

Medicago Interactions with Cotton Root Rot

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Phymatotrichopsis omnivora (Duggar) Hennebert is a destructive root pathogen of many dicotyledonous plants. The disease caused by this pathogen, best known as cotton root rot (CRR) or *Phymatotrichum* root rot (PRR), has greatly hindered the production of cotton and alfalfa in the southwestern USA. An extensive study to understand the interaction of *P. omnivora* with alfalfa (*Medicago sativa*), and the model legume, *Medicago truncatula*, has been initiated by the Consortium for Legume Research. The Consortium consists of researchers from the Samuel Roberts Noble Foundation, Oklahoma State University and the University of Oklahoma, who have developed an interdisciplinary program targeted towards understanding CRR disease of alfalfa. The objectives of the consortium are to characterize CRR at the biological, chemical and genetic levels with a long term goal of developing resistant alfalfa varieties. This presentation will provide an overview of the Consortium project and describe current progress.

Multigene phylogenetic analysis has recently reclassified *P. omnivora* as an ascomycete in the class Pezizomycetes (operculate cup fungi). The *P. omnivora* genome is currently being sequenced using '454' technology to gain further insight into the genome structure and organization of this fungus. Although the *P. omnivora* sequence has been difficult to assemble, possibly due in part to a large genome size, and the multinucleate and heterokaryotic nature of this fungus, we have now achieved an approximate 40 Mb draft sequence of the genome.

Microarray analysis of susceptible *M. truncatula* roots infected with *P. omnivora*, identified up-regulated genes involved in ROS generation, phytohormone signaling and pathogenesis-related class I and class IV chitinases. Gene expression and metabolite profiling further demonstrated that during later stages of infection the plant defense response system seems to be suppressed. Typically, isoflavonoid and pterocarpin biosynthesis are induced during fungal interactions with *Medicago*. However, *P. omnivora* appears to be circumventing this traditional defense mechanism whereby the major antifungal metabolite medicarpin does not accumulate and the biosynthetic genes are not induced.

An extensive screen of a *M. truncatula* core collection has resulted in the identification of four ecotypes with increased tolerance to CRR. Mapping populations of these genotypes will be generated to identify the resistance loci. To date, we have been unable to identify a CRR-resistant alfalfa variety and have extended the screen to include the alfalfa core collection and other forage legumes.