

**USDA-ARS/  
U.S. Wheat and Barley Scab Initiative  
FY12 Final Performance Report  
July 16, 2013**

**Cover Page**

<b>PI:</b>	Jose Gonzalez
<b>Institution:</b>	South Dakota State University
<b>Address:</b>	Plant Science Department 280 Northern Plains Biostress Building 1110 Rotunda Lane N. Brookings, SD 57007
<b>E-mail:</b>	jose.gonzalez@sdstate.edu
<b>Phone:</b>	605-688-6907
<b>Fax:</b>	605-688-4452
<b>Fiscal Year:</b>	FY12
<b>USDA-ARS Agreement ID:</b>	59-0790-8-066
<b>USDA-ARS Agreement Title:</b>	Molecular Characterization and Pyramiding of Novel Scab Resistance Sources Adapted to the Northern Plains Growing Region.
<b>FY12 USDA-ARS Award Amount:</b>	\$ 27,837*

**USWBSI Individual Project(s)**

<b>USWBSI Research Category**</b>	<b>Project Title</b>	<b>ARS Award Amount</b>
HWW-CP	Pyramiding and Validating Multiple FHB Resistance QTLs in Different Winter Wheat Backgrounds.	\$ 14,071
VDHR-SPR	Pyramiding and Validating Multiple FHB Resistance QTLs in Different Spring Wheat Backgrounds.	\$ 13,766
	<b>Total ARS Award Amount</b>	<b>\$ 27,837</b>

\_\_\_\_\_  
Principal Investigator

\_\_\_\_\_  
Date

\* Partial funding for this research is under ARS agreement # 59-0206-9-052

\*\* MGMT – FHB Management

FSTU – Food Safety, Toxicology, & Utilization of Mycotoxin-contaminated Grain

GDER – Gene Discovery & Engineering Resistance

PBG – Pathogen Biology & Genetics

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: Pyramiding and Validating Multiple FHB Resistance QTLs in Different Winter Wheat Backgrounds.**

**1. What major problem or issue is being resolved relevant to Fusarium head blight (scab) and how are you resolving it?**

The main goal of the project is to combine multiple sources of resistance into multiple genetic backgrounds while at the same mapping and validating putative QTL locations associated with resistance to FHB.

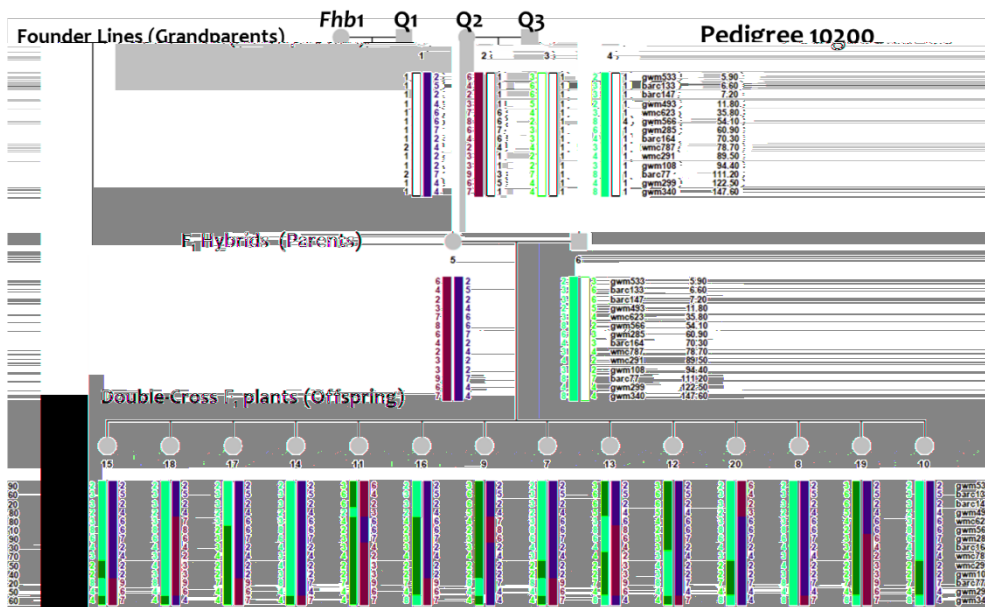
The project makes use of a family-based mapping approach based on the development of multiple segregating families derived from 3- and 4-ways crosses. All crosses had at least one elite line carrying the *fhb1* locus. The F1 progeny is genotyped for mapping. The phenotype comes from greenhouse and field evaluations over 2-3 generations.

