

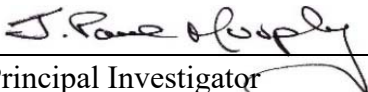
USDA-ARS
U.S. Wheat and Barley Scab Initiative
FY17 Final Performance Report
Due date: July 31, 2018

Cover Page

Principle Investigator (PI):	J. Paul Murphy
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Fiscal Year:	2017
USDA-ARS Agreement ID:	59-0206-7-009
USDA-ARS Agreement Title:	Genotyping Breeding Lines for FHB Resistance.
FY17 USDA-ARS Award Amount:	\$ 71,279
Recipient Organization:	North Carolina State University Office of Contracts & Grants Box 7214 Raleigh, NC 27695-7214
DUNS Number:	04-209-2122
EIN:	56-6000756
Recipient Identifying Number or Account Number:	572204-06050
Project/Grant Reporting Period:	6/1/17 - 5/31/18
Reporting Period End Date:	05/31/18

USWBSI Individual Project(s)

USWBSI Research Category*	Project Title	ARS Award Amount
VDHR-NWW	Genotyping Lines for FHB Resistance - Northern.	\$ 21,802
VDHR-SWW	Genotyping Lines for FHB Resistance - Southern.	\$ 21,802
VDHR-NWW	Support for Genomic Selection in the Eastern Soft Wheat Region.	\$ 27,675
	FY17 Total ARS Award Amount	\$ 71,279


 Principal Investigator

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* 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.*

Objective 1: to characterize entries in the Northern (NUWWSN and PNUWWSN) scab screening nurseries with markers linked to FHB QTL

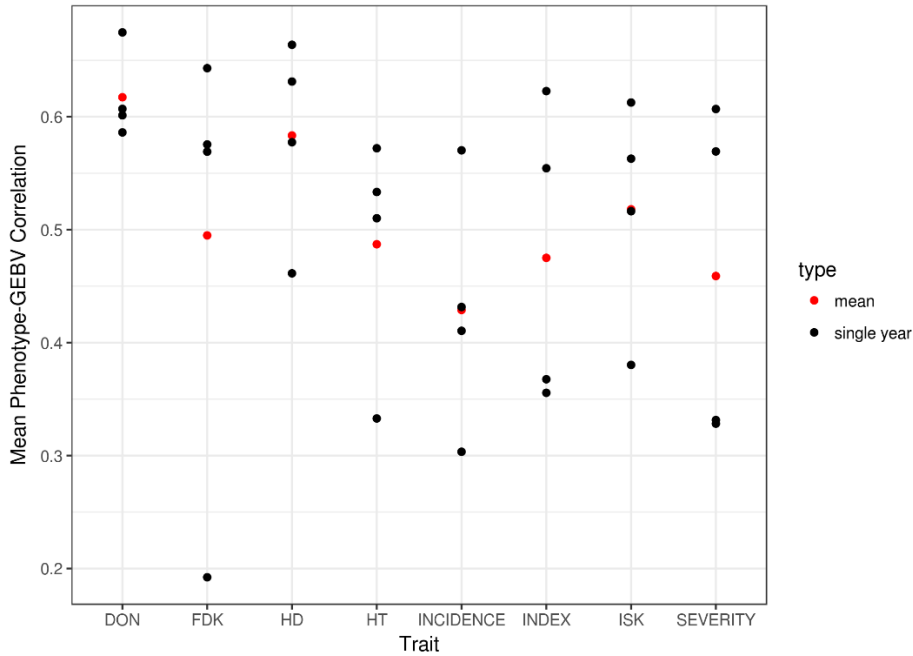
- 1) Major activities: Genomic DNA was isolated from entries in the 2018 NUWWSN and PNUWWSN. KASP assays developed for markers linked to FHB resistance QTL including QTL from Asian sources (Fhb1, QTL on chromosome 5A and 2D) as well as six QTL identified from soft red winter wheat sources Bess, NC-Neuse 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.

Objective 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

- 1) Major activities – Genomic DNA was isolated from entries in the 2018 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 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.

Objective 3: to use next generation sequencing (NGS) analysis to genotype SRWW to identify QTL associated with FHB resistance and perform genomic selection (GS).

