USDA-ARS/
U.S. Wheat and Barley Scab Initiative
FY09 Final Performance Report
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Cover Page

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Fiscal Year:	2009
USDA-ARS Agreement ID:	59-0790-6-071
USDA-ARS Agreement Title:	Genes Regulated by the GMPK1 Pathway and Pathogenesis in *Fusarium graminearum*.
FY09- USDA-ARS Award Amount:	$ 29,268

USWBSI Individual Project(s)

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

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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 Winter Wheat Region
    SWW – Southern Sinter 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?**

Our research aims to identify fungal genes that are essential for regulating DON production or developmental processes related to plant infection. Results from such studies will be useful to 'develop new strategies for reducing impact of FHB disease and mycotoxin contamination in barley and wheat'. In previous studies, we found that the FgHos2 and FgRpd3 histone deacetylase (HDAC) genes are important for plant infection. In addition, FgHos2 is important for DON production and sexual reproduction. FgRpd3 is critical for conidiation.

To further characterize these HDAC genes, we have generated the FgHos2 FgHda1 and FgHos2 FgHos3 double mutants. In infection assays with flowering wheat heads, these double mutants were significantly reduced in virulence and DON production. Only the inoculated wheat kernels rarely developed scab symptoms. We also have conducted microarray analysis with the FgHos2 and FgRpd3 mutants using the new Fusarium Affymetrix GeneChip. Data analysis and functional characterization of selected genes are in progress. Several genes down-regulated in the FgHos2 and FgRpd3 mutants were putative protein kinase genes that were found to be important for virulence in *F. graminearum*. Overall, over data indicate that inhibiting HDAC genes can be used to control the head blight disease. Identifying and characterizing genes regulated by FgHos2 and FgRpd3 HDACs will be helpful to understand the regulatory mechanisms of DON production and plant infection.

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:

The FgHos2 FgHda1 and FgHos2 FgHos3 double mutants were generated and found to be almost completely blocked in DON production and infection of flowering wheat heads. FgHos3, FgHda1, and FgHos3 are the only type II HDAC genes in *F. graminearum*.

Microarray analysis was used to identify genes regulated by FgHos2 and FgRpd3 in *F. graminearum*. Several putative protein kinase genes down-regulated in these mutants were found to be important for plant infection.

Impact:

Our data with the double mutants indicate that type II HDAC genes have overlapping functions. Although FgHos2 is the dominant type II HDAC gene in *F. graminearum*, a general type II HDAC inhibitor rather than FgHos2-specific inhibitor should be more effective in controlling wheat scab disease development and DON production.

Some of these genes regulated by FgHos2 and FgRpd3 HDACs that were identified in this study function as novel fungal virulence factors. Further characterization of these genes will be helpful to understand the regulatory mechanisms of DON production and plant infection in *F. graminearum*.

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., Wang, G., Liu, W., Kang, Z., Kistler, H. C., and Xu, J. -R. 2010. Systematic Characterization of Type II HDAC Genes in *Fusarium graminearum.* Submitted to *Eukaryotic Cell.*
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.* Submitted to Molecular Plant-Microbe Interactions.
3) Ding, S., Liu, W., Iliuk, A., Ribot, C., Vallet, J., Wang, Y., Tao, A., Lebrun, M., and **Xu, J. –R**. 2010. The *TIG1* HDAC complex regulates infectious growth in the rice blast fungus *Magnaporthe oryzae*. Plant Cell. In press. (This work was initiated with a gene identified in Fusarium with a project funded by the scab initiative)
4) Ma, L., Rep, M., Borkovich, K. A., Coleman, J. J., Daboussi, M., DiPietro, A., Dufresne, M., Freitag, M., Grabherr, M., Henrissat, B., Kang, S., Park, J., Shim, W., Woloshuk, C. Xie, X., **Xu, J. –R**., Antoniw, J., ……, Cuomo, C. A., and Kistler, H. C. 2010. *Fusarium* comparative genomics reveals pathogenicity related lineage-specific genome expansion. *Nature*. 464: 367-373.
5) Choi, Y. E. and Xu, J. -R. 2010. The cAMP signaling pathway in *Fusarium verticillioides* is important for conidiation, plant infection, and stress responses but not fumonisin production. Molecular Plant-Microbe Interactions. 23: 522-533.
6) Zhou, X., Heyer, C., Choi, Y., Mehrabi, R., and **Xu, J. –R**. *CID1* is important for plant infection in *Fusarium verticillioides.* 2010. *Fungal Genetics and Biology*. 47: 143–151.
7) Ding, S., Mehrabi, R., Koten, C., Kang, Z., Wei, Y., Seong, K., Kistler, H. C., and **Xu, J. –R**. 2009. The transducin beta like gene *FTL1* is essential for pathogenesis in *Fusarium graminearum*. Eukaryotic Cell. 8: 867–876.
8) Seong, K.Y., Pasquali, M., Zhou, X., Song, J., Hilburn, K., McCormick, S.P., 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. *Molecular Microbiology*. 72: 354-367.