USDA-ARS/
U.S. Wheat and Barley Scab Initiative
FY08 Final Performance Report (approx. May 08 – April 09)
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Cover Page

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Fiscal Year:	2008
USDA-ARS Agreement ID:	NA
USDA-ARS Agreement Title:	Fungal Genes involved in DON Accumulation in Wheat.
FY08 USDA-ARS Award Amount:	$ 34,755

USWBSI Individual Project(s)

USWBSI Research Category*	Project Title	ARS Adjusted Award Amount
PBG	Fungal Genes involved in DON Accumulation in Wheat.	$34,755
	Total Award Amount	**$ 34,755**

H. C. Kistler July 8, 2009

Principal Investigator Date

* MGMT – FHB Management
FSTU – Food Safety, Toxicology, & Utilization of Mycotoxin-contaminated Grain
GDER – Gene Discovery & Engineering Resistance
PBG – Pathogen Biology & Genetics
BAR-CP – Barley Coordinated Project
HWW-CP – Hard Winter Wheat Coordinated Project
VDHR – Variety Development & Uniform Nurseries – Sub categories are below:
SPR – Spring Wheat Region
NWW – Northern Winter Wheat Region
SWW – Southern Sinter Wheat Region

Project 1: *Fungal Genes involved in DON Accumulation in Wheat.*

1. **What major problem or issue is being resolved relevant to Fusarium head blight (scab) 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 (i.e. how is it being used) to minimize the threat of Fusarium head blight or to reduce mycotoxins. Complete both 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. 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**. 2009. Global gene regulation by *Fusarium* transcription factors *Tri6* and *Tri10* reveals adaptations for toxin biosynthesis. Mol. Microbiol. 72: 354-367.

Menke, J.R., Dong, Y. and Kistler, H.C. 2008. Comparative gene expression analysis of *Fusarium graminearum* in *Triticum aestivum* and *Oryza sativa* spp. *japonica*. Proceedings of the 2008 National Fusarium Head Blight Forum. p.88.

Menke, J.R., Dong, Y. and Kistler, H.C. 2009. Comparative gene expression analysis of *Fusarium graminearum* in *Triticum aestivum* and *Oryza sativa* spp. *japonica*. Fungal Genetics Reports 56 (Supplement) 253.

If your FY08 USDA-ARS Grant contained a VDHR-related project, include below a list all germplasm or cultivars released with full or partial support of the USWBSI. List the release notice or publication. Briefly describe the level of FHB resistance. If this is not applicable (i.e. no VDHR-related project) to your FY08 grant, please insert 'Not Applicable' below.

Not Applicable