**Comparative and Functional Genomics of the Morchellaceae**

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The Ascomycete genus *Morchella* is fascinating for a number of reasons. *Morchella* species are globally popular mushrooms collected for the table so they represent a curious recreational activity and a potential income source for mushroom growers. Despite this popularity and a concerted effort to understand their propagation, they have not been consistently cultivated on a large scale. Perhaps this is because the life history of *Morchella* species remains elusive. It has been hypothesized that they form mycorrhizal associations with plant roots, but these associations have not been unequivocally proven. By using a comparative genomics approach, we are sequencing numerous taxa, including *Morchella esculenta*, *Morchella conica*, *Morchella rufobrunnea*, *Morchella americana*, and three strains on unknown lineage. In addition to this sequencing, we have used numerous members of the Morchellaceae to characterize the evolution of family specific metabolic pathways. Phylogenetic analyses reveal the relative position of each strain within *Morchella* and the Ascomycetes. Gene annotation methods were used to identify candidate genes for interaction with plants (effectors and other small secreted protein production), novel biochemical pathways, and secondary metabolite production. In addition to these genomic approaches, we have data mined 18S & ITS amplicon data, as well as binned metagenomic reads, from plant endophyte studies. This data clarifies the role of *Morchella* as plant endophytes in the Poaceae and other plant lineages.