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# **Extensive sampling of basidiomycete genomes demonstrates inadequacy of the white rot/ brown rot paradigm for wood decay fungi**

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# Extensive sampling of basidiomycete genomes demonstrates inadequacy of the white rot/brown rot paradigm for wood decay fungi

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## Abstract

Basidiomycota (basidiomycetes) make up 32% of the described fungi and include most wood decaying species, as well as pathogens and mutualistic symbionts. Wood-decaying basidiomycetes have typically been classified as either white rot or brown rot, based on the ability (in white rot only) to degrade lignin along with cellulose and hemicellulose. Prior genomic comparisons suggested that the two decay modes can be distinguished based on the presence or absence of ligninolytic class II peroxidases (PODs), as well as the abundance of enzymes acting directly on crystalline cellulose (reduced in brown rot). To assess the generality of the white rot/brown rot classification paradigm we compared the genomes of 33 basidiomycetes, including four newly sequenced wood decayers, and performed phylogenetically-informed Principal Components Analysis (PCA) of a broad range of gene families encoding plant biomass-degrading enzymes. The newly sequenced *Botryobasidium botryosum* and *Jaapia argillacea* genomes lack PODs, but possess diverse enzymes acting on crystalline cellulose, and they group close to the model white rot species *Phanerochaete chrysosporium* in the PCA. Furthermore, laboratory assays showed that both *B. botryosum* and *J. argillacea* can degrade all polymeric components of woody plant cell walls, a characteristic of white rot. We also found expansions in reducing polyketide synthase genes specific to the brown rot fungi. Our results suggest a continuum rather than a dichotomy between the white rot and brown rot modes of wood

decay. A more nuanced categorization of rot types is needed, based on an improved understanding of the genomics and biochemistry of wood decay.