- 1) Major activities – Sequence based genotyping was performed on entries in the 2014 through 2018 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 2017 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. The mean correlation between the GEBV and observed values varied for each trait and over years of the nursery as noted in the scatter plot below. Encouragingly, the mean correlation for DON was quite high each year, with an overall mean of 0.62.
- 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 PhD student and two post-doctoral scientists have been directed towards this project. The post-doctoral researcher Martin Sarinelli presented results of these analysis at USWBSI Forum during December, 2017.

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 have been provided to the nursery coordinate for inclusion in the NUWWSN and PNUWWSN reports.

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 (USFHBN) 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). We will also genotype three-way F1 plants to be sent for doubled haploid production. 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.*

Objective 1: to characterize entries in the Southern (USFHBN) scab screening nurseries with markers linked to FHB QTL

1) Major activities: Genomic DNA was isolated from entries in the 2018 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: 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

1) Major activities: Genomic DNA was isolated from entries in the 2018 Uniform Southern Soft Red Winter Wheat Scab Nursery. KASP assays developed for markers linked to genes

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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 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.

Objective 3: to use next generation sequencing (NGS) analysis to genotype SRWW to identify QTL associated with FHB resistance and perform genomic selection (GS)

1) Major activities: Genomic DNA was isolated from entries in the 2011 to 2018 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 2011-2018 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 2011-2017 nurseries as a training population, GEBVs were determined and reported for entries in the 2018 Uniform Southern Soft Red Winter Wheat Scab Nursery report. Comparison of predicted values and phenotypes of the 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. During 2018, models were used to predict FHB traits for approximately 3,200 breeding lines provided by programs at North Carolina State University, University of Arkansas, Louisiana State University, University of Georgia, and Texas A&M University.

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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 post-doctoral scientist and student have established relationships with nursery coordinators and regional wheat breeders to facilitate collaborative research.

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 2017 Uniform Southern Soft Red Winter Wheat Scab Nursery report and will also be included in the 2018 report.

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Project 3: *Support for Genomic Selection in the Eastern Soft Wheat Region.*

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

The overall goal of this project was to augment funding for projects Genotyping Lines for FHB Resistance – Northern and Southern and to facilitate use of genomic selection in the Eastern Soft Wheat Region.

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 2011 to 2018 Uniform Southern Soft Red Winter Wheat Scab Nursery and entries in the 2014 through 2018 NUWWSN and PNUWWSN. Next generation sequencing was done to identify genome-wide SNP markers. Phenotypic data were obtained from the nursery coordinator. Genotypic and phenotypic data were also obtained for 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 (GS).

3) Significant results: When genotypic data from the Uniform Southern Soft Red Winter Wheat Scab Nursery and the NUWWSN and PNUWWSN were combined, highly significant markers associated with FHB resistance were not identified. However, accuracies from cross validation for FHB traits were high, although there did not seem to be an advantage to using the combined nurseries as a training population.

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 PhD student and a post-doctoral scientist have been directed towards this project. The post-doctoral scientist and student have established relationships with nursery coordinators and regional wheat breeders to facilitate collaborative research. The post-doctoral researcher Martin Sarinelli presented results of these analysis at USWBSI Forum during December 2017.

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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 Uniform Southern Soft Red Winter Wheat Scab Nursery report. Genomic predications for FHB traits have been provided to the nursery coordinate for inclusion in the NUWWSN and PNUWWSN reports.

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Training of Next Generation Scientists

Instructions: Please answer the following questions as it pertains to the FY17 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 FY17 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 FY17 award period?** yes

If yes, how many? 1

3. **Have any post docs who worked for you during the FY17 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 FY17 award period and were supported by funding from your USWBSI grant gone on to take positions with private ag-related companies or federal agencies?** Yes; Martin Sarinelli was hired by DonMario Group Seeds as the director for cultivar development for the United States.

If yes, how many? 1

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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 FY17 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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Publications, Conference Papers, and Presentations

Instructions: Refer to the FY17-FPR_Instructions for detailed instructions for listing publications/presentations about your work that resulted from all of the projects included in the FY17 grant. Only include citations for publications submitted or presentations given during your award period (6/1/17 - 5/31/18). 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.

Journal publications.

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

Other publications, conference papers and presentations.

Sarinelli, J. Martin, JP Murphy, R. Acharya, C. Sneller and G. Brown-Guedira. 2017. Regional Approach to Genomic Selection for Scab Resistance. In: Proceedings of 2017 National Fusarium Head Blight Forum, Milwaukee, WI.

Status: Abstract published and invited talk presented

Acknowledgement of Federal Support: YES (presentation), YES (abstract)