

FY22 Performance Progress Report

Due date: July 26, 2023

Cover Page

USDA-ARS Agreement ID:	N/A
USDA-ARS Agreement Title:	Development of Wheat PHG for FHB Resistance
Principle Investigator (PI):	Katherine Jordan
Institution:	USDA-Agricultural Research Service
Institution UEI:	N/A
Fiscal Year:	2022
FY22 USDA-ARS Award Amount:	\$70,000
PI Mailing Address:	1712 Claflin Rd. 4008 Throckmorton Plant Science Center Manhattan, KS 66506-0121
PI E-mail:	Katherine.Jordan@usda.gov
PI Phone:	785-532-1344
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
TSCI	Haplotype-Informed Prediction of FHB Resistance in US Wheat Breeding Programs	\$70,000
FY22 Total ARS Award Amount		\$70,000

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.



7-18-2023

Principal Investigator Signature

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: Haplotype-Informed Prediction of FHB Resistance in US Wheat Breeding Programs

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

- 1- Expand the diversity of PHG database by incorporating soft and spring wheat germplasm.
- 2- Map novel FHB-resistance QTLs using BLUPs by GWAS and develop diagnostic markers for FHB resistance QTLs for use in breeding programs.
- 3- Build a GS model for FHB resistance for HWW using field-generated phenotypic data
- 4- Test/optimize the GS model on two sets of breeding lines from Kansas and the Great Plains region.

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

1- Expand the diversity of PHG database by incorporating soft and spring wheat germplasm.

a) What were the major activities?

We have added ~15x exome coverage sequencing data of 60 soft and 25 spring wheat varieties to include in the PHG database creation for more informed haplotype representation of the US breeding programs. In addition, we have successfully captured the hard winter wheat varieties that were planted in the field but did not yield DNA for capture. There is now a total of 291 varieties that built the PHG database using exome capture, which include all marker classes. Also, we are currently adding promoter capture sequencing data for the 291 lines to increase variants for mapping and selection.

b) What were the significant results?

By adding the additional ~90 lines of exome capture data we have detected > 1.028 million variants ($MAF \geq 0.01$) across the wheat genome using the PHG database for variant detection. For comparison, we mapped the same exome capture data to CSv2.1 RefSeq reference genome and called variants for same lines using GATK and found 454,075 high quality (HQ) variants with $MAF \geq 0.01$, and het calls < 0.03. The pilot batch (48 lines) of promotor capture additionally detected ~35,000 HQ variants using the GATK variant caller, producing variants outside of the exome region. We are waiting on the subsequent results of the remaining lines for promotor capture, and will add to PHG database.

c) List key outcomes or other achievements.

Using these 290 wheat lines, we have detected over 1 million variants to use with in genome wide association studies (GWAS) and will filter down to include in genomic selection (GS) models for FHB incidence, severity, FDK, and DON. The PHG variant calling method increased the number of HQ variants by more than double with traditionally used variant detection methods. Overall, we feel each marker class is represented in our database, and using $MAF > 0.01$, we will detect associations and find markers to run in a GS models.

2- Map novel FHB-resistance QTLs using BLUPs by GWAS and develop diagnostic markers for FHB resistance QTLs for use in breeding programs.

a) What were the major activities?

From May 2022-July 2022, we completed the first season of field phenotyping at the KSU FHB nursery for heading date, FHB incidence and severity, FDK, and DON content. Field phenotyping season for year 2 (May 2023- July 2023) has just ended and seeds were harvested July 2023. This represents the second year this population has been grown and phenotyped in the KSU FHB nursery. We are ready to score FDK and then will send out samples for DON content. Once the data for both years is collected, we will produce BLUPs to run GWAS on those data.

b) What were the significant results?

Preliminary GWAS results from year one data were obtained using the PHG variants with FDK, DON content, and normalized area under disease curve (AUDPC) that incorporates heading date and FHB severity from days 20-32 post heading. Significant GWAS associations ($p < 10^{-5}$) were detected for all traits measured, including AUDPC. We detected significant associations in the region of FHB1 (3BS) providing proof of concept that our data normalization for heading date was achieved, that our lines contain QTL, and we have the power to detect QTL. We are in the initial phase of analyzing 2023 data, which will include running the same analysis as we did on year 1 data, and generating BLUPs to combine both years to ensure these QTL were repeatable. In addition, the population was grown in the greenhouse (including spring varieties not grown in the field) to provide additional phenotype data for GWAS and GS modeling.

c) List key outcomes or other achievements.

