

Transcriptomics and co-expression network analysis revealing candidate genes for the laccase activity of *Trametes gibbosa*

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【Objective】 *Trametes gibbosa*, which is a white-rot fungus of the Polyporaceae family found in the cold temperate zone, causes spongy white rot on wood. Laccase can oxidize benzene homologs and is one of the important oxidases for white rot fungi to degrade wood. However, the pathway of laccase synthesis in white rot fungi is unknown. **【Result】** The peak value of laccase activity reached 135.75 U/min/L on the 9th day. For laccase activity and RNA-seq data, gene expression was segmented into 24 modules. Turquoise and blue modules had greater associations with laccase activity (positively 0.94 and negatively -0.86, respectively). For biology function, these genes were concentrated on the cell cycle, citrate cycle, nicotinate, and nicotinamide metabolism, succinate dehydrogenase activity, flavin adenine dinucleotide binding, and oxidoreductase activity which are highly related to the laccase synthetic pathway. Among them, gene_8826 (MW199767), gene_7458 (MW199766), gene_61 (MW199765), gene_1741 (MH257605), and gene_11087 (MK805159) were identified as central genes.

【Conclusion】 Laccase activity steadily increased in wood degradation. Laccase oxidation consumes oxygen to produce hydrogen ions and water during the degradation of wood. Some of the hydrogen ions produced can be combined by Flavin adenine dinucleotide (FAD) to form reduced Flavin dinucleotide (FADH₂), which can be transmitted. Also, the fungus was starved of oxygen throughout fermentation, and the NADH and FADH₂ are unable to transfer hydrogen under hypoxia, resulting in the inability of NAD and FAD to regenerate and inhibit the tricarboxylic acid cycle of cells. These key hub genes related to laccase activity play important roles in the molecular mechanisms of laccase synthesis for exploring industrial excellent strains.