Identification of Pathogenicity Factors Produced by Phymatotrichopsis omnivora

Description
The soil-borne plant pathogen Phymatotrichopsis omnivora, causal agent of cotton root rot, is a recalcitrant organism for which no economical or consistently efficacious control strategy exists. The pathogen has a very broad host range, including economically important crops such as cotton, alfalfa, grapes, pecans, and numerous ornamentals. With advances in proteomics and bioinformatics and the availability of the genomic sequence of P. omnivora (University of Oklahoma), the prospect of using these technologies to identify the pathogenicity factors of this organism is opportune. For a pathogen with such a broad host range, a similar and consistent pattern of infection among different hosts, and limited infection stages, there may be a subset of proteins (e.g. toxins, enzymes, antibiotics) that are responsible for its ability to ingress and decimate host roots. We will use proteomic and bioinformatic approaches to identify these factors and demonstrate their role in plant demise. Such factors have the potential for use as targets in novel breeding efforts (introduce genes to detoxify or resist these targets) or synthetic compounds to disrupt their action or that of the pathogen.

Process
Extract proteins from a hydroponic system containing cotton and the pathogen; analyze the proteins using Difference Gel Electrophoresis and DeCyder software to identify proteins unique to the pathogen-plant interaction; identify proteins of interest using MALDI-TOF and LC/MS/MS mass spectrometric approaches, resolved masses from the MS study will be used to search the genome sequence of P. omnivora to identify potential proteins involved in pathogenicity; confirm role of proteins in pathogenicity by gene expression analysis during the infection process.

Objectives
Determine the qualitative and quantitative differences in secreted proteins from Phymatotrichopsis omnivora grown with and without cotton roots; identify unique or up-regulated proteins from cultures of the pathogen with cotton roots; perform in silico database searches to establish homology with known proteins; analyze expression of genes encoding potential pathogenic factors; initiate a proteomic study to compare the proteins in strands on cotton roots to strands in soil cultures.

Outcomes
Identification of secreted proteins that are involved in the infection process by P. omnivora; knowing compounds involved in pathogenicity will provide targets for control strategies to manage this pathogen.

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