


**USDA-ARS**  
**U.S. Wheat and Barley Scab Initiative**  
**FY18 Performance Report**  
**Due date: July 12, 2019**

**Cover Page**

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<b>Fiscal Year:</b>	2018
<b>USDA-ARS Agreement ID:</b>	59-0206-7-009
<b>USDA-ARS Agreement Title:</b>	Genotyping Breeding Lines for FHB Resistance.
<b>FY18 USDA-ARS Award Amount:</b>	\$ 51,720
<b>Recipient Organization:</b>	North Carolina State University Office of Contracts & Grants Box 7214 Raleigh, NC 27695-7214
<b>DUNS Number:</b>	04-209-2122
<b>EIN:</b>	56-6000756
<b>Recipient Identifying Number or Account Number:</b>	572204
<b>Project/Grant Reporting Period:</b>	6/1/18 - 5/31/19
<b>Reporting Period End Date:</b>	05/31/19

**USWBSI Individual Project(s)**

<b>USWBSI Research Category*</b>	<b>Project Title</b>	<b>ARS Award Amount</b>
VDHR-NWW	Genotyping FHB Nurseries - Northern.	\$ 27,011
VDHR-SWW	Genotyping FHB Nurseries- Southern.	\$ 24,709
	<b>FY18 Total ARS Award Amount</b>	<b>\$ 51,720</b>



July 9, 2019

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

FY18 Performance Report  
PI: Murphy, J. Paul  
USDA-ARS Agreement #: 59-0206-7-009  
Reporting Period: 6/1/18 - 5/31/19

**Project 1:** *Genotyping FHB Nurseries - Northern.*

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

The overall goal of the project is to utilize the capacity of the genotyping lab to work cooperatively with breeding programs to identify genomic regions involved in disease resistance and develop GS models.

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.

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

Objective 1

- 1) Major activities – Genomic DNA was isolated from entries in the 2019 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 six QTL identified from soft red winter wheat sources Bess, NC-Neuse and Jamestown. In addition, these KASP assays were assessed on entries in other collaborative nurseries, including the Uniform Eastern Winter Wheat Regional Nursery, Mason-Dixon, Five State and Soft White Winter Wheat nurseries and advanced lines provided by one public and one private breeding program.
- 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.

FY18 Performance Report

PI: Murphy, J. Paul

USDA-ARS Agreement #: 59-0206-7-009

Reporting Period: 6/1/18 - 5/31/19

Objective 2

- 1) Major activities – Genomic DNA was isolated from entries in the 2019 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 48 loci and reports were shared with contributors. Data are available on USDA-ARS website.
- 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.

Objective 3

- 1) Major activities – Sequence based genotyping was performed on entries in the 2014 through 2019 NUWWSN and PNUWWSN. Phenotypic data were obtained from the nursery coordinator. These data were combined with the genotypic and phenotypic data available from the Northern SRWW Coordinated Multi-PI Project (MPI4) to develop a large training set.
- 2) Specific objective: To use next generation sequencing (NGS) analysis to genotype SRWW to identify QTL associated with FHB resistance and perform genomic selection.
- 3) Significant results: Genotyping of all entries in the 2014 to 2018 NUWWSN and PNUWWSN identified more than 30,000 polymorphic SNP markers. Genomic estimated breeding values were calculated for entries of each year of the NUWWSN and PNUWWSN separately, using the remaining years and the MPI4 data as the training population. Encouragingly, the mean correlation between observed and predicted values for DON was quite high each year, with an overall mean of 0.62. These materials were used to calculate GEBVs of entries in the 2018 and 2019 NUWWSN and PNUWWSN that were provided to breeders and the nursery coordinators.
- 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 can be used to predict FHB resistance in earlier generation breeding lines provided by breeders.

FY18 Performance Report

PI: Murphy, J. Paul

USDA-ARS Agreement #: 59-0206-7-009

Reporting Period: 6/1/18 - 5/31/19

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

Partial efforts of two post-doctoral scientists have been directed towards this project. Post-doctoral researcher Dr. Brian Ward has gained experience with analysis of DNA sequence data and building GS model and has interacted with breeder to present results of these analysis at USWBSI Forum during December 2018.

Dr. Luis Rivera-Burgos has gained experience with analysis of DNA sequence data, construction of linkage maps, and QTL analysis for FHB resistance.

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

Genomic predictions for FHB traits have been provided to the nursery coordinator for inclusion in the NUWWSN and PNUWWSN reports. For 2019, GEBVs were also sent directly to the breeders at the end of the growing season.

