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# Evolution of symbiosis genes in an invasive ectomycorrhizal fungus

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**ABSTRACTS** - Oral Presentations

**Evolution of symbiosis genes in an invasive ectomycorrhizal fungus**

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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.