USDA-ARS/
U.S. Wheat and Barley Scab Initiative
FY07 Final Performance Report (approx. May 07 – April 08)
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Cover Page

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Fiscal Year:	2007
USDA-ARS Agreement ID:	59-0790-3-078
USDA-ARS Agreement Title:	Characterization of Resistance to Fusarium Head Blight in Wheat and Its Relatives.
FY07 ARS Award Amount:	$ 70,509

USWBSI Individual Project(s)

USWBSI Research Area*	Project Title	ARS Adjusted Award Amount
HGR	Enhancing Resistance to Fusarium Head Blight in Wheat Using Alien Species.	$38,314
HGG	Fine Mapping of Qfhs.ndsu-3AS in Durum Wheat.	$ 32,195
	Total Award Amount	**$ 70,509**

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
IIR – Integrated/Interdisciplinary Research
PGG – Pathogen Genetics & Genomics
VDUN – Variety Development & Uniform Nurseries

(Form – FPR07)

PI: Cai, Xiwen
USDA-ARS Agreement #: 59-0790-3-078
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 lack of effective resistance to FHB and the complex inheritance of currently identified sources of resistance limit the progress of breeding for FHB resistance in wheat. We have developed and identified wheat-alien species derivatives with FHB resistance and have been introgressing resistance genes from the derivatives into adapted wheat backgrounds through chromosome manipulation. Alien introgression for FHB resistance is a time-consuming research project due to the quantitative nature of resistance and the genomic distinction between wheat and alien species. To ensure success in the alien introgression, we have been increasing the generation of the progeny derived from the crosses, manipulating wheat and alien chromosomes in the progeny, and extensively evaluating the materials of interest in each generation for FHB resistance in the greenhouse and fields. We selected 422 lines (F_{5-7}) that exhibited a FHB severity of less than or equal to 15% and favorable agronomic characteristics for seed increase in the greenhouse Summer 2007. A total of 195 advanced lines were re-evaluated for FHB resistance with three replications in the greenhouse Spring 2008. Meanwhile, these introgression lines have been grown at three locations to verify their resistance and to evaluate their agronomic performance under different field conditions. We grew 281 lines in the FHB nursery at Jianyang, China Fall 2007. Most of the lines showed similar levels of resistance as what we observed in the greenhouse screening experiments. Currently, 154 lines have been grown with three replications in the FHB nursery with a mist system in Langdon, ND. We will evaluate their reaction to FHB under that environment. Also, we have grown 285 advanced lines for seed increase and further evaluation of agronomic traits in Prosper, ND. Moreover, we haplotyped most of the introgression lines at 7 molecular marker loci linked to several FHB resistance QTL, including *fhb1* on 3BS. It appears that some of the lines may contain novel resistance genes according to their haplotypes.

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 developed and identified over 200 advanced alien introgression lines (BC_2F_{6-9}) with FHB resistance under the greenhouse environments. Most of these lines consistently exhibited resistance under a field condition (Jiangyang, China). Importantly, many of the lines showed favorable agronomic characteristics, including plant height, maturity, resistance to other diseases, and yield potential, etc., in addition to FHB resistance. An obvious linkage drag has not been observed in these lines. We have been increasing seed of these lines in the field and anticipate releasing several spring wheat germplasm with FHB resistance next year.

Impact: The alien introgression lines with FHB resistance and other desirable agronomic traits represent a useful source of resistance for the development of superior wheat cultivars. Utilization of these germplasm in wheat breeding will broaden the genetic basis of FHB resistance and enhance resistance of wheat cultivars to FHB. Deployment of the alien resistance genes in wheat cultivars will reduce the economic losses caused by 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 the resistance genes from the relatives directly in wheat breeding. A pre-breeding effort like what we have been doing in this project is needed to make the alien resistance genes available to wheat breeders. Thus, this research project has been building a "bridge" for wheat breeders to exploit the alien gene pool for enhancing resistance of wheat to FHB.

