U.S. Wheat and Barley Scab Initiative
Annual Progress Report
September 15, 1999

Cover Page

PI:	**Bob Bowden**
Institution:	**Kansas State University**
Address:	**4604 Throckmorton Hall** **Manhattan, KS 66502**
Email:	**rbowden@plantpath.ksu.edu**
Phone:	**785-532-5810**
Fax:	**785-532-5692**
Year:	**FY1999**
Grant Number:	**59-0790-9-029**
Grant Title:	**Fusarium Head Blight Research**
Amount Granted:	**$34,146.00**

Project

Program Area	Objective	Requested Amount
Epidemiology	Develop a genetic map of G. zeae.	$35,000
	Requested Total	$35,000[1]

_____

Principle Investigator Date

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

Project 1: Develop a genetic map of *G. zeae*.

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

   Although *Gibberella zeae*, the causal agent of Fusarium head blight, is one of the most important plant pathogens in the world, little is known about its genetics. Techniques for crossing this homothallic fungus were recently developed by our group. This advance made it possible to construct a genetic map of *G. zeae*. A genetic map would improve population genetic studies by removing the bias created by linkage between molecular markers used to monitor genetic recombination, gene flow, mutation, and genetic drift. It could also be used for map-based cloning of important genes related to aggressiveness, competitive ability, sensitivity to fungicides, etc. A genetic map can be used for detecting quantitative trait loci (QTL) controlling adaptive traits such as aggressiveness, growth rate, etc. Finally, a genetic map of *G. zeae* can be compared to maps of other fungi to study the degree of gene synteny and the evolution of chromosome rearrangements. Toward that end, we have produced a mapping population by crossing a deoxynivalenol (DON) mycotoxin-producing strain from Kansas with a nivalenol mycotoxin-producing strain from Japan. Ninety-six progeny were scored for 1083 AFLP markers using 36 primer pairs. MapManager was used to construct the linkage map.

2. Please provide a comparison of the actual accomplishments with the objectives established.
   Objectives:
   1. Produce a mapping population by crossing two diverse strains of *G. zeae*
      a. Accomplished.
   2. Construct a genetic linkage map using molecular markers
      a. Preliminary map accomplished. We are now checking for markers mis-scored or misplaced on the map.
   3. Correlate linkage groups to physical chromosomes
      a. Not yet started.

3. What were the reasons established objectives were not met? If applicable.
   At this date (9/15/1999), excellent progress has been made on objectives 1 and 2, but there has been insufficient time to meet the third objective.

4. What were the most significant accomplishments this past year?

   So far we have mapped 1038 AFLP markers on nine linkage groups that range from 105 to 530 cM. The total map distance is 2741 cM. Skewed segregation ratios were associated with five linkage groups. Two of these were attributable to selection for *nit* markers used in the cross. The others could be due to chromosome rearrangements or segregation distortion loci. In joint studies with our collaborators in the USDA mycotoxicology group at Peoria, we have found that mycotoxin type and quantity segregate in this cross.

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.

Bowden, R. L. and Leslie, J. F. 1999. Sexual recombination in *Gibberella zeae*. Phytopathology 89:182-188.