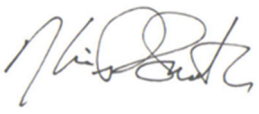
USDA-ARS
U.S. Wheat and Barley Scab Initiative
FY18 Final Performance Report
Due date: July 12, 2019

Cover Page

Principle Investigator (PI):	Kevin Smith
Institution:	University of Minnesota
E-mail:	smith376@umn.edu
Phone:	612-625-1211
Fiscal Year:	2018
USDA-ARS Agreement ID:	59-0206-4-020
USDA-ARS Agreement Title:	Breeding and Genetics of Fusarium Head Blight Resistance in Barley.
FY18 USDA-ARS Award Amount:	$ 179,206
Recipient Organization:	Regents of the University of Minnesota Suite 450 Sponsored FIN RPT-P10010000 Minneapolis, MN 55455-2003
DUNS Number:	555917996
EIN:	41 -6007513
Recipient Identifying Number or Account Number:	CON000000048320
Project/Grant Reporting Period:	5/13/18 - 5/12/19
Reporting Period End Date:	05/12/19

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.	$ 37,305
	FY18 Total ARS Award Amount	$ 179,206



7-12-19

Principal Investigator 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

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Project 1: *Developing Malting Barley varieties with Enhanced FHB Resistance and Lower DON.*

1. **What are the major goals and objectives of the 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 more 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?** *Address items 1-4) below for each goal or objective.*
   1) major activities
   We conducted FHB evaluation in misted and inoculated field nurseries at Crookston and St. Paul, MN for totaling over 7,600 plots. We evaluated FHB severity and harvested selected plots for DON. These nurseries included trials for the second year of 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. We initiated over 200 new crosses in our spring six-row, spring two-row, and winter two-row breeding programs.

   2) specific objectives
   - Develop breeding populations segregating for FHB resistance.
   - Implement early generation genomic selection on F3 plants for DON concentration and other relevant traits.
   - Evaluate breeding lines in replicated field disease nurseries. Field FHB trials were conducted at two locations in Minnesota that utilize overhead mist irrigation and inoculum applied as either grain spawn or as a suspension of conidia with backpack sprayers.

   3) significant results
   One of our spring six-row variety candidates, S6M176 was rated satisfactory in its first year of industry malt evaluations. This line is near isogenic with Lacey and was derived by marker assisted backcrossing a resistance allele from the variety Chevron at a QTL located on chromosome 6H. S6M175 is 37% lower in DON, 2.0% higher in yield, 0.5 days later heading, and slightly taller compared to Lacey.
   We submitted our first three two-row variety candidates for AMBA Pilot testing with the 2018 crop. Two of the three were rated as satisfactory. S2M178 had 13% lower DON, was 0.5% lower in yield, 1.7 days later heading, substantially shorter (11 cm), and better lodging resistance compared to ND Genesis. S2M179 was 39% lower DON, 2.5% higher in yield, 1.4 days earlier heading, shorter, and had better lodging resistance compared to ND Genesis.

4) key outcomes or other achievements

While our six-row variety candidate, S6M175, did well in industry testing, we will not be moving this line forward due to industry preference for two-row barley. Our two spring two-row variety candidates, S2M178 and S2M179 are being grown for a second year of AMBA pilot scale testing with the 2019 crop. We have also started seed increases to allow for possible plant scale testing in 2020.

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

Two undergraduate students and two graduate students participated in FHB research and learned about the breeding challenges and approaches that we use thus contributing to their training and development as scientists.

4. 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 Variety Trials Bulletin and in the publication Prairie Grains. I also discuss FHB breeding research at field days in Minnesota. We have updated 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 project?

The overall goal of the project is to empirically evaluate the effectiveness of genomic selection to improve the breeding of FHB resistant varieties and to develop and evaluate methods to improve prediction accuracy.

2. What was accomplished under these goals? *Address items 1-4) below for each goal or objective.*

1) major activities

We used a training population of 787 lines and 15,066 SNP markers for prediction of spring two rows and 129 lines and 6,755 markers for spring six-rows. We made predictions on F3 breeding lines in the fall of 2018. We conducted cross-validation assessment of accuracy for DON in the spring two-row of 0.47 and 0.23 for parent training population predicting off-spring.