**2. List the most important accomplishment and its impact (i.e. how is it being used) to minimize the threat of Fusarium head blight or to reduce mycotoxins. Complete both sections (repeat sections for each major accomplishment):**

**Accomplishment (1):**

**Population development (progress = 100%):**

Four-way crosses were conducted amongst 20 FHB resistant hard red spring wheat lines to develop 44 “four-way F1” segregating populations. Fifteen of these lines were experimental lines from the SDSU breeding program carrying *Fhb1*, a major effect resistance QTL, while the remaining lines provided novel sources of resistance. Crosses were conducted such that each population was segregating for *Fhb1* as well as 2 to 3 other novel resistance loci. These four-way cross populations can be construed as 3 generation pedigrees consisting of grandparents, parents and offspring. The average pedigree contained 26 individuals (4 founders and 22 non-founders), combining to form a mapping population of 994 non-founders. An example of one small spring wheat pedigree is shown below.



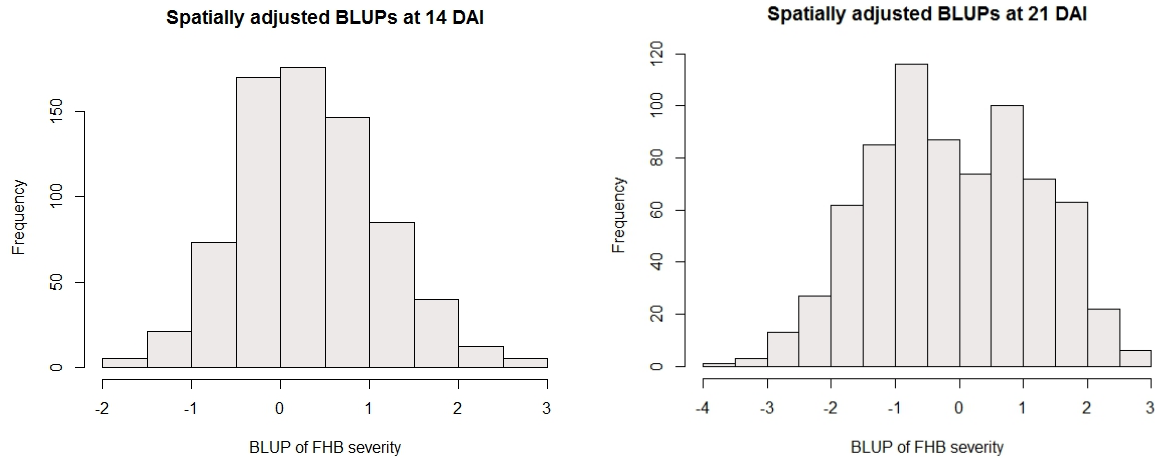
**Impact:**

These lines have been made available to breeding programs in the region. The SDSU Hard Red Spring Wheat Breeding program has fully incorporated these lines into their selection pipelines. Previous projects making use of only one source of FHB resistance have originated several elite lines used as parental materials.

**Accomplishment (2):**

**Phenotypic evaluation (progress = 95%)**

Four-way F1 plants were planted in the greenhouse and spray inoculated with *Fusarium graminearum*. A total of 1413 spikes were inoculated on 742 plants. Disease severity was evaluated at 14 and 21 days after inoculation (dai). Spatial analysis and binomial mixed models were used to analyze disease severity and estimate best linear unbiased predictions for individual four-way F1 plants (shown below).



During the 2012 growing season, 744 F2 lines derived from the four-way F1 plants were established in inoculated disease nurseries for progeny testing. Testing was a collaborative effort, in which 462 F2 lines evaluated in Brookings SD by South Dakota State University, 485 F2 lines were evaluated in Volga SD by South Dakota State University, 347 F2 lines were evaluated in St. Paul MN by University of Minnesota and 341 F2 lines were evaluated in Prosper ND by North Dakota State University. Approximately 200 entries were in common between each disease nursery. Linear mixed models were used to analyze the 2012 field data and provide best linear unbiased predictions of the genotypic value of the four-way F1 parent plants. Based on these results 125 F2 lines were selected and advanced to winter nurseries in the SDSU Spring Wheat Breeding Program. Due to low FHB severity in South Dakota in 2012, 684 F3 lines were established in Brookings SD in 2013 and are currently being evaluated.

**Impact:**

These evaluations are used both for QTL mapping purposes and breeding.

