UNVEILING MICROBIAL NETWORKS: FUNGI AND BACTERIA RESPONSES TO POLLUTION IN THE GULF OF VENICE

Fateme Sadeghian*†[1], Francesco Venice[1], Michael Tangherlini[2], Tiziano Vendrame[3], Alessandro Benassi[3], Antonio Dell'anno[4], and Giovanna Varese‡[1]

[1]Department of Life Sciences and Systems Biology [University of Turin] – Italy
[2]Research Infrastructures for marine biological resources, Department - Stazione Zoologica Anton Dohrn Napoli, Italy – Italy
[3]Regional Department for Environment Quality, ARPAV, Regional agency for Environmental Protection and Prevention of the Veneto, Padova, Italy – Italy
[4]Department of Life and Environmental Sciences, Polytechnic University of Marche, Italy – Italy

Abstract

Microbial communities are crucial for marine ecosystem health and understanding their structural and metabolic adaptations to stressors like Persistent Organic Pollutants (POPs), microplastics, and heavy metals is essential. We used metabarcoding to assess the impact of pollutants on fungal and bacterial communities in Adriatic Sea sediments, marking one of the first studies to investigate both in polluted marine environments.
Our research focuses on three areas in the Gulf of Venice (Italy) along a pollution gradient, with heavy metal concentrations ranging from 62–143 mg/kg s.s. and polycyclic aromatic hydrocarbons from 54–352 μg/kg s.s. Methodologically, we applied an advanced approach to study fungal communities using 18S primers with blocking primers, enabling the quantification of typically overlooked taxa such as Chytridiomycota, Cryptomycota, Aphelidiomycota, and the LJKM11 clade, alongside Dikarya and Mucoromycota. These "fungal dark matter" taxa have unexplored ecological roles but were prominent in our study.
Surprisingly, the impact of pollution on microbial communities was lower than expected; alpha diversity was not reduced, and beta diversity did not show a dramatic shift in community composition. Using co-occurrence networks, we explore the hypothesis that high pollution drives microbial diversification and fosters new metabolic interactions. Our study enhances understanding of how human impact shapes marine ecosystems.

Keywords: Pollution gradients, DNA metabarcoding, Microbial interaction, Fungi, Bacteria

*Speaker
†Corresponding author: f.sadeghian@unito.it
‡Corresponding author: cristina.varese@unito.it