

## Patterns of genome evolution underlying differential wood-decay mechanisms in Polyporales

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**Purpose:** The Polyporales is a diverse group of saprotrophic Agaricomycetes playing a major role in terrestrial carbon cycle. The order includes white- and brown-rot species that use different strategies to decompose woody plant material. To explore changes in the genetic toolkit leading to a great variety of differential wood-decay mechanisms in Polyporales, we aimed to reconstruct historical patterns of genome evolution, with special emphasis on gene families related to wood-decay.

**Methods:** To investigate genome-wide catalogs of gene families of Polyporales, we first generated a dataset containing the whole proteomes of 107 agaricomycetes fungi. Taxa were sampled so as to cover all major wood decayer Agaricomycetes clades. Protein sequences were clustered into gene families and then aligned. Next we inferred maximum likelihood gene trees and used a concatenated alignment of single-copy orthogroups with at least 70% taxon occupancy to infer a species tree. Then we carried out gene tree-species tree reconciliation and reconstructed gene duplication/loss histories in across all families using the COMPARE pipeline.

**Results and conclusions:** Our reconstructions of the evolution of 107 fungal genomes including 47 Polyporales species revealed historical genome expansion and contraction events along the phylogeny. Gene duplication/loss history shows distinct patterns in the Polyporales, many of which with clear connections to lifestyle transitions in the order. Consistent with previous studies, our analysis revealed differential evolution of wood-decay related gene families in brown- and white-rot lineages, but also several novel families that show lifestyle-associated gene duplication/loss patterns in the Polyporales.