USDA-ARS/
U.S. Wheat and Barley Scab Initiative
FY06 Final Performance Report (approx. May 06 – April 07)
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Cover Page

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Fiscal Year:	2006
USDA-ARS Agreement ID:	NA
USDA-ARS Agreement Title:	Fusarium Head Blight Research.
FY06 ARS Award Amount:	$ 102,114

USWBSI Individual Project(s)

USWBSI Research Area*	Project Title	ARS Award Amount
PGG	Heterogeneity and Selection in the F. graminearum Species Complex in the U.S.	$ 52,984
PGG	Identifying Fungal Gene Expression Vital to FHB Infection and DON Accumulation.	$ 49,130
	Total Award Amount	**$ 102,114**

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Principal Investigator Date

* CBCC – Chemical, Biological & Cultural Control
EEDF – Etiology, Epidemiology & Disease Forecasting
FSTU – Food Safety, Toxicology, & Utilization of Mycotoxin-contaminated Grain
GET – Genetic Engineering & Transformation
HGR – Host Genetics Resources
HGG – Host Genetics & Genomics
PGG – Pathogen Genetics & Genomics
VDUN – Variety Development & Uniform Nurseries

Project 1: *Heterogeneity and Selection in the F. graminearum Species Complex in the U.S.*

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

The re-emergence of FHB in past 15 years 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 potentially important factor for the disease is the level of genetic variation in the pathogen. In order to assist plant breeding and disease management programs, it is essential to understand the sources and extent of genetic variation in the head blight pathogen both in the U.S. and worldwide.

Genetic diversity of populations of *F. graminearum* is being characterized from pathogen collections gathered in the U.S. Genetic data on strains have been arranged into geographic populations corresponding to defined regions within the U.S. and analyzed according to geographic source. These studies present an up-to date snapshot of pathogen genetic diversity in the United States.

2. List the most important accomplishment and its impact (how is it being used?). Complete all three sections (repeat sections for each major accomplishment):

Accomplishment:
From a previous study of diversity in *Fusarium graminearum* collected in Midwestern states we identified a small population in North Dakota and Minnesota that have an experimentally verified 3-acetyl, deoxynivalenol (3ADON) chemotype that were genetically distinct from the predominant 15-acetyl, deoxynivalenol (15ADON) chemotype strains. Collections in 2003, 2004 and now in 2006 have verified that this population is increasing in frequency and spreading southward. From the 2006 collection we observed 3ADON strains in South Dakota for the first time. The 3ADON chemotype strains also were found to have greater mycotoxin potential as these strains produce on average ~60% more DON on inoculated wheat than 15ADON strains. This year we may have encountered the first real evidence for recombination between the previously separate 3ADON and 15ADON populations and are currently working to determine the impact of recombination on mycotoxin potential and fitness. We have also continued to document the establishment of nivalenol producing strains in the south central US and now have evidence for their presence in Arkansas as well as previously reported in Louisiana.

Impact:
We are now expanding our studies, not only characterizing genetic diversity of strains, but also testing the significance of chemotype and mycotoxin potential on disease and DON accumulation on wheat cultivars. Using strains of different chemotype, we have tested DON accumulation on the eight most commonly planted varieties of wheat in Minnesota. Our preliminary results indicate little correlation between disease reaction and DON accumulation.

Our studies demonstrate the need for continual monitoring of the population composition, as *F. graminearum* in the U.S. is changing over time and is not as homogeneous as previously believed.

As a result of that accomplishment, what does your particular clientele, the scientific community, and agriculture as a whole have now that they didn't have before?

As a result of our reports on pathogen diversity, other scientists now know that distinct populations of the pathogen exist in the United States and the geographic distribution of those strains. These conclusions will assist other scientists involved wheat and barley improvement by alerting them to this diversity so that the entire spectrum of pathogen and toxin types may be accounted for in plant variety improvement efforts.

Project 2: *Identifying Fungal Gene Expression Vital to FHB Infection and DON Accumulation.*

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 understand pathogenicity. Our genomic project for the scab fungus provides a unique opportunity to harness this technology for the study of the disease cycle of this important fungus.

