab Screening Nurseries. In: *Proceedings of the 2016 National Fusarium Head Blight Forum*. S. Canty, K. Wolfe, D. Van Sanford (eds.). December 4-6, 2016. Hyatt Regency St. Louis, MO. Saint Louis, MO. P. 75.

Status: Abstract Published and Poster Presented

Acknowledgement of Federal Support: YES (poster), NO (abstract)

Murphy P., J. Lyerly, J. M. Sarinelli, P. Tyagi and G. Brown-Guedira. The 2016 Uniform Southern Soft Red Winter Wheat Scab Nursery. In: *Proceedings of the 2016 National Fusarium Head Blight Forum*. S. Canty, K. Wolfe, D. Van Sanford (eds.). December 4-6, 2016. Hyatt Regency St. Louis, MO. PP. 83-84.

Status: Abstract Published and Poster Presented

FY16 Final Performance Report
PI: Brown-Guedira, Gina

Acknowledgement of Federal Support: YES (poster), NO (abstract)