U.S. Wheat and Barley Scab Initiative
FY00 Final Performance Report (approx. May 00 – April 01)
July 30, 2001

Cover Page

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Year:	**FY2000 (approx. May 00 – April 01)**
Grant Number:	**59-0790-0-068**
Grant Title:	**Fusarium Head Blight Research**
2000 ARS Award Amount:	**$48,780**

Project

Program Area	Project Title	Requested Amount
Biotechnology	Genomics of Gibberella zeae, the head scab fungus.	$36,000.00
	Requested Total	$36,000.00[1]

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Principal Investigator Date

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

Project 1: Genomics of Gibberella zeae, the head scab fungus.

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

To better understand the wheat scab fungus, it is important to identify fungal genes expressed during different development and infection stages. One of our objectives is to construct two cDNA libraries with RNAs isolated from *Gibberella zeae* strain PH-1 mycelia starved for carbon and nitrogen, which are two culture conditions that mimic the fungal *in planta* growth environment. The other objective is to sequence 5000 random clones from these libraries and make the sequences and clones available to *G. zeae* researchers.

In the past year, we have accomplished all the objectives we proposed. Both nitrogen-starved and carbon-starved cDNA libraries contain over 1 million original plaques with insertion size of 0.5-3 kb. Around 4500 clones from the nitrogen starved library and 800 clones from the carbon starved library have been sequenced as ESTs (Expressed Sequence Tags). Additional 9216 clones from the nitrogen starved library and 6912 clones from the carbon starved library were picked into 384 well plates. All these clones have been arrayed with Q-Pix on high-density membranes. These clones can be used for sequencing more ESTs when additional funding is available.

All the sequences (original and processed) and BLASTX results are available at the web site (http://www.genomics.purdue.edu/~jxu/Fgr). Contig assembly has been done with CAP3. We have also distributed over 20 EST clones to a number of *G. zeae* researchers.

In addition, we have generated a 10X BAC library with the average insert size larger than 70 Kb. A PH-1 cosmid library was also constructed in the vector pMocosX, which contains the hygromycin resistance marker suitable for *G. zeae* transformation.

2. What were the most significant accomplishments?

We have accomplished all the objectives we proposed. Before this EST project, there is very limited sequence information in GenBank about *G. zeae*. We now have estabalished an EST database consisting of around 10,000 entries. Thousands of additional clones from these cDNA libraries are ready for future EST sequencing. We have also constructed a BAC library and a cosmid library. Materials and sequence information generated in this project will be very useful for future genomics studies on fungal pathogenesis in *G. zeae*.

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.

There is no publication resulted from the project yet. Two manuscripts are in preparation. One is on the ESTs (in collaboration with Frances Trail and Corby Kistler). The other one is on a MAP kinase gene (*CHM1*) we knocked out. *CHM1*, an homologue of *MPS1* in *Magnaporthe*, is critical for fungal virulence in *G. zeae*.