PI: Jaehyuk YuPI's E-mail: jyu1@wisc.eduProject ID: 0506-YU-090FY04 ARS Agreement #: NewResearch Area: EDMDuration of Award: 1 YearProject Title: Functions of Two Regulators of G Protein Signaling Fusarium graminearum.

PROJECT 1 ABSTRACT (1 Page Limit)

The filamentous fungus *Fusarium graminearum* is one of the most important pathogenic and toxigenic fungi that cause serious crop disease and produce various kinds of highly toxic mycotoxins. The long-term goal of this study is to provide basis for the development of effective control measures to eliminate or prevent infestation of wheat and barley by *F. graminearum*.

As one of supplementary approaches to prevent or minimize fungal and mycotoxin problems, we are focusing on upstream global signaling mechanisms that can be manipulated to disarm fungal defense, dispersion and toxicogenesis systems. This project is focused on understanding the roles of proper control of G protein-mediated signaling on toxicogenesis and sporulation of *F. graminearum*. In the future, plant pathogenesis test will be carried out.

It has been shown that deletion of the *flbA* gene encoding a regulator of G protein signaling (RGS) resulted in un-controlled activation of a heterotrimeric G protein-mediated vegetative growth signaling, which caused the blockage of sporulation, the absence of the mycotoxin (sterigmatocystin) production, and hyphal disintegration (autolysis) in *Aspergillus nidulans*. We hypothesized that the disruption of necessary control of the homologous G protein pathway would result in perturbations in toxicogenesis and sporulation in *F. graminearum*. While all *Aspergillus* species examined has only one FlbA homolog, two genes (*RGS1* and *RGS2*) that encode putative FlbA homologs are identified in the genome of *F. graminearum*. Employing our PCR-based gene disruption cassette construction technique, we generated deletion constructs for these two RGS genes. Our preliminary studies suggest that deletion of the *F. graminearum RGS1* gene may cause abnormal hyphal growth and abolished sporulation. We propose to delete individual RGS genes and test effects of deletion on vegetative growth, morphogenesis, development, and toxin (DON) production in *F. graminearum*.

Outcomes of this research will likely, at a minimum, provide novel insights into the mechanisms of Gprotein signaling influencing (various) toxin production and sporulation in this pathogenic/toxigenic fungus. It is anticipated that this information could, in the future, lead to the development of strategies to control infection and toxin production during growth on crop plants by *F. graminearum*. Understanding upstream regulatory mechanisms controlling fungal growth, sporulation and toxin production would be of great impact on wheat and barley protection/improvement and sustainability programs as well as on human and animal health.