

Evolution of nutritional modes in Agaricomycetes: Phylogenetic and comparative genomic perspectives

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Agaricomycetes (mushroom-forming Fungi) obtain nutrition from both living and non-living substrates, principally plants. Phylogenetic analyses indicate that numerous transitions have occurred between saprotrophic and mycorrhizal nutritional modes, as well as between white rot and brown rot forms of saprotrophy. The white rot mode of decay (which involves decomposition of lignin, cellulose, and hemicellulose components of plant cell walls) may be plesiomorphic for Agaricomycetes as a whole. Brown rot (in which lignin is modified, but not extensively degraded) and ectomycorrhizal lifestyles have evolved repeatedly, possibly with some reversals. Genome sequences of diverse Agaricomycetes with white rot, brown rot, and ectomycorrhizal nutritional modes now provide opportunities to study the functional basis of shifts in trophic ecology. The independently-evolved brown rot species *Postia placenta* (Polyporales) and *Serpula lacrymans* (Boletales) are both characterized by losses of genes encoding lignin-degrading class II peroxidases as well as glycoside hydrolases. Similar patterns of gene loss have occurred in the lineage leading to the ectomycorrhizal *Laccaria bicolor* (Agaricales). Thus, it appears that the ancestral white rot mechanism has been repeatedly and convergently modified to give rise to brown rot and mycorrhizal nutritional modes through reduction of the lignocellulose-degrading apparatus.