

FY22 Performance Progress Report

Due date: July 26, 2023

Cover Page

USDA-ARS Agreement ID:	N/A
USDA-ARS Agreement Title:	Genotyping Eastern Wheat Line for FHB Resistance
Principle Investigator (PI):	Gina Brown-Guedira
Institution:	USDA-Agricultural Research Service
Institution UEI:	N/A
Fiscal Year:	2022
FY22 USDA-ARS Award Amount:	\$50,000
PI Mailing Address:	4114 WILLIAMS HALL NCSU RALEIGH, NC 27695-7620
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Period of Performance:	May 1, 2022 - April 30, 2023
Reporting Period End Date:	April 30, 2023

USWBSI Individual Project(s)

USWBSI Research Category*	Project Title	ARS Award Amount
VDHR-NWW	Genotyping Lines for FHB Resistance - Northern	\$25,000
VDHR-SWW	Genotyping Breeding Lines for FHB Resistance - Southern	\$25,000
FY22 Total ARS Award Amount		\$50,000

I am submitting this report as an: Annual Report

I certify to the best of my knowledge and belief that this report is correct and complete for performance of activities for the purposes set forth in the award documents.



Principal Investigator Signature

July 25, 2023

Date Report Submitted

† BAR-CP – Barley Coordinated Project
 DUR-CP – Durum Coordinated Project
 EC-HQ – Executive Committee-Headquarters
 FST-R – Food Safety & Toxicology (Research)
 FST-S – Food Safety & Toxicology (Service)
 GDER – Gene Discovery & Engineering Resistance
 HWW-CP – Hard Winter Wheat Coordinated Project

MGMT – FHB Management
 MGMT-IM – FHB Management – Integrated Management Coordinated Project
 PBG – Pathogen Biology & Genetics
 TSCI – Transformational Science
 VDHR – Variety Development & Uniform Nurseries
 NWW –Northern Soft Winter Wheat Region
 SPR – Spring 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 research project?

This proposal supports collaborative genomics-assisted selection efforts by the Northern soft winter wheat programs. This project addresses the need to provide breeders with information about the genetic basis of resistance to FHB and other traits in locally adapted and newly introduced germplasm and to improve their ability to select for FHB resistance in cultivars using new breeding approaches. Specific objectives of this continuing research are: (1) to characterize entries in the Southern scab screening nurseries with markers linked to FHB QTL; (2) to characterize entries with diagnostic markers for genes having major effects on plant development and genes conferring resistance to other pests; (3) to implement genome-wide markers analyses to identify QTL associated with FHB resistance and perform genomic selection (GS); (4) to investigate new methodology for collecting genome-wide marker data; and (5) collaborate with complimentary projects to implement genomic selection in eastern soft winter wheat breeding programs.

2. What was accomplished under these goals or objectives? (For each major goal/objective, address these three items below.)

a) What were the major activities?

In support of objectives 1, 2 & 4, a pool of primers for amplicon sequencing targeting markers linked to FHB resistance 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, was used to evaluate eastern germplasm. Markers linked to genes for plant growth and development, disease resistance genes, and quality traits are also included in the primer panel. Genomic DNA was isolated from entries in the 2021 NUWWSN and PNUWWSN and the marker pool evaluated on all entries. In addition, entries in other collaborative nurseries, including the Uniform Eastern Winter Wheat Regional Nursery, the newly established “Big Six” test and advanced lines provided by the NorGrains breeding group were evaluated. This included data for new assays that were added to the trait marker set.

In support of objectives 3 & 5, tissue was received for 3360 breeding lines from collaborators in the Northern VDHR (Ohio State University, Purdue University, University of Illinois University of Kentucky). An additional 2876 samples were received from University of Maryland and Virginia Tech. DNA was isolated, quantified, normalized and libraries prepared. Libraries were also prepared for entries in the Northern FHB nurseries as well as other collaborative tests targeted to this region. Pooled libraries were sent to Michigan State University for sequencing and SNP calling was completed during March 2023. Data were provided the coordinator of the genomic selection and genome-wide association studies for the northern group. Libraries for a subset of lines was also prepared using the Allegro mid-density genotyping platform and sequenced. Data analysis is on-going.

b) What were the significant results?

