USDA-ARS/
U.S. Wheat and Barley Scab Initiative
FY05 Final Performance Report (approx. May 05 – April 06)
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Cover Page

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Fiscal Year:	**2005**
FY05 ARS Agreement ID:	**59-0790-5-184**
Agreement Title:	**Functions of Two Regulators of G Protein Signaling Fusarium graminearum.**
FY05 ARS Award Amount:	**$ 37,073**

USWBSI Individual Project(s)

USWBSI Research Area*	Project Title	ARS Adjusted Award Amount
EDM	Functions of Two Regulators of G Protein Signaling Fusarium graminearum.	$ 37,073
	Total Award Amount	**$ 37,073**

7/12/2006

Principal Investigator Date

* BIO – Biotechnology
CBC – Chemical & Biological Control
EDM – Epidemiology & Disease Management
FSTU – Food Safety, Toxicology, & Utilization
GIE – Germplasm Introduction & Enhancement
VDUN – Variety Development & Uniform Nurseries

Project 1: *Functions of Two Regulators of G Protein Signaling Fusarium graminearum.*

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

Fusarium head blight (FHB: scab) of barley and wheat caused by *Fusarium graminearum* is significant and devastating disease in the US and Canada. Infection not only results in decreased yield but also reduced quality of grains by the contamination of grains with mycotoxins. As the goal of the U.S. Wheat and Barley Scab Initiative states, it is highly urgent to develop effective control measures that minimize the threat of FHB to the producers, processors, and consumers of wheat and barley. The long-term goal of this project is to provide a basis for the development of novel strategies to eliminate or prevent *Fusarium graminearum* infestation and associated toxin production in wheat and barley. We are focusing on upstream regulation of G protein signaling that can be manipulated to disarm fungal pathogenicity, defense, dispersion and toxigenesis systems.

In previous studies, it has been shown that heterotrimeric G protein (G protein)-mediated signal transduction and its tight regulation by regulators of G protein signaling (RGS) is extremely important for growth, mating, differentiation, pathogenicity and other cellular responses to external/internal cues in various plant pathogenic fungi including *F. graminearum*. We showed that proper control of a G alpha-mediated vegetation signaling pathway is crucial for the maintenance of hyphal integrity, formation of asexual/sexual spores and toxigenesis in a number of *Aspergillus* species. Moreover, a serious of studies strongly suggested that G protein signaling components play an important role in controlling development, mating and pathogenicity in *Fusarium* species. However, functions of these important RGS proteins in spore formation and toxin production in *F. graminearum* have not been studied. We have identified five genes encoding RGS proteins in the genome of *F. graminearum* and characterized functions of two RGS genes by gene deletion.

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: Deletion of RGS1, one of the major RGS protein genes, and other RGS protein genes have been completed sing geneticin or hygromycin resistant markers. Importantly, deletion of *RGS1* resulted in the absence of macroconidia (asexual spores) or sexual spore formation in various culture conditions tested. Several lines of preliminary data suggest that this *RGS1* gene may also be required for DON production. Deletion of *RGS2* appears to affect red pigment accumulation in *F. graminearum*. Precise determination of toxin and pigment production as well as additional quantitative analyses for spore formation are in progress. Moreover, these mutant strains will be sent to Dr. Jin-Rong Xu's lab for testing altered pathogenicity in barley and wheat.

Impact: This is the first time that functions of RGS proteins are determined in *F. graminaerum.* Moreover, this is an excellent example that an (or two) upstream regulatory

gene significantly affecting the *Fusarium* life cycle, aggressiveness, and disease processes; and, that mutational studies directed at understanding mechanisms of pathogenicity and targets for intervention strategies. Outcomes of our research will provide a basis for the development of new intervention tools that block spore formation and toxin production in *F. graminearum*, thereby eliminating dispersion, infestation and toxin (DON) contamination in barley and wheat.

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?:

Thus far, most approaches to control fungi have been primarily focused on targeting fungal cell wall, membrane or essential genes. Currently, scientists search for antifungal proteins that directly disrupt fungal membrane with a hope to introduce such genes into a crop plant to make it resistant to fungal infection. Our studies provide crucial alternative approaches, which employ manipulation and/or control of membrane-bound upstream signaling components that globally affect spore formation and toxin production. By functioning as negative regulators, RGS proteins fine-tune vital G protein-mediated signaling. Such tight control of the degree and time of signals is essential for basic cellular functions including survival of an organism. As a result of our accomplishment, we now know that RGS proteins play critical roles in formation of spores that are the primary agent for infecting host plants. These RGS protein genes will be excellent targets to inhibit or eliminate fungal propagation and subsequent infection. These mutant strains are shared with other Fusarium research groups including Drs. Jin-Rong Xu (Perdue University) and Robert Proctor (USDA, Peoria, IL).

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.

This project began just a year ago and by nature requires extensive genetic, molecular biological, biochemical and physiological studies. A number of important publications are expected in year 2007.