USDA-ARS/
U.S. Wheat and Barley Scab Initiative
FY06 Final Performance Report (approx. May 06 – April 07)
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Cover Page

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Fiscal Year:	2006
USDA-ARS Agreement ID:	59-0790-3-078
USDA-ARS Agreement Title:	Characterization of Resistance to Fusarium Head Blight in Wheat and Its Relatives.
FY06 ARS Award Amount:	$ 72,184

USWBSI Individual Project(s)

USWBSI Research Area[*]	**Project Title**	**ARS Award Amount**
HGR	Enhancing Resistance to Fusarium Head Blight in Wheat using Alien Species.	$ 33,937
HGG	Fine Mapping of QFHS.NDSU-3AS in Durum Wheat.	$ 38,248
	Total Award Amount	**$ 72,184**

Principal Investigator Date

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[*] CBCC – Chemical, Biological & Cultural Control
EEDF – Etiology, Epidemiology & Disease Forecasting
FSTU – Food Safety, Toxicology, & Utilization of Mycotoxin-contaminated Grain
GET – Genetic Engineering & Transformation
HGR – Host Genetics Resources
HGG – Host Genetics & Genomics
PGG – Pathogen Genetics & Genomics
VDUN – Variety Development & Uniform Nurseries

Project 1: *Enhancing Resistance to Fusarium Head Blight in Wheat using Alien Species.*

1. What major problem or issue is being resolved and how are you resolving it?

The wheat-alien species derivatives we previously produced and identified as resistant to Fusarium head blight (FHB) either contain large amounts of alien chromatin or have undesirable wheat genetic backgrounds. Thus it is difficult to utilize these resistant derivatives directly in breeding for FHB resistance although they may represent novel sources of resistance. This is the biggest challenge for the utilization of alien genes in wheat improvement. To make these sources of resistance accessible by breeders, we have been developing breeder-friendly germplasm lines from these resistant derivatives in this project. This has been done by inducing recombination between wheat and alien chromatin using a *Ph* inhibitor gene (Ph^I) and eliminating unwanted alien chromatin from the derivatives. Meanwhile we have hybridized the recombinant lines with reduced alien chromatin to the adapted spring wheat cultivars, including Alsen, Russ, Reeder, Steele, Glenn, and ND2710. To date we have produced and identified 411 BC_2F_4 and BC_2F_5 progeny and lines with significantly reduced alien chromatin through this approach. We evaluated these 411 genotypes for FHB resistance and identified 228 lines as resistant to FHB in the greenhouse Fall 2006. We re-evaluated these resistant lines in three replications in the greenhouse Spring 2007 and found 148 of them consistently exhibited resistance. These resistant lines are much more breeder-friendly than the original derivatives in terms of agronomic characteristics and the amount of alien chromatin. They may be utilized directly in breeding for FHB resistance.

2. List the most important accomplishment and its impact (how is it being used?). Complete all three sections (repeat sections for each major accomplishment):

Accomplishment: We produced and identified 148 BC_2F_5 and BC_2F_6 lines with FHB resistance based on our disease data from two greenhouse screening seasons. Most of them exhibited resistance levels comparable to ‘Sumai 3’, a Chinese common wheat cultivar widely used as a major source of resistance in breeding, and contain minimal alien chromatin. Many of these resistant lines have one or more wheat-alien chromosome translocations and appear to be stabilized genetically. We are increasing seeds of these lines in the greenhouse right now and will verify their resistance in the field.

Impact: These resistant alien introgression lines represent potential novel sources of resistance to FHB for both spring and durum wheat. Many of these lines are breeder-friendly and can be utilized directly in breeding. Deployment of FHB resistance genes derived from wild species in wheat cultivars will enhance and diversify resistance of wheat to this devastating disease.

As a result of that accomplishment, what does your particular clientele, the scientific community, and agriculture as a whole have now that they didn’t have before?

Fusarium head blight resistance has been identified from relatives of wheat. It is, however, difficult to utilize resistant genes from alien species directly in wheat breeding. The breeder-friendly wheat germplasm lines we have developed in this project allow wheat breeders to have access to the FHB resistance genes in the relatives of wheat.

Project 2: *Fine Mapping of QFHS.NDSU-3AS in Durum Wheat.*

1. What major problem or issue is being resolved and how are you resolving it?

The primary goals of this project are to construct a fine map of the major FHB resistance QTL *Qfhs.ndsu-3AS* in durum wheat and to develop effective user-friendly markers tagging this QTL for marker-assisted selection in breeding and germplasm development. To approach these goals, we have generated new PCR-based markers closely linked to the QTL, placed the QTL within a smaller chromosomal region, and developed a large segregating population (>2,000 individuals) for high resolution mapping. We detected four new wheat EST-derived STS marker loci near the QTL. Based on the ETSs mapped to the QTL region, we identified a genomic region on rice chromosome 1 collinear with the chromosomal region harboring the QTL on the short arm of wheat chromosome 3A (3AS). We identified 279 unmapped wheat ESTs that might reside within the QTL region according to this collinearity. A total of 279 STS and 22 SSR primer pairs were designed from the unmapped wheat EST sequences. Through this approach, one new SSR and eight new STS markers were mapped to chromosome 3A, four of the STS markers are closely linked to the QTL. Assignment of these new markers to the QTL region led to the identification of new recombinants within this region and the placement of the QTL within a smaller chromosomal interval. Meanwhile we developed a large F2 population from a cross between the susceptible parent Langdon (LDN) and a recombinant we recently identified with the smallest chromosomal fragment harboring the resistance QTL. We have been using this population to increase map resolution of this QTL region.

