USDA-ARS/
U.S. Wheat and Barley Scab Initiative
FY05 Final Performance Report (approx. May 05 – April 06)
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Cover Page

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Fiscal Year:	**2005**
FY05 ARS Agreement ID:	**59-0790-3-078**
Agreement Title:	**Characterization of Resistance to Fusarium Head Blight in Wheat and its Reltives.**
FY05 ARS Award Amount:	**$ 71,215**

USWBSI Individual Project(s)

USWBSI Research Area*	Project Title	ARS Adjusted Award Amount
BIO	Fine Mapping of QFHS.NDSU-3AS in Durum Wheat.	$ 37,068
GIE	Enhancing Resistance to Fusarium Head Blight in Wheat Using Alien Species.	$ 34,147
	Total Award Amount	**$ 71,215**

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Principal Investigator Date

* BIO – Biotechnology
CBC – Chemical & Biological Control
EDM – Epidemiology & Disease Management
FSTU – Food Safety, Toxicology, & Utilization
GIE – Germplasm Introduction & Enhancement
VDUN – Variety Development & Uniform Nurseries

Project 1: *Fine Mapping of QFHS.NDSU-3AS in Durum Wheat.*

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

Lack of effective sources of resistance has been a major hurdle of breeding for FHB resistance in durum wheat (*Triticum turgidum* ssp. *durum*, genomes AABB). The major FHB resistance QTL, *Qfhs.ndsu-3AS*, identified from *T. turgidum* ssp. *dicoccoides* (genomes AABB), a tetraploid relative of durum, could play an important role in enhancing resistance of durum to FHB. This FHB resistance QTL was previously mapped to the short arm of chromosome 3A (3AS). The density of molecular markers and resolution within the QTL region in the previous genetic map are not sufficient for effective utilization of this QTL in breeding and further understanding of the molecular mechanism of FHB resistance. We have detected more molecular marker loci near the QTL and placed the QTL within a smaller chromosomal interval.

A large number of ESTs have been developed in wheat and many of them have been assigned to chromosomal deletion bins. The SSR marker locus *Xgwm2* that defined the QTL peak was assigned to the chromosome bin 3AS 0.45-1.00 using Chinese Spring (CS) (*T. aestivum* L.) deletion lines of 3AS. We have used the ESTs mapped to this chromosome bin as reference sequences to identify TRAP (target region amplified polymorphism), STS (sequence tagged site), and SSR (simple sequence repeat), and SNP (single nucleotide polymorphism) marker loci near *Qfhs.ndsu-3AS* for saturation mapping of the chromosomal region harboring the QTL. Meanwhile, we have been constructing a RFLP map of the ESTs assigned to the chromosome bin 3AS 0.45-1.00. This will allow us to identify rice genomic regions colinear with the QTL region and to generate more molecular markers closely linked to the QTL using rice genomic sequences as references. In addition, we have been generating more recombinants in the QTL region by screening a large F_2 population (over 4,000 individuals) derived from the cross between LDN and a LDN(Dic)-3A RICL that is resistant to FHB and carries the smallest T. *turgidum* ssp. *dicoccoides* chromosomal fragment. We also re-evaluated the mapping population of 83 recombinant inbred chromosome lines (RICLs) over two seasons in the greenhouse. The resulting phenotype data validated the map position of this FHB resistance QTL. In summary, we have been making significant progress toward fine mapping of this QTL via the approaches mentioned above.

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

<u>Accomplishment I:</u>

We saturated the genomic region containing the QTL using EST-derived TRAP, STS, SSR, and SNP markers. A total of 45 new molecular marker loci were detected on chromosome 3A and the resulting linkage map consisted of 55 markers spanning a genetic distance of 277.2 cM. *Qfhs.ndsu-3AS* was positioned within a chromosomal interval of 11.5 cM and is flanked by the two PCR-based molecular marker loci, *Xfcp399* (STS) and *Xfcp397.2* (TRAP). To date, the average map distance between the marker loci within this QTL region has been reduced to 3.5 cM.

