

PMI Convergent losses of decay mechanisms and rapid turnover of symbiosis genes in mycorrhizal mutualists

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Background

- An improved understanding of ectomycorrhizal fungi is needed to resolve mechanisms of nutrient cycling in forests, especially the ability to decompose lignocellulose. Phylogenomic and comparative genomic analyses of newly sequenced fungal genomes, along with 31 other fungal genomes were performed to elucidate the genetic bases of mycorrhizal lifestyle evolution.

Science

- Newly sequenced fungal genomes included 13 ectomycorrhizal (ECM), orchid (ORM) and ericoid (ERM) species, and 5 saprotrophs.
- ECM fungi have a reduced complement of genes encoding plant cell-wall degrading enzymes, yet, have retained a distinct suite of these enzymes indicating that they possess diverse capabilities to decompose lignocellulose.
- The symbiosis development between ECM fungi and host-plant development and immunity requires lineage-specific genes encoding small secreted effector proteins (SSEPs). Of induced genes, 7-38% are orphan genes, including genes that code for SSEPs.

Significance

- Convergent evolution of mycorrhizal habit in fungi occurred via the repeated evolution of a “symbiosis toolkit”, with reduced numbers of plant cell-wall degrading enzymes and lineage-specific suites of mycorrhiza-induced genes.

Kohler *et al.* 2015, Convergent losses of decay mechanisms and rapid turnover of symbiosis genes in mycorrhizal mutualists. *Nature Genetics*. 47(4): 410-415; Doi: 10.1038/ng.3223

Figure 5. Evolution of mycorrhizal symbiosis inferred from 49 fungal genomes.

