USDA-ARS / USWBSI
FY04 Final Performance Report
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Cover Page

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Year:	**FY2004** (approx. May 04 – April 05)
FY04 ARS Agreement ID:	**59-0790-3-078**
FY04 ARS Agreement Title:	**Characterization of Resitance to Fusarium Head Blight in Wheat and its Relatives.**
FY04 ARS Award Amount:	**$ 60,863**

USWBSI Individual Project(s)

USWBSI Research Area*	Project Title	ARS Adjusted Award Amount
BIO	Fine Mapping of Qfhs.ndsu-3AS in Durum Wheat.	$ 33,446
GIE	Enhancing Resistance to Fusarium Head Blight in Wheat Using Alien Species.	$ 27,418
	Total ARS Award Amount	**$ 60,863**

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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?

Qfhs.ndsu-3AS is a major FHB resistance QTL identified in tetraploid wheat and was mapped on the chromosome 3A using *T. durum* cv. Langdon (LDN)-*T. dicoccoides* chromosome 3A recombinant inbred chromosome lines (RICL). The chromosomal region spanning the QTL seems to be a region with low recombination. We have tried various PCR-based marker techniques, such as SSR, STS, SSCP, and TRAP (Target Region Amplification Polymorphism), to saturate this chromosomal region. These PCR-based markers were derived from the ESTs assigned to the QTL region. We have designed 345 TRAP primer pairs and amplified polymorphism at 130 loci. So far we have assigned 60 markers to this chromosome. The total map distance is 162.2 cM. Twenty-eight markers were assigned to the QTL region with a map distance of 17.0 cM.

We have been generating more recombinants within the QTL region in order to increase the resolution of the QTL map. We identified two co-dominant TRAP markers that are 12.3 cM apart and flank the QTL. These two flanking markers have been used to screen the large F_2 population (over 1,000 individuals) for recombinants in this chromosomal region. The F_2 population was derived from the cross between LDN and a LDN(Dic)-3A RICL that is resistant to FHB and carries the smallest *T. dicoccoides* chromosomal fragment. So far we have identified 3 recombinants within the QTL region. Heterozygous recombinants are being allowed to self in order to obtain homozygous recombinants. Homozygous recombinants will be evaluated for FHB resistance. This will allow for placing the QTL within a smaller chromosomal interval and generating more useful markers for MAS (marker-assisted selection) in breeding. Meanwhile, we have been making efforts to generate more markers to further saturate the QTL region. We ran 13 new SSR primer pairs (wmc, cfa, and cfd) mapped on the chromosome 3A in our population. Unfortunately, none of them was mapped in the QTL region. Also, we amplified the DNA sequences flanking the SSR locus closely linked with the QTL peak, *Xgwm2*, using TAIL-PCR (thermal asymmetric interlaced PCR). We have been using these sequences to screen LDN BAC library and trying to identify positive clones to generate more markers in the QTL region. We have been using PCR-based markers closely linked with the QTL to screen breeding lines for FHB resistance.

2. What were the most significant accomplishments?

We have further saturated this QTL region using new molecular markers. We re-evaluated the mapping population for FHB resistance for two more greenhouse seasons. This allowed us to obtain more accurate phenotyping data for fine mapping of the QTL. Two co-dominant markers flanking the QTL were generated to identify recombinants within the QTL region. We have used the flanking markers to identify 3 recombinants in the QTL region from a large F_2 population (800 F_2 individuals). We have been screening more F_2 individuals for recombinants. We should be able to construct a finer map of the QTL after the recombinants are genotyped and phenotyped. In addition, we have been using molecular markers to assist selection of breeding materials in which *Qfhs.ndsu-3AS* is involved for FHB resistance. Therefore, this project has been making a significant progress toward the construction of a fine map of the FHB resistance QTL and the development of molecular markers for MAS in breeding for FHB resistance.

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 evaluated over 300 wheat-alien species derivatives with replications over two greenhouse seasons. Seventy-four of the derivatives were identified as resistant to Fusarium head blight (FHB) as Sumai 3, a widely used source of resistance from China. These wheat-alien species derivatives represent a potential source of novel genes to enhance resistance of both durum and common wheat to FHB. We have grown 25 of the resistant derivatives that are morphologically like wheat and may carry less alien chromatin in their genomes than others in the field to verify their resistance under field conditions. Three of the 25 derivatives that have exhibited high levels of resistance and desired agronomic traits have been released to the spring wheat breeding program at North Dakota State University.

