



# Distribution, Community Composition, and Potential Metabolic Activity of Bacterioplankton in an Urbanized Mediterranean Sea Coastal Zone

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**ABSTRACT** Bacterioplankton are fundamental components of marine ecosystems and influence the entire biosphere by contributing to the global biogeochemical cycles of key elements. Yet, there is a significant gap in knowledge about their diversity and specific activities, as well as environmental factors that shape their community composition and function. Here, the distribution and diversity of surface bacterioplankton along the coastline of the Gulf of Naples (GON; Italy) were investigated using flow cytometry coupled with high-throughput sequencing of the 16S rRNA gene. Heterotrophic bacteria numerically dominated the bacterioplankton and comprised mainly *Alphaproteobacteria*, *Gammaproteobacteria*, and *Bacteroidetes*. Distinct communities occupied river-influenced, coastal, and offshore sites, as indicated by Bray-Curtis dissimilarity, distance metric (UniFrac), linear discriminant analysis effect size (LEfSe), and multivariate analyses. The heterogeneity in diversity and community composition was mainly due to salinity and changes in environmental conditions across sites, as defined by nutrient and chlorophyll *a* concentrations. Bacterioplankton communities were composed of a few dominant taxa and a large proportion (92%) of rare taxa (here defined as operational taxonomic units [OTUs] accounting for <0.1% of the total sequence abundance), the majority of which were unique to each site. The relationship between 16S rRNA and the 16S rRNA gene, i.e., between potential metabolic activity and abundance, was positive for the whole community. However, analysis of individual OTUs revealed high rRNA-to-rRNA gene ratios for most (71.6% ± 16.7%) of the rare taxa, suggesting that these low-abundance organisms were potentially active and hence might be playing an important role in ecosystem diversity and functioning in the GON.

**IMPORTANCE** The study of bacterioplankton in coastal zones is of critical importance, considering that these areas are highly productive and anthropogenically impacted. Their richness and evenness, as well as their potential activity, are very important to assess ecosystem health and functioning. Here, we investigated bacterial distribution, community composition, and potential metabolic activity in the GON, which is an ideal test site due to its heterogeneous environment characterized by a complex hydrodynamics and terrestrial inputs of varied quantities and quality. Our study demonstrates that bacterioplankton communities in this region are highly diverse and strongly regulated by a combination of different environmental factors leading to their heterogeneous distribution, with the rare taxa contributing to a major proportion of diversity and shifts in community composition and potentially holding a key role in ecosystem functioning.

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