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Old dogs, new tricks: Investigating the genomics of adaptation to new niches within the Serpulaceae

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Ecological transitions, for example from a free-living, saprotrophic nutritional mode to one that is dependent on a symbiotic partner, are not uncommon in fungi. Ectomycorrhizal (ECM) symbiosis, for instance, has evolved repeatedly, in phylogenetically distant lineages, and from different nutritional strategies. Comparative genomics has been instrumental in highlighting the commonalities and differences among the genomic architectures of different ECM species. Yet, due to the general plasticity of fungal genomes, hundreds if not thousands of genes may be differentially duplicated or lost between any two species, and often the most pronounced changes involve gene families with broad functional classification such as signaling proteins or proteins containing protein-protein interaction domains. Unsurprisingly, it can be difficult to pinpoint the genes that are most important for success in the new niche. The family Serpulaceae (Basidiomycota/Agaricomycota/Boletales) comprises the polyphyletic saprotrophic genus *Serpula* and, nested within, two ECM genera: *Austropaxillus* and *Gymnopaxillus*. While most *Serpula* species are free-living brown rotters, the genus' most well-known member, *Serpula lacrymans* is adapted to a life in human-built environments where it aggressively degrades timber construction. Unlike its relatives, *S. lacrymans* is rarely found in the wild and has thus also undergone an ecological transition. We hope that by comparing the signatures of adaptation between the ECM species *A. statuum* and the house-invader *S. lacrymans*, we will be able to begin to distinguish a more general pattern of adaptation to a new environment from those that are specific to their respective ecologies. To achieve this, we have sequenced and assembled the genomes of *A. statuum* and the brown rot species *S. incrassata*, an outgroup to *A. statuum* and *S. lacrymans*. Preliminary data suggests that *A. statuum* has an expanded genome compared to both *S. lacrymans* and *S. incrassata*.