U.S. Wheat and Barley Scab Initiative
Annual Progress Report
September 18, 2000

Cover Page

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Year:	**FY2000**
Grant Number:	**59-0790-9-049**
Grant Title:	**Fusarium Head Blight Research**
Amount Granted:	**$55,000.00**

Project

Program Area	Objective	Requested Amount
Biotechnology	Develop disease resistance-like markers for Fusarium QTL.	$65,727.00
	Requested Total	$65,727.00[1]

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Principal Investigator Date

[1] Note: The Requested Total and the Amount Granted are not equal.

Project 1: Develop 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. We are resolving this issue by isolating, mapping on genetic and physical maps, and sequencing Resistance Gene Analog (RGA) markers. These markers and all data will be provided to breeders for use in marker assisted selection. The sequencing will facilitate development of user friendly PCR methods for use of these markers. We have advanced the Foster x CI4196 mapping population to the F7 generation and are using this population for mapping. The CI4196 line is one of the most Fusarium Head Blight resistant lines available.

2. Please provide a comparison of the actual accomplishments with the objectives established.
   Our proposed objectives were to isolate, sequence and map resistance gene analogs (RGAs). To date we have isolated 20 new RGAs, which map to 31 genetic loci. These RGAs, plus 11 additional ones developed and mapped by Dr. Saghai Maroof, have been used to isolate barley Bacterial Artificial Chromosome clones (physical mapping). Genetic mapping is in progress for 26 additional RGA probes received from Dr. Gary Muehlbauer. These have been mapped to the barley physical map by Gary. Thus, a minimum of 67 new RGA loci have been placed on the barley map. All of the above RGAs were confirmed by sequencing and the sequence is available for PCR primer development. A total of 582 BAC clones have been identified with these probes from a 6.3X Morex BAC library. This represents approximately 92 loci (582 divided by 6.3), a number somewhat larger than the 67 new loci that have been mapped. This discrepancy is due to the fact that some of the probes have not been mapped yet and it is also an indication of the existence of more loci than the genetic mapping can identify due to lack of polymorphism or closely linked loci.

   We have focused on developing techniques to facilitate large scale RGA isolation. RGA isolation is a slow and tedious procedure and faster, more efficient techniques are required to approach saturation of the 1,000 (or so) RGA genes that are estimated to reside in plant genomes. As explained in our proposal, we developed a technique for RGA isolation from our Bacterial Artificial Chromosome (BAC) genomic library. The technique worked, but it also isolated a lot of non-RGA genes. Therefore it was slow and tedious because many fragments had to be sequenced to identify the real RGAs. We now have applied a similar technique to the many cDNA libraries that we have developed under an EST (expressed sequence tag) sequencing grant from USDA-NRI. This technique is working much better and we have now isolated many new RGAs that need to be mapped. We will complete mapping of additional RGAs before this grant period is over.

3. What were the reasons established objectives were not met? If applicable.
   The established objectives were, or will be, met before the grant period is completed.

4. What were the most significant accomplishments this past year?
   The most significant accomplishment was the development of a technique to allow rapid and efficient isolation of RGA clones.

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. Brueggeman, R., A. Druka, D. Kudrna, and A. Kleinhofs (1999) Isolation and characterization of resistance gene analogs from barley. 16th American Barley Researchers Workshop, p54, Idaho Falls, Idaho, July 11-15, 1999.
2. Kanazin, V., T. Blake, A. Kleinhofs, and G. Muehlbauer (1999) Cloning and characterization of disease resistance gene analog clusters in barley. 16th American Barley Researchers Workshop, p63, July 11-15, 1999, Idaho Falls, Idaho.
3. Brueggeman, R., A. Druka, D. Kudrna, and A. Kleinhofs (2000) Novel resistance gene analogs from barley. Plant and Animal Genome VIII p108, Jan. 9-12, 2000, San Diego, CA.
4. Kanazin, V., T. Blake, A. Kleinhofs, and G. Muehlbauer (2000) Cloning and characterization of the disease resistance genes analogs in barley. Plant and Animal Genome VIII p83, Jan. 9-12, 2000, San Diego, CA.