U.S. Wheat and Barley Scab Initiative
FY02 Final Performance Report (approx. May 02 – April 03)
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Cover Page

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Year:	**FY2002 (approx. May 02 – April 03)**
Grant Number:	**NA**
Grant Title:	**Fusarium Head Blight Research**
FY02 ARS Award Amount:	**$ 82,927**

Project

Program Area	Project Title	USWBSI Recommended Amount
EDM	Diversity of Gibberella zeae populations from the U.S., China and Italy.	$53,000
EDM	Use of gene expression analysis to study pathogenicity in Gibberella zeae.	$32,000
	Total Amount Recommended	**$85,000**

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Principal Investigator Date

Project 1: Diversity of *Gibberella zeae* populations from the U.S., China and Italy.

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

The re-emergence of FHB in past decade is likely due to a combination of factors including unfavorable climatic conditions, changes in agronomic practices and the lack of high levels of genetic resistance in currently planted wheat and barley. Another unknown but potentially important factor for the disease is the level of genetic variation in the pathogen. In order to assist effective plant breeding and disease management programs, it is essential to understand the the sources and extent of genetic variation in the head blight pathogen both in the U.S. and worldwide.

Genetic diversity of populations from China, the U.S. and Italy have been inferred based on allele differences at polymorphic, single copy loci defined by RFLPs and multilocus haplotypes have been constructed for each strain. Genetic data on strains have been arranged into geographic populations corresponding to the country of origin or defined regions within each country (e.g. state, county, field etc.) and analyzed according to geographic source. In order to determine the degree of outcrossing in the fungus, the extent of linkage disequilibrium between pairs of loci were calculated.

2. What were the most significant accomplishments?

We have completed the first comprehensive population genetic survey of *Fusarium graminearum* in the United States, using co-dominant genetic markers. Contrary to previously reports that used smaller sample sizes and/or less informative genetic markers, we discovered that population subdivision does exist within the United States and the rate of outcrossing is much less than previously inferred. Our results indicate that a new population of the pathogen has been recently introduced into North Dakota and Northwestern Minnesota. The new population, which has not yet been assimilated into the resident pathogen population, produces a different spectrum of trichothecene toxins than the resident population.

Project 2: Use of gene expression analysis to study pathogenicity in *Gibberella zeae*.

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 ESTs from libraries created from *Fusarium graminearum*-infected wheat heads subtracted with wheat heads infected with a low virulence strain of the fungus or mock inoculated plants.

2. What were the most significant accomplishments?

Based on differences in aggressiveness we selected two strains with high (NRRL 31084) and low (NRRL 28303) virulence for genomic studies. cDNA libraries were created by suppression subtractive hybridization to compare mRNA populations from wheat heads inoculated with them in order to identify genes specific to each interaction. EST sequences from both the forward and reverse libraries revealed marked differences in gene expression among strains during pathogenesis. Several of them had matches with sequences from the whole genome sequence assembly of *Fusarium graminearum,* indicating that they were *Fusarium* genes expressed *in planta*. Another subtracted cDNA library also has been constructed using wheat inoculated with NRRL 31084 and mock inoculated wheat heads to further characterize fungal genes expressed during the disease interaction. Ultimately, we anticipate that this information will be vital for identification, isolation and functional analysis of genes related to pathogenicity.

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.

Trail, F., J.R. Xu, P. San Miguel, R. G. Halgren, and H.C. Kistler. 2003. Analysis of expressed sequence tags from *Gibberella zeae* (anamorph *Fusarium graminearum*). Fungal Genetics and Biology 38:187-197.

Hou, Z., Xue, C., Peng,Y., Katan, T., Kistler, H.C., and Xu, J.R. 2002. A MAP kinase gene (MGV1) from *Fusarium graminearum* involved in mycotoxin production, female fertility, heterokaryon formation, and plant infection. Molecular Plant Microbe Interactions 15:1119-1127.

Gale, L.R., C. A. Hernick, K. Takamura, L.-F. Chen, and H. C. Kistler. 2002. Population analysis of *Fusarium graminearum* from wheat fields in eastern China. Phytopathology 92:1315-1322.

Gale, L.R., Ward, T., Balmas, V. and Kistler, H.C. Population subdivision in *Fusarium graminearum* lineage 7 in the U.S. is correlated with toxin chemotype. Fungal Genetics Newsletter 50 (Suppl): 145. 2003.

Goswami, R.S., Trail, F., Xu, J.R. and Kistler, H.C. Fungal genes expressed during plant disease development in the *Fusarium graminearum*/wheat interaction. Fungal Genetics Newsletter 50 (Suppl): 106. 2003.

O'Donnell, K., Ward, T.J., and Kistler, H.C. Discordant evolution of trichothecene toxins and species within the *Fusarium graminearum* species complex: Phylogenetic evidence from multigene genealogies. IXth International Fusarium Workshop Abstracts. 27-30 January 2003.

Trail, F., Xu, J.R., and Kistler, H.C. The *Fusarium graminearum* Genomics Project. 2002 National *Fusarium* Head Blight Forum Proceedings. p. 186. 2002.

Tracy, M., Hou, Z., Kistler, H.C. and Xu, J.R. REMI mutagenesis in the wheat scab fungus, *Fusarium graminearum*. 2002 National *Fusarium* Head Blight Forum Proceedings. p. 185. 2002.
Chen, L.-F., Yao, H.-Y., Yu,G., Xie, W.-P. and Kistler, H.C. Metabolism of trichothecenes by wheat.2002 National *Fusarium* Head Blight Forum Proceedings. p. 189. 2002.

Goswami, R.S., and Kistler, H.C. Assessment of the differential ability of *Fusarium* strains to spread on wheat and rice. 2002 National *Fusarium* Head Blight Forum Proceedings. p. 163. 2002.