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**Identification of Genes Differentially Expressed During Early Interactions
Between the White Mold Fungus, *Sclerotium rolfii* and Peanut**

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Objective: To identify and characterize genes in the *Sclerotium rolfii* (white mold fungus) and peanut genomes that are differentially expressed during early interactions between the fungus and plant.

Project Overview: The goal of this project is to identify plant and fungal genes that are expressed differently during the initial contact phase of the plant-pathogen interaction. Highly virulent and weakly virulent strains of *S. rolfii* will be compared on a highly susceptible cultivar. Understanding the different genetic and biochemical pathways expressed early in the infection process will potentially provide new targets to disrupt the life cycle of *S. rolfii*, stopping or slowing infection by this significant peanut disease-causing organism. Additionally, identification of pathogen responsive genes in peanut will add to the understanding gene expression in peanut and could identify valuable promoter sequences useful in potential future transgenic disease control strategies.

Progress: Ms. Ansuya Jogi came on board in the Gold laboratory in August 2009 on this project as part of her Master of Plant Pathology research. Ansuya determined the best conditions under which to isolate RNAs. She collected RNA from growth chamber grown infected peanut plants using four cultivars of varying susceptibility. Additionally, Dr. Brenneman is carrying out peanut field trials and Ansuya plans to collect field material for RNA extraction, for real time PCR confirmation of sequencing results. We have just received the 454 sequencing results and Ansuya is beginning analysis. The sequencing results will provide targets for real-time PCR assays for further investigation of the temporal expression of interesting genes. This is the core portion of Ms. Jogi's MS research and we expect to publish the results upon her degree completion in late 2011.

Expected Results: Some identified genes will represent potential control targets. By focusing on the early phase of the interaction we expect to identify primary recognition events and cell signaling mechanisms. Using high and low virulence isolates we expect differences in gene expression in both the plant and pathogen that may point toward important components in pathogen fitness and in host early defense. We may be able to identify conserved regulation of sets of host genes involved in early response to this important pathogen.