USDA-ARS/
U.S. Wheat and Barley Scab Initiative
FY10 Final Performance Report
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Cover Page

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Fiscal Year:	FY10
USDA-ARS Agreement ID:	NA
USDA-ARS Agreement Title:	Identification and Deployment of FHB Resistance QTL in US Hard Winter Wheat.
FY10 USDA-ARS Award Amount:	$ 74,233

USWBSI Individual Project(s)

USWBSI Research Category[*]	**Project Title**	**ARS Award Amount**
HWW-CP	Mapping and Deploying FHB Resistance QTL in US Hard Winter Wheat.	$ 55,608
HWW-CP	Using Association Mapping to Identify and Validate New FHB Resistance QTL and Integrate the QTL into HWW.	$ 18,625
	Total ARS Award Amount	**$ 74,233**

6/28/2011

Principal Investigator Date

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[*] 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: *Mapping and Deploying FHB Resistance QTL in US Hard Winter Wheat.*

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

Effective utilization of FHB resistant resources relies on identification of new resistance genes and understanding the inheritance. A major FHB resistance QTL (*Fhb1*) from Sumai 3 has been mapped and widely used in breeding programs. FHB1 can significantly improve the resistance in diverse genetic backgrounds. However, it only provides 20-40% reduction in FHB severity in different genetic backgrounds, thus more resistance genes are needed to enhance the levels of resistance and to provide sufficient protection from severe FHB epidemics. Thus, identification of additional resistance genes from other new sources may enrich FHB resistance gene diversity and provide new resistance genes to enhance FHB resistance levels through gene pyramiding. We used two approaches: 1) continue searching new genes from Chinese landraces that might have different genes from Sumai 3 and 2) search resistance gene/QTL from US native FHB resistant germplasm. We evaluated FHB resistance in mapping populations developed using two Chinese FHB resistant landraces, Huangcandou and Baisanyuehuang, and a US moderately resistant cultivar Heyne as resistant parents. The results are expected to provide breeders with selectable markers for breeding wheat cultivars with low DON and high levels of FHB resistance to speed up breeding process. Meanwhile, we are using marker-assisted backcross method to transfer major FHB resistance QTL FHB1 and other QTL from Asian sources into adopted hard winter wheat cultivars to quickly deploy these QTL in hard winter wheat germplasm and cultivars.

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. Two F7 RIL populations from the crosses between two Chinese resistant landraces, Huangcandou (HCD) and Baisanyuehuang (BSYH), and Jagger (a highly susceptible parent) were evaluated for FHB resistance. The data were analyzed and primarily QTL analysis showed that both sources have two major QTL on 3BS and explained about 15-30% of phenotypic variation for PSS.
2. RIL mapping population with local source of FHB resistance (Heyne/Trego) was evaluated for FHB in both field and greenhouse for FHB resistance. Heyne is a local HWW cultivar with moderate resistance to FHB. Primary analysis identified three QTL on 3AS, 4AL and 4DL based on both field and greenhouse data.
3. Twenty-five selected backcross lines with FHB1 in Wesley background were tested for FHB in greenhouse and field at Manhattan KS. These lines showed good yield in 2010 South Dakota and Nebraska yield trials. Markers were rechecked in these lines to confirm they contain Fhb1. Some of the selected lines have been sent to breeding programs in OK, KS, NE and SD for further crosses.
4. In another MAS project, FHB1 and several other FHB resistance QTL were transferred into HWW Jagger (KS), Overland (NE) and Overley (KS). About 4000 Bc3F2 plants

were screened for markers potentially linked to QTL on 3B, 5A, 7A, 6B, 5D and 4B and about 2000 plants with at least one QTL were selected and subjected initial FHB screening.

1. **Impact:**

Huangcandou and Baisanyuehuang are two highly resistant landraces from China. The FHB resistance QTL from both accessions has not been reported before. The QTL on 3BS centromere has not been reported before from Chinese sources. This QTL combined with Fhb1 provide a very high level of resistance in these landrace. These QTL can be used to improve the level of FHB resistance in currently used cultivars after further validation in different genetic backgrounds.

The germplasm or cultivars from marker-assisted backcross will be important for breeding programs in OK, NE, SD and KS as FHB resistant parents. Some selected Wesley lines can be directly used as a cultivar to quickly relieve FHB damage in HWW growing region where FHB resistant cultivar currently is not available because Wesley is still a popular cultivar growing in SD and NE. In addition, this is first time to demonstrate that marker-assistant backcross can a powerful tool to quickly deploy FHB QTL when breeding programs closely collaborate with a USDA genotyping lab.

