USDA-ARS/
U.S. Wheat and Barley Scab Initiative
FY05 Final Performance Report (approx. May 05 – April 06)
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Cover Page

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Fiscal Year:	**2005**
FY05 ARS Agreement ID:	**NA**
Agreement Title:	**Genomics and Population Genetics of Gibberella zeae.**
FY05 ARS Award Amount:	**$ 107,792**

USWBSI Individual Project(s)

USWBSI Research Area*	Project Title	ARS Adjusted Award Amount
EDM	Distribution, Survival and Discovery of New Populations of *Fusarium graminearum* in the U.S.	$ 63,000
EDM	Genomics of *Gibberella zeae*, the Head Scab Fungus.	$ 44,792
	Total Award Amount	**$ 107,792**

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Principal Investigator Date

* BIO – Biotechnology
CBC – Chemical & Biological Control
EDM – Epidemiology & Disease Management
FSTU – Food Safety, Toxicology, & Utilization
GIE – Germplasm Introduction & Enhancement
VDUN – Variety Development & Uniform Nurseries

Project 1: *Distribution, Survival and Discovery of New Populations of Fusarium graminearum 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 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 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 yearly pathogen surveys in the U.S. Genetic data on strains have been arranged into geographic populations corresponding to defined regions within the U.S. (e.g. state, county, etc.) and analyzed according to geographic source. These studies are the most comprehensive survey of pathogen genetic diversity and change in pathogen populations conducted in the United States in the last six years.

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 survey of diversity in *Fusarium graminearum* collected nine Midwestern states in 1999 and 2000, we identified a small population in North Dakota and Minnesota (7%) that produced 3-acetyl, deoxynivalenol (3ADON) that were genetically distinct (Nm = 0.5) from the predominant 15-acetyl, deoxynivalenol (15ADON) producing *F. graminearum*. Collections in 2003 and 2004 in North Dakota and Minnesota indicates the 3ADON type was widespread and at high frequency (21% in ND, 24% in MN). Further analysis demonstrated that recombination in *F. graminearum*, although occurring, may be an infrequent event, as only 70 potential recombinants between the two populations were identified. Chemotyping in collections from 2001-2003 indicates that 15ADON is still the only type in other Midwestern states, although the nivalenol type was the most frequent in isolates from Louisiana. The predominance of the nivalenol type in Louisiana and the build-up of the 3ADON type in Minnesota and North Dakota suggest that selection is a principal evolutionary force acting on populations of *F. graminearum*.

Impact:

Contrary to prior reports on pathogen diversity, at least three distinct populations of *F. graminearum* have been found in the United States since the year 2000. Each of these pathogen populations is correlated with the predominance of a distinct profile of trichothecene mycotoxin. At the same time 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. 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: *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 understand 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.

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:

We have described the first studies utilizing a DNA microarray based on the genome sequence of *F. graminearum*. Microarrays allow us to study how genes are turned on and off during developmental processes such as reproduction and plant infection.

Impact:

Microarray design for the FHB fungus was commercialized by Affymetrix, Inc. as the USDA *Fusarium graminearum* GeneChip. The microarray and data derived from it will be useful to other scientists engaged in research to improve disease management on small grain crops. From these resources we hope to identify novel genes or gene regulation patterns that may be critical for pathogenicity in the fungus and thus may be targets for novel disease control measures.

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?:

Microarray data from the FHB fungus during infection of barley 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 may purchase *F. graminearum* microarrays from private sector distributors or make 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., Bryant, J.D., Calvo, S., Giese, H., Katan, T., O'Donnell, K., Suga, H., Taga, M., Usgaard, T.R., Ward, T.J. and **Kistler, H.C**. 2005. Chromosome complement of the fungal plant pathogen *Fusarium graminearum* based on genetic and physical mapping and cytological observations. Genetics 171: 985-1001.

Goswami, R.S. and **Kistler, H.C**. 2005. Pathogenicity and *in planta* mycotoxin accumulation among members of the *Fusarium graminearum* species complex on wheat and rice. Phytopathology 95:1397-1404.

Güldener, U., Seong, K.-Y., Boddu, J., Cho, S., Trail, F., Xu, J.-R., Adam, G., Mewes, H.-W., Muehlbauer, G.J., and **Kistler, H.C.** 2006. Development of a *Fusarium graminearum* Affymetrix GeneChip for profiling fungal gene expression *in vitro* and *in planta*. Fungal Genet. Biol. 43: 316-325.

Seong, K., Li, L., Tracy, M., **Kistler, H.C.** and Xu, J.-R. 2006. Cryptic promoter activity in the coding region of the HMG-CoA reductase gene in *Fusarium graminearum*. Fungal Genet. Biol. 43: 34-41.

Presentations and non-peer reviewed articles:

Gale, L.R., Bryant, J.D., Ochocki, G.E., Ward, T.J., and **Kistler, H.C.** *Fusarium graminearum* in the U.S.: heterogeneous and in flux. Fungal Genet. Newsl. 52 (Suppl): 63. 2005.

Cuomo, C., Ma, L.-J., Butler, J., Calvo, S., DeCaprio, D., Elkins, T., Galagan, J., Xu, J.-R., Trail, F., **Kistler, C.**, and Birren, B. Sequencing and analysis of the *Fusarium graminearum* genome. Fungal Genetics Newsletter 52 (Suppl): 81. 2005.

Gale, L.R., Bryant, J.D., Giese, H., Katan, T., O'Donnell, K., Suga, H., Usgaard, T.R., Ward, T.J. and **Kistler, H.C.** A genetic map of *Gibberella zeae* using sequence-tagged sites and AFLPs. Fungal Genetics Newsletter 52 (Suppl): 82. 2005.

Seong, K.-Y., Yao, J., **Kistler, H.C.**, Xu, J.-R. REMI mutagenesis and identification of infection defective mutants in Wheat Scab Fungus *Fusarium graminearum*. Fungal Genetics Newsletter 52 (Suppl): 106. 2005.

Chang, Y.-L., Cho, S., **Kistler, C.,** Sheng, H.-C., and Muehlbauer, G. Bacterial artificial chromosome-based physical map of *Gibberella zeae* (*Fusarium graminearum*). Plant and Animal Genome XII. San Diego, CA. Final Abstract Guide p. 94, 2005.

Birren, B., **Kistler, H.C.**, Xu, J. R. and Trail, F. Genomics of *Fusarium graminearum*. NSF/USDA Microbial Genome Sequencing Program Awardee Workshop. San Diego, CA. Final Program. p. 52-53, 2005.

Gale, L.R., L.E. O'Leary, J.D. Bryant, G.E. Ochocki, T.J. Ward and **H.C. Kistler**. 2005. Displacement of the native population of *Fusarium graminearum* in North Dakota and parts of Minnesota by a genetically divergent and more toxigenic population. 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. 158.

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*. 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. 159.

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., J.-R. Xu, and **H. C. Kistler**. 2005. Gene expression analysis of conidium maturation and germination on *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. 168.

Xu, J.R., F. Trail, and **H. C. Kistler**. 2005. Functional genomic studies of pathogenicity in *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.171.