**Accomplishment (3):**

**Marker genotyping (progress = 95%)**

Founder lines and four-way F1 plants have been genotyped with 74 SSR markers have been genotyped targeting putative QTL containing chromosomes 2A, 2B, 3A, 3B, 3D, 4D and 7B. Single cross F1 “parent” genotypes were inferred from the founder lines. Additional genomic regions with putative trait loci, including chromosomes 2D, 5A and 6B, may be targeted using singleplex SNP assays. Genotypic data is currently being error checked to prepare for analysis.

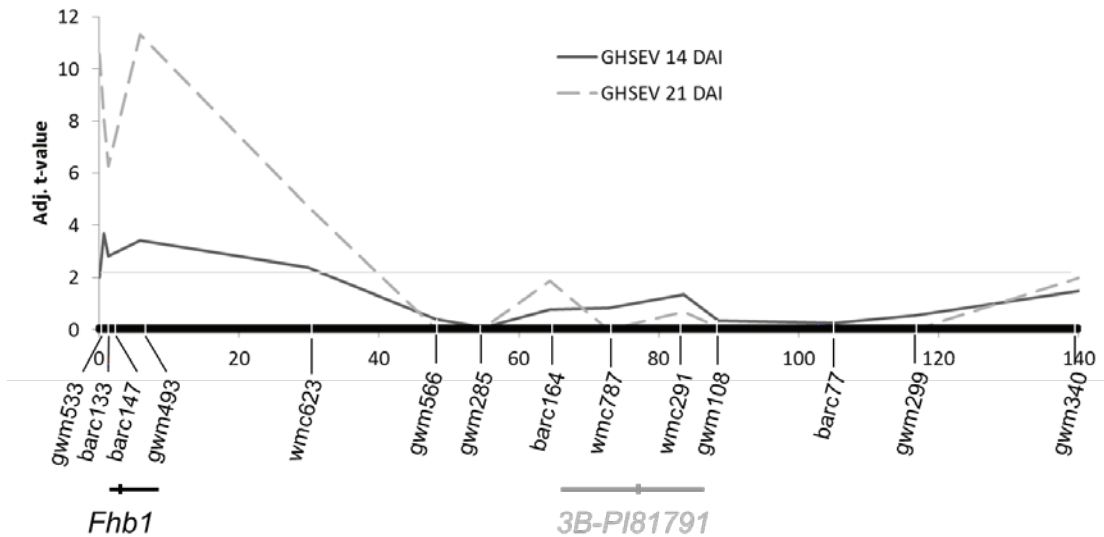
**Impact:**

This is the second component of the mapping component of the project. Additionally significant markers can be used as selections tools.

**Accomplishment (4):**

**QTL Mapping Data Analysis (progress = 20%)**

Extensive review of available software for trait locus mapping in large pedigrees has been conducted. CRI-MAP V2.5 (<http://www.animalgenome.org/tools/share/crimap/>) is being used construct de novo linkage maps from the pedigree and marker data to ensure reliable marker ordering and genetic distances. Approximate IBD estimation and non-parametric linkage analyses are being conducted in S.A.G.E. (<http://darwin.cwru.edu/sage/>). For example; Preliminary non-parametric linkage analysis for chromosome 3B using sib-pair regression on greenhouse phenotypes resulted proper localization of *Fhb1*, and peaks near a putative segregating QTL derived from a Japanese landrace (PI81791). A more thorough analysis will be conducted using all marker and phenotypic data once the data are compiled and processed.



**Impact:**

Once complete (we estimate this will be completed by end of 2013) significant markers will be available to aid in selection.

**Project 2: Pyramiding and Validating Multiple FHB Resistance QTLs in Different Spring Wheat Backgrounds.**

**1. What major problem or issue is being resolved relevant to Fusarium head blight (scab) and how are you resolving it?**

The main goal of the project is to combine multiple sources of resistance into multiple genetic backgrounds while at the same mapping and validating putative QTL locations associated with resistance to FHB.

The project makes use of a family-based mapping approach based on the development of multiple segregating families derived from 3- and 4-ways crosses. All crosses had at least one elite line carrying the *fhb1* locus. The F1 progeny is genotyped for mapping. The phenotype comes from greenhouse and field evaluations over 2-3 generations.

