

Title: Bacterial Communities in Association to Specific Tissues in Wild Morels

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Project Goals: The goal of this SFA is to obtain mechanistic insights into Bacterial-Fungal Interactions to inform predictive models of their function in soil and their responses to environmental perturbations, such as changing climate and agricultural practices.

Abstract Text: The fungal genus *Morchella* is an iconic fungal group with great ecological and economic importance. Because of their widespread consumption, they represent some of the most emblematic fungal groups known to humankind. In this study the bacterial communities associated with different types of tissues (fruiting bodies, mycelium, and sclerotia) in a diverse collection of morels (including wild individuals) were investigated. The fungi collected included representatives of the black and yellow morel clades. Regardless of the species investigated, *Pseudomonas* spp. were detected as the most prevalent associate bacterium in mycelium and sclerotia. Together with *Ralstonia* spp. (mycelium and sclerotia) and *Methylobacterium* spp. (sclerotia), they represented the core associated bacterial community. In contrast, a highly diverse bacterial community was found associated with fruiting bodies, with representatives of *Pedobacter* spp., *Deviosa* spp. and *Bradyrhizobium* spp. constituting the core bacterial community. Multiple strains from *Pseudomonas* spp. were isolated from mycelia during the cultivation process. Confrontation assays with *Morchella* spp. for these *Pseudomonas* spp. resulted in multiple types of positive or negative interactions. The sequencing of the genomes of these *Pseudomonas* spp. allowed the identification of gene clusters relevant to promote positive interactions with morels, including secretion systems and toxin-antitoxin systems. This study offers the first *in-vivo* evidence linking observations from soils and confrontation studies suggesting the relevance of *Pseudomonas* spp. on the physiology and development of morels.

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