U.S. Wheat and Barley Scab Initiative
FY02 Final Performance Report (approx. May 02 – April 03)
July 15, 2003

Cover Page

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Year:	**FY2002 (approx. May 02 – April 03)**
Grant Number:	**59-0790-1-070**
Grant Title:	**Fusarium Head Blight Research**
FY02 ARS Award Amount:	**$ 29,268**

Project

Program Area	Project Title	USWBSI Recommended Amount
BIO	Saturation Mapping and Contig Development for Qfhs.ndsu-3AS, a Major FHB Locus in Durum Wheat.	$30,000
	Total Amount Recommended	**$30,000**

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Principal Investigator Date

Project 1: Saturation Mapping and Contig Development for Qfhs.ndsu-3AS, a Major FHB Locus in Durum Wheat.

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

Fusarium head blight (FHB) is a major disease affecting the wheat industry. Developing resistant varieties is one of the best means of control against FHB. Wild varieties offer the best resistance for durum wheat, especially *Triticum turgidum* L. var. *dicoccoides*. Previously, a linkage map was constructed using the RICL population Langdon-dicoccoides-3A. A major QTL for resistance to FHB, *Qfhs.ndsu-3AS*, was found on the short arm of chromosome 3A, as well as a marker, *Xgwm2,* tightly linked to the QTL peak. In order to facilitate the isolation of the gene or genes responsible for the resistance, saturation mapping of the region around this QTL is being carried out using a combination of approaches, which include wheat EST (expressed sequence tag)-derived markers designed from the NSF-Wheat Genomics project. Another resource for markers is by using synteny of wheat with other members of the Poacea. ESTs that map to regions in rice orthologous to wheat chromosome 3A surrounding the QTL of interest are being targeted for designing primers. Various databases (i.e. GRAMENE, TIGR) contain information for aligning wheat markers to rice bacterial artificial chromosomes.

2. What were the most significant accomplishments?

Thirty-six individuals who show recombination in the *Qfhs.ndsu-3AS* region were selected from the original recombinant inbred chromosome line (RICL) population. This sub-set was screened in the greenhouse for reaction to *Fusarium* in a randomized complete block design with two replications. The added data was used for a more accurate phenotypic characterization of these individuals reducing the error associated with quantitative trait mapping and more precise placement of *Qfhs.ndsu-3AS*. We have used an individual which contains the region surrounding *Qfhs.ndsu-3AS* to cross with Langdon-16 (the original susceptible parent). We generated over 120 F_1 lines, planted 40 of those individuals for selfing and have generated over 2,000 F_2 individuals. Since the *T. dicoccoides* segment was in Langdon-16 background, these lines should only segregate for the region of interest. If need be we can increase the number of F_2 individuals to a much higher level. Flanking PCR markers are being used to identify recombinations within the region of interest. Only recombinants will be phenotypically characterized. We have identified 15 bacterial artificial chromosome (BAC) clones by screening the *T. monococcum* BAC high-density filters (Lijavetzky et al. 1999) with the DNA-based probe *NDSU.fhb.3A* derived from the microsattelite marker *Xgwm2* tightly linked with *Qfhs.ndsu-3AS*. These BAC clones are currently being characterized.

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.

Saturation Mapping of a Major Fusarium Head Blight QTL in Tetraploid Wheat. M.M. Osenga, V.S. Kalavacharla, C.D. Otto, E.M. Elias, S. Kianian. 2002 ASA-CSSA-SSSA Annual Meetings. November 10-14, 2002. Indianapolis, Indiana