Extremotolerant Yeasts in Bioremediation

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ABSTRACT

Bioremediation represents a crucial strategy for the removal of contaminants, such as polycyclic aromatic hydrocarbons (PAHs), which are toxic to biota in various environments. Among these, phenanthrene (Phe) and benzo(a)pyrene (BaP) are commonly used as model compounds for studying the degradation of low- and high-molecular-weight PAHs, respectively, due to their mutagenic and carcinogenic properties. As an oil producer, Mexico experiences frequent incidents of oil spills and illegal extraction activities, leading to significant ecological damage. In recent decades, fungi have emerged as an effective tool for the removal or degradation of such contaminants. The aim of the present study was to explore the metagenomic and genomic potential of fungi isolated from contaminated soils. In this work, we report the isolation of two yeast strains and four bacterial strains from soil continuously contaminated with crude oil derivatives. These microorganisms were identified through phenotypic and molecular analyses as *Exophiala* sp. LBMH1012 and *Rhodotorula mucilaginosa* LBMH1013. Both strains exhibited the ability to metabolize monoaromatic and polyaromatic hydrocarbons, with a distinct preference for either group. Furthermore, both yeasts demonstrated growth across a wide pH range and tolerance to temperatures up to 30°C and NaCl concentrations up to 1M. To determine whether these preferences could be explained by genomic factors, we sequenced the genomes of both yeasts. The results supported this hypothesis, as *Exophiala* sp. LBMH1012 exhibited a higher number of cytochrome P450 oxidase genes compared to *Rhodotorula mucilaginosa*. Additionally, the strain *LBMH1012* was identified as a novel species, which we named *Exophiala chapopotensis*. Notably, metagenomic analysis of the soil from which these yeasts were isolated revealed an enriched gene pool associated with the degradation of xenobiotics. In conclusion, the yeasts identified in this study possess significant potential

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for application in bioremediation processes, offering promising avenues for the remediation of hydrocarbon-contaminated environments.

Keywords: Hydrocarbonoclast, Yeasts, Fungi, Crude oil, PAHs

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