U.S. Wheat and Barley Scab Initiative
Annual Progress Report
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Cover Page

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Year:	**FY2000**
Grant Number:	**59-0790-0-068**
Grant Title:	**Fusarium Head Blight Research**
Amount Granted:	**$50,000.00**

Project

Program Area	Objective	Requested Amount
Biotechnology	Study the disease cycle of the head scab fungus Gibberella zeae using genomics technology.	$36,000.00
	Requested Total	$36,000.00[1]

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Principal Investigator Date

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

Project 1: Study the disease cycle of the head scab fungus Gibberella zeae using genomics technology.

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. Two cDNA libraries were constructed 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. Around 2000 clones from the nitrogen starved library and 800 clones from the carbon starved library have been sequenced as ESTs (Expressed Sequence Tags). All the sequences (original and processed) and BLASTX results are available at the web site (http://www.genomics.purdue.edu/~jxu/Fgr).

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. More ESTs will be sequenced from the nitrogen starved cDNA library after removing the highly redundant clones. Microarray analysis will be used to identify fungal genes expressed in different processes when more ESTs are sequenced.

We have also generated a BAC library consisting of 9, 000 clones with the average insert size of 60 Kb. Currently, efforts to construct a BAC library with bigger average insert size are under the way. A PH-1 cosmid library was constructed in the vector pMocosX, which contains the hygromycin resistance marker suitable for *G. zeae* transformation.

2. Please provide a comparison of the actual accomplishments with the objectives established.

We have accomplished the objective to construct a nitrogen starved cDNA library and sequenced 2000 ESTs from this library. Additional 9,000 clones from this library have been picked and will be ready for sequencing soon to meet the goal of 5000 ESTs. A carbon starved cDNA library was also constructed (it is not listed in the objectives) for future EST sequencing. As planned, all the original sequences and BLASTX search results were posted on the web.

For the objective to construct a BAC library, currently, we have a BAC library with an average insert size of 60 Kb and is in the process of generating more BAC clones with bigger insert size.

3. What were the reasons established objectives were not met? If applicable.

Progressing towards accomplishing the established objectives by the end of the funding period.

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

Construct the cDNA libraries, establishing the EST database, and constructing a BAC library.

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 out of this research yet.

I am a new faculty member at Purdue University. This project did not start until I moved into my lab in May.