Seasonality of the marine microbiome in the Blanes Bay Microbial Observatory (NW Mediterranean)

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The oceans are ecosystems dominated by microbes, in which bacteria and archaea play key roles in biogeochemical cycling. In temperate oceans, seasonal changes in environmental conditions deeply influence the marine microbiome. Here, we analyse the seasonality of the marine microbiome of a coastal ocean site, using the long-term time series of the Blanes Bay Microbial Observatory (BBMO). First, using amplicons of the 16S rRNA gene, we evaluate the dynamics of the main bacterial groups in this coastal oligotrophic station during 11 years and test how similar the temporal niches of closely related taxa are, and what are the environmental parameters modulating their patterns of seasonality. We further explore how conserved the niche is at higher taxonomic levels. The community presents recurrent seasonality for 297 out of 6825 amplicon sequence variants (ASVs), which constitute almost half of the total relative abundance (47%). For certain genera, niche similarity decreases as nucleotide divergence in the 16S rRNA gene increases, a pattern compatible with the selection of similar taxa through environmental filtering. Additionally, we observe evidence of seasonal differentiation within various genera as seen by the distinct seasonal patterns of closely related taxa. Then, we focus on the seasonal patterns of a relevant functional group in the marine microbial food web, the aerobic anoxygenic phototrophic bacteria (AAPs), and evaluate their long-term temporal dynamics through multivariate and co-occurrence analyses. Diversity indices show a clear seasonal trend, with maximum values in winter, which is inverse to that of AAP abundance. Finally, we extend the seasonality analyses to 21 biogeochemical relevant functions by using 7 years of metagenomic data from the BBMO and identify the main taxa driving each function in each season. We show that, for some groups, the seasonality of bacterial families is different than that of their gene repertoire, so that different taxa within the same group present different functional specialization. Overall, this study provides new insights into the seasonal patterns of key taxonomic and functional groups in the coastal surface ocean through the integration of information obtained using several molecular techniques applied to a long-term time series.

Keywords: marine prokaryotes, time series, amplicon sequencing, metagenomics