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Diversity of ligninolytic enzymes and their genes in the genus Ganoderma - application for biodegradation of xenobiotic compounds

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White Rot Fungi (WRF) and their ligninolytic enzymes are considered promising biotechnological tools to remove persistent organic pollutants from industrial waste waters and polluted ecosystems. A high diversity within the genus Ganoderma has been reported in Cuba; in spite of this, the diversity of their ligninolytic enzymes, their genes and the biotechnological potential of well adapted autochthonous strains belonging to genus Ganoderma remains underexplored. The objectives of this study were: To analyze the diversity of ligninolytic enzymes and genes of Cuban native strains from the genus Ganoderma and to evaluate their potential for degradation of textile dyes and polycyclic aromatic hydrocarbons (PAHs). Thirteen WRF strains were isolated from decayed wood in urban ecosystems in Havana and identified as Ganoderma sp. using a multiplex ITS-based PCR-method. The strains were cultured in SB-U medium with sugarcane molasses and the ligninolytic enzymes activities as well as isozyme analyses were measured on extracellular enzyme extracts. The diversity of genes encoding laccases and peroxidases was determined using a PCR and cloning approach with basidiomycete specific primers. The results showed that Ganoderma sp. strains isolated differed in their ligninolytic enzyme activities, isozymatic profiles, laccase and peroxidase gene repertoires. A high diversity of laccase genes was found among the strains; while only one gene encoding manganese or versatile peroxidases were detected. The translated laccases and peroxidases amino acid sequences have not been described before. The strains were able to significantly degrade textile dyes, naphthalene, phenanthrene and fluorene. We found that the PAH oxidation performed by their extracellular enzymes generated non-toxic intermediate metabolites; the possible degradation pathways of these PAHs were determined. These findings hold promises for the development of a practical application for the treatment of textile industry wastewaters, as well as for bioremediation of polluted ecosystems by well-adapted native WRF strains.

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