



ABSTRACT

Title:

A multi-omics characterization of marine basidiomycete yeasts with plastic-degrading potential

Authors:

Florio Furno Matteo^a, Venice Francesco^a, Fateme Sadeghian^a, Chiarello Matteo^b, Spina Federica^a, Torchia Costanza^a, Laera Angelica^a and Varese Giovanna Cristina^a

Affiliations:

^a University of Turin (UNITO), Department of Life Sciences and Systems Biology, Turin, Italy.

^b University of Turin (UNITO), Department of Chemistry, Turin, Italy

Presenting: Florio Furno Matteo

Abstract content:

Microplastic (MP) pollution represents a critical environmental challenge, severely impacting marine ecosystems and biodiversity. This study investigates the genomic, metabolomic and phenotypical traits of four marine basidiomycete yeasts isolated from sediment-associated MPs in the Livorno region (Italy), highlighting their potential role in plastic depolymerization. The genomes of *Cystobasidium slooffiae* and *Sakaguchia dacryoidea* (Cystobasidiomycetes), *Vishniacozyma carnescens* (Tremellomycetes), and *Kondoa aerea* (Agaricostilbomycetes) revealed a high abundance of genes encoding putative plastic-degrading enzymes, including esterases, laccases, and hydrophobins potentially involved in MP adhesion. Notably, evidence of horizontal gene transfer, such as a bacterial-derived plastic depolymerase identified in *C. slooffiae*, suggests evolutionary adaptation to MP-rich environments. Metabolomic profiling by mass spectrometry revealed a diverse array of bioactive compounds, including terpene-like molecules with potential biotechnological relevance. In parallel, transcriptomic (RNA-based) analyses are currently ongoing to identify the enzymes actively involved in the degradation of polyurethane, including both polyester- and polyether-based formulations. Overall, these findings support the contribution of marine yeasts to MP degradation processes and provide new insights into their adaptive strategies in polluted marine ecosystems. The studied strains emerge as promising candidates for sustainable bioremediation approaches and bio-based innovation.