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 and FHB QTL were also made available on the USDA-ARS Plant Science Research website <https://www.ars.usda.gov/southeast-area/raleigh-nc/plant-science-research/docs/small-grains-genotyping-laboratory/regional-nursery-marker-reports/cooperative-uniform-winter-wheat-scab-nurseries/>

**Project 2: Genotyping FHB Nurseries- Southern.**

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

The overall goal of the project is to utilize the capacity of the genotyping lab to work cooperatively with breeding programs to identify genomic regions involved in disease resistance and develop GS models.

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.

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

Objective 1

- 1) Major activities – Genomic DNA was isolated from entries in the 2019 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.

Objective 2

- 1) Major activities – Genomic DNA was isolated from entries in the 2019 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.

FY18 Performance Report

PI: Murphy, J. Paul

USDA-ARS Agreement #: 59-0206-7-009

Reporting Period: 6/1/18 - 5/31/19

- 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 48 loci and reports were shared with contributors. Data are available on USDA-ARS website.
- 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.

Objective 3

- 1) Major activities – Genomic DNA was isolated from entries in the 2011 to 2019 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 entries in the 2011-2019 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. Based on GS models using the 2011-2018 nurseries as a training population, GEBVs were determined and reported for entries in the 2019 Uniform Southern Soft Red Winter Wheat Scab Nursery report.
- 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. During 2019, models were used to predict FHB traits for approximately 4,000 breeding lines provided by programs at North Carolina State University, University of Arkansas, Louisiana State University, University of Georgia, University of Kentucky and Texas A&M University.

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

The efforts of a post-doctoral scientist have been directed towards this project. The post-doctoral researcher Dr. Brian Ward has interacted with a Research Associate in Dr. Murphy's group to develop genomic predictions, has interacted with breeders, and presented results of analysis at USWBSI Forum during December 2018.

FY18 Performance Report

PI: Murphy, J. Paul

USDA-ARS Agreement #: 59-0206-7-009

Reporting Period: 6/1/18 - 5/31/19

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

Genomic predictions for FHB traits have been provided to the nursery coordinator for inclusion in the SUWWSN report. Genomic estimated breeding values for FHB resistance traits were provided to breeders during the growing season.

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 and FHB QTL were also made available on the USDA-ARS Plant Science Research website

<https://www.ars.usda.gov/southeast-area/raleigh-nc/plant-science-research/docs/small-grains-genotyping-laboratory/regional-nursery-marker-reports/cooperative-uniform-winter-wheat-scab-nurseries/>

FY18 Performance Report  
PI: Murphy, J. Paul  
USDA-ARS Agreement #: 59-0206-7-009  
Reporting Period: 6/1/18 - 5/31/19

## **Training of Next Generation Scientists**

**Instructions:** Please answer the following questions as it pertains to the FY18 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 FY18 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 FY18 award period?**

No

**If yes, how many?**

- 3. Have any post docs who worked for you during the FY18 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 FY18 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?**



FY18 Performance Report  
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 USDA-ARS Agreement #: 59-0206-7-009  
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### 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 FY18 award period. All columns must be completed for each listed germplasm/cultivar. Use the key below the table for Grain Class abbreviations.

*NOTE: 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

FY18 Performance Report  
PI: Murphy, J. Paul  
USDA-ARS Agreement #: 59-0206-7-009  
Reporting Period: 6/1/18 - 5/31/19

## **Publications, Conference Papers, and Presentations**

**Instructions:** Refer to the FY18-FPR\_Instructions for detailed instructions for listing publications/presentations about your work that resulted from all of the projects included in the FY18 grant. Only include citations for publications submitted or presentations given during your award period (6/1/18 - 5/31/19). If you did not have any publications or presentations, state 'Nothing to Report' directly above the Journal publications section.

**NOTE:** Directly below each reference/citation, you must indicate the Status (i.e. published, submitted, etc.) and whether acknowledgement of Federal support was indicated in publication/presentation. See example below for a poster presentation with an abstract:

Conley, E.J., and J.A. Anderson. 2018. Accuracy of Genome-Wide Prediction for Fusarium Head Blight Associated Traits in a Spring Wheat Breeding Program. In: Proceedings of the XXIV International Plant & Animal Genome Conference, San Diego, CA.  
Status: Abstract Published and Poster Presented  
Acknowledgement of Federal Support: YES (poster), NO (abstract)

Nothing to report.

**Journal publications.**

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

**Other publications, conference papers and presentations.**