

USDA-ARS
U.S. Wheat and Barley Scab Initiative
FY20 Annual Performance Progress Report
Due date: July 29, 2021

Cover Page

Principle Investigator (PI):	Gina Brown-Guedira
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Phone:	919-513-0696
Fiscal Year:	2020
USDA-ARS Agreement ID:	N/A
USDA-ARS Agreement Title:	Genotyping Breeding Lines for FHB Resistance
FY20 USDA-ARS Award Amount:	\$ 72,813
Project/Grant Reporting Period:	5/1/20 - 4/30/21
Reporting Period End Date:	4/30/2021

USWBSI Individual Project(s)

USWBSI Research Category*	Project Title	ARS Award Amount
VDHR-NWW	Genotyping Lines for FHB Resistance - Northern	\$ 50,313
VDHR-SWW	Genotyping Lines for FHB Resistance - Southern	\$ 22,500
FY20 Total ARS Award Amount		\$ 72,813

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Principal Investigator

Date

* MGMT – FHB Management
FST – Food Safety & Toxicology
R- Research
S – Service (DON Testing Labs)
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 research 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 or objectives? (For each major goal/objective, address these three items below.)

a) What were the major activities?

Objective 1) Genomic DNA was isolated from entries in the 2020 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.

Objective 2) Genomic DNA was isolated from entries in the 2020 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.

Objective 3) Sequence based genotyping has been performed on entries in the 2014 through 2020 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 too obtained for the 2020 nursery entries and all genotyped selection candidates.

b) 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 2020 NUWWSN and PNUWWSN and 2020 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.

c) List key outcomes or other achievements.

Objective 1) Data for 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. Was this research impacted by the COVID-19 pandemic (i.e. university shutdowns and/or restrictions, reduced or lack of support personnel, etc.)? If yes, please explain how this research was impacted or is continuing to be impacted.

Laboratory reagents and supplies for preparation of NGS libraries were often delayed or unavailable. Manual preparation of thousands of samples was required since supplies for automated liquid handlers were not available. Supply chain issues coupled with limits on

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the number of staff allowed in the laboratory and the amount of time allowed on-site severely affected our ability to perform this mission critical work in a timely manner. We continue to be impacted by supply chain issues and shortage of staff hours to get lab work done.

4. 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 this new training as part of this research.

Graduate Student Noah DeWitt has been enrolled in the USDA Pathways Program for students. As part of this training, Noah is responsible for implementing the SNP calling pipeline for genomic selection samples in this research.

5. 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 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

1. What are the major goals and objectives of the research 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 Southern (SUWWSN) 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.

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?

Objective 1) Genomic DNA was isolated from entries in the 2020 SUWWSN. 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 Southern Winter Wheat Regional Nursery, Gulf-Atlantic Wheat Nursery, Uniform Bread Wheat Trial and the SunWheat nurseries and advanced lines provided by two public and one private breeding program.

Objective 2) Genomic DNA was isolated from entries in the 2020 SUWWSN. KASP assays developed for markers linked to genes for plant growth and development, disease resistance genes, and quality traits were evaluated on all entries.

Objective 3) Sequence based genotyping has been performed on entries in the 2020 SUWWSN. Libraries were prepared and analyzed for approximately 7,500 breeding lines (selection candidates) provided by northern programs. Genotypes were provided to Jeanette Lylery, data scientist on the Southern Collaborative project. Using the genotypic and phenotypic data available from the prior years' SUWWSN as a training

population, GEBV were to obtained for the 2020 nursery entries and all genotyped selection candidates.

b) 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 2020 SUWWSN and selection candidates identified more than 30,000 polymorphic SNP markers. Genomic estimated breeding values were calculated for entries of each year of the SUWWSN separately, using the remaining years as the training population. Encouragingly, the mean correlations between observed and predicted values for FHB traits continue to be high each year.

c) List key outcomes or other achievements.

Objective 1) Data for 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, particularly for crosses entered in the double-haploid project. They are also used to track frequency and effects of resistance alleles in the nurseries over time.

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 continues to provide valuable data to make selections for scab resistance on thousands of breeding prior to entry into the FHB nurseries.

3. Was this research impacted by the COVID-19 pandemic (i.e. university shutdowns and/or restrictions, reduced or lack of support personnel, etc.)? If yes, please explain how this research was impacted or is continuing to be impacted.

Laboratory reagents and supplies for preparation of NGS libraries were often delayed or unavailable. Manual preparation of thousands of samples was required since supplies for automated liquid handlers were not available. Supply chain issues coupled with limits on the number of staff allowed in the laboratory and the amount of time allowed on-site

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severely affected our ability to perform this mission critical work in a timely manner. We continue to be impacted by supply chain issues and shortage of staff hours to get lab work done.

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Graduate Student Noah DeWitt has been enrolled in the USDA Pathways Program for students. As part of this training, Noah is responsible for implementing the SNP calling pipeline for genomic selection samples in this research.

