U.S. Wheat and Barley Scab Initiative
FY01 Final Performance Report (approx. May 01 – April 02)
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Cover Page

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Year:	**FY2001 (approx. May 01 – April 02)**
Grant Number:	**59-0790-9-049**
Grant Title:	**Fusarium Head Blight Research**
FY01 ARS Award Amount:	**$ 43,806**

Project

Program Area	Project Title	Requested Amount
Biotech	Disease resistance-like markers for fusarium QTL	$ 60,204
	Total Amount Requested	**$ 60,204**

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Principal Investigator Date

(Form – FPR01)

Project 1: Disease resistance-like markers for fusarium 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, and sequencing Resistance Gene Analog (RGA) markers. 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. Sequencing will facilitate development of user friendly PCR methods for use of these markers.

2. What were the most significant accomplishments?

We have completed mapping approximately 120 new RGA loci and identified BAC clones for most of them. Many more remain to be mapped, particularly the wheat and rice RGAs. There are a number of duplications of the barley RGAs among these.

- We developed techniques for large scale RGA isolation. RGA isolation is a slow and tedious procedure and the more efficient techniques we developed will facilitate saturation of the barley genome. This technique involves the use of cDNA libraries and RGA conserved PCR primers. This worked much better than previous approaches, however the technique is limited because many RGAs are expressed at a very low level and may not be represented in the libraries used. Many more new RGAs are also coming from the rice genome sequencing effort. Thus, additional efforts in RGA isolation from barley may not be warranted. In fact, we have so many putative RGAs now that we can not process all of them. Clearly, mapping is now the major bottleneck to further genome saturation.
- We advanced the Foster x CI4196 mapping population to the F7 generation and have developed an anchor map. This population is used for mapping RGAs that are polymorphic. 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.
- We completed physical and genetic mapping of the maize rust resistance barley homologue gene RGA families.
- We completed map-based cloning of the barley stem rust resistance gene Rpg1. This project was funded primarily by a USDA/NRI grant. However, the identification of the gene as a member of receptor kinase gene family opens new possibilities for isolation of disease resistance gene analogs.

We have also mapped other genes that may be involved with disease resistance. These include the germin-like genes and the hypersensitive induced reaction genes.

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., J. M. Zale, J. Soul, R. Brueggeman, A. Druka, D. Kudrna, B. Steffenson, and A. Kleinhofs (2002) A barley gene family homologous to the maize rust resistance gene Rp1-D. Theor Appl Genet (2002) 104: 1298-1306.
2. Druka, A., D. Kudrna, C. G. Kannagara, D. von Wettstein, and A. Kleinhofs (2002) Physical and genetic mapping of barley (Hordeum vulgare) germin-like cDNAs. Proc. Natl. Acad. Sci. USA 99:850-855.
3. Rostoks, N., D. Kudrna, and A. Kleinhofs (2002) Mapping and sequencing putative barley hypersensitive induced reaction genes. Plant, Animal, and Microbe Genomes X P407.
4. Kanazin, V., T. Blake, A. Kleinhofs, and G. Muehlbauer (2002) Characterization of the barley resistance gene analogs. Plant, Animal, and Microbe Genomes X P405.