

genera within the Rhodobacteraceae. During summer the sampling site experienced blooms of cyanobacteria, with *Synechococcus* as the dominant genus, and of the Actinobacterium DS001. In Autumn, the genus *Actinomarina* of the Actinobacteria reached its highest RA; at the same time archaeal abundances (mostly *Nitrosopumilus*) started to rise, reaching their maxima during winter. In the coldest months also the sulfur oxidizer group SUP05 of the Gammaproteobacteria displayed the highest values.

Water masses age and origin drive the diversity of pelagic prokaryotes and dissolved organic matter dynamics: the Mediterranean Sea case

Gian Marco Luna (1)*, Grazia Marina Quero (1), Simona Retelletti Brogi (2), Chiara Santinelli (2)

(1) Institute for Biological Resources and Marine Biotechnologies, National Research Council (IRBIM-CNR), Largo Fiera della Pesca 2, 60125, Ancona, Italy

(2) Biophysics Institute, National Research Council (IBF-CNR), Via G. Moruzzi, Pisa 56124, Italy

* email corresponding author: gianmarco.luna@cnr.it

The deep sea is among the largest, yet still poorly known, ecosystems on Earth. This knowledge gap is particularly evident for the deep Mediterranean Sea, characterized by peculiar conditions at meso- and bathypelagic depths, likely selecting for unique microbial assemblages. We collected seawater samples, from the surface to the bathypelagic layers, in basins of the Western Mediterranean Sea (Algero-Provençal Basin, Alboran Sea and Gulf of Lion) characterized by different trophic regimes, and described the composition of pelagic prokaryotic communities, the main physical-chemical variables, and the concentration and optical properties of dissolved organic matter (DOM). The main goal was to test the hypothesis that assemblages vary in the different water masses, and that they are structured by the quantity/quality of DOM. Communities were significantly different among layers (epi-, meso- and bathypelagic) and water masses. Richness and diversity (as Shannon index) increased significantly with depth, with highest richness in mesopelagic stations. Our data show that spatially separated microbial communities, belonging to different water masses, are associated with different DOM properties (different DOM quality), even if at similar DOC concentration, suggesting a different role played by communities in the DOM cycling, that needs to be further elucidated also in light of the changing conditions of the entire basin.

The sweet tooth of marine microbiomes: potential and expression patterns of prokaryotic glycosyl-hydrolases across the global ocean

Vincenzo Manna*, Elisa Banchi, Mauro Celussi

Istituto Nazionale di Oceanografia e Geofisica Sperimentale – OGS, Via Auguste Piccard 54, 34151, Trieste

* email corresponding author: vmanna@ogs.it

Polysaccharides constitute a large fraction of the organic matter produced and degraded in the ocean, representing a pivotal nutritional source for heterotrophic microbes. Extracellular enzymes are the essential tool used by heterotrophic prokaryotes to access this resource. According to the foraging theory, extracellular enzymes should be cell-associated in dilute systems but secreted into the surrounding environment in diffusion-limited systems (e.g., organic particles). Aiming to characterise abundance and expression patterns of cell-associated and cell-free carbohydrate-degrading enzymes (glycosyl-hydrolases, GHs) across the global ocean, we queried the Tara Oceans metagenomic and metatranscriptomic datasets searching for prokaryotic GHs sequences. Distinguishing between secretory and non-secretory GHs, we aimed to assess the importance of microbial lifestyle for carbohydrate cycling in the ocean. Secretory GHs showed a clear latitudinal pattern, mostly evident for surface and deep chlorophyll maximum samples, with

higher abundance and expression observed in polar samples. According to GHs expression data, mesopelagic samples gathered in a distinct cluster, regardless of their climatic zone, significantly defined by secretory GHs involved in chitin degradation. These results indicate that a consistent fraction of carbohydrates cycling at high latitudes and in the mesopelagic ocean is channelled through dissolved exoenzymes, highlighting the importance of microscale carbon fluxes in these environments.

Trends of fecal pollution along the coasts of Marche Region (Adriatic Sea) over a decade (2011-2021)

Grazia Marina Quero*, Stefano Guicciardi, Pierluigi Penna, Gian Marco Luna

CNR IRBIM, National Research Council – Institute of Marine Biological Resources and Biotechnologies, Largo Fiera della Pesca, 60125, Ancona (Italy)

* email corresponding author: grazia.quero@irbim.cnr.it

A general increase of fecal pollution has been reported worldwide over the last decades, with predictions suggesting a further rise by the end of this century in response to global change and increasing pressure on coasts. For these reasons, clarifying the trends and factors related to fecal pollution over relatively large spatial and temporal scales is of paramount importance. In this study, we retrospectively evaluated and analyzed Fecal Indicator Bacteria (FIB) abundance data along a coastal section of the Marche region – an area characterized by intense tourism, maritime traffic and industrial activities – over a decade (2011-2021) and related such data to precipitations levels, rivers' flow and drainage basins discharge, with the primary objectives of: i) assessing the temporal variation of the overall fecal contamination along the Marche Region coasts and ii) clarifying the possible factors explaining the fecal contamination.

In the light of climate change scenarios and considering the need to clarify environmental and human health under the One Health approach, our study represents a step forward the understanding of the future variability of fecal contamination and in designing effective management plans to limit microbial pollution in coastal waters.

The role of intraspecific morpho-functional trait variability in marine phytoplankton responses to changing nutrient scenarios

Silvia Pulina (1)*, Jorin Hamer (2), Giannina S. I. Hattich (2,3), Julia Romberg (2), Cecilia T. Satta (1), Birte Matthiessen (2)

(1) Aquatic ecology group, University of Sassari, Dipartimento di Architettura, Design e Urbanistica, via Piandanna 4, 07100 Sassari, Italy

(2) GEOMAR Helmholtz Centre for Ocean Research, Düsternbrooker Weg 20, 24105 Kiel, Germany

(3) Åbo Akademi University, Environmental and Marine Biology, Artillerigatan 6A, 20520 Åbo/Turku, Finland

* email corresponding author: pulinasi@uniss.it

Nutrient limitation is expected to increase in the future ocean driven by intensified water column stratification due to increasing temperature. High variability in phytoplankton morphology at inter- and intra-specific level is a powerful strategy to cope with changing nutrient conditions. Nine genotypes of the diatom *Chaetoceros affinis* were incubated in the short-term at seven nitrate regimes to study the intraspecific morphological trait dynamics. Preliminary results suggest a significant intraspecific cell size and S/V variability of the diatom which can be explained by both plasticity of genotypes and to a larger extent by differences in mean trait values among genotypes. This significant variability allowed to group the cells into four morphotypes diverging in diameter size. Comparable intraspecific morphological variability of the diatom was also observed over a previous long-term experiment with a community consisting of *C. affinis* and the