USDA-ARS / USWBSI
FY03 Final Performance Report (approx. May 03 – April 04)
July 15, 2004

Cover Page

PI:	**Xiwen Cai**
Institution:	**North Dakota State University**
Address:	**Department of Plant Sciences** **Box 5051** **166 Loftsgard** **Fargo, ND 58105-5051**
E-mail:	**xiwen.cai@ndsu.nodak.edu**
Phone:	**701-231-7404**
Fax:	**701-231-8474**
Year:	**FY2003 (approx. May 03 – April 04)**
FY03 ARS Agreement ID:	**59-0790-3-078**
FY03 ARS Agreement Title:	**Characterization of resitance to Fusarium head blight in wheat and its relatives.**
FY03 ARS Award Amount:	**$ 56,355**

USWBSI Individual Project(s)

USWBSI Research Area*	**Project Title**	**ARS Adjusted Award Amount**
BIO	Saturation and Physical mapping of Qfhs.ndsu-3AS in durum wheat.	$ 33,446
GIE	Enhancing resistance to Fusarium head blight in wheat using alien species.	$ 22,909
	Total Amount Recommended	**$ 56,355**

_Xiwen Cai_______________________________July 12, 2004_________________
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

(Form – FPR03)

Project 1: *Saturation and Physical mapping of Qfhs.ndsu-3AS in durum wheat.*

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

We have assigned 30 new markers to chromosome 3A in durum wheat using different marker techniques, including SSR, STS, RFLP and TRAP (Target Region Amplification Polymorphism) etc. Ten of them were mapped within a 29.3 cM chromosomal interval spanning the Fusarium head blight (FHB) resistance QTL, *Qfhs.ndsu-3AS* on this chromosome. Assignment of the new markers to the region surrounding the QTL on chromosome 3A has extended the map distance from 155.2 cM to 248.4 cM. New markers flanking the QTL have been identified and the QTL has been placed within a smaller chromosomal interval. A large F_2 population (over 1,000 individuals) has been developed to generate more recombinants for fine mapping of this QTL region. F_3 offspring of the heterozygous recombinant F_2 individuals were produced to generate homozygous recombinants for FHB evaluation. We assigned the microsatellite marker closely linked with the peak of the QTL, *Xgwm2*, to the deletion bin 3AS-4. About 200 ESTs mapped in this deletion bin have been used as a source to generate markers to saturate this QTL region. We have designed 38 SSR primer pairs and 96 STS primer pairs based on the EST sequences and conserved domains of disease resistance genes in the ESTs. Only one STS marker has been mapped within the QTL region through this approach. A total of 248 primer pairs have been designed to generate TRAP markers within this chromosomal region using bulked segregant analysis. Seven TRAP markers have been assigned to the QTL region. We have been also generating more markers to saturate this chromosomal region based on the synteny between wheat chromosome 3A and rice chromosome 1. We recovered the polymorphic band of the SSR marker *Xgwm 2* and sequenced the fragment. The flanking sequences of *Xgwm 2* locus were obtained using TAIL-PCR (thermal asymmetric interlaced PCR). We have been trying to assign these sequences to our map through RFLP. In the meantime, these sequences are being used to screen the BAC libraries of *Triticum monococcum*, durum wheat cultivar 'Langdon', and *T. tauschii*. This may allow for generating more markers within this QTL region. We assigned 10 of the markers closely linked with another FHB resistance QTL (*Qfhs.ndsu-3BS*) region on chromosome 3B to the outside of the QTL (*Qfhs.ndsu-3AS*) region on chromosome 3A. This result suggested that these two FHB resistance QTLs might not be alleles at homoeologous loci.

2. What were the most significant accomplishments?

We have assigned 10 new molecular markers within the FHB resistance QTL region. The map distance has been extended from 155.2 cM to 248.4 cM in the current map of chromosome 3A. We have identified new markers flanking the QTL and placed the QTL within a 9.4 cM chromosomal interval which is over three times smaller than the previous interval (29.3 cM) spanning the QTL. We have had TAIL-PCR work for chromosome walking in the wheat genomes. This provides a new approach to access the QTL.