In support of objectives 1 & 2, nursery reports were provided to cooperators and will be posted on the Plant Science Research Unit website.

In support of objectives 3 & 5, genomic estimated breeding values for FHB resistance traits were provided to breeding programs in time for in field selection of lines.

From objective 4, the amplicon sequencing approach available from the commercial company Agriplex Genomics continues to be robust. Data from the Allegro mid-density platform underdevelopment indicates that reliable library preparation can be done at reduced volumes that are cost effective.

c) List key outcomes or other achievements.

From Objective 1, our analysis indicates that over all eastern nurseries evaluated, 29% of lines have the resistance allele of the *Fhb1* locus, with the percentage being somewhat higher in northern winter wheat germplasm (43%). The Jamestown haplotype associated with resistance on chromosome 1B was present in 31% of northern lines.

Data from objectives 1 & 2, data were used for selection of parents for crossing and tracking the frequency of key alleles in the nurseries. Genotypes of major genes can also be utilized as co-variables to improve efficiency of genomic selection models.

Research in Objective 4 has resulted in a commercially available Agriplex platform that is publicly available so it can be utilized by the wheat research community.

Our results from Objectives 3 & 5, overall, suggest that GS for FHB resistance can be utilized to streamline variety selection and evaluation. This effort includes genotyping thousands of selection candidates at earlier generations to allow for selection prior to entry into the FHB nurseries.

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

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

Joy Horowitz was hired as a technician in the NCSU Department of Crop and Soil Sciences funded by this project. While providing valuable lab assistance, Joy is enrolled in classes at NCSU with the goal of obtaining skills in data science and a certificate in computer science. She is given opportunities to use her computer science training as part of this research.

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

Genotypic data are provided to the coordinators of the genomic selection project. Nursery coordinators include the genomic estimated breeding values for nursery entries in the SUWWSN report and provide GEBVs on breeding lines to the collaborating breeding programs in GA, LA, FL, AR, TX, NC, and SC.

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 will be 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 Breeding Lines for FHB Resistance - Southern

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

This proposal supports collaborative genomics-assisted selection efforts by the Southern soft winter wheat programs. This project addresses the need to provide breeders with information about the genetic basis of resistance to FHB and other traits in locally adapted and newly introduced germplasm and to improve their ability to select for FHB resistance in cultivars using new breeding approaches. Specific objectives of this continuing research are: (1) to characterize entries in the Southern scab screening nurseries with markers linked to FHB QTL; (2) to characterize entries with diagnostic markers for genes having major effects on plant development and genes conferring resistance to other pests; (3) to implement genome-wide markers analyses to identify QTL associated with FHB resistance and perform genomic selection (GS); (4) to investigate new methodology for collecting genome-wide marker data; and (5) collaborate with complimentary projects to implement genomic selection in eastern soft winter wheat breeding programs.

2. What was accomplished under these goals or objectives? (For each major goal/objective, address these three items below.)

a) What were the major activities?

In support of objectives 1, 2 & 4, a pool of primers for amplicon sequencing targeting markers linked to FHB resistance 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, was used to evaluate eastern germplasm. Markers linked to genes for plant growth and development, disease resistance genes, and quality traits are also included in the primer panel. Genomic DNA was isolated from entries in the 2021 SUWWSN and the marker pool evaluated on all entries. In addition, entries in other collaborative nurseries, including the Uniform Southern Winter Wheat Regional Nursery, Gulf Atlantic Wheat Nursery and advanced lines provided by the SunGrains breeding cooperative were evaluated. This included data for new assays that were added to the trait marker set.

