

**USDA-ARS/  
U.S. Wheat and Barley Scab Initiative  
FY19 Performance Progress Report - NCE  
Due date: July 29, 2021**

**Cover Page**

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<b>Fiscal Year:</b>	2019
<b>USDA-ARS Agreement ID:</b>	59-0206-7-153
<b>USDA-ARS Agreement Title:</b>	Genetic and Molecular Characterization of New Sources of FHB Resistance in Wheat
<b>FY19 USDA-ARS Award Amount:</b>	\$ 99,142
<b>Recipient Organization:</b>	North Dakota State University Office of Grant & Contract Accounting NDSU Dept 3130, PO Box 6050 Fargo, ND 58108-0650
<b>DUNS Number:</b>	80-388-2299
<b>EIN:</b>	45-6002439
<b>Recipient Identifying Number or Account Number:</b>	FAR0028058
<b>Project/Grant Reporting Period:</b>	5/1/19 - 4/30/21
<b>Reporting Period End Date:</b>	4/30/2021

**USWBSI Individual Project(s)**

<b>USWBSI Research Category*</b>	<b>Project Title</b>	<b>ARS Award Amount</b>
DUR-CP	Identify and Map Novel QTL for FHB Resistance in Durum Wheat	\$ 41,821
VDHR-SPR	Genetic and Molecular Characterization of Novel FHB Resistance QTL in Spring Wheat	\$ 57,321
<b>FY19 Total ARS Award Amount</b>		<b>\$ 99,142</b>

*Shaobin Zhong*

07/29/2021

Principal Investigator

Date

\* MGMT – FHB Management  
 FST – Food Safety & Toxicology  
 R – Research  
 S – Service (DON Testing Lab)  
 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: Identify and Map Novel QTL for FHB Resistance in Durum Wheat**

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

The major goal of this project was to identify, map, and deploy QTLs for FHB resistance in the emmer wheat (*Triticum turgidum* L. subsp. *dicoccum*) line PI 254188. Therefore, the specific objectives are:

- 1) Develop a mapping population with recombinant inbred lines (RILs) derived from the cross between Divide and PI 254188;
- 2) Phenotype FHB resistance and morphological traits of the mapping population from the Divide/PI 254188 cross in greenhouse and field;
- 3) Construct a genetic linkage map of the population using 90k-SNP chips;
- 4) Identify DNA markers linked to QTL for FHB resistance in PI 254188;
- 5) Transfer and pyramid the FHB resistance QTL into adapted durum wheat cultivars.

**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?**

We evaluated ~200 RILs (F2:7) derived from the cross between Divide and PI 254188 for FHB resistance in three greenhouse seasons and two field experiments. We genotyped the RIL population using the genotyping by sequencing (GBS) approach and identified SNP markers. We constructed a genetic linkage map for the Divide/PI 254188 population with the SNP markers generated from the GBS genotyping. We conducted QTL analysis using the constructed linkage genetic map and the phenotype data from all greenhouse and field experiments. We also raised another RIL population from the cross between Joppa and one FHB resistant RIL derived from the cross between Divide and PI 254188. We backcrossed seven of the highly resistant RILs to Joppa and ND Riveland to improve the quality and yield of the transgression lines.

**b) What were the significant results?**

The RIL mapping population derived from the Divide/PI 254188 cross segregated for FHB resistance in the greenhouse evaluation; Some RILs had a high level of FHB resistance better than the resistant parent PI 254188 while some other RILs were very susceptible. GBS of the RIL mapping population and the parents generated over 8,000 SNP markers, and after filtration of low-quality ones, 4,192 SNP markers were used to construct a genetic linkage map, which consisted of 16 linkage groups corresponding to 14 chromosomes of the durum wheat genome. The total map size was 2653.47 cM. A major QTL on chromosome 2A and a minor QTL on chromosome 5A were detected in the Divide/PI 254188 RIL population. Interestingly, it appeared that Divide contains the 2A QTL contributing FHB resistance while PI 254188 has the 5A QTL conferring the FHB resistance. These QTL will be validated using the RIL population from the cross

between Joppa and one FHB resistant RIL derived from the cross between Divide and PI 254188.

**c) List key outcomes or other achievements.**

- (1) A large number of SNP markers were generated for the RIL population derived from the Divide/PI 254188 cross.
- (2) A genetic linkage map with 4,192 SNP markers have been developed.
- (3) FHB phenotyping data were collected from both greenhouse and field inoculation experiments for multiple years and seasons.
- (4) One major QTL and one minor QTL for FHB resistance were detected in the RIL population based on phenotype data from both greenhouse and field experiments.
- (5) After several cycles of backcrosses with durum wheat cultivars, agronomic traits of the introgression lines with a high level of FHB resistance have been significantly improved. These lines will be used directly in durum wheat breeding programs.

