USDA-ARS/
U.S. Wheat and Barley Scab Initiative
FY10 Final Performance Report
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Cover Page

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Fiscal Year:	FY10
USDA-ARS Agreement ID:	59-0790-6-071
USDA-ARS Agreement Title:	Genes Regulated by the GMPK1 Pathway and Pathogenesis in *Fusarium graminearum*.
FY10 USDA-ARS Award Amount:	$ 29,268

USWBSI Individual Project(s)

USWBSI Research Category[*]	Project Title	ARS Award Amount
PBG	Role of Histone Deacetylation and Chromatin Modification in *Gibberella zeae*.	$ 29,268
	Total ARS Award Amount	**$ 29,268**

7/12/2011

Principal Investigator Date

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[*] 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 Soft Winter Wheat Region
    SWW – Southern Soft Red Winter Wheat Region

Project 1: *Role of Histone Deacetylation and Chromatin Modification in Gibberella zeae.*

1. **What major problem or issue is being resolved relevant to Fusarium head blight (scab) and how are you resolving it?**

Head blight caused by *Fusarium graminearum* is an important disease of wheat and barley. Although a number of virulence factors and the *TRI* cluster have been characterized in this important pathogen, it is not clear what are the molecular mechanisms regulating the plant infection processes and global regulation of secondary metabolism. In this study, we functionally characterized all three class II histone deacetylase genes in *F. graminearum* and found one of them, *HDF1*, is important for plant infection and mycotoxins production. The Hdf1 HDAC enzyme may play a critical role in regulating chromatin modifications related to the expression of infection-related genes.

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:

In this study, we characterized the *HDF1* histone deacetylase (HDAC) gene that is orthologous to yeast *HOS2*. Deletion of *HDF1* resulted in a 60% reduction in HDAC activity and a significant reduction in virulence and DON production. The *hdf1* deletion mutant failed to spread from the inoculation site to other parts of wheat heads or corn stalks. Microarray analysis revealed that 149 and 253 genes were down- and up-regulated, respectively, over 5-fold in the *hdf1* mutant. Deletion of the other two class II HDAC genes had no obvious effect on vegetative growth and resulted in only a minor reduction in conidiation and virulence in the Δ*hdf2* mutant. In yeast two-hybrid assays, *HDF1* physically interacts with *FTL1*, which is a component of the Set3 HDAC complex and a known fungal pathogenicity factor.

Impact:

Our results indicate that *HDF1* is the major class II HDAC histone deacetylase gene in *F. graminearum.* It may function as a component in a well conserved HDAC complex in the regulation of conidiation, DON production, and pathogenesis. The genome of *F. graminearum* contains chromosomal regions with higher genetic variation and enriched for genes expressed *in planta*. The *HDF1* HDAC complex may play a critical role in regulating chromatin modifications related to the expression of infection-related genes.

HDAC is one of the targets for developing pharmaceutical compounds. Our results indicate that HDAC inhibitors also can be used to control plant diseases and mycotoxin contamination caused by fungal pathogens.

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.

1) Li, Y., Wang, C., Liu, W., Wang, G., Kang, Z., Kistler, H. C., and Xu, J. -R. 2011. Systematic Characterization of Type II HDAC Genes in *Fusarium graminearum. Molecular Plant-Microbe Interactions.* 24: 487-496.

2) Wang, Y., Liu, W., Hou, Z., Wang, C., Zhou, X., Jonkers, W., Ding, S., Kistler, H. C., and Xu, J. –R. 2010. A novel transcriptional factor important for pathogenesis and ascosporogenesis in *Fusarium graminearum.* Molecular Plant-Microbe Interactions. 24: 118-128.