

# Russulaceae: a new genomic dataset to study ecosystem function and evolutionary diversification of ectomycorrhizal fungi with their tree associates

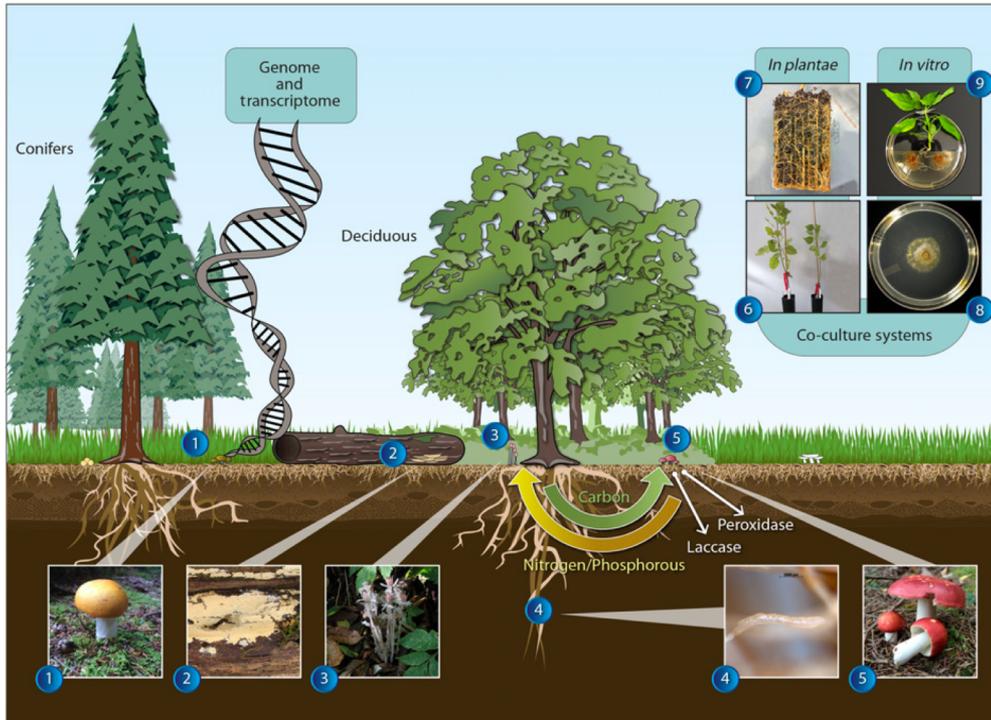


Contact: Jessy Labbé ([labbejj@ornl.gov](mailto:labbejj@ornl.gov)); (865) 576-3478

Funding Source: DOE Office of Biological and Environmental Research, Genomic Sciences Program

## Background

- The fungal family Russulaceae are ubiquitous ectomycorrhizal symbionts and play an important role as plant root mutualists, but much is still unknown about their functional diversity.
- This review presents the evolutionary history and ecosystem function of the family and their specific role in nutrient cycling and plant health as part of the Russulaceae Genome Initiative (RGI).



Schematic representation of key ecological roles played by Russulaceae in forested ecosystems

## Science

- Dense genomic sampling was conducted on several members of Russulaceae as part of the RGI, which suggest that:
  - Russulaceae species originated in the Palaeogene period (60 Myr ago)
  - Many of the ectomycorrhizal species appear to be host generalists
  - These ectomycorrhizal species are specialized in the uptake of ammonium giving them a competitive advantage in Nitrogen-rich ecosystems
  - Plant hosts act as bridges for ectomycorrhizal Russulaceae to disperse and diversify by occupying novel niches in new habitats
  - They have lost many genes capable of accessing carbon (C) from C-rich biopolymers and have retained a core set of genes that define a particular ecological strategy for scavenging nutrients from target biopolymers, e.g., lignin
  - There is less variation in gene copy number within families of oxidative enzymes and carbohydrate active enzymes than found between lineages of ectomycorrhizal and saprotrophic fungi.

## Significance

- The reference genomes & cultures produced by this project signifies a promising resource for the identification of potential genetic controls for ectomycorrhizal association and decomposition.