

**0203-TR-082 Use of gene expression analysis to study pathogenicity in *Gibberella zeae*.**

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Research Area: EDM

PROJECT ABSTRACT

(1 Page Limit)

*Gibberella zeae* (anamorph *Fusarium graminearum*) causes head scab of wheat and barley and stalk rot and ear rot of corn. As conventional control measures have not produced effective control of this devastating pathogen, a deeper understanding of the life cycle and biology of the fungus is necessary. Our long-term goal is to understand the production and spread of inoculum for head scab, and the role of the two types of spores (sexual and asexual) in completing the disease cycle. Studies on the development and mechanisms of dispersal of the inoculum will provide valuable insight into effective control procedures for this disease. Our goals are to understand the biology of the *F. graminearum* especially with regard to spore production and to develop strategies for elimination of the inoculum of the scab disease. Specifically, this research will provide (1) an understanding how field colonized vegetative host tissue supports perithecial production over the course of 1 year; (2) identification of genes and gene products involved early in perithecial initiation and development. Using strains with mutations involved in initial stages of perithecial production or lacking perithecia, we can begin the genetic and physiological analysis of this early phase on inoculum production. Our approach is twofold: to combine basic, laboratory research with field research aimed at the ultimate control of inoculum production. Our research combines studies of the basic biology of *G. zeae* with behavior of the fungus in the field. These two approaches will result in novel approaches to interruption of the disease cycle.

**0203-TR-083 Genetics and morphology of perithecium development in *Gibberella zeae* on wheat and in vitro.**

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PROJECT ABSTRACT

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*Gibberella zeae* (anamorph: *Fusarium graminearum*) causes head scab, or head blight of wheat, barley, and oats, and foot and crown rot of corn. Recent scab outbreaks in Asia, Canada, Europe, South America and the United States highlight the increased threat this disease poses to food supplies worldwide. Conventional control methods for this disease organism have not resulted in effective control. Therefore, a more developed understanding of the organism is warranted. Our longterm goals are: (1) to understand the genetic basis for inoculum development, mycotoxin production and pathogenicity; (2) to use genomics to develop a biology-based control program for scab, using the genomics programs of wheat and corn to enhance this program. We have sequenced and analyzed a cohort of 12351 ESTs from different growth states of *G. zeae*. The objective of this proposal is to use the sequence information and genetic/genomics materials generated in earlier studies to further characterize molecular mechanisms of fungal pathogenicity, inoculum production, and secondary metabolism. Additional funding for full sequencing for the genome is being sought. We will determine whether the genes we have indicated may be used to develop novel controls. We believe that the two-fold approach presented here, to establish a scaffold for long-term genomics studies as well as generating functional genomics information, will provide the most benefits to scab control both long-term and short-term.