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?**

Qfhs.ndsu-3AS is a major FHB resistance QTL identified in tetraploid wheat. The map resolution of this QTL was not high enough to allow one to effectively access this locus in terms of molecular cloning and marker-assisted selection of the QTL. We have saturated the genomic region harboring *Qfhs.ndsu-3AS* with newly developed EST- and BAC end-derived STS and SSR markers. Also, we have generated CAPS (cleaved amplified polymorphic sequences) markers for saturation mapping of this genomic region. By collaborating with the wheat physical mapping and sequencing of 3AS project led by Dr. B. S. Gill (Kansas State University), we have identified contigs and BACs spanning the genomic region containing *Qfhs.ndsu-3AS*. Also, we have identified rice and *Brachypodium distachyon* genomic regions collinear with the QTL region on 3AS. All these efforts have significantly facilitated saturation and fine mapping of this QTL. To date, a total of 28 new molecular marker loci have been detected near the QTL. Meanwhile, we developed an $F_{2:3}$ population with 1,207 F_2 individuals/F_3 families from the cross of a resistant recombinant containing the smallest *T. diccocoides* chromosomal fragment containg *Qfhs.ndsu-3AS* in LDN background with LDN. We have been continuously developing molecular markers residing within the QTL region and using the large population to increase the resolution of the QTL map.

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 detected 28 new EST- and BAC end-derived STS and SSR marker loci on 3AS. Eight of them reside near *Xgwm2*, a SSR marker locus tightly linked to the highest point of the QTL peak. We identified contigs and BACs harboring the marker loci in the QTL region, including *Xgwm2*, *Xwgc501*, *Xwgc774*, *Xwgc716*, and *Xwgc1127*, and have been assembling the contigs within this region according to the genetic map. We identified the rice and *Brachypodium* genomic regions collinear with the QTL region on 3AS. Also we developed a large population to further increase the resolution of the QTL map.

Impact: The newly developed PCR-based molecular markers residing within the QTL region are useful for marker-assisted selection (MAS) of *Qfhs.ndsu-3AS* in wheat breeding and germplasm development. Some of the markers have been provided to wheat breeding programs for MAS and gene pyramiding of FHB resistance QTL. The genetic map we have constructed has been used to assemble the contigs on 3AS. These physical mapping results and the microcollinearity identified with rice and *Brachypodium* genomes enhance knowledge of this genomic region harboring the QTL and facilitate cloning and understanding of this QTL 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?:

We developed new user-friendly molecular markers tagging the FHB resistance QTL *Qfhs.ndsu-3AS* and more precisely positioned the QTL on 3AS. This will make MAS and gene pyramiding more efficient in breeding for FHB resistance. In addition, this is the research project to first time identify the microcollinearity between the chromosomal interval containing *Qfhs.ndsu-3AS* and the genomic regions of rice and *Brachypodium*. Moreover, all the molecular markers we developed have been made available to the USDA-NRI funded project on the physical mapping and sequencing of 3AS.

PI: Cai, Xiwen
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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.

Refereed Journal Articles:

Oliver, R.E., **X. Cai**, R.W. Stack, T. Friesen, S. Halley, and S.S. Xu. 2008. Fusarium head blight resistance in tetraploid wheat (*Triticum turgidum* L.). Crop Sci 48: 213-222

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.

Proceedings:

Cai, X., S.S. Xu, R.E. Oliver, Q. Zhang, R.W. Stack,, S. Zhong, T.L. Friesen, S. Halley, and E.M. Elias. 2008. Alien Introgression for FHB Resistance in Wheat - Challenges and Strategies. Proc. 11th Intern. Wheat Genet. Symp., Brisbane, Australia, August 24-29, 2008.

Xu, S.S., R.E. Oliver, **X. Cai,** T.L. Friesen, S. Halley, and E.M. Elias. 2007. Searching for new sources of FHB resistance in the relatives of wheat. *In* Proc. 2007 National Fusarium Head Blight Forum (abstr.), Kansas City, MO, December 2-4, 2007.

Invited Oral Presentations:

Zhu, X., X. Chen, J.D., Faris, J. Hu, R.W. Stack, T. Adhikari, M.E. Elias, S.F. Kianian, and **X. Cai.** 2007. Toward a better understanding of a major FHB resistance QTL in tetraploid wheat (abstr.). Proc. National Wheat Genomics Conference, November 30 – December 2, 2007. Kansas City, MO.

Cai, X. 2008. Molecular characterization of pest resistance and meiotic restitution in wheat. Wheat Cytogenetics Institute, Nanjing Agricultural University, Nanjing, P. R. China, April 22-23, 2008.

Cai, X. 2008. Wheat genetics project: identification, characterization, and introgression of desirable genes. Annual Meeting of ND SBARE and ND Wheat Commission, April 4, 2008.