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:	**N/A**
Grant Title:	**Fusarium Head Blight Research**
FY01 ARS Award Amount:	**$ 20,003**

Project

Program Area	Project Title	Requested Amount
Epid/Dis. Mgt.	Genomics of *Gibberella zeae*, the head scab fungus	$ 31,852
Epid/Dis. Mgt.	Genetics of pathogenicity in *Fusarium graminearum*	
	Total Amount Requested	**$ 31,852**

Principal Investigator Date

(Form – FPR01)

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?

There is a lack of knowledge concerning the way in which the head blight pathogen, *Fusarium graminearum* causes disease in plants. This basic knowledge will be required to develop novel strategies for the control of the disease and the mycotoxins produced by the fungus. Genomics technology makes it possible to study the expression of potentially all of the genes in an organism. Agricultural scientists have begun using this technology to improve crops and study pathogenicity. A genome project for the scab fungus provides a unique opportunity to harness this technology for the study of the disease cycle of this important fungus. One direct method to access a large number of expressed genes is to partially sequence individual clones from a cDNA library, called Expressed Sequence Tags (ESTs). Our goal was to sequence 7000 ESTs, from three separate libraries each representing a different developmental stage of the pathogen: perithecial development, DON production in culture, and infection hyphae in wheat heads. Another goal was to document the function of some genes with respect to the ability of the fungus to cause disease.

2. What were the most significant accomplishments?

a) The DNA sequence of 19 kb of the trichothecene biosynthetic cluster for 39 strains of *Fusarium graminearum* and related species was determined and shown to correspond to the strain's chemotype (the type of mycotoxin produced whether nivalenol, or deoxynivalenol with 3-acetyl deoxynivalenol, or 15-acetyl deoxynivalenol). DNA polymorphisms correspond to chemotype rather than species. This trans-species polymorphism is consistent with balancing selection for chemotype. See Ward et al., 2002.
b) The DNA sequence for nearly 8,000 ESTs from various stages of the fungus were sequenced and analysis of these data were presented for publication along with F. Trail and J.Xu. These sequences are posted on the web: http://www.crl.umn.edu/scab/gz-consort.html
c) Knockout mutants of the gene for a MAP kinase (*MGV*1) were shown to reduce the aggressiveness of the fungus. The gene also appears to be involved in cell wall formation and vegetative compatibility. These data were presented for publication along with J. Xu.

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.

Ward, T.J., J.P. Bielawski, H.C. Kistler, E. Sullivan, and K. O'Donnell. Evidence of ancient polymorphism and adaptive evolution in the trichothecene gene cluster of phytopathogenic *Fusarium*. Proc. Natl. Acad. Sci. USA, 99:9278-9283. 2002.
http://www.pnas.org/cgi/reprint/99/14/9278.pdf

Trail, F., Xu, J.R., San Miguel, P., Gaffoor, I. and Kistler, H.C. Expressed sequence tags from developmental stages of *Gibberella zeae*. Proceedings of the 2001 National Fusarium Head Blight Forum. p. 37.

Hou, Z., Xue, C., Kistler, H.C. and Xu, J.R. MGV1 regulates female fertility and plant infection in *Fusarium graminearum*. Proceedings of the 2001 National Fusarium Head Blight Forum. p. 127.

Trail, F., Xu, J.R., San Miguel, P., and Kistler, H.C. Genomics of the mycotoxin producing fungus, *Fusarium graminearum* (*Gibberella zeae*). Proceedings of the 14th Aflatoxin Elimination Workshop. p. 37. 2001.

Goswami, R.S., Trail, F., Xu, J.R. and Kistler, H.C. Differential expression of genes in *Fusarium graminearum* with high and low virulence for wheat. Phytopathology 92:S31. 2002.

Tracy, M., Hou, Z., Kistler, H.C. and Xu, J.R. REMI mutagenesis in the wheat scab fungus *Fusarium graminearum*. Phytopathology 92:S81. 2002.

Hou, Z., Xue, C., Peng,Y., Katan, T., Kistler, H.C., and Xu, J.R. A MAP kinase gene (MGV1) from *Fusarium graminearum* involved in mycotoxin production, female fertility, heterokaryon formation, hyphal growth and plant infection. Submitted to Molecular Plant Microbe Interactions. In review.

Trail, F., Xu, J.R., San Miguel, P. Halgren, R. and Kistler, H.C. Analysis of expressed sequence tags from *Fusarium graminearum*. Submitted to Fungal Genetics and Biology. In review.