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

Genotypic data are provided to the coordinators of the genomic selection project and to individual breeding programs. 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 VA, NC, SC, GA, LA, TX and MD.

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/>

Training of Next Generation Scientists

Instructions: Please answer the following questions as it pertains to the FY20 award period (5/1/20 - 4/30/21). 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 FY20 award period?**

Yes No

If yes, how many? [Click to enter number here.](#)

- 2. Did any graduate students in your research program supported by funding from your USWBSI grant earn their Ph.D. degree during the FY20 award period?**

Yes No

If yes, how many? [Click to enter number here.](#)

- 3. Have any post docs who worked for you during the FY20 award period and were supported by funding from your USWBSI grant taken faculty positions with universities?**

Yes No

If yes, how many? [Click to enter number here.](#)

- 4. Have any post docs who worked for you during the FY20 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 No

If yes, how many? [Click to enter number here.](#)

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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 FY20 award period (5/1/20 - 4/30/21). 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	FHB Rating (0-9)	Year Released
Not applicable to this project.	Select Grain Class	Select what represents your most resistant check	Enter as text 0-9 rating	Select Year
Click here to enter text.	Select Grain Class	Select what represents your most resistant check	Enter as text 0-9 rating	Select Year
Click here to enter text.	Select Grain Class	Select what represents your most resistant check	Enter as text 0-9 rating	Select Year
Click here to enter text.	Select Grain Class	Select what represents your most resistant check	Enter as text 0-9 rating	Select Year
Click here to enter text.	Select Grain Class	Select what represents your most resistant check	Enter as text 0-9 rating	Select Year
Click here to enter text.	Select Grain Class	Select what represents your most resistant check	Enter as text 0-9 rating	Select Year
Click here to enter text.	Select Grain Class	Select what represents your most resistant check	Enter as text 0-9 rating	Select Year
Click here to enter text.	Select Grain Class	Select what represents your most resistant check	Enter as text 0-9 rating	Select Year
Click here to enter text.	Select Grain Class	Select what represents your most resistant check	Enter as text 0-9 rating	Select Year
Click here to enter text.	Select Grain Class	Select what represents your most resistant check	Enter as text 0-9 rating	Select Year
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Click here to enter text.	Select Grain Class	Select what represents your most resistant check	Enter as text 0-9 rating	Select Year
Click here to enter text.	Select Grain Class	Select what represents your most resistant check	Enter as text 0-9 rating	Select Year
Click here to enter text.	Select Grain Class	Select what represents your most resistant check	Enter as text 0-9 rating	Select Year

NOTE: List the associated release notice or publication under the appropriate sub-section in the 'Publications' section of the FPR.

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Publications, Conference Papers, and Presentations

Instructions: Refer to the PR_Instructions for detailed more instructions for listing publications/presentations about your work that resulted from all of the projects included in the FY20 grant award. Only citations for publications published (submitted or accepted) or presentations presented during the **award period (5/1/20 - 4/30/21)** should be included. If you did not publish/submit or present anything, state 'Nothing to Report' directly above the Journal publications section.

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

Z.J. Winn, R. Acharya, J. Lyerly, G. Brown-Guedira, C. Cowger, C. Griffey, J. Fitzgerald, R.E. Mason and J.P. Murphy. 2020. "Mapping of Fusarium Head Blight Resistance in NC13-20076 Soft Red Winter Wheat." In: S. Canty, A. Hoffstetter, and R. Dill-Macky (Eds.), *Proceedings of the 2020 National Fusarium Head Blight Forum* (p. 12.), Virtual; December 7-11. Online: https://scabusa.org/pdfs/NFHB20_Proceedings.pdf.

Status: Abstract Published and Poster Presented

Acknowledgement of Federal Support: YES (Abstract and Poster)

Journal publications.

Carmack, W.J., Clark, A., Dong, Y., Brown-Guedira, G. and Van Sanford, D., 2020. Optical Sorter-Based Selection Effectively Identifies Soft Red Winter Wheat Breeding Lines with *Fhb1* and Enhances FHB Resistance in Lines With and Without *Fhb1*. *Frontiers in Plant Science*, 11, 1318. <https://doi.org/10.3389/fpls.2020.01318>

Status: Paper published

Acknowledgement of Federal Support: YES

Gaire, R., Sneller, C., Brown-Guedira, G., Van Sanford, D.A., Mohammadi, M., Kolb, F.L., Olson, E., Sorrells, M. and Rutkoski, J., 2021. Genetic trends in Fusarium head blight resistance due to 20 years of winter wheat breeding and cooperative testing in the Northern US. *Plant Disease*

Status: Paper published – online first

Acknowledgement of Federal Support: YES

Gaire, R., Brown-Guedira, G., Dong, Y., Ohm, H. and Mohammadi, M., 2021. Genome-wide association studies for Fusarium head blight resistance and it's trade-off with grain yield in soft red winter wheat. *Plant Disease*

Status: Paper published – online first

Acknowledgement of Federal Support: YES

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

None

Other publications, conference papers and presentations.

None