In support of objectives 3 & 5, tissue was received for 3936 breeding lines from collaborators in the Southern VDHR (North Carolina State University, Clemson, University of Georgia, Louisiana State University, University of Florida, University of Arkansas, Texas A&M). DNA was isolated, quantified, normalized and libraries prepared. Libraries were also prepared for entries in the Southern FHB nurseries as well as other collaborative tests targeted to this region. Pooled libraries were sent to Michigan State University for sequencing and SNP calling was completed during February 2023. Data were provided to Jeanette Lyerly, coordinator of the genomic selection and genome-wide association studies for the southern group. Libraries for a subset of lines was also prepared using the Allegro mid-density genotyping platform and sequenced. Data analysis is on-going.

b) What were the significant results?

In support of objectives 1 & 2, nursery reports were provided to cooperators and will be posted on the Plant Science Research Unit website.

In support of objectives 3 & 5, genomic estimated breeding values for FHB resistance traits were provided to breeding programs in time for in field selection of lines.

From objective 4, the amplicon sequencing approach available from the commercial company Agriplex Genomics continues to be robust. Data from the Allegro mid-density platform underdevelopment indicates that reliable library preparation can be done at reduced volumes that are cost effective.

c) List key outcomes or other achievements.

From Objective 1, our analysis indicates that over all eastern nurseries evaluated, 29% of lines have the resistance allele of the *Fhb1* locus, with the percentage being somewhat lower in southern germplasm (19%). Ongoing analysis of the QTL effects indicate that the Jamestown haplotype on chromosome 1B that is present in 32% of southern lines is significantly associated with improved resistance in the Southern Uniform Winter Wheat Scab Screening nursery.

Data from objectives 1 & 2, data were used for selection of parents for crossing and tracking the frequency of key alleles in the nurseries. Genotypes of major genes can also be utilized as co-variates to improve efficiency of genomic selection models.

Research in Objective 4 has resulted in a commercially available Agriplex platform that is publicly available so it can be utilized by the wheat research community.

Our results from Objectives 3 & 5, overall, suggest that GS for FHB resistance can be utilized to streamline variety selection and evaluation. This effort includes genotyping thousands of selection candidates at earlier generations to allow for selection prior to entry into the FHB nurseries.

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

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

Joy Horowitz was hired as a technician in the NCSU Department of Crop and Soil Sciences funded by this project. While providing valuable lab assistance, Joy is enrolled in classes at NCSU with the goal of obtaining skills in data science and a certificate in computer science. She is given opportunities to use her computer science training as part of this research.

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Publications, Conference Papers, and Presentations

Please include a listing of all your publications/presentations about your FHB work that were a result of funding from your FY22 grant award. Only citations for publications published (submitted or accepted) or presentations presented during the **award period** should be included.

Did you publish/submit or present anything during this award period May 1, 2022 – April 30, 2023?

Yes, I've included the citation reference in listing(s) below.

No, I have nothing to report.

Journal publications as a result of FY22 award

List peer-reviewed articles or papers appearing in scientific, technical, or professional journals. Include any peer-reviewed publication in the periodically published proceedings of a scientific society, a conference, or the like.

Identify for each publication: Author(s); title; journal; volume; year; page numbers; status of publication (published [include DOI#]; accepted, awaiting publication; submitted, under review; other); acknowledgement of federal support (yes/no).

Winn, Z.J., Lyerly, J.H., Brown-Guedira, G., Murphy, J.P. and Mason, R.E., 2023. Utilization of a publicly available diversity panel in genomic prediction of Fusarium head blight resistance traits in wheat. *The Plant Genome*, p.e20353. <https://doi.org/10.1002/tpg2.20353>. Acknowledged federal support: Yes

Books or other non-periodical, one-time publications as a result of FY22 award

Report any book, monograph, dissertation, abstract, or the like published as or in a separate publication, rather than a periodical or series. Include any significant publication in the proceedings of a one-time conference or in the report of a one-time study, commission, or the like.

Identify for each one-time publication: Author(s); title; editor; title of collection, if applicable; bibliographic information; year; type of publication (book, thesis, or dissertation, other); status of publication (published; accepted, awaiting publication; submitted, under review; other); acknowledgement of federal support (yes/no).

Other publications, conference papers and presentations as a result of FY22 award

Identify any other publications, conference papers and/or presentations not reported above. Specify the status of the publication.