



Microorganisms have central roles in biogeochemical processes in marine environments, but our understanding of the composition of these communities and the ecological factors that determine community structure on a global scale is limited. Now, 5 studies report the initial findings of the international Tara Oceans consortium, which sampled plankton at 210 sites across the world's major oceanic regions from 2009 to 2013.

Oceanic plankton is composed of viruses, prokaryotes, microbial eukaryotes, phytoplankton and zooplankton; these form complex networks that are determined by abiotic factors — such as depth, temperature, oxygen and nutrient availability — as well as biotic factors, such as grazing, symbiosis and pathogenicity. To better understand these networks and the factors shaping them, seawater was sampled from three different depths: the surface water and the deep chlorophyll maximum layers (both of which are within the epipelagic layer), and the deeper mesopelagic zone. Furthermore, samples were fractionated according to plankton size, enabling the independent study of prokaryotes, viruses and eukaryotes.

Sunagawa *et al.* used metagenomic sequencing on the prokaryote-enriched fractions and determined the composition of 243 samples from 68 locations; these data were used to create the global Ocean Microbial Reference Gene Catalogue, which includes more than 40 million genes from viruses, prokaryotes and picoeukaryotes. The authors found that temperature is the main driver of community composition in the surface layers of the ocean, with geography having a less important

role. These findings led the authors to propose that community structure is determined by the potential of microorganisms to disperse on a global scale, with local environmental conditions selecting for those species that are adapted to the new conditions.

Brum *et al.* determined the viral composition of 43 samples from 26 sites, mostly from the epipelagic layers of different oceans. They analysed double-stranded DNA viromes using metagenomic sequencing and found that viral populations were rarely endemic to a location