0203-VA-088 Role of a Colletotrichum graminicola pathogenicity gene homologue in F. graminearum.

PI: Vaillancourt, Lisa J.; E-mail: vaillan@uky.edu
University of Kentucky, Department of Plant Pathology, Lexington, KY 40546-0091
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PROJECT ABSTRACT
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A novel pathogenicity gene in the fungus *Colletotrichum graminicola* was recently identified in our laboratory using a random insertional mutagenesis approach. *C. graminicola* causes anthracnose leaf blight and stalk rot diseases of corn. Normal expression of the *C. graminicola* pathogenicity gene, named *CPR1*, is necessary for necrotrophic colonization of host tissues and for induction of disease symptoms. The predicted product of the *CPR1* gene is similar to a family of proteins that comprise one subunit of the eukaryotic microsomal signal peptidase. One possibility is that the CPR1 mutant does not secrete sufficient quantities of extracellular pectolytic enzymes to efficiently colonize its host. *F. graminearum* is closely related to *C. graminicola*, and there is evidence that it has a homologue of the *CPR1* gene. A fragment of this putative homologue was cloned by degenerate PCR in our laboratory. Like *C. graminicola*, *F. graminearum* causes a stalk rot disease of corn, in addition to causing the very important wheat scab disease. The goal of the work proposed here is to define the role of the homologue of this novel *Colletotrichum graminicola* pathogenicity gene in the wheat scab fungus *Fusarium graminearum*. The specific objectives will be: (1) isolate and characterize the homologous gene; (2) produce mutations that will eliminate or reduce the expression of the gene; and (3) test the resulting mutants for pathogenicity to wheat. This work is significant because it could provide a unique fungal target for disease therapies. In addition, it could provide a useful tool to better understand the nature of host-pathogen interactions in the wheat scab disease, leading to better management protocols.