FY21 Performance Progress Report

Due date: July 26, 2022

Cover Page

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Phone:	919-513-0696
Fiscal Year:	2021
USDA-ARS Agreement ID:	N/A
USDA-ARS Agreement Title:	Genotyping Breeding Lines for FHB Resistance
FY20 USDA-ARS Award Amount:	$45,000
Recipient Organization:	USDA-ARS Eastern Regional Small Grains Genotyping Lab NCSU-Crop Science, Campus Box 7620 Raleigh, NC 27695-7620
DUNS Number:	N/A
EIN:	N/A
Project/Grant Period:	5/1/21 - 4/30/22
Reporting Period End Date:	4/30/2022

USWBSI Individual Project(s)

USWBSI Research Category[*]	Project Title	ARS Award Amount
VDHR-NWW	Genotyping Lines for FHB Resistance - Northern	$22,500
VDHR-SWW	Genotyping Lines for FHB Resistance - Southern	$22,500
FY21 Total ARS Award Amount		$45,000

I am submitting this report as an: ☒ Annual Report   ☐ Final 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.

[signature: Gina Brown-Guedira]

_____   July 26, 2022 _____
Principal Investigator Signature   Date Report Submitted

Project 1: Genotyping Lines for FHB Resistance - Northern

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1. What are the major goals and objectives of the research project?
The overall goal of the project is to provide genotyping data to cooperating 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 utilize a database of historical phenotypes on entries in FHB screening nurseries with conjunction with genome-wide SNP data to train genomic selection models and to perform association analysis for identification of QTL associated with FHB resistance; (4) to investigate new methodology for collecting genome-wide marker data; and (5) collaborate with complimentary project "Implementing genomic selection within the NWW Coordinated Project" to implement genomic selection in Northern 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?
Objectives 1 and 2) In collaboration with AgriPlex Genomics, we developed a pool of primers for amplicon sequencing that targeted 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. Markers linked to genes for plant growth and development, disease resistance genes, and quality traits were 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, Mason-Dixon, Five State and Soft White Winter Wheat nurseries and advanced lines provided by one public and one private breeding program were evaluated.

Objective 3) Sequence based genotyping has been performed on entries in the 2014 through 2021 NUWWSN and PNUWWSN. Libraries were prepared and analyzed for approximately 7,500 breeding lines (selection candidates) provided by northern programs. Genotypes were provided to Dr. Brian Ward, post-doc on the Northern Collaborative project. Using the genotypic and phenotypic data available from the prior years' NUWWSN, PNUWWSN and the Northern SRWW Coordinated Multi-PI Project (MPI4) as a training population, GEBV were obtained for the 2021 nursery entries and all genotyped selection candidates.

What were the significant results?
Objective 1) Analyses indicate that the new QTL from SRWW sources contribute significantly to reducing FHB levels.

Objective 2) Nurseries were evaluated with markers linked to 48 loci and reports were shared with contributors. Data will be posted on USDA-ARS website.

Objective 3) Genotyping of entries in the 2014 to 2021 NUWWSN and PNUWWSN and 2021 selection candidates 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 correlations between observed and predicted values for FHB traits continue to be high each year.

List key outcomes or other achievements.
Objectives 1 and 2) An amplicon sequencing approach is available from a commercial company (Agriplex Geomics) that can be utilized by USDA-ARS genotyping labs as well as other interested programs. Markers linked to FHB resistance QTL are now evaluated on all entries in the eastern uniform and collaborative nurseries and other materials submitted by breeders. Data are used for selection of parents for targeted crossing to improve FHB resistance and tracking the frequency of resistance alleles in the nurseries.

Objective 2) Data are 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.

Objective 3) Overall, our results suggest that GS for FHB resistance can be utilized to streamline variety selection and evaluation. The work was greatly expanded this year to included 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 as at NCSU with the goal of obtaining skills in data science and a certificate in computer science. She is given opportunities to use this new 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 NUWWSN

(Form – PPR21)

and PNUWWSN reports and provide GEBVs on breeding lines to the collaborating breeding programs in KY, OH, IN, IL, MI, and NY.

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 Lines for FHB Resistance - Southern

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1.   What are the major goals and objectives of the research project?
The overall goals of the project are:
1 - Characterize entries in the FHB screening nurseries with DNA markers linked to genes/QTL, including those associated with FHB resistance.

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 utilize a database of historical phenotypes on entries in FHB screening nurseries with conjunction with genome-wide SNP data to train genomic selection models and to perform association analysis for identification of QTL associated with FHB resistance; (4) to investigate new methodology for collecting genome-wide marker data; and (5) collaborate to implement genomic selection in southern soft winter wheat breeding programs.

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

What were the major activities?
Objectives 1 and 2) In collaboration with AgriPlex Genomics, we developed a pool of primers for amplicon sequencing that targeted 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. Markers linked to genes for plant growth and development, disease resistance genes, and quality traits were 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.

Objective 3) Sequence based genotyping has been performed on entries in the 2008 through 2021 SUWWSN. Libraries were prepared and analyzed for approximately 4,500 breeding lines (selection candidates) provided by southern programs. Genotypes were provided to Jeanette Lyerly, research associate at NCSU and data analyst for the southern collaborative project. Using the genotypic and phenotypic data available from the prior years' SUWWSN GEBV were obtained for the 2021 nursery entries and all genotyped selection candidates.

What were the significant results?

Objective 1) Analyses indicate that the new QTL from SRWW sources contribute significantly to reducing FHB levels.
Objective 2) Nurseries were evaluated with markers linked to 48 loci and reports were shared with contributors. Data will be posted on USDA-ARS website.

Objective 3) Genotyping of entries in the 2008 to 2021 NUWWSN and PNUWWSN and 2021 selection candidates identified more than 30,000 polymorphic SNP markers. Genomic estimated breeding values were calculated for entries of each year of the SUWWSN, using the remaining years and the MPI4 data as the training population. Encouragingly, the mean correlations between observed and predicted values for FHB traits continue to be high each year.

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Objective 2) Data are 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.

Objective 3) Overall, our results suggest that GS for FHB resistance can be utilized to streamline variety selection and evaluation. The work was greatly expanded this year to included thousands of selection candidates at earlier generations to allow for selection prior to entry into the FHB nurseries.

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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 as at NCSU with the goal of obtaining skills in data science and a certificate in computer science. She is given opportunities to use this new 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 reports and provide GEBVs on breeding lines to the collaborating breeding programs in NC, VA, SC, FL, AR, GA, TX and LA.

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/

Publications, Conference Papers, and Presentations

Please include a listing of all your publications/presentations about your <u>FHB work</u> that were a result of funding from your FY21 grant award. Only citations for publications <u>published</u> (submitted or accepted) or presentations <u>presented</u> during the **award period** should be included.

Did you publish/submit or present anything during this award period?

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

☒ No, I have nothing to report.

Journal publications as a result of FY21 grant 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).

Books or other non-periodical, one-time publications as a result of FY21 grant 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 FY21 grant award

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