U.S. Wheat and Barley Scab Initiative
FY01 Final Performance Report (approx. May 01 – April 02)
July 15, 2002

Cover Page

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Grant Number:	**59-0790-1-070**
Grant Title:	**Fusarium Head Blight Research**
FY01 ARS Award Amount:	**$ 28,230**

Project

Program Area	Project Title	Requested Amount
Biotech	Development of a BAC contig spanning a major FHB QTL in durum wheat	$ 59,430
	Total Amount Requested	**$ 59,430**

_Venugopal S. Kalavacharla_____July 15, 2002__
Principal Investigator Date

(Form – FPR01)

Project 1: Development of a BAC contig spanning a major FHB QTL 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 of 19 markers 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. The GRAMENE database contains information for aligning wheat markers to rice bacterial artificial chromosomes.

2. What were the most significant accomplishments?
ESTs: 29 primers were designed by selecting ESTs that have been mapped to Group 3A, as part of the Wheat EST mapping effort. All these ESTs map to the chromosomal bin 3AS4-0.45-1.00. Forward and reverse primers have been designed from these ESTs sequences using the Primer3 software. The optimal annealing temperature was established and PCR was run on the parents, a small sample of the population, and controls. The primers that showed polymorphism on the sample population was used on the entire LDN(Dic-3A) population, run on a PAGE gel, silver stained, and scored. Not all primers showed polymorphism. Markers showing polymorphism are currently being mapped.

Ten primers have been designed using the consensus contig sequence information available on the NSF EST database. Polymorphism seen in the parents and a sample population allow the use of that primer on the complete population. These markers will then be added to the 3A map as well.

Thirty-six individuals which show recombination in the region of interest have been selected from the original recombinant inbred chromosome line (RICL) population. This sub-set is being re-screened in the greenhouse for reaction to *Fusarium* in a randomized complete block design with two replications. The added data should help in more accurate phenotypic characterization of these individuals reducing the error associated with quantitative trait mapping and more precise placement of *Qfhs.ndsu-3AS*. This population will then be targeted with the above molecular markers for saturation mapping. Additionally, one member of the RICL population, LDN (Dic-3A)-72, that contains the smallest region of the *T. dicoccoides* segment, and shows good tolerance to scab is being crossed to normal Langdon durum in order to generate a large population segregating for recombinants in this region. This population will be screened with flanking molecular markers and then targeted for saturation mapping and phenotypic characterization.

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.

Otto, C.D., Kalavacharla, V., Kianian, S.F., Elias, E.M., Stack, R.W., Joppa, L.R., Doehler, E.T. Molecular Analysis of a major *Fusarium* head blight QTL in a RICL population of tetraploid wheat. International Plant & Animal Genome Conference, January 13-17, 2001.

Kalavacharla, V.S., Goreham, J., Spaeth, K., Osenga, M., Elias, E.M., and Kianian, S.F. Progress towards saturation mapping and BAC contig development for *Qfhs.ndsu-3AS*, a major FHB QTL in durum wheat. National *Fusarium* Head Blight Forum, Erlanger, KY. December 2001.

Osenga, M., Kalavacharla, V., Otto, C., Kianian, S. Saturation Mapping of a Major Fusarium Head Blight QTL in Tetraploid Wheat. 18th Annual Graduate Student Symposium. March 8-9, 2002. University of Saskatchewan, Saskatoon, SK, Canada. Oral presentation:

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