There are wheat-alien species amphiploids, chromosome addition, substation, and translocation lines among the 74 resistant derivatives. Some of these derivatives carry a large amount of alien chromatin in their genomes. Alien chromatin in these derivatives may contain desirable genes, such as FHB resistance genes, and undesirable genes as well, such as the genes conditioning late maturity and low yield. We have manipulated chromosomes in these derivatives to eliminate unwanted alien chromatin and develop breeder-friendly germplasm lines. This has been done by hybridizing these derivatives to the Ph^I lines that carry a *Ph* gene inhibitor and promote homoeologous chromosome pairing. Progeny from these crosses has been crossed and backcrossed to the resistant and susceptible spring wheat cultivars, Alsen, Steele, Reeder, and Dapps. The BC1F2 and BC1F3 materials are being grown in the greenhouse to increase generation or to further backcross to the wheat cultivars. Genetically stabilized lines with desired agronomic traits will be evaluated for FHB resistance. Chromosome constitutions of the resistant lines will be characterized using molecular cytogenetic techniques. This will lead to the development of breeder-friendly germplasm lines resistant to FHB.

2. What were the most significant accomplishments?

We have identified 74 FHB resistant lines derived from the crosses of wheat with a number of relatives of wheat, including *T. tauschii* (Coss.) Schmal., *Roegneria kamoji* C. Koch, *R. ciliaris* (Trin.) Nevski, *Leymus racemosus* Lam., *Thinopyrum ponticum* (Podp.) Barkworth & D.R. Dewey, *Th. elongatum* (Host) D.R. Dewey, *Th. junceum* (L.) Love, *Th. intermedium* (Host) Barkworth & D.R. Dewey, *Dasypyrum villosa* L., *Secale cereale* L., and oat *(Avena sativa* L.). These lines could serve as a novel source of resistance to manage FHB in both durum and common wheat. We have characterized chromosome constitutions for some of the resistant derivatives using fluorescence in situ hybridization (FISH). Four of the derivatives were identified as partial wheat-*Th. ponticum* amphiploids with 56 chromosomes. These amphiploids contain a large amount of alien chromatin and unwanted traits. We have been performing chromosome manipulation in order to eliminate unwanted alien chromatin and reduce the linkage drag in the resistant derivatives. We have produced a large number of lines from multiple crosses in which the resistant derivatives were involved. These lines are being served as a foundation to develop breeder-friendly germplasm lines resistant to FHB.

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

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

Xu, S.S., J.D. Faris, **X**. **Cai**, and D.L. Klindworth. 2005. Molecular cytogenetic characterization and seed storage protein analysis of 1A/1D translocation lines in durum wheat. Chromosome Research (in press).

Chen, X., **X. Cai**, J. Hu, and S. Kianian. 2004. Saturation mapping of the Fusarium head blight resistance QTL *Qfhs-ndsu-3A* in durum wheat. p. 240. *In* S.M. Canty, T. Boring, K. Versdahl, J. Wardwell, and R.W. Ward (ed.) Proc. 2nd Int. Symp. on Fusarium Head Blight, Orlando, FL. 11-15 Dec. 2004. Michigan State University, East Lansing, MI.

Chen, X., J.G. Hernandez, J. Hu, S. Kianian, and **X. Cai**. 2004. Comparative mapping of the Fusarium head blight resistance QTLs *Qfhs-ndsu-3AS* and *Qfhs-ndsu-3BS* in wheat. *In* Agronomy Abstracts (CD-ROM), ASA, Madison, WI.

Oliver, R.E., **X. Cai**, S.S. Xu, R.W. Stack, and Y. Jin. 2004. Fusarium head blight reaction and cytogenetic characterization of four wheat-*Thinopyrum ponticum* amphiploids. *In* Agronomy Abstracts (CD-ROM), ASA, Madison, WI.

Oliver, R.E., S.S. Xu, **X. Cai**, R.W. Stack, and Y. Jin. 2004. Fusarium head blight resistance in wheat-alien species derivatives. p. 139. *In* S.M. Canty, T. Boring, K. Versdahl, J. Wardwell, and R.W. Ward (ed.) Proc. 2nd Int. Symp. on Fusarium Head Blight, Orlando, FL. 11-15 Dec. 2004. Michigan State University, East Lansing, MI.

Oliver, R.E., S.S. Xu, **X. Cai**, and R.W. Stack. 2004. Evaluation of tetraploid wheat germplasm for resistance to Fusarium head blight. p. 138. *In* S.M. Canty, T. Boring, K. Versdahl, J. Wardwell, and R.W. Ward (ed.) Proc. 2nd Int. Symp. on Fusarium Head Blight, Orlando, FL. 11-15 Dec. 2004. Michigan State University, East Lansing, MI.