

USDA-ARS
U.S. Wheat and Barley Scab Initiative
FY19 Performance Report
Due date: July 24, 2020

Cover Page

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Fiscal Year:	2019
USDA-ARS Agreement ID:	59-0206-9-118
USDA-ARS Agreement Title:	Breeding and Genetics of Fusarium Head Blight Resistance in Barley
FY19 USDA-ARS Award Amount:	\$ 183,858
Recipient Organization:	Regents of the University of Minnesota Suite 450 Sponsored FIN RPT-P100100001 Minneapolis, MN 55455-2003
DUNS Number:	555917996
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Project/Grant Reporting Period:	5/13/19 - 5/12/20
Reporting Period End Date:	5/12/2020

USWBSI Individual Project(s)

USWBSI Research Category*	Project Title	ARS Award Amount
BAR-CP	Developing Malting Barley varieties with Enhanced FHB Resistance and Lower DON	\$ 141,901
BAR-CP	Developing and Testing Genome-Wide Marker Methods to Optimize Prediction Accuracy	\$ 41,957
FY19 Total ARS Award Amount		\$ 183,858



Principal Investigator

7/28/2020

Date

* 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: *Developing Malting Barley varieties with Enhanced FHB Resistance and Lower DON*

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

The overall goal of this project is to develop malting barley varieties with enhanced resistance to FHB and lower concentration of the mycotoxin deoxynivalenol (DON). To accomplish this goal, we are conducting a comprehensive FHB breeding effort utilizing greenhouse for crossing and single-seed advance, extensive field trials for FHB evaluation, various uses of markers to improve selection, regional yield and quality testing, and collaborative regional nurseries to evaluate elite breeding lines. Our breeding efforts have concentrated on two-row barley in response to industry needs. We have added a winter barley program to explore more sustainable production systems and potential avoidance of FHB.

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

Objective 1. Create new breeding populations by crossing parents that carry resistance to FHB and other desirable traits;

a) What were the major activities?

In the fall of 2019, we identified a set of 70 parents from our breeding program to make crosses to develop new breeding populations. Most of these 200 new crosses have at least one parent that is lower in DON concentration compared to ND Genesis or is predicted based on genomic selection modeling to have progeny that are lower in DON compared to ND Genesis

b) What were the significant results?

These crosses resulted in the advancement and planting of 138 F2 populations in the spring of 2020.

c) List key outcomes or other achievements.

These activities maintain the steady flow of breeding lines created and advanced to field trials, marker genotyping, and FHB field screening to improve resistance to FHB.

Objective 2. Conduct selection for FHB resistance and lower DON concentration in segregating breeding populations using genetic markers and field screening

a) What were the major activities?

In the summer of 2019, we conducted FHB evaluation in misted and inoculated field nurseries at Crookston and St. Paul, MN totaling just under 5,000 plots. We evaluated FHB severity and harvested selected plots for DON. These nurseries included trials with a selected set of lines from a genetic study of population variance for FHB severity, first year yield trial entries for our spring two-row and spring six-row breeding programs, and advanced breeding lines and varieties. This data was used to select parents and advance

lines in our breeding program. We genotyped 1,400 F3 breeding lines in the Fall of 2019 with genome-wide markers to produce predictions for agronomic performance, malting quality, FHB severity, and DON concentration. This genotypic data was used to select 300 new lines to be entered into first year yield and FHB evaluations for the 2020 growing season.

b) What were the significant results?

Based on re-evaluation of parents, observed phenotype in the New Zealand winter nursery, and marker-based prediction for seven traits including DON, 330 of these lines were harvested and the seed used to plant preliminary yield trials at three locations and FHB nurseries at two locations in the spring of 2020.

c) List key outcomes or other achievements.

We successfully met our target of generating new first year breeding lines for evaluation and evaluating advanced breeding lines for industry evaluation and consideration as new variety candidates.

Objective 3. Advance lines to regional testing and industry evaluation that are candidates for new cultivar releases.

a) What were the major activities?

Four advanced lines (S2M177, S2M179, S2M180, S2M182) from crop year 2019 were advanced to American Malting Barley industry pilot testing for malting quality.

b) What were the significant results?

Advanced line S2M177 was rated satisfactory in AMBA pilot testing with the 2019 crop. It was rated unsatisfactory in the 2018 crop and with multiple years of data, it shows slightly higher DON compared to ND Genesis. We have removed it from release consideration.

Advanced breeding line S2M179 is about 25% lower DON, but with similar agronomic performance compared to ND Genesis. S2M179 was rated satisfactory for quality with the 2018 crop and unsatisfactory for the 2019 crop in AMBA pilot testing. Unfortunately, its diastatic power was too low for adjunct brewing and the FAN was too high for all-malt brewing. We have removed it from release consideration, however the line has been used as a parent in current breeding populations.

Advanced line S2M180 also showed promise with about 20% lower DON compared to ND Genesis, but it was rated unsatisfactory with the 2019 crop in AMBA Pilot testing and also removed from release consideration.

Advanced line S2M182 was rated as satisfactory and has good agronomic performance, however, based on multiple years of DON testing this line is not improved for FHB resistance and has been removed from release consideration.

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c) List key outcomes or other achievements.

While our top two candidates for release this year were removed from consideration for release due to industry evaluation of malting quality, these lines have been used in crosses and should be good parents for future breeding lines.

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

We did not receive DON data back from some of our 2019 grain samples until July which was too late to consider that data for selecting entries for 2020 trials. This was due to all labs being shut down at our University in March. Fortunately, we were able to plant all of our FHB nurseries as planned, but are short handed to assess disease and harvest grain for DON analysis. We are dealing with that situation currently.