PI: Bai, Guihua
USDA-ARS Agreement #: NA

Project 2: *Using Association Mapping to Identify and Validate New FHB Resistance QTL and Integrate the QTL into HWW.*

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

Major scab epidemics have occurred in the HWW region. Genetically improved seed coupled with appropriate management practices are the quickest and most cost effective way to reduce DON in the grain supply. However, little is known concerning the genetic basis of native resistance in the Great Plains germplasm and how best to effectively utilize it. Using associationmapping techniques, we will be able to validate reported QTL and identify new QTLs in HWW germplasm, and move from molecular mapping to marker-assisted breeding. For this research we used selected lines from numerous sources that we have identified as being important in the creation of hard winter FHB tolerant lines. The key to this research will be to maximize the information we are already collected from our existing FHB screening nurseries, such as, advanced regional lines and lines that were tested in our state variety trials. Our goal is to use 188 wheat lines including native sources of resistance (e.g. Henye. Lakin, Arapahoe, Everest, Overland, Settler CL, Lyman, Art, Hitch); DON accumulators (e.g. Harry and Trego); a series of backcross lines (Fhb1 and/or Fhb3 in Trego, Wesley, Harding, Overley, Jagger and Overland) and some accessions with various levels of FHB resistance from China and/or Japan (to look for new alleles and increase our diversity). ***Phenotypic data:*** All accessions are phenotyped for FHB resistance by needle inoculation in the greenhouse at KSU and SD, respectively and irrigated FHB winter wheat nurseries in KS, NE, and SD. Bulk samples from these phenotyping nurseries are submitted for objective FHB evaluation and DON analysis (in cooperation with Dr. Floyd Dowell). ***Genotyping Using Molecular Markers:*** For marker analysis, all accessions will be analyzed for structure with at least 100 genome-wide SSR markers at the USDA Genotyping Lab in Manhattan. We will also genotype the accessions using all reported markers linked to known FHB QTLs (about 50) and 9K single nucleotide polymorphism (SNP) chip for higher resolution QTL mapping. The diversity of lines should be adequate for association mapping studies and allow most important alleles to be identified, as well as some of their epistatic interactions. We believe that between the SSR and SNP markers (as well as some STS markers linked to QTL) we will have adequate genome coverage for association mapping. ***Data Analysis:*** The data will be analyzed using the software developed by Dr. Dong Wang to identify major genes and epistatic gene interactions that control FHB tolerance and help reduce DON. PowerMarker software will be used to calculate values of gene diversity, and distance-based cluster analysis using the UPGMA algorithm. A model-based (Bayesian) software package Structure 2.1 (Pritchard and others 2000) will be used to assess the number of subpopulations among all accessions. Information on marker distribution in wheat genomes was obtained from the consensus map Somers et al 2004. Pair-wise LD will be calculated using TASSEL 1.9.4 (http://www.maizegenetics.net). A database with all marker allele information will be developed for all the evaluated accessions and breeders will use them to select appropriate parents for crosses. We have chosen this approach because it directly compares our native sources of resistance (including our commercial lines), with known Asian sources of resistance at both phenotypic and genotypic levels.

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:

Phenotypic data for FHB have been done one field for and two greenhouse experiments in Manhattan, KS. About 110 SSR markers have been screened for the population. In addition, the population was also screened with 9K SNP chip from Illumina and data scoring and analysis are in progressing.

Impact:

The phenotypic data of the population collected from both field and greenhouse environment will be important for breeders to select right parents for crosses because the population mainly consisted of elite breeding materials and new varieties that they use most often as parents in their crosses. The 9K SNP data for the population will be a useful resource for developing SNP markers linked to important QTL in HWW.

Include below a list of all germplasm or cultivars released with full or partial support of the USWBSI. List the release notice or publication. Briefly describe the level of FHB resistance.

(Several Wesley Fhb1 lines were informally released to breeding programs in SD, NE, KS and OK as a source of Fhb1 for crosses.)

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.

1. Amy N. Bernardo, Hongxiang Ma, Dadong Zhang, and Guihua Bai. 2011. Single Nucleotide Polymorphism in Wheat Chromosome Region Harboring Fhb1 for Fusarium Head Blight Resistance. Mol Breed. DOI 10.1007/s11032-011-9565-y
2. Tao Li, Guihua Bai, Shuangye Wu and Shiliang Gu. 2011. Quantitative Trait Loci for Resistance to Fusarium Head Blight in a Chinese Wheat Landrace Haiyanzhong. Theor Appl Genet. DOI 10.1007/s00122-011-1549-0
3. Tao Li, Guihua Bai, Shuangye Wu and Shiliang Gu. 2011. Quantitative Trait Loci for Resistance to Fusarium Head Blight in a Chinese Wheat Landrace Huangfangzhu. Mol Breed. (Submitted)
4. Jayatilake DV, Bai GH, and Dong YH. 2011. A novel quantitative trait locus for Fusarium head blight resistance in chromosome 7A of wheat. Theor Appl Genet. DOI 10.1007/s00122-1523-2
5. D.D. Zhang, G.H. Bai, C.S. Zhu, J.M. Yu, W. Bockus, S. Baenziger and P. St. Amand. 2010 Association Studies Validate and Discover Genetic Loci for Fusarium Head Blight Resistance in Wheat. 2010 National Fusarium Head Blight Forum