

{rokbox title=| Contribution of phylotypes to (a) total and (b) actively dividing communities in different depth layers :: Image:
Authors|images/stories/ieo/imagenespublicaciones/centro-oceanografico-baleares-ieo-csic-dynamics-actively-dividing-mena-2022-thumb-et-al.jpg|images/stories/ieo/imagenespublicaciones/centro-oceanografico-baleares-ieo-csic-dynamics-actively-dividing-mena-2022-et-al.jpg{/rokbox}

Catalina Mena, Patricia Reglero, Rosa Balbín, Melissa Martín, Rocío Santiago and Eva Sintes, 2022.

[Dynamics of actively dividing prokaryotes in the western Mediterranean Sea.](#)

Scientific Reports. Volume 12. Article number:2064 (2022).

<https://doi.org/10.1038/s41598-022-06120-y>

Abstract: Microbial community metabolism and functionality play a key role modulating global biogeochemical processes. However, the metabolic activities and contribution of actively growing prokaryotes to ecosystem energy fluxes remain underexplored. Here we describe the temporal and spatial dynamics of active prokaryotes in the different water masses of the Mediterranean Sea using a combination of bromodeoxyuridine labelling and 16S rRNA gene Illumina sequencing. Bulk and actively dividing prokaryotic communities were drastically different and depth stratified. Alteromonadales were rare in bulk communities (contributing 0.1% on average) but dominated the actively dividing community throughout the overall water column (28% on average). Moreover, temporal variability of actively dividing Alteromonadales oligotypes was evinced. SAR86, Actinomarinales and Rhodobacterales contributed on average 3–3.4% each to the bulk and 11, 8.4 and 8.5% to the actively dividing communities in the epipelagic zone, respectively. SAR11 and Nitrosopumilales contributed less to the actively dividing than to the bulk communities during all the study period. Noticeably, the large contribution of these two taxa to the total prokaryotic communities (23% SAR11 and 26% Nitrosopumilales), especially in the meso- and bathypelagic zones, results in important contributions to actively dividing communities (11% SAR11 and 12% Nitrosopumilales). The intense temporal and spatial variability of actively dividing communities revealed in this study strengthen the view of a highly dynamic deep ocean. Our results suggest that some rare or low abundant phylotypes from surface layers down to the deep sea can disproportionally contribute to the activity of the prokaryotic communities, exhibiting a more dynamic response to environmental changes than other abundant phylotypes, emphasizing the role they might have in community metabolism and biogeochemical processes.

Keywords: Microbial communities, Environmental microbiology, Marine microbiology, Microbial

ecology