2. List the most important accomplishment and its impact (how is it being used?). Complete all three sections (repeat sections for each major accomplishment):

Accomplishment:

DNA microarrays allow us to study how genes are turned on and off during developmental processes such as reproduction and plant infection. We have used a DNA microarray based on the genome sequence of *F. graminearum* to study pathogen gene expression during infection of wheat and barley and during sporulation.

Impact:

We now have a comprehensive knowledge of the genes expressed by the fungus during reproduction and plant infection. Using this information we have discovered a gene in the fungus that controls the ability to reproduce, accumulate DON and cause head blight disease. This gene makes a novel regulatory connection between spore formation and toxin accumulation that may be exploited as a new target for disease and pathogen control.

As a result of that accomplishment, what does your particular clientele, the scientific community, and agriculture as a whole have now that they didn't have before?

Data from ongoing microarray experiments of the FHB fungus are freely available on the internet at www.barleybase.org and www.plexdb.org and thus are accessible to scientists in both the public and private sector. Additionally, based on our work, other researchers are now purchasing *F. graminearum* microarrays from private sector distributors, or making their own based on information available on the internet at http://mips.gsf.de/genre/proj/fusarium/ .

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.

Publications:

Gale,L.R., Ward,T.J., Balmas,V., and **Kistler, H.C.** 2007. Population subdivision of *Fusarium graminearum sensu stricto* in the Upper Midwestern United States. Phytopathology 97: In press.

Starkey, D.E., Ward, T.J., Aoki, T., Gale, L.R., **Kistler, H.C**., Geiser, D.M., Suga, H., Toth, B., Varga, J. and O'Donnell, K. 2007. Global molecular surveillance reveals novel Fusarium head blight species and trichothecene toxin diversity. Fungal Genet.Biol., In press. Available online 12 March 2007.

Goswami, R.S., Xu, J.R., Trail, F., Hilburn, K.S., and **Kistler, H.C.** 2006. Genomic analysis of host-pathogen interaction between *Fusarium graminearum* and wheat during early stages of disease development. Microbiology 152: 1877-1890.

Seong, K., Li, L., Tracy, M., **Kistler, H.C.** and Xu, J.-R. 2006. Cryptic promoter activity of the HMR1 coding region in the wheat scab fungus *Fusarium graminearum*. Fungal Genetics and Biology 43: 34-41.

Presentations and non-peer reviewed articles:

Kistler, H.C. 2006. Profiles in Scourge: Gene expression analysis of a crop killer. Society for In vitro Biology Meeting. Minneapolis, MN. June 3, 2006.

Gale, L.R., L.E. O'Leary, J.D. Bryant, G.E. Ochocki, T.J. Ward and **H.C. Kistler**. 2006. Population shifts in *Fusarium graminearum sensu stricto* in the Upper Midwest. Joint Meeting of APS-CPS-MSA

Seong, K.Y., J.-R. Xu, and **H. C. Kistler**. 2005. Gene expression analysis of conidium maturation and germination on *Fusarium graminearum.* Proceedings of the National Fusarium Head Blight Forum; 2005 Milwaukee, WI. East Lansing: Michigan State University. p. 168.

Xu, J.R., F. Trail, and **H. C. Kistler**. 2005. Functional genomic studies of pathogenicity in *Fusarium graminearum* Proceedings of the National Fusarium Head Blight Forum; 2005 Milwaukee, WI. East Lansing: Michigan State University. p.171.

Hilburn, K.L.B. and **H.C. Kistler** 2005. Deletion of the trichothecene gene cluster of *Fusarium graminearum*. In: Canty, S.M., Boring, T., Wardwell, J. Siler, L. and Ward, R.W. (eds.) Proceedings of the National Fusarium Head Blight Forum; 2005 Milwaukee, WI. East Lansing: Michigan State University. p. 163.

Seong, K.-Y., Xu, J.-R., and **Kistler, H.C.** 2006. Genome-wide RNA expression analysis during conidial maturation and germination in the filamentous fungus *Fusarium graminearum.* 8th Europeaon Conference on Fungal Genetics.

Gale, L.R., T.J. Ward, K. O'Donnell, S.A. Harrison, and **H.C. Kistler**. 2005. Fusarium head blight of wheat in Louisiana is caused largely by nivalenol producers of *Fusarium graminearum* and *Fusarium asiaticum.* Proceedings of the National Fusarium Head Blight Forum; 2005 Milwaukee, WI. East Lansing: Michigan State University. p. 159.