Short Communication

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Understanding the biology and pathology of a soilborne fungus *Rhizctonia solani* through proteomic investigations

[1] **Dilip K. Lakshman and [2]Savithiry S. Natarajan**

[1]*Floral and Nursery Plants Research Unit, Agricultural Research service, USDA, Beltsville, Maryland, USA.*

[2]*Soybean Genomics and Improvement Laboratory, USDA, USA*

Soilborne pathogens account for the largest percentage of losses in commercial production and the fungus *Rhizoctonia* (*sensu lato*) is a major cause of seedling and root disease of cultivated crops, ornamentals, turfgrasses and forest trees. The pathogen also causes aerial blights and postharvest losses. The fungus includes destructive plant pathogen, saprophytes important for decomposing soil organic matter, mycorrhizac symbiotically associated with roots, and biocontrol agents. *R. solani* (Teleomorph: *Thanatephorus cucumeris*) displays several hyphal anastomosis (fusion) groups (AGs). Each AG is genetically isolated and shows distinct host plant specialization. The pathogen is known to release various enzymes to dissolve host barriers to invade plan tissues. Elucidating the nature and dynamics of released enzymes is critical to our understanding of its pathogenicity. Although there are reports on the physiological and histological basis of *Rhizoctonia*-host interactions, very little is known about the molecular biology and control of gene expression during infection by this pathogen. In this vein, we are investigating the Expressed Sequence Tags (ESTs) and proteins of a wide host-range isolate of *R. solani*, AG-4 on a global scale (i.e., proteomics). We have optimized two protein extraction protocols suitable for proteomic investigations and resolved several *R. solani* proteins by two-dimensional (2-D) gel electrophoresis (1). Following those protocols, we resolved over 500 *R. solani* proteins in 2-D protein gels covering pH 4-7 and size range 6.5 to 205 kDa. In demonstration of the suitability of this technique for proteomic studies, we have identified about 150 gel-separated proteins by Matrx-Assisted Laser Desorption/Ionization Time-of-Flight Mass Spectrometry (MALDI-TOF-MS) and Liquid Chromatography-Mass Spectrometry/Mass Spectrometry (LC-MS/MS). Some of the *Rhizoctomia* proteins were related to other fungal proteins with established roles in pathogenesis, Currently, we are investigating the protein profiles exuded by the fungus in the presence of a susceptible host. We are also differentiating the protein profiles of a virulent and a hypovirulent (i.e., avirulent) isolate of *R. solani* to better understand its virulence mechanism. Investigations using proteomics and related molecular tools should give us a better understanding of what makes *R. solani* a successful pathogen, saprophyte, symbiont or a biocontrol agent.

Literature Cited

1. Lakshman DK Natarajan SS Garrett W Lakshman S Dhar AK. 2008 Optimized proyein extraction methods for proteomic analysis of *Rhizoctonia solani Mycologia* 100: 867-75