Combined 'Omics Approaches for the Study of Ectomycorrhizal Symbiosis between Suillus and Pinaceae, with Emphasis on their Role in Nutrient Cycling

Hui-Ling Liao (PI)[1], Rytas Vilgalys (Co-PI)[1], Sara Branco[2], Thomas Bruns[3], Peter Kennedy[4], Nhu Nguyen[5], Kabir Peay[6], Jennifer M. Talbot[7], John W. Taylor[3]

[1]Duke University, [2]Montana State University, [3]University of California, Berkeley, [4]University of Minnesota, [5]University of Hawaii, [6]Stanford University, [7]Boston University

Abstract: This study will explore the genetics of obligately symbiotic interactions between conifers (Pinaceae) and their host-specific ectomycorrhizal fungi in the mushroom genus Suillus, and their effects on ecological cycling of forest carbon. Using conifer seedlings experimentally inoculated with different Suillus species, we will employ integrated metatranscriptomic / metaproteomic / metabolomic approaches identify key fungal in EMF-Pinaceae roots for the species represent samples of the widely co-distribution across their natural habitats. Here we request metatranscriptomic sequencing of root/rhizosphere soil samples using newly developed methods that preferentially enrich fungal and plant mRNA (JGI). Sequenced transcriptome reads will be mapped to Suillus genomes (curated by JGI) or plant reference EST databases (publicly available and/or sequenced during this project). Comparative meta'omics analysis (JGI/EMSL) will allow us to investigate the genetic basis of host specificity between compatible/incompatible species pairs of Suillus-Pinaceae, and also identify their roles in soil nutrient cycling. This study will provide the first ever assessment of molecular functioning and core genes involved in ectomycorrhizal formation at the genus and species level (Suillus) across a phylogenetically diverse sampling of conifers (Pinaceae). Meta'omic analyses of mycorrhizal functioning in soil will also help us to better define the roles these species play in soil nutrient turnover.