

**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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<b>Year:</b>	<b>FY2002 (approx. May 02 – April 03)</b>
<b>Grant Number:</b>	<b>59-0790-9-049</b>
<b>Grant Title:</b>	<b>Fusarium Head Blight Research</b>
<b>FY02 ARS Award Amount:</b>	<b>\$ 48,780</b>

**Project**

<b>Program Area</b>	<b>Project Title</b>	<b>USWBSI Recommended Amount</b>
BIO	Saturation mapping of a chromosome 3(3H) Fusarium head blight resistance QTL.	\$50,000
	<b>Total Amount Recommended</b>	<b>\$50,000</b>

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 Principal Investigator

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 Date

### **Project 1: Saturation mapping of a chromosome 3(3H) Fusarium head blight resistance QTL.**

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

The major issue being resolved is to provide molecular markers, that are closely associated with Fusarium Head Blight (FHB) resistance, to breeders for use in marker assisted selection in their work towards development of FHB resistant cultivars. More and more efforts are going into moving resistance QTL to adapted cultivars using molecular markers and availability of multiple markers is essential for this work. We are resolving this issue by isolating, mapping on genetic and physical maps Expressed Sequence Tags (ESTs). There are approximately 341,000 barley and 415,000 wheat ESTs deposited. These probably represent more than half of all the genes in barley. We target these ESTs to the region of choice (chromosome 3H short arm telomeric region) by identifying homology with sequenced rice genomic DNA from the region syntenous to the target region. This allows us to saturate the region with markers and thus facilitate their utilization for molecular marker assisted selection of specific QTL. The long term goal is to try to identify candidate genes that might be involved in the Fusarium head blight resistance. The mapping data is available on my web site <http://barleygenomics.wsu.edu> and will be provided to breeders, who can not access the internet, on request.

2. What were the most significant accomplishments?

The Foster x CI4196 mapping population was advanced to the F7 generation and an anchor map developed. We continue to improve this map. Recently, Dr. Horsley's group used this map to identify a major Fusarium Head Blight (FHB) QTL on chromosome 2H. The Foster x CI4196 population is used for mapping selected ESTs that are polymorphic. We also integrate the SSR markers mapped by Dr. Horsley's group in this overall map. The CI4196 line is one of the most Fusarium Head Blight resistant lines available and a good map together with good molecular markers will facilitate the exploitation of the genes carried by this line.

Due to the identification of the major FHB QTL on chromosome 2H, we have shifted our major emphasis from chromosome 3H to chromosome 2H. To facilitate high resolution mapping, we have identified cross-overs in the FHB QTL region. These selected cross-over lines are used to facilitate rapid mapping. We have also initiated fractionation of this QTL by moving molecularly identified fragments into a uniform genetic background in order to test their contribution to the overall resistance. This work is in progress.

We have also mapped other genes that may be involved with disease resistance. These include the germin-like genes, resistance gene analogs and the hypersensitive induced reaction genes. Genes that facilitate cell death may actually increase the organism's susceptibility to FHB. Therefore it is important to identify the negative regulators of cell death. This work is also in progress.

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.

1. Rostoks, N., D. Schmierer, D. Kudrna, and A. Kleinhofs (2003) Barley putative hypersensitive induced reaction genes: genetic mapping, sequence analyses and differential expression in disease lesion mimic mutants. *Theor. Appl. Genet.* (in press).
2. Schmierer, D., D. Kudrna, T. Drader, and A. Kleinhofs (2002) Saturation genetic and physical mapping of chromosome 3 *Fusarium* Head Blight QTL region. Presented at the Scab Forum 2002, Holiday Inn Cincinnati-Airport, Erlanger, KY Dec. 7-9, 2002.
3. Schmierer, D., D. Kudrna, T. Drader, and A. Kleinhofs (2002) Genetic Linkage Map of cv. Foster x *Fusarium* Resistant Line CI4196. Poster presented at North American Barley Researchers Workshop Fargo, ND Fall 2002.