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:	59-0790-3-081
USDA-ARS Agreement Title:	Genetic Mechanisms to Control Head Scab.
FY07 ARS Award Amount:	$ 22,630

USWBSI Individual Project(s)

USWBSI Research Area*	Project Title	ARS Adjusted Award Amount
PGG	Global Regulation of Fusarium Toxins.	$22,630
	Total Award Amount	**$ 22,630**

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

Project 1: *Global Regulation of Fusarium Toxins.*

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

One of the most severe mycotoxin problems in the U.S. is trichothecene contamination of small grains by *Gibberella zeae* (anamorph *Fusarium graminearum*) in a disease called scab or Fusarium head blight (FHB). Our lab is attempting to find genes and gene products important in either *Gibberella zeae* sporulation or toxin production. Such genes and gene products would provide needed knowledge of virulence factors in the fungus and possibly provide insight into control strategies. . Recent progress in fungal toxin clusters has suggested that these clusters, as well as spore formation, is globally regulated by higher order chromatin conformation. For this grant, we have initiated studies to identify global regulators of secondary metabolite (e.g. mycotoxin) gene clusters in *Fusarium* based on our findings from the genus *Aspergillus*. Specifically we have identified and inactivated *hepA*, a putative heterochromatin protein 1 involved in heterochromatin formation in *F. graminearum.* We will now examine our hypothesis that deletion of *hepA* increases toxin formation through activation of chromatin. We also have identified demethylase genes that we predict will decrease toxin formation through repression of chromatin.

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: Toxin genes in fungi are typically arranged in clusters and our work in *Aspergillus* species shows these clusters are located in facultative heterochromatic regions that when activated (euchromatin format) result in increased toxin production but when silenced (heterochromatin format), decreased toxin formation. Our initial results suggest toxin formation may also be regulated by heterochromatin in *Fusarium* spp,

Impact: This is the first identification of *F. graminearum* histone remodeling genes, a topic that has become of interest in international laboratories. While it is yet too early to assess the role of these genes on fungal toxin production, we expect there will be significant effects. Several other labs have shown that chromatin remodeling proteins and interacting partners affect *Fusarium* mycotoxin production and spore production based on our findings in *Aspergillus*.

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?:

An important contribution of this work the importance of chromatin remodeling on toxin gene cluster expression which appears to be taken up by the research community world wide. Several of the proteins we have identified can be considered for fungicide targeting.

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.

From past and present SCAB funding, the *Fusarium hepA* work is not yet completed

Palmer J, Perrin R, Keller NP (submitted) H3K9 methylation regulates growth and development in *Aspergillus fumigatus*. Euk Cell

Tsitsigiannis D I, Keller NP (2007) Oxylipins as developmental and host-fungal communication signals. Trends in Microbiology Mar;15(3):109-18.

Brodhagen M, Keller NP (2006) Signaling pathways connecting mycotoxin production and sporulation. Molecular Plant Pathology 7:285-301.

McDonald T, Devi T, Shimizu K, Sim S-C, Keller NP (2004) Signaling events connecting mycotoxin biosynthesis and sporulation in *Aspergillus* and *Fusarium spp.* In New Horizon of Mycotoxicology for Assuring Food Safety, Proceedings of the International Symposium of Mycotoxicology (Editor: Takumi Yoshizawa) pp 139-147.