2) specific objectives

- Evaluate parent selection based on genomewide marker effects to increase genetic variance and reduce unfavorable trait correlations;
- Initiate new work to Map FHB resistance and DON accumulation in elite two-row by six-row crosses and
- Introgress six-row resistance into two-row barley using genome-wide markers.

3) significant results

We released a panel of spring two-row barley lines that can be used for mapping and genomic selection for a large number of traits (including FHB and DON) evaluated at many locations. All of the data is available on T3.

We published a paper (see below) where we empirically validated predictions of genetic variance and superior progeny mean for 27 crosses. We concluded that accurate predictions for specific crosses of genetic variance and superior progeny mean are feasible, but as with any implementation of genomewide selection, reliable phenotypic data are critical. Prediction accuracy was lower for traits with lower heritability such as FHB severity.

We are in the process of collecting DON data from two-row by six-row progeny that can be used for association analysis. We have identified two-row lines that have six-row parents with disease resistance in their pedigrees and have initiated crosses with them.

4) key outcomes or other achievements

We are now beginning to use predictions of cross performance in our breeding program.

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

One graduate student is primarily involved in this research. However, we discuss this work in lab meetings so that other students and post-docs can be involved in learning from this project.

4. 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. We will be preparing a draft of a manuscript describing the population variance work once all of the data from this summer have been collected.

Training of Next Generation Scientists

Instructions: Please answer the following questions as it pertains to the FY18 award period. 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 FY18 award period?** No
   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 FY18 award period?**
   Yes
   If yes, how many? 1

3. **Have any post docs who worked for you during the FY18 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 FY18 award period and were supported by funding from your USWBSI grant gone on to take positions with private ag-related companies or federal agencies?**

   If yes, how many? No

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 FY18 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**
S2MET Mapping and Genomic Selection Panel	BAR	range	NA	2019

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

Publications, Conference Papers, and Presentations

Instructions: Refer to the FY18-FPR_Instructions for detailed instructions for listing publications/presentations about your work that resulted from all of the projects included in the FY18 grant. Only include citations for publications submitted or presentations given during your award period (5/13/18 - 5/12/19). If you did not have any publications or presentations, state 'Nothing to Report' directly above the Journal publications section.

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

Conley, E.J., and J.A. Anderson. 2018. Accuracy of Genome-Wide Prediction for Fusarium Head Blight Associated Traits in a Spring Wheat Breeding Program. In: Proceedings of the XXIV International Plant & Animal Genome Conference, San Diego, CA.
Status: Abstract Published and Poster Presented
Acknowledgement of Federal Support: YES (poster), NO (abstract)

Journal publications.

Neyhart, J.L. and Smith, K.P. 2019. Validating the Use of Genomewide Marker Effects and Simulated Populations to Inform Cross Selection in a Contemporary Breeding Program. Crop Sci 59:1062-1072. doi:10.2135/cropsci2018.11.0716
Status: Manuscript Published
Acknowledgement of Federal Support: YES

Neyhart J.L., A. Mills, C. Sellmer, M. Sorrells, D. Sweeney, C. Kapp, A. McFarland, L. Elmore, J. Sherman, R. Horsley, E. Stockinger, P. Hayes, M. Mohammadi, J. Goudet, L. Lukens, H. Darby, P. González, L. Gutierrez, C. Duley, C. Evans, G. Hu, and K. P. Smith. 2019. Registration of the S2MET Barley Mapping Population for Multi-Environment Genomewide Selection. J. Plant Registrations 13:270-280. doi:10.3198/jpr2018.06.0037crmp
Status: Manuscript Published
Acknowledgement of Federal Support: YES

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

Other publications, conference papers and presentations.

Jeffrey L. Neyhart and Kevin P. Smith. 2018. Using Genomewide Markers and Simulated Populations to Predict Genetic Variance and Correlation for Fusarium Head Blight Resistance in Barley. Proceedings of the 2018 National Fusarium Head Blight Forum Hyatt Regency St. Louis at the Arch St. Louis, Missouri, USA December 2-4, 2018.
Status: Proceedings Paper Published
Acknowledgement of Federal Support: YES