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The scales at which microbiomes of marine hosts vary in time and space, and the biotic and abiotic drivers of variation are poorly understood. Functional redundancy can maintain key microbe-mediated processes despite taxonomic variation, but it is unclear if these functions are stable following changes in the host or host environment. We repeatedly sampled the microbiome of the same *Fucus distichus* individuals through time and compared host-associated bacterial (16S rRNA gene), eukaryotic (18S rRNA gene), and functional (shotgun metagenomic) diversity to source pools of microbes in the surrounding environment. Temporal variation in biotic filters (the host) and the abiotic environment were partially decoupled by sampling co-occurring host individuals at different life stages over time. Synchronous temporal turnover in microbial taxa occurred at the host population-level but interindividual variation in specific ASVs was high and minimally explained by differences in host ontogeny or spatial distance within the host population. In contrast, interindividual variation in microbial functional repertoire was low, suggesting high functional redundancy. We also observed consistent and habitat-specific temporal turnover in microbial functions indicating functional change is driven by seasonal variation across host-associated and abiotic intertidal habitats. This research makes a novel contribution to understanding the selective filters determining microbiome compositional dynamics and functions in an ecologically important marine host.

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DIATOMS AND DINOFLAGELLATES DIVERSITY INHABITING A COASTAL UPWELLING SYSTEM: A METABARCODING APPROACH

Small eukaryotic plankton has been traditionally characterized using conventional microscopy techniques. Current advances in sequencing technologies allow the cost-effective study the diversity within microbial plankton based on DNA sequences. This technique has been implemented in the last 15 years for investigating prokaryotic diversity, but its application to unravel the diversity and ecology of eukaryotic organisms is still incipient. In this study we analyze the diversity of the diatoms and dinoflagellates in the marine communities using rDNA sequencing techniques, as well as the taxonomic resolution provided by the V4 region of the 18S rRNA gene. Twenty monthly 6L seawater samples for DNA metabarcoding were collected and filtered through 3 µm polycarbonate filter in a station off the Ría de A Coruña (NW Iberian Peninsula). DNA was extracted, the V4 region of the 18S rRNA was PCR amplified and subsequently sequenced using the High Throughput Sequencing (HTS) platform Illumina. Amplicon sequence variants (ASVs) were differentiated using DADA2 implemented in R. Sequences were aligned against PR2 v4.12.0 and SILVA 132 18S rRNA databases as references, as well as studied using BLAST and phylogenetic trees. *Sequence*-based *taxonomic* approach found 128 and 416 metabarcodes corresponding to diatoms and dinoflagellates, respectively. Sequences had limited resolution at species or even genus level, and overall the taxonomic resolution of diatoms was substantially higher than those of dinoflagellates.

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