

## Comparative genomics of *Ceriporiopsis subvermispora* and *Phanerochaete chrysosporium* provide insight into selective ligninolysis.

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### Abstract

Efficient lignin depolymerization is unique to the wood decay basidiomycetes, collectively referred to as white rot fungi. *Phanerochaete chrysosporium* simultaneously degrades lignin and cellulose, whereas the closely related species, *Ceriporiopsis subvermispora*, also depolymerizes lignin but may do so with relatively little cellulose degradation. To investigate the basis for selective ligninolysis, we conducted comparative genome analysis of *C. subvermispora* and *P. chrysosporium*. Genes encoding manganese peroxidase numbered 13 and five in *C. subvermispora* and *P. chrysosporium*, respectively. In addition, the *C. subvermispora* genome contains at least seven genes predicted to encode laccases, whereas the *P. chrysosporium* genome contains none. We also observed expansion of the number of *C. subvermispora* desaturase-encoding genes putatively involved in lipid metabolism. Microarray-based transcriptome analysis showed substantial up-regulation of several desaturase and MnP genes in wood-containing medium. MS identified MnP proteins in *C. subvermispora* culture filtrates, but none in *P. chrysosporium* cultures. These results support the importance of MnP and a lignin degradation mechanism whereby cleavage of the dominant nonphenolic structures is mediated by lipid peroxidation products. Two *C. subvermispora* genes were predicted to encode peroxidases structurally similar to *P. chrysosporium* lignin peroxidase and, following heterologous expression in *Escherichia coli*, the enzymes were shown to oxidize high redox potential substrates, but not Mn(2+). Apart from oxidative lignin degradation, we also examined cellulolytic and hemicellulolytic systems in both fungi. In summary, the *C. subvermispora* genetic inventory and expression patterns exhibit increased oxidoreductase potential and diminished cellulolytic capability relative to *P. chrysosporium*.

### Identifier

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