USDA-ARS/
U.S. Wheat and Barley Scab Initiative
FY09 Final Performance Report
July 15, 2010

Cover Page

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Fiscal Year:	2009
USDA-ARS Agreement ID:	NA
USDA-ARS Agreement Title:	Fungal Genes for DON Accumulation in Wheat.
FY09- USDA-ARS Award Amount:	$ 34,500

USWBSI Individual Project(s)

USWBSI Research Category*	Project Title	ARS Adjusted Award Amount
PBG	Fungal Genes Involved in DON Accumulation in Wheat.	$ 34,500
	Total Award Amount	**$ 34,500**

July 1, 2010

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
DUR-CP – Durum 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 pathogenic fungus *Fusarium graminearum* causes disease 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 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:

Discovery of fungal growth conditions that induce the accumulation of DON in culture have led to the ability to study the mechanisms of toxin production in greater detail. We have tagged several proteins involved in toxin production with the fluorescent proteins GFP and m-Cherry, and localized the site of toxin biosynthesis within the cell. The localization of these proteins suggests ways in which the cell sequesters toxic pathway intermediates and a mechanism for toxin export from the cell may be inferred from these results.

Impact:

Previous studies in our lab supported by the USWBSI have shown that the FHB pathogen is remarkably adapted for producing vomitoxin, by precisely regulating the genes unique to toxin synthesis in order to promote toxin accumulation. We have now found, by labeling proteins for toxin synthesis with fluorescent proteins, that previously uncharacterized genes result in the production of “toxin factories;” subcellular vesicles that appear to serve as the staging area for components of the toxin biosynthetic assembly line. Alterations in components the cellular factory can reduce levels of vomitoxin in grain. These alterations point out potential targets for control strategies designed to reduce toxin concentrations in the food supply.

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.

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.

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.