Impact:

The FHB resistance QTL *Qfhs.ndsu-3AS* has been placed within a smaller chromosomal interval (11.5 cM). The two PCR-based molecular markers (*Xfcp401* and *Xfcp397.2*) flanking this interval are useful in assisting selection of this QTL in breeding and the allelism tests of FHB resistance QTLs. This will facilitate utilization of this QTL in breeding for FHB resistance in durum and pyramiding of different resistance QTLs to enhance resistance of durum to FHB. In addition, this accomplishment will lead to the construction of a high resolution map of *Qfhs.ndsu-3AS*, a major FHB resistance QTL non-homoeologous to *Qfhs.ndsu-3BS* derived from hexaploid wheat cultivar "Sumai 3", and ultimately cloning of this QTL. This will enhance the knowledge of molecular mechanisms of FHB resistance and facilitate our breeding efforts to combat this destructive disease in 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?:

This project has developed PCR-based molecular markers closely linked to the major FHB resistance QTL *Qfhs.ndsu-3AS* in tetraploid wheat. Some of the molecular markers developed in this project have been provided to other laboratories for MAS and allelism tests.

Accomplishment II:

We identified a recombinant line that is resistant to FHB and contains a smallest T. *turgidum* spp. *dicoccoides* chromosome 3A fragment via substitution mapping. Linkage drag in this line was significantly reduced comparing to other resistant lines.

Impact:

This resistant line carries only a small chromosomal fragment containing FHB resistance QTL from T. *turgidum* ssp. *dicoccoides* and the major portion of its genomes is from the durum cultivar "Langdon (LDN)". Serious linkage drag has not been found in this line. This resistant line, therefore, could be used directly in breeding for FHB resistance in durum.

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 could represent a potential source of resistance for durum.

Project 2: *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?

We have identified over 70 wheat-alien species derivatives with resistance to FHB. They carry varied amounts of alien chromatin that may contain both the genes of interest, such as FHB resistance genes, and the genes we do not want, such as the gene conditioning late maturity. They cannot be utilized directly in breeding for FHB resistance in wheat due to genetic complexity and undesirable genes in the alien chromatin. However, we can develop breeder-friendly germplasm from these resistant derivatives via chromosome manipulation. We have hybridized some of these resistant derivatives with the wheat genetic stock having the *Ph* inhibitor gene Ph^I to induce recombination between wheat and alien chromosomes. The progeny from these crosses were crossed and backcrossed with the spring wheat cultivars and breeding lines, including Alsen, Russ, Reeder, Steele, Glenn, and ND2710, to eliminate unwanted alien chromatin and to integrate the alien resistance genes into the adapted genetic backgrounds. This will lead to the development of elite breeder-friendly germplasm with enhanced FHB resistance. A large number of F_3 and F_4 progeny have been produced. We selected over 800 progeny for evaluation of FHB reaction based on morphology and genetic stability. Eighty-five of the progeny evaluated exhibited an FHB reaction similar to Sumai 3. Chromosome constitution in some of these resistant progeny has been characterized using fluorescent *in situ* hybridization (FISH). Preliminary FISH results indicated these resistant progeny contain 1-2 alien chromosomes or chromosome fragments in their genomes. These progeny will be further manipulated cytogenetically, if necessary, to eliminate unwanted alien chromatin and to develop elite breeding lines resistant to FHB.

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 identified 74 wheat-alien species derivatives resistant to FHB and characterized chromosome constitution in some of the derivatives using FISH.

Impact:

These resistant derivatives represent potential novel sources of FHB resistance for wheat breeding. Alien resistance genes in the derivatives can be integrated into wheat genomes via chromosome translocation or substitution. Understanding of chromosome constitution in the resistant derivatives provides critical information for the production of elite germplasm via chromosome manipulation. The wheat-alien chromosome translocation and substitution lines could be utilized directly in breeding. Pyramiding of the alien resistance genes and other resistance genes currently identified in wheat will facilitate the development of germplasm with robust and durable 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 accomplishment provides wheat breeders an access to the secondary and tertiary gene pool in breeding for FHB resistance. Utilization of alien FHB resistance genes in breeding could lead to the development of wheat cultivars with enhanced FHB resistance.

