

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

Fernandez-Fueyo E, Ruiz-Dueñas FJ, Ferreira P, Floudas D, Hibbett DS, Canessa P, Larrondo LF, James TY, Seelenfreund D, Lobos S, Polanco R, Tello M, Honda Y, Watanabe T, Watanabe T, Ryu JS, San RJ, Kubicek CP, Schmoll M, Gaskell J, Hammel KE, St John FJ, Vanden Wymelenberg A, Sabat G, Splinter BonDurant S, Syed K, Yadav JS, Doddapaneni H, Subramanian V, Lavín JL, Oguiza JA, Perez G, Pisabarro AG, Ramirez L, Santoyo F, Master E, Coutinho PM, Henrissat B, Lombard V, Magnuson JK, Kües U, Hori C, Igarashi K, Samejima M, Held BW, Barry KW, LaButti KM, Lapidus A, Lindquist EA, Lucas SM, Riley R, Salamov AA, Hoffmeister D, Schwenk D, Hadar Y, Yarden O, de Vries RP, Wiebenga A, Stenlid J, Eastwood D, Grigoriev IV, Berka RM, Blanchette RA, Kersten P, Martinez AT, Vicuna R, Cullen D (2012) Comparative genomics of *Ceriporiopsis subvermispora* and *Phanerochaete chrysosporium* provide insight into selective ligninolysis. *Proc Natl Acad Sci U S A* 109, 5458-5463.

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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*.

Beteiligte Forschungseinheiten

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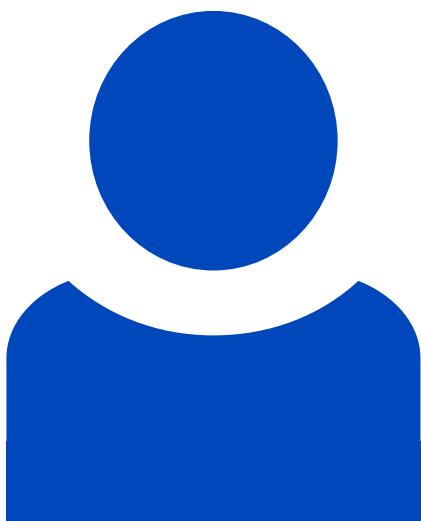
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Identifier

doi: 10.1073/pnas.1119912109

PMID: 22434909