**USDA-ARS/**
**U.S. Wheat and Barley Scab Initiative**
**FY09 Final Performance Report**
**July 15, 2010**

# Cover Page

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| **Fiscal Year:** | 2009 |
| **USDA-ARS Agreement ID:** | NA |
| **USDA-ARS Agreement Title:** | Mapping Novel QTL in Chinese Landraces and Deploying FHB-resistance QTL in Hard Winter Wheat. |
| **FY09- USDA-ARS Award Amount:** | $ 55,608 |

**USWBSI Individual Project(s)**

| **USWBSI Research Category**[*] | **Project Title** | **ARS Adjusted Award Amount** |
|---|---|---|
| HWW-CP | Mapping Novel QTL in Chinese Landraces and Deploying FHB-resistance QTL in Hard Winter Wheat. | $ 55,608 |
| | **Total Award Amount** | **$ 55,608** |

7/1/2010

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 Winter Wheat Region
    SWW – Southern Sinter Wheat Region

**Project 1:** *Mapping Novel QTL in Chinese Landraces and Deploying FHB-resistance QTL in 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 Sumai 3 source and 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 Sumai 3 source and 2) to identify new resistant sources that might be different from Sumai 3. We evaluated FHB resistance in mapping populations with two Chinese landraces Haiyanzhong and Huangfangzhu as resistant parents. We also developed Chinese Spring-Sumai 3 substitution lines to dissect QTL into individual chromosomes. We found 7A substitution showed the same resistance as Sumai 3. Therefore, we used the this line developed Chinese Spring 7A chromosome recombinant inbred lines and used the population to evaluate the QTL effect in chromosome 7A. The results are expected to provide breeders with quality 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 landraces, Haiyanzhong and Huangfangzhu, and Wheaton (a highly susceptible parent) were evaluated for FHB resistance. The data were analyzed and primarily QTL analysis showed that HYZ has a major QTL on 7D and explained about 22-30% of phenotypic variation for PSS. In Huangfangzhu, two QTL with major effects on PSS were mapped on 3BS (Fhb1) and 7AL. The manuscripts for the mapping work are in preparation.
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. Parents were screened with 1000 SSR to identify polymorphism.
3. About 109 backcross progenies with FHB1 in Wesley background were tested in field at Manhattan KS. These lines containing FHB1 showed low FHB severity after corn kernel and needle inoculation. Data for soil born mosaic virus were collected for further selection of resistant lines to be released as resistant germplasm.

4. In another MAS project, FHB1 and several other FHB resistance QTL were transferred into HWW Jagger (KS), Overland (NE) and Overley (KS). About 200 crosses were remade between marker-assisted selected plants and recurrent parents.
5. A new QTL was mapped on chromosome 7A centromere using population of 200 Chinese Spring-Sumai 3 7A chromosome recombinant inbred lines. This QTL showed larger effect on PSS and explained 25% phenotypic variation.

**Impact:**

Haiyanzhong and Huangfangzhu are two highly resistant landraces from China. The FHB resistance QTL from both accessions has not been reported before. The new QTL from 7D of HYZ and 7A of Sumai 3 are new major QTL for FHB resistance. These QTL can be used with Fhb1 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 NE, SD and KS to use as parents. Some selected lines can be further tested and released as a cultivar to quickly relieve FHB damage in HWW growing region where FHB resistant cultivar currently is not available. 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 USDA genotyping lab.

**Include below a list 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.**

**No.**

**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. D.D. Zhang, G. H. Bai, C.S. Zhu, J.M. Yu, W. Bockus , S. Baenziger. 2009. Association Mapping of Fusarium Head Blight Resistance in Asian and U.S.A. Wheat. 2009 National Fusarium Head Blight Forum, December 2 - 4, 2009. Orlando, FL.
2. A.N. Bernardo, D-D. Zhang, H-X. Ma and G-H. Bai. 2009 Development, Mapping and Haplotype Analysis of EST-based SNPs in the Wheat *Fhb1* Region. 2009 National Fusarium Head Blight Forum, December 2 - 4, 2009. Orlando, FL.
3. D.V. Jayatilake and G-H. Bai, 2009. Mapping QTL for Fusarium Head Blight Resistance in Wheat Chromosome 7A. 2009 National Fusarium Head Blight Forum, December 2 - 4, 2009. Orlando, FL.
4. D.V. Jayatilake and G-H. Bai, 2010. A Novel QTL for Fusarium Head Blight Resistance in Wheat Chromosome 7A. National Wheat Genomics Conference. March 7-9, Lincoln, NE.