The associations that we see in our initial GWAS correspond to some known FHB genomic regions (FHB1), while others are in novel locations. We hope these associations will replicate with year 2 of our data collection. Providing replication is achieved, markers will be designed, and developed to run diagnostic KASP assays for breeding program selection.

3- Build a GS model for FHB resistance for HWW using field phenotypic data

4- Test/optimize the GS model on two sets of breeding lines from Kansas and the Great Plains region.

- **I am going to combine these objectives, as they are directly tied to each other, and dependent on the GS models based on BLUPs we are currently generating.**

a) What were the major activities?

Two years of field data have been obtained spring 2022 and spring 2023. We are going to generate BLUPs to use as the phenotype for the GS models for normalized AUDPC, FDK, and DON content.

b) What were the significant results?

No significant results yet, but we are hoping to produce predictive models using our field data, which we will extrapolate to other Kansas breeding programs. We will split our dataset into 2 random sets, 70% training data and 30% testing data using BLUP

phenotypes. Models will be run on a subset of PHG markers that will be thinned based on frequency, GWAS signal, and LD across the genome, and tested in the testing population.

c) List key outcomes or other achievements.

No outcomes yet, but we will choose the most predictive model using our training/testing data, and then using that model test our predictions on Kansas wheat breeding programs. In conjunction with Allan Fritz (KSU wheat breeder), we will gather genotype data on the lines he plants in KSU FHB nursery fall 2023 and validate with field season data beginning spring 2024. Similar plans are in place to work with Guorong Zhang (KSU wheat breeder) on his breeding program.

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

Graduate Student, Lawrence Tidakbi began his studies at Kansas State University in the Plant Pathology Department in August 2022. He presented a poster of our preliminary phenotyping and GWAS results at the FHB Forum in Tampa in December 2022, and in San Deigo at PAG in January 2023. Both conferences gave him a chance to discuss our project with research scientists and improve collaborative relationships.

Lawrence also has been added to the WheatCap graduate student cohort, which provides a monthly learning and network-building opportunity for the next generation of graduate students interested in studying quantitative traits to boost yield in wheat. This included his attendance to the WheatCap student workshop that took place the day before PAG began in San Deigo, which gave him a chance to give an oral presentation on this project.

PI Katherine Jordan attended the FHB Forum in Tampa, in December 2022, where we were able to talk future collaborations with this genotype database with other SCAB Initiative scientists.

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

In addition to the posters presented at professional conferences (FHB Forum and PAG), we have shared PHG variant data with some of the breeders that supplied lines to be used in our field study for their use in their own breeding programs for other phenotypic traits. We are waiting on second year results (for replication and BLUPs) before we publish the association results formally.

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).

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.

L. Tidakbi, G. Bai, J. Rupp, K.W. Jordan. (2022). Haplotype-Informed Prediction of Fusarium Head Blight Resistance in USA Wheat Breeding Programs. Proceedings of the National Fusarium Head Blight Forum; Tampa, Florida. December 4-6, 2022. Retrieved from: <https://scabusa.org/forum/2022/2022NFHBFForumProceedings.pdf>

Poster presentation, Acknowledgment of federal support: yes.

L. Tidakbi, K.W. Jordan. Haplotype-Informed Prediction of Fusarium Head Blight Resistance in USA Wheat Breeding Programs. Presented to WheatCap cohort, San Diego, CA, January 13, 2023. **Oral presentation**, acknowledgement of federal support: yes.

L. Tidakbi, G. Bai, J. Rupp, K.W. Jordan. Haplotype-Informed Prediction of Fusarium Head Blight Resistance in USA Wheat Breeding Programs. Presented at Plant and Animal Genomes 30, San Diego, CA, January 16, 2023. **Poster presentation**, acknowledgement of federal support: yes.

L. Tidakbi, G. Bai, J. Rupp, K.W. Jordan. Haplotype-Informed Prediction of Fusarium Head Blight Resistance in USA Wheat Breeding Programs. Presented at Kansas State University Graduate Student Forum, Manhattan, Kansas, March 2023. **Poster presentation**, acknowledgement of federal support: yes.