2. List the most important accomplishment and its impact (how is it being used?). Complete all three sections (repeat sections for each major accomplishment):

Accomplishment I: We assigned 4 new STS markers (*Xwgc500*, *Xwgc716*, *Xwgc501*, and *Xwgc510*) to the chromosomal region (7.3 cM) harboring the FHB resistance QTL *Qfhs.ndsu-3AS*, which makes the average map distance between markers reduced to 1.2 cM within the QTL region. This QTL was positioned within a much smaller chromosomal interval (3.5 cM).

Impact I: More markers were developed and assigned to the QTL region and the QTL was positioned more precisely within the chromosomal region. The newly developed user-friendly markers are closely linked to the QTL and have been provided to breeders for marker-assisted selection and pyramiding of resistance genes. This will facilitate utilization of this resistance QTL in breeding, especially in durum wheat.

As a result of that accomplishment, what does your particular clientele, the scientific community, and agriculture as a whole have now that they didn't have before?

The results we have obtained in this project provide a more precise location of this FHB resistance QTL on 3AS. This will facilitate cloning and comparative genomic analysis of this QTL. More importantly this project has developed effective user-friendly molecular markers closely linked to the QTL for marker-assisted selection and genetic analysis of the QTL.

Accomplishment II: We identified microcolinearity between the QTL region on 3AS and a chromosomal region on rice chromosome 1.

Impact II: Colinearity between these two chromosomal regions allows for the development of more markers to saturate the QTL region and comparative analysis of the genes residing in these two genomic regions. This will facilitate fine mapping and cloning of this QTL and enhance knowledge of the molecular mechanism of FHB resistance.

As a result of that accomplishment, what does your particular clientele, the scientific community, and agriculture as a whole have now that they didn't have before?

This project has enhanced knowledge of the homology between rice chromosome 1 and wheat chromosome 3A, especially for the collinear regions we identified in this study.

Accomplishment III: We identified a new recombinant with a smaller *Triticum dicoccoides* chromosomal fragment harboring the FHB resistance QTL.

Impact III: This resistant recombinant can be utilized directly in breeding for FHB resistance in durum wheat because it contains minimal *T. dicoccoides* DNA without obvious linkage drag.

As a result of that accomplishment, what does your particular clientele, the scientific community, and agriculture as a whole have now that they didn't have before?

A source of effective resistance to FHB has not been identified in durum. This resistant line with an exotic resistance gene in a durum background may be a potential source of resistance for durum.

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.

Peer-Reviewed Articles

Chen, X., J.D., Faris, J. Hu, R.W. Stack, T. Adhikari, M.E. Elias, S.F. Kianian, and **X. Cai.** 2007. Saturation and comparative mapping of a major Fusarium head blight resistance QTL in tetraploid wheat. Molecular Breeding 19: 113-124.

Oliver, R.E., R.W. Stack, J.D. Miller, and **X. Cai.** 2007. Reaction of wild emmer wheat accessions to Fusarium head blight. Crop Sci 47: 891-897.

Oliver, R.E., **X. Cai**, R.W. Stack, T. Friesen, S. Halley, and S.S. Xu. 2007. Fusarium head blight resistance in tetraploid wheat (*Triticum turgidum* L.). Crop Sci (accepted 5/6/07).

Oliver, R.E., S.S. Xu, R.W. Stack, T.L. Friesen, Y. Jin, and **X. Cai.** 2006. Molecular cytogenetic characterization of four partial wheat-*Thinopyrum ponticum* amphiploids and their reactions to Fusarium head blight, tan spot, and Stagonospora nodorum blotch. Theor Appl Genet 112: 1473-1479.

Abstracts in Proceedings

Oliver, R.E., S.S. Xu, R.W. Stack, and **X. Cai.** Introgression and Genetic Characterization of Alien Fusarium Head Blight Resistance in Wheat (abstr.). *In* Proc. 2006 National Fusarium Head Blight Forum (abstr.), Durham, NC, December 10-12, 2006.

Chen, X., J.D. Faris, J. Hu, R.W. Stack, T. Adhikari, M.E. Elias, S.F. Kianian, and **X. Cai.** 2006. Saturation mapping of the major FHB resistance QTL *Qfhs.ndsu-3AS* in tetraploid wheat. p. 174 (abstr.). Proc. Plant & Animal Genomes XIV Conference, January 14-18, 2006. San Diego, CA.