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TITLE: Planktonic prokaryote and protist communities in a submarine canyon system in the Ligurian Sea (NW Mediterranean)

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ABSTRACT:

Submarine canyons are large geomorphological features that incise continental margins and act as highly dynamic conduits of sediments from shallow to the deep-sea regions. They are often regarded as biodiversity and biomass hotspots, but their role in influencing plankton communities is still poorly known. We studied the ecology of planktonic deep-sea microbes in a submarine canyon system (Polcevera and Bisagno canyons) in the Ligurian Sea (NW Mediterranean Sea), aiming at testing whether these large-scale incisions are peculiar systems, in comparison to the overlying water and the adjacent uncarved slope, in terms of biogeochemical and biological features. We analysed microbial communities? composition by high-throughput sequencing of 16S and 18S rRNA genes and their functional attributes by measuring heterotrophic carbon production, dissolved inorganic carbon fixation, respiration and the activity of the exoenzymes leucine aminopeptidase, alkaline phosphatase, beta-glucosidase and lipase. We found that both prokaryotic and eukaryotic communities were not significantly different inside the canyons (if compared to the close slope and overlying water), but they were rather shaped by the water masses dynamics in the area. The shallowest Modified Atlantic Waters, Levantine Intermediate Waters and Winter Intermediate Waters hosted higher percentages of Alphaproteobacteria, Bacteroidetes and Dinophyta, while the deepest Western Mediterranean Deep Waters hosted a higher fraction of Gammaproteobacteria, Chloroflexi, Discoba and Fungi. Among the functional measurements, only leucine aminopeptidase activity showed higher rates within the canyons. However, local hotspots within the canyons characterised by high particulate matter loads and high C:N ratio (interpreted as refractory material from sediment local resuspension) displayed pronounced degradation activities.

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