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

I have one post-doc (not paid from the USWBSI) that is currently gaining experience with barley breeding and FHB by working with materials and data from this project.

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

All of our raw data is uploaded to the public database, T3 Barley, and is freely available to researchers. Results of the North American Barley Evaluation Nursery (NABSEN) are posted on the USWBSI website. We report the FHB rating for all varieties grown in Minnesota in the MAES Minnesota Field Crop Trials extension publication and in Prairie Grains Magazine. I also discuss FHB breeding research at field days in Minnesota. We provide annual updates to Scab Smart with current variety information.

Project 2: *Developing and Testing Genome-Wide Marker Methods to Optimize Prediction Accuracy*

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

The overall goal of this research is to continue to improve and optimize the ways that we use genome-wide markers in breeding for FHB resistance. Our specific objectives are to continue our work to: 1. Evaluate parent selection based on genome-wide marker effects to increase genetic variance and reduce unfavorable trait correlations; and initiate new work to 2. Map FHB resistance and DON accumulation in elite two-row by six-row crosses and 3. Introgress six-row resistance into two-row barley using genome-wide markers.

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

Objective 1. Evaluate parent selection based on genome-wide marker effects to increase genetic variance and reduce unfavorable trait correlations.

a) What were the major activities?

We generated over 200 crosses in the fall of 2019. In the spring program, 114 of these F2 populations were selected to go to the field in 2020. Thirty of these crosses were designed based on marker-based predictions of parent combinations that should produce progeny with lower DON or reduced correlation of DON with heading date and plant height. The same set of parents that generated the marker-based parent combinations were also used to produce a set of populations based on traditional parent selection.

b) What were the significant results?

We successfully designed and carried out crosses that will allow us to evaluate parent combination selection strategies.

c) List key outcomes or other achievements.

As the lines from these populations move through the breeding program, we will assess the relative success of the marker-based predictions compared to traditional parent selection. We will be able to begin to assess the impact of this parent selection method following the summer of 2021.

Objective 2. Map FHB resistance and DON accumulation in elite two-row by six-row crosses.

a) What were the major activities?

We generated a mapping population between one of our best lines from our six-row FHB breeding program (6MS16_5044-007) and an elite two-row from the NDSU breeding program (2ND32529). Both parents have lower DON, but different breeding histories and presumably different genes for disease resistance. We advanced the lines by single seed descent and selected only two row lines to conform with our breeding program plan and to avoid the confounding effects of spike type on disease resistance. We planted this

mapping population (155 lines) in two FHB nurseries (St. Paul and Crookston) in the spring of 2020.

- b) What were the significant results?
We will have our first results for DON and FHB severity from the 2020 field season. Genotyping of these lines has been put on hold due to lab closures for COVID-19.
- c) List key outcomes or other achievements.
The mapping population was developed and evaluated for the first year.

Objective 3. Introgress six-row resistance into two-row barley using genome-wide markers.

- a) What were the major activities?
This objective will utilize information on the genetic architecture of resistance as determined for the mapping population described in objective 2 and existing genomic selection training populations for two-row and six row barley. We will conduct backcrossing and/or genomic selection to introgress resistance from six-row into two-row barley in selected crosses. We are in the early stages of this project.
- b) What were the significant results?
No results yet.
- c) List key outcomes or other achievements.
None to report

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

We were unable to conduct genotyping for the mapping population described in objective 2. We anticipate that we will be able to complete it this year, but not in time to use that information for selection, thus the selection will be delayed until 2021.

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

One post-doc (not paid from the USWBSI) is currently working with materials and data from this project.

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

All of our raw data is uploaded to the public database, T3 Barley, and is freely available to researchers. A manuscript entitled “Multi-Trait Improvement by Predicting Genetic Correlations in Breeding Crosses” was published in the journal G3 this year.

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Training of Next Generation Scientists

Instructions: Please answer the following questions as it pertains to the FY19 award period (5/13/19 - 5/12/20). 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 FY19 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 FY19 award period?**

Yes

If yes, how many? 1

- 3. Have any post docs who worked for you during the FY19 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 FY19 award period and were supported by funding from your USWBSI grant gone on to take positions with private ag-related companies or federal agencies?**

No

If yes, how many?

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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 FY19 award period. 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 (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 FY19-FPR_Instructions for detailed more instructions for listing publications/presentations about your work that resulted from all of the projects included in the FY19 grant award. Only citations for publications published (submitted or accepted) or presentations presented during the **award period (5/13/19 - 5/12/20)** 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.

Journal publications.

Neyhart, J.L., A.J. Lorenz, and K.P. Smith. 2019. Multi-trait improvement by predicting genetic correlations in breeding crosses. *G3*, 9:3153-3165. <https://doi.org/10.1534/g3.119.400406>.
Status: Manuscript Published
Acknowledgement of Federal Support: YES

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

Other publications, conference papers and presentations.

Neyhart, J.L., Aaron Lorenz and K.P. Smith. 2019. Applied Breeding Simulations: Using Genomewide Markers to Predict Genetic Correlations. Plant and Animal Genome Conference XXVII, January 12-16, 2019, San Diego, CA.
Status: Abstract Published and Poster Presented
Acknowledgement of Federal Support: YES (Abstract and Poster)

Smith, K.P., Neyhart, J.L., Aaron Lorenz and. 2019. “Implementing Cross Selection using Genomewide Predictions for Superior Progeny Mean and Trait Correlations with Fusarium Head Blight Severity.” In: S. Canty, A. Hoffstetter, H. Campbell and R. Dill-Macky (Eds.), *Proceedings of the 2019 National Fusarium Head Blight Forum* (p. 118), Milwaukee, WI; December 8-10. University of Kentucky, Lexington, KY.
Status: Short report Published
Acknowledgement of Federal Support: YES