BIODEGRADATION POTENTIAL AND METABOLOMIC INSIGHTS OF MARINE PLASTISPHERE YEASTS

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Abstract

Microplastic (MP) pollution represents a critical environmental challenge, impacting marine ecosystems and their biodiversity. In this study, we investigated the genomic and metabolomic traits of four marine basidiomycete yeasts associated with sediment MPs from the Livorno region (Italy), highlighting their potential in plastic depolymerization. The genomes of *Cystobasidium slooffiae* and *Sakaguchia dacryoidea* (Cystobasidiomycetes), *Vishniacozyma carnescens* (Tremellomycetes), and *Kondoa aeria* (Agaricostilbomycetes) exhibit a high abundance of gene linked to plastic-degrading enzymes, including esterases, laccases, and hydrophobins that enhance MP adhesion. Additionally, horizontally acquired genes, such as a bacterial-derived plastic depolymerase in *C. slooffiae*, further suggest their adaptation for MP breakdown.

Metabolomic analyses via Mass Spectrometry revealed a diverse profile of bioactive compounds, including terpene-like molecules with potential biotechnological applications. These findings not only underscore the ability of marine yeasts to contribute to MP degradation but also provide insight into their evolutionary adaptations in marine environments. This study positions these strains as promising candidates for sustainable bioremediation strategies and bio-based innovation.

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