**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.**

Yes, the COVID-10 pandemic caused the university to partially close the campus and the research activities had to be reduced to the minimum. The FHB phenotyping in greenhouse was impacted because access to greenhouse is limited and number of people working in the same room is limited to one for keeping social distancing.

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

The project provided trainings to two research associate and two Ph.D. students on FHB phenotyping, QTL mapping and marker development. The PI and the participants of this project have attended three seminars and two conferences.

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

Nothing to report

**Project 2:** *Genetic and Molecular Characterization of Novel FHB Resistance QTL in Spring Wheat*

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

Our overall goal is to characterize novel FHB resistance quantitative trait loci (QTL) at both genetic and molecular levels in spring wheat. The specific objectives of this project are to:

- 1) Clone and characterize the major FHB resistance QTL on chromosome 5AL in wheat line PI 277012.
- 2) Identify novel QTL for FHB resistance in PI 185843, a Brazil wheat cultivar with a higher level of FHB resistance.
- 3) Develop user-friendly DNA markers for the novel QTLs and deploy them in selection of FHB resistance in 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?**

- (1) To clone the major QTL on 5AL for FHB resistance in the wheat line PI 277012, we collected 5A chromosomes from both Grandin and PI 277012 by chromosome sorting technology in collaboration with Dr. Jaroslav Dolezel at the Institute of Experimental Botany, Czech Republic. We extracted DNA samples from the sorted 5A chromosomes from the two wheat genotypes and generated paired-end sequence reads from them by Illumina sequencing platform. We assembled the sequence reads into a 5A scaffold using the Chinese Spring 5A pseudomolecule as reference. Due to the highly repetitive genome sequence, the quality of assemblies with the short-reads was not good. Therefore, we prepared high molecular weight DNA of PI 277012 and sent it to Mayo Clinic Genome Analysis Core Facility for HiFi whole genome sequencing. Eight SMRT cells were used, HiFi sequence reads with 12x genome coverage were generated, and whole genome assembly was conducted with the HiFi reads. We identified chromosome 5A contigs covering the whole region containing the target FHB resistance QTL and identified genes showing polymorphisms between Grandin and PI 277012. We also screened EMS mutants generated from PI 277012 in the greenhouse.
- (2) To map the QTL in PI 185843, we finished the genotyping and genotyping of 200 RILs derived from the Wheaton/PI 185843 cross, and conducted QTL analysis.
- (3) To develop user-friendly DNA markers for the novel QTLs for FHB resistance, we identified additional SNP markers for the 5AL QTL region. These SNP markers were converted into PCR-based markers for fine mapping and introgression of the 5AL QTL.

**b) What were the significant results?**

(1) A total of 122.3 and 206.4 million paired-end reads (250 bp and 150 pb) were generated for the Grandin 5A chromosome, which were assembled into an 872.38 Mb scaffold. A total of 313.6 million paired-end reads (150 pb) were generated for the PI 277012 5A chromosome, which were assembled into a 933.66 Mb scaffold.

(2) Whole genome sequencing of PI 277012 with the PacBio HiFi sequencing technology resulted in a high-quality genome assembly of 5827 contigs with N50=9.11 Mb. Analysis of sequences in the region flanked by the DNA markers flanking the 5A QTL detected two large contigs covering the QTL region. Comparative genomic analysis identified genes with polymorphism between Grandin and PI 277012. These genes will be further characterized for marker development and candidate gene identification for the QTL.

(3) Screening approximately 400 M2 progenies derived from EMS M1 plants of PI 277012 in greenhouse identified several mutants that were much more susceptible to FHB compared to the parent PI 277012.

(4) Genetics analysis identified four QTLs (genes) for type II FHB resistance on chromosome 2A, 3B, and 4D, respectively. The largest effect QTL was mapped on chromosome 4D and explained 15.8% of the phenotypic variation. QTLs detected on chromosome 2A and 3B are different from previously reported QTLs and may be novel.

(5) Fifteen additional PCR-based SNP markers were developed in the 5AL QTL region of PI 277012 and have been used in selection of the QTL in the process of introgression of the FHB resistance into adapted wheat cultivars.

**c) List key outcomes or other achievements.**

(1) Genome sequences of chromosome 5A were generated from the resistant PI 277012 and susceptible Grandin. Also, whole genome sequence assembly was generated with PacBio HiFi sequence data. The 5A genome assemblies are very useful for identification of candidate genes for the 5AL QTL.

(2) More EMS mutants susceptible to FHB were identified from PI 277012, which will be useful for validation of the candidate genes for the QTL.

(3) Novel QTL were identified from PI 185843, which will be used to develop FHB resistant wheat varieties.

(4) The PCR-based SNP markers developed will facilitate the quick transfer of the FHB resistance into adapted wheat breeding lines.

FY19 Performance Progress Report - NCE

PI: Zhong, Shaobin

USDA-ARS Agreement #: 59-0206-7-153

Reporting Period: 5/1/19 - 4/30/21

**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.**

Yes, the COVID-10 pandemic caused the university to partially close the campus and the research activities had to be reduced to the minimum. The FHB phenotyping in greenhouse was impacted because access to greenhouse is limited and number of people working in the same room is limited to one for keeping social distancing.

