# Diversity of endo- and exo-bacteria associated with soil fungi

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**Project Goals: Interactions between bacteria and fungi are important determinants of ecosystem function, yet little is known about these interactions or how they operate. This is a critical knowledge gap as these interactions are important in addressing multiple DOE priorities including developing renewable energy sources, understanding the possible effects of Earth system change, and understanding how these interactions may help overcome energy and environmental challenges. Here we present preliminary results of the diversity and function of bacterial:fungal interactions in soil ecosystem. Using a combination of single cell isolation and cultivation techniques, as well as bioinformatics-based data mining of 16S rRNA and ITS sequences, we are beginning to understand the diversity of bacteria that form associations with fungi, and how these associations affect both fungal and bacterial growth.**

**Abstract**

Fungi are cosmopolitan microorganisms with complex genetic make-up and metabolism.[1, 2] Furthermore, this group of microorganisms possesses important roles in ecology, agriculture, forestry and human health. In soil, fungi are one of the most abundant group of microorganisms and are known to interact with different microorganisms, including bacteria. Bacterial:fungal interactions in soils can be positive or negative (synergistic or antagonistic). In the present study, we obtained 45 fungal isolates and 53 exobacteria associated with the fungal isolates from soil microcosms from six different locations. These fungi were obtained with different growth media of plant origin, namely cornmeal, oatmeal, sorghum grain, and potato carrot. The fungal isolates were also investigated via real-time PCR for endobacteria. Out of the 45 fungal isolates, 41 were associated with endobacteria. From this culture collection, four fungal isolates (*Didymella* spp., *Neopestalotiopsis* spp., *Staphylotrichum coccosporum*, *Aspergillus* spp.) and four bacterial isolates (*Exiguobacterium sp.,* two *Paenibacillus spp.*, and *Pseudomonas sp.*) associated with these fungi with synergistic and antagonistic interactions from the same microcosm were selected for further investigation. The selection was based on confrontational assays. These confrontational assays allowed us to distinguish bacteria that would inhibit or enhance fungal growth. In addition to the exobacteria interaction with fungi, another five fungi were selected to further investigate for the endo-bacteria association based on the real time PCR results. The fungi selected were *Didymella glomerata*, *Cladosporium sp.*, *Aspergillus fumigatus*, *Aspergillus sp.* and *Byssochlamys spectabilis*. Hydrophobicity analyses via contact angle and surface composition via Attenuated total reflection Fourier transform infrared (ATR-FTIR) were also employed to better understand the physical interactions of the bacteria with these fungi. All nine fungal isolates presented cell

surfaces with moderate to high hydrophobicity. The main functional groups observed on the surface of these fungi belonged to polysaccharides as well as phosphate compounds and proteins. Further investigations of the metabolites involved in the communication between the fungi and the bacteria triggering negative and positive interactions are underway.

**References**

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