Accomplishment II:

We produced FHB resistant progeny with 1-2 alien chromosomes or chromosome fragments in the adapted genetic backgrounds.

Impact:

We have been increasing generations of the resistant progeny with reduced alien chromatin. Genetically stabilized lines derived from these progeny will be evaluated for FHB resistance in the greenhouse and field. Resistant lines will be released and utilized in breeding for FHB resistance. They could play an important role in enhancing resistance of wheat to FHB.

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?:

Resistant wheat-alien species derivatives with large amounts of alien chromatin cannot be used directly in breeding. This accomplishment leads to the production of resistant germplasm lines with minimal alien chromatin. Availability of these resistant germplasm lines to breeders will facilitate utilization of alien resistance genes in the development of wheat cultivars with high levels of FHB resistance.

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.

Oliver, R.E., Xu, S.S., Stack, R.W., Friesen, T.L., Jin, Y., and Cai, X. 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.

Oliver, R.E., Cai, X., Xu, S.S., Chen, X., and Stack, R.W. 2005. Wheat-alien species derivatives: A novel source of resistance to Fusarium head blight in wheat. Crop Sci 45: 1353-1360.

Cai, X., Chen, P.D., Xu, S.S., Oliver, R.E., and Chen, X. 2005. Utilization of alien genes to enhance Fusarium head blight resistance in wheat: A review. Euphytica 142: 309-318.

Chen, X., Faris, J.D., Hu, J., Stack, R.W., Adhikari, T., Elias, M.E., Kianian, S. F., and Cai, X. 2006. Saturation and comparative mapping of a major Fusarium head blight resistance QTL in tetraploid wheat. Molecular Breeding (submitted).

Oliver, R.E., Cai, X., Friesen, T.L. Halley, S., Stack, R.W., and Xu, S.S. 2006. Fusarium head blight resistance in tetraploid wheat (*Triticum turgidum* L.) (in preparation).

Oliver, R.E., Stack, R.W., Miller, J.D., and Cai, X. 2006. Reaction of wild emmer wheat accessions to Fusarium head blight (in preparation).

Chen, X., Faris, J.D., Hu, J., Stack, R.W., Adhikari, T., Elias, M.E., Kianian, S. F., and Cai, X. 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.

Cai, X., Xu, S.S. Oliver, R.E., and Stack, R.W. 2005. The alien gene could be one of the 'fighters' against Fusarium head blight in wheat. p. 21 (abstr.). *In* S.M. Canty, T. Boring, J. Wardwell, L. Siler, and R.W. Ward (ed.) Proc. 2005 National Fusarium Head Blight Forum (abstr.), Milwaukee, WI. 11-13 Dec. 2005. Michigan State University, East Lansing, MI. (invited presentation)

Oliver, R.E., X. Cai, R. Stack, T. Friesen, S. Halley, and S.S. Xu. 2005. Fusarium head blight resistance in tetraploid wheat. p. 79 (abstr.). *In* S.M. Canty, T. Boring, J. Wardwell, L. Siler, and R.W. Ward (ed.) Proc. 2005 National Fusarium Head Blight Forum, Milwaukee, WI. 11-13 Dec. 2005. Michigan State University, East Lansing, MI.

McArthur, R.I., R.E. Oliver, S.S. Xu, R. Stack, R.R.C.Wang, and X. Cai. 2005. Molecular characterization of wheat-alien species amphiploids and chromosome addition lines resistant to Fusarium head blight. p. 60 (abstr.). *In* S.M. Canty, T. Boring, J. Wardwell, L. Siler, and R.W. Ward (ed.) Proc. 2005 National Fusarium Head Blight Forum, Milwaukee, WI. 11-13 Dec. 2005. Michigan State University, East Lansing, MI.