

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

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Grant #: NA; \$32,000; 1 Year

Research Area: EDM

PROJECT ABSTRACT

(1 Page Limit)

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.