**2. List the most important accomplishment and its impact (i.e. how is it being used) to minimize the threat of Fusarium head blight or to reduce mycotoxins. Complete both sections (repeat sections for each major accomplishment):**

**Accomplishment (1):**

**Population development (progress = 100%):**

Four-way crosses were conducted amongst 10 hard and soft red winter wheat lines to develop 28 “four-way F1” segregating populations. Two of these lines were Wesley backcross lines carrying the *Fhb1* QTL, while the remaining lines contributed novel sources of resistance or desirable agronomic traits. Crosses were conducted such that each population was segregating for *Fhb1*, as well as 2 to 3 other novel resistance loci. These four-way cross populations can be construed as 3-generation pedigrees consisting of grandparents, parents and offspring. The average pedigree contained 26 individuals (4 founders and 22 non-founders), forming a combined mapping population of 621 non-founders.

**Impact:**

These lines have been made available to Winter Wheat breeding programs in the region for selections purposes.

**Accomplishment (2):**

**Phenotypic evaluation (progress = 75%)**

Four-way F1 plants were planted in the greenhouse and spray inoculated with *Fusarium graminearum*. A total of 838 spikes were inoculated on 452 plants. Disease severity was evaluated at 7, 14 and 21 days after inoculation (dai). Spatial analysis and binomial mixed models were used to analyze disease severity and estimate best linear unbiased predictions for individual four-way F1 plants.

During the 2013 growing season, 542 F2 lines derived from the four-way F1 plants were established in the inoculated disease nurseries for progeny testing. The testing effort was collaborative, with 501 F2 lines evaluated in Volga SD by South Dakota State University, 380 F2 lines evaluated in Manhattan KS by Kansas State University, and 201 F2 lines evaluated in Carrington ND by NDSU. Evaluation of this material is currently underway.

**Impact:**

These evaluations are part of the QTL mapping. They are also useful for selection purposes.

**Accomplishment (3):****Marker genotyping (progress = 90%)**

Founder lines and four-way F1 plants have been genotyped for 9,000 SNP loci at the USDA-NDSU Biosciences Research Lab using a custom Illumina Infinium array (as collaborative effort with Dr. S. Chao). Of these, 2,795 polymorphic SNP loci with reliable allele calling were selected for further analysis. Additionally, 26 SSR markers around putative QTL regions are being genotyped at the USDA-KSU Hard Winter Wheat Genetics Research Unit.

**Impact:**

The genotyping is the second component of the QTL mapping.

**Accomplishment (4):****Mapping trait loci (progress = 5%)**

Given no prior information on marker positions for the SNPs, current efforts are underway to map these 2,975 loci in the 28 winter wheat pedigrees. Several software packages have been evaluated for this purpose. Locusmap V1.1 (<http://animalgene.umn.edu/locusmap/>) has been found to providing reliable maximum likelihood estimates of pairwise recombination fractions and identification of linkage groups. These linkage groups will then be used in CRI-MAP V2.5 to order the markers and develop the framework linkage map. Non-parametric linkage analysis will be conducted using MCMC IBD estimation methods to map resistance loci segregating in these pedigrees.

**Impact:**

Once complete (by end of 2013), markers significantly associated with FHB resistance QTLs will be available as selection tools.

**Include below a list of the publications, presentations, peer-reviewed articles, and non-peer reviewed articles written about your work that resulted from all of the projects included in the grant. Please reference each item using an accepted journal format. If you need more space, continue the list on the next page.**

J.T. Eckard, J.L. Gonzalez-Hernandez\*, K.D. Glover and W.A. Berzonsky. 2012. Mapping and pyramiding scab resistance QTL in early generation spring and winter wheat breeding populations using family-based mapping approach. In: S. Canty, A. Clark, A. Anderson-Scully and D. Van Sanford (Eds.), Proceedings of the 2012 National Fusarium Head Blight Forum (pp. 58). East Lansing, MI/Lexington, KY:U.S. Wheat & Barley Scab Initiative.

J.T. Eckard, J.L. Gonzalez-Hernandez\*, K.D. Glover, W.A. Berzonsky, JA Anderson and M Mergoum. 2012. Generalized linear models for genetic prediction of scab resistance from regional disease nurseries. In: S. Canty, A. Clark, A. Anderson-Scully and D. Van Sanford (Eds.), Proceedings of the 2012 National Fusarium Head Blight Forum (pp. 57). East Lansing, MI/Lexington, KY:U.S. Wheat & Barley Scab Initiative.

J. Gonzalez. Molecular Breeding in Grasses at Delaware State University. Nov 27, 2012. Food and Fuel. (Invited presentation)