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ABSTRACTS (MASTER THESIS)

Transcriptional response of a selective white-rot fungus to a lignin fragment

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White rot fungi are the only microorganism in nature that can mineralize lignin in wood. Some of fragments generated during lignin degradation are putative signal molecules that regulate the mechanism of wood decay. In a model species of white-rot fungus, *Phanerochaete chrysosporium*, its cellular response to vanillin, has been analyzed in detail [1]. Vanillin is one of the key intermediates found during lignin biodegradation. *P. chrysosporium* exposed to vanillin drastically changes the metabolic flux from the glyoxylate cycle to the tricarboxylic acid cycle and then activates the heme biosynthesis pathway.

On the other hand, a white-rot fungus, *Ceriporiopsis subvermispora*, has very different characteristics from *P. chrysosporium*: i) selective ligninolysis without serious damage to cellulose; ii) secretion of large amounts of fatty acids and their peroxidation at an early stage of wood decay; iii) high resistance to growth inhibition by vanillin; iv) no activity of lignin peroxidase; v) possession of a suppression mechanism of cellulolytic hydroxyl radical; vi) no activity of cellobiohydrolase.

In this study, the author focuses on cellular response of *C. subvermispora* to vanillin, and tried to analyze genes that were up-regulated by exogenous addition of vanillin.

Reference

[1] Shimizu, M., Yuda, N., Nakamura, T., Tanaka, H., and Wariishi. (2005) Metabolic regulation at the tricarboxylic acid and glyoxylate cycles of the lignin-degrading basidiomycete *Phanerochaete chrysosporium* against exogenous addition of vanillin. *Proteomics* **5**, 3919-3931.