USDA-ARS/
U.S. Wheat and Barley Scab Initiative
FY09 Final Performance Report
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Cover Page

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Fiscal Year:	2009
USDA-ARS Agreement ID:	59-0790-8-068
USDA-ARS Agreement Title:	Characterization of Resistance to Fusarium Head Blight in Wheat and its Realives.
FY09- USDA-ARS Award Amount:	$ 66,071

USWBSI Individual Project(s)

USWBSI Research Category[*]	Project Title	ARS Adjusted Award Amount
DUR-CP	Fine Mapping of Qfhs.ndsu-3AS in Durum Wheat.	$ 31,195
VDHR-SPR	Enhancing Resistance to Fusarium Head Blight in Wheat Using Alien Species.	$ 34,876
	Total Award Amount	**$ 66,071**

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: *Fine Mapping of Qfhs.ndsu-3AS in Durum Wheat.*

1. **What major problem or issue is being resolved relevant to Fusarium head blight (scab) and how are you resolving it?**
User-friendly diagnostic molecular markers closely linked to a FHB resistance QTL can be used to assist effective selection of FHB resistance in the development of superior cultivars and elite germplasm. However, low polymorphisms and high percentage of repetitive DNA sequences within the wheat genome often impede the development of such markers near a QTL. We identified the genomic sequences of rice and *Brachypodium distachyon*, which are collinear with the QTL region on the short arm of wheat chromosome 3A (3AS), using DNA sequences of the EST-derived STS (sequence tagged site) marker loci near the FHB resistance QTL *Qfhs.ndsu-3AS* and used those rice and *Brachypodium distachyon* genomic sequences to identify more wheat ESTs/genes within the QTL region for marker development. Also, we used other molecular marker techniques, such as SSCP (single strand conformation polymorphism) and CAPS (cleaved amplified polymorphic sequences), to identify more marker loci near the QTL. Meanwhile, we used a large mapping population with 1,896 F_2 individuals to more precisely position the FHB resistance QTL on 3AS. Through these approaches, we further saturated the QTL region with newly-developed molecular markers and increased map resolution of the QTL region.

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:

A total of 813 pairs of STS primers and 42 pairs of SSR primers had been designed from tentative consensus sequences (TCs) and singletons of wheat ESTs identified based on collinear genomic sequences of rice and *Brachypodium distachyon*. As a result, 56 polymorphic STS and SSR markers had been developed and 45 of them mapped to a genomic region of 232 cM on chromosome 3A. Of the 45 markers, 23 mapped to a chromosomal interval of 14.9 cM harboring *Qfhs.ndsu-3AS* in the population of 83 recombinant inbred chromosome lines (RICLs). The average map distance between maker loci was reduced from 4.9 cM in the previous study to 1.24 cM in the QTL region. Five co-segregating markers were 0.6 cM proximal to *Xgwm2*, a SSR locus closely linked to the QTL peak. Co-segregating markers in the initial mapping population of 83 RICLs have been resolved in the large F_2 population.

Impact:

More new PCR-based molecular markers were identified within the QTL region and resolution of the genetic map for this genomic region has been increased. These results have positioned this FHB resistance QTL on 3AS more precisely in the durum genome. Several newly-developed STS markers closely linked to *Qfhs.ndsu-3AS* have been used to genotype durum materials for selection of this FHB resistance QTL. This work has provided more effective markers to assist selection of this QTL in durum breeding and germplasm development. Furthermore, results generated in this project facilitates understanding of the genomic interval harboring *Qfhs.ndsu-3AS* and adjacent genomic regions on chromosome 3A.

Project 2: *Enhancing Resistance to Fusarium Head Blight in Wheat Using Alien Species.*

1. **What major problem or issue is being resolved relevant to Fusarium head blight (scab) and how are you resolving it?**
   The polygenic nature of FHB resistance and strong genetic background effect of FHB resistance QTL complicate FHB resistance gene introgression, especially from relatives of wheat. Resistance levels often dilute after FHB resistance genes are transferred to adapted wheat backgrounds. To confront this problem, we have used multiple adapted wheat cultivars as recipients and increased population size for FHB screening and selection in this project. Also, we have grown a portion of segregating materials in the field under high FHB disease pressure for selection of segregants with high levels of FHB resistance. To date, we have obtained over 600 spring wheat segregants in early generations with favorable FHB resistance derived from different alien sources. Advanced spring wheat lines have been validated for FHB resistance at several field locations in ND and China. Meanwhile, we have evaluated agronomic performance and grain quality of advanced introgression lines under those environments.

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:
   To date, we have developed over 100 advanced spring wheat breeding lines with FHB resistance. These lines have been evaluated for resistance to FHB and other diseases under the greenhouse and field conditions. Five of these lines exhibited favorable FHB resistance as well as high yield and good quality characteristics. Also, several lines showed significantly reduced DON levels comparing to their spring wheat parents. These advanced spring wheat breeding lines are being grown in the field for further evaluation of FHB resistance and agronomic performance. Some of these advanced introgression lines have been provided to wheat breeding programs for use in the development of superior wheat cultivars. I anticipate releasing several more spring wheat germplasm lines with FHB resistance and other favorable traits late this year or early next year.

   Impact:
   The advanced spring wheat introgression lines we have developed exhibited favorable or acceptable agronomic and quality characteristics in addition to FHB resistance in our field experiments. Some of them also showed resistance to other diseases, such as tan spot, Stagonospora nodorum blotch (SNB), and rusts. Obvious linkage drag derived from alien species has not been observed in these lines. Thus, they can be utilized directly for cultivar development without any pre-breeding effort. These germplasm can be used to broaden and diversify genetic basis of FHB resistance in wheat and enhance resistance of wheat to this disease.

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.

We will release 2-3 hard red spring wheat germplasm with a FHB resistance level (Type II) similar as Alsen or better than Alsen at some locations late this year or early next year. These advanced breeding lines also exhibited resistance to other diseases (tan spot, SNB, and rusts) in addition to FHB. One of the lines showed significantly higher yield than Alsen at Prosper, ND.

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.

Zhu, X., Chao, S., Gu, Y. Q., Elias, M. E., Kianian, S. F., and Cai, X. 2009. Comparative mapping of the chromosomal region harboring the Fusarium head blight resistance QTL *Qfhs.ndsu-3AS* in durum wheat. p165 (abstr.). *In* Proc. 2009 National Fusarium Head Blight Forum, Orlando, FL, 7-9 December, 2009.

Xu**,** S. S., Friesen**,** T. L., Chu**,** C. G., Halley**,** S., Zhong**,** S. B., Cai, X., Elias**,** E. M. 2009. Development of durum wheat germplasm with enhanced resistance to Fusarium head blight derived from emmer wheat**.** p160 (abstr.). *In* Proc. 2009 National Fusarium Head Blight Forum, Orlando, FL, 7-9 December, 2009.

McArthur, R. I., Oliver, R. E., Xu, S. S., Wang, R. R.-C., Cai, X. 2010. Molecular and cytogenetic characterization of alien chromosomes in wheat-*Elymus rectisetus* and wheat-*Thinopyrum junceum* amphiploids and disomic addition lines with resistance to Fusarium head blight, tan spot, and Stagonospora nodorum blotch. In preparation.