4-2019

Evolution of symbiosis genes in an invasive ectomycorrhizal fungus

Brooke Allen  
*University of Mississippi*

Jason Hoeksema  
*University of Mississippi*

Rytas Vilgalys  
*Duke University*

Follow this and additional works at: [https://trace.tennessee.edu/masmc](https://trace.tennessee.edu/masmc)

Recommended Citation  
https://trace.tennessee.edu/masmc/24

This Presentation is brought to you for free and open access by the Conferences at UT at Trace: Tennessee Research and Creative Exchange. It has been accepted for inclusion in Middle Atlantic States Mycological Conference 2019 by an authorized administrator of Trace: Tennessee Research and Creative Exchange. For more information, please contact trace@utk.edu.
Evolution of symbiosis genes in an invasive ectomycorrhizal fungus
Brooke Allen¹, Jason Hoeksema¹, Rytas Vilgalys²
¹Department of Biology, University of Mississippi, ²Department of Biology, Duke University

The molecular mechanisms of ectomycorrhizal formation are still poorly understood, and the molecules involved in the “molecular crosstalk” between partners are still being discovered. One class of molecules that may play an underappreciated role is the terpenes. Liao and colleagues have found that genes involved in terpene production are differentially expressed in ectomycorrhizal symbiosis between pines and the ectomycorrhizal fungus Piloderma. Indeed, terpenes may be involved in most forms of plant-microbe and microbe-microbe signaling. For example, Schmidt and colleagues found that a soil bacterium and pathogenic fungi use terpenes to communicate with each other. Terpenes are the largest class of secondary metabolites and are widespread in plants and fungi. However, they have been studied almost exclusively from the pharmaceutical perspective and little is known about their roles in nature. Here, we investigate the evolution of symbiosis signaling by comparing terpene synthesis gene clusters in Suillus luteus, an invasive ectomycorrhizal fungus, from its native and introduced regions. In introduced regions decreased fungal diversity, novel hosts, and novel pathogens may all drive rapid evolution in terpene synthesis pathways and may also alter the fitness consequences of the symbiosis for the plant and fungal symbionts. We will present preliminary results from analyses of S. luteus genomic data using the fungiSMASH platform.