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 screened a total of 327 genotypes for Type II resistance to FHB in the greenhouse for two seasons. There are wheat cultivars, synthetic hexaploid wheat lines, and wheat lines derived from the crosses between wheat and its wild relatives from the genera *Triticum, Elymus, Roegneria, Thinopyrum, Leymus, Dasypyrum,* and *Avena* among the 327 genotypes evaluated. Forty-eight of the 327 genotypes showed resistance as high as the resistant check 'Sumai 3' in the greenhouse. Twenty-five of them were planted in the field in the spring 2004 to confirm their resistance. Molecular cytogenetic characterization indicated that the resistant wheat-alien species derivatives included amphiploids, addition, substitution, and translocation lines. They carry variable amount of alien chromatin in their genomes. In the meantime, hundreds of crosses have been made between the adapted wheat cultivars and the resistant lines in order to transfer the resistance to wheat. Chromosome manipulation has been carried out to eliminate unwanted alien chromatin from the progeny. Fluorescence *in situ* hybridization (FISH) has been used to characterize chromosome constitutions of the resistant lines. The wheat-alien species chromosome translocation lines consistently show resistance in the greenhouse and field evaluation will be released to breeders to develop wheat cultivars having higher levels of resistance or more durable resistance to this disease.

We have evaluated a number of accessions of the wild species, *Th. ponticum, Th. elongatum, Th. intermedium, Leymus racemosus,*and *Elymus humidus* for Type II FHB resistance. Some of the accessions showed high level of resistance to the disease. These resistant accessions have been hybridized to both common wheat and durum wheat using embryo rescue techniques. This will allow for introduction of the FHB resistance from the wild species to wheat.

2. What were the most significant accomplishments?

We have identified novel sources of FHB resistance from wheat-alien species derivatives. Alien chromatin conferring resistance to FHB has been integrated into the wheat genomes and characterized using molecular cytogenetic techniques. Some of the resistance sources identified are synthetic hexaploid wheat lines (Langdon-*T.tauschii* amphiploids, 2n=AABBDD=42) and wheat-alien species chromosome translocation lines (2n=42). These resistant lines either have the same genomes as common wheat or carry the least alien chromatin in their genomes. They are desirable materials for breeders to directly utilize the novel sources of resistance to develop varieties resistant to this disease. We have been characterizing the alien chromatin conferring FHB resistance in these lines. This will assist breeders to pyramid the novel sources of resistance with the previously identified resistance sources and enhance resistance of wheat to this disease.

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.

Cai, X., Stack, R.W., Froberg R.C., and Maan, S.S. (2003) Genetic Characterization of Fusarium Head Blight Resistance in Spring Wheat. In: Proc. 10th Intern. Wheat Genet. Symp., Italy, pp1108-1110

Chen, X., Cai, X., Hu, J., Kianian, S. (2004) Saturation mapping of the Fusarium head blight resistance QTL *Qfhs-ndsu-3A* in durum wheat (abstract). In: Proc. 2nd Intern. Symp. on Fusarium Head Blight, Orlando, Florida (submitted).

Chen, X., Hernandez, J.G., Hu, J., Kianian, S., Cai, X., (2004) Comparative mapping of the Fusarium head blight resistance QTLs *Qfhs-ndsu-3AS* and *Qfhs-ndsu-3BS* in wheat (abstract). Proc. 2004 ASA-CSSA-SSSA Intern. Annual Meetings, Seattle, WA (submitted)

Chen, X., Hu, J., Kianian, S., and Cai, X. (2003) Saturation mapping of a major Fusarium head blight resistance QTL region in tetraploid wheat (abstract). In: Natl FHB Forum Proc, Bloomington, MN, pp11

Oliver, R.E., Cai, X., Xu, S.S., Stack, R.W., and Jin, Y. (2004) Fusarium head blight reaction and cytogenetic characterization of four wheat-*Thinopyrum ponticum* amphiploids (abstract). Proc. 2004 ASA-CSSA-SSSA Intern. Annual Meetings, Seattle, WA (submitted)

Oliver, R.E., Xu, S.S., Cai, X., Stack, R.W., and Jin, Y. (2004) Fusarium head blight resistance in wheat-alien species derivatives (abstract). In: Proc. 2nd Intern. Symp. on Fusarium Head Blight, Orlando, Florida (submitted).

Oliver, R.E., Xu, S.S., Cai, X., and Stack, R.W. (2004) Evaluation of tetraploid wheat germplasm for resistance to Fusarium head blight (abstract). In: Proc. 2nd Intern. Symp. on Fusarium Head Blight, Orlando, Florida (submitted).

Oliver, R.E., Cai, X., Xu, S.S., Chen, X., and Stack, R.W. (2004) Wheat-alien species derivatives- Novel sources of resistance to Fusarium head blight. Crop Sci. (in preparation).

Oliver, R.E., Chen, X., Xu, S.S., Stack, R., Jin, Y., and Cai, X. (2003) Identification of novel sources of Fusarium head blight resistance from wheat-alien species derivatives (abstract). In: Natl FHB Forum Proc, Bloomington, MN, pp225