USDA-ARS/
U.S. Wheat and Barley Scab Initiative
FY07 Final Performance Report (approx. May 07 – April 08)
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Cover Page

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Fiscal Year:	2007
USDA-ARS Agreement ID:	NA
USDA-ARS Agreement Title:	Fungal Genes in DON Biosynthesis.
FY07 ARS Award Amount:	$ 34,964

USWBSI Individual Project(s)

USWBSI Research Area[*]	**Project Title**	**ARS Adjusted Award Amount**
PGG	Identifying Fungal Genes and Plant Factors Involved in DON Production.	$34,964
	Total Award Amount	**$ 34,964**

Principal Investigator Date

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[*] 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
IIR – Integrated/Interdisciplinary Research
PGG – Pathogen Genetics & Genomics
VDUN – Variety Development & Uniform Nurseries

(Form FPR07)

Project 1: *Identifying Fungal Genes and Plant Factors Involved in DON Production.*

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

The fungus *Fusarium graminearum* causes extensive losses on wheat and barley crops world-wide and contaminates harvested grain with a compound known as DON, whose levels in grain are strictly regulated. In addition to factors reducing the impact of Fusarium head blight, novel methods for reduction of DON accumulation in grain are desirable. Currently, little is known about the pathogen factors that influence the accumulation of DON in plants. This study directly addresses the issue by identifying genes responsive the fungal regulatory pathways known to influence DON accumulation in both wheat and barley.

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:

To elucidate their genome-wide impact on gene regulation, *Tri6* and *Tri10* deletion mutants were constructed in *F. graminearum* and used for microarray analyses with RNA isolated from infected wheat heads with the wildtype as the control. While only a total of 37 genes had expression levels altered ≥ two-fold in the Δtri10 mutant, 208 genes were altered ≥ two-fold the Δtri6 mutant including transcript levels for nearly all known Tri genes. Among those also reduced were genes coding for enzymes in the isoprenoid biosynthetic pathway from acetyl CoA to farnesyl pyrophosphate, the latter being the immediate molecular precursor to all trichothecenes.

Impact:

This study demonstrates that the FHB fungus is remarkably adapted for producing DON, not only by precisely regulating the genes unique to toxin synthesis but also by modifying gene expression in basic house-keeping functions of the cell to promote toxin accumulation. Fungal cells thus become finely tuned "toxin factories" distinct from their non-toxin producing cousin species. This study also shows that alterations in the cellular factory's toxin assembly line can drastically reduce production of DON and the amount of disease caused by the fungus. These alterations have the potential to be used by FHB researchers as potential targets for designing control strategies aimed at reducing toxin concentrations in grain.

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?:

The published data on *F. graminearum* genes regulated by *Tri6* and *Tri10*, as well as the accompanying microarray data has been submitted to the Plant Expression Database (plexdb.org), and represent an important transfer of technology because FHB researchers now have access to the entire suite of genes regulated by these trichothecene biosynthetic cluster genes.

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.

Seong, K., Pasquali, M., Song, J., Hilburn, K., McCormick, S., Dong, Y., Xu, J.-R. and **Kistler, H.C**. 200x. Global gene regulation by *Fusarium* transcription factors *Tri6* and *Tri10* reveals adaptations for toxin biosynthesis. In revision for Mol. Microbiol.

Pasquali, M., Lysoe, E., Seong, K.-Y., Xu, J.-R., Ma, L.-J., **Kistler, H.C**. 2008. Global gene expression during plant infection and toxin biosynthesis in *Fusarium graminearum*. Journal of Plant Pathology 90 (3, Supplement): S3.11 – 12. Abstract.

Pasquali, M., Seong, K.-Y., Menke, J., Lysoe, E., Hilburn, K., Xu, J.-R., and **Kistler, H.C.** 2007. Spore development and trichothecene mutants of *Fusarium graminearum*. In: Proceedings of the 2007 National Fusarium Head Blight Forum, Kansas City, MO, 2-4 December, 2007. Page 32. Abstract.