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

The project provided one research associate and three Ph.D. students with training on QTL mapping and marker development as well as map-based gene cloning. The PI and the participants of this project have attended three seminars and two conferences.

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

The FHB resistant wheat lines developed and DNA markers associated with the FHB resistance have been provided to and used by other wheat researchers and breeders.

## Training of Next Generation Scientists

**Instructions:** Please answer the following questions as it pertains to the **FY19 award period (5/1/19 - 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 FY19 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 FY19 award period?**

Yes     No

**If yes, how many?** one

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?**

Yes     No

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

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?**

Yes     No

**If yes, how many?** one

### 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 (5/1/19 - 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	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

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



FY19 Performance Progress Report - NCE

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## Publications, Conference Papers, and Presentations

**Instructions:** Refer to the 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 (5/1/19 - 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](https://scabusa.org/pdfs/NFHB20_Proceedings.pdf).  
Status: Abstract Published and Poster Presented  
Acknowledgement of Federal Support: YES (Abstract and Poster)

### Journal publications.

Shrestha, S., Poudel, R. S., \***Zhong, S.** 2021. Identification of fungal species associated with crown and root rots of wheat and evaluation of plant reactions to the pathogens in North Dakota. *Plant Dis.* (Accepted; first look)

Status: Published

Acknowledgement of Federal Support: YES

Wit, M., Leng, Y., Du, Y., Cegiełko, M., Jabłońska, E., Wakuliński, W., \***Zhong, S.** 2021. Genome sequence resources for the maize pathogen *Fusarium temperatum* isolated in Poland. *Mol. Plant-Microbe Interact.* 34:214-217.

Status: Published

Acknowledgement of Federal Support: No

Wan, J., Jin, Z., **Zhong, S.**, Schwarz, P., Chen, B., and Rao, J. 2020. Clove oil-in-water nanoemulsion mitigates growth of *Fusarium graminearum* and trichothecene mycotoxin production during the malting of Fusarium infected barley. *Food Chemistry* 312:312120.

Status: Published

Acknowledgement of Federal Support: YES

Liu, Y., Evan, S., Fiedler, J. D., Hegstad, J. B., Green, A., Mergoum, M., **Zhong, S.**, Li, X. 2019. Genetic mapping and prediction analysis of FHB resistance in a hard red spring wheat

FY19 Performance Progress Report - NCE

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breeding population. *Front. Plant Sci.* 10:1007.

<https://doi.org/10.3389/fpls.2019.01007>.

Status: Published

Acknowledgement of Federal Support: YES

Wu, D., Lu, J., **Zhong, S.**, Schwarz, P., Chen, B., Rao, J. 2019. Physical stability, antifungal and mycotoxin inhibitory activities of lecithin stabilized cinnamon oil emulsions in the presence of chitosan. *Food & Function* 10:2817-2827.

Status: Published

Acknowledgement of Federal Support: YES

Wan, J., **Zhong, S.**, Schwarz, P., Chen, B., and Rao, J. 2019. Enhancement of antifungal and mycotoxin inhibitory activities of food-grade thyme oil nanoemulsions with natural emulsifiers. *Food Control* 106: 106709.

Status: Published

Acknowledgement of Federal Support: YES

Wan, J., **Zhong, S.**, Schwarz, P., Chen, B., and Rao, J. 2019. Physical properties, antifungal and mycotoxin inhibitory activities of five essential oil nanoemulsions: impact of oil compositions and processing parameters. *Food Chemistry* 291:199-206.

Status: Published

Acknowledgement of Federal Support: YES

Szabo-Hever, A., Zhang, Q., Friesen, T. L., Zhong, S., Elias, E. M., Cai, X., Jin, Y., Chao, S., and Xu, S. S. 2018. Genetic diversity and resistance to Fusarium head blight in synthetic hexaploid wheat derived from *Aegilops tauschii* and diverse *Triticum turgidum* subspecies. *Front. Plant Sci.* 9:1829. doi: 10.3389/fpls.2018.01829.

Status: Published

Acknowledgement of Federal Support: YES

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

Nothing to report.

### **Other publications, conference papers and presentations.**

Leng, Y., Poudel, B., Bernardo, A., Bian, R., Karmacharya, A., Mullins, J., Bai, G., Xu, S.S., Zhong, S. 2020. Identification and molecular mapping of a major QTL on chromosome 2A conferring resistance to Fusarium head blight in emmer wheat (p19, Poster #7). In: Canty, S., A. Hoffstetter, and R. Dill-Macky (Eds.), *Proceedings of the 2020 National Fusarium Head Blight Forum*. East Lansing, MI: U.S. Wheat & Barley Scab Initiative.

Status: Abstract Published and Poster Presented

Acknowledgement of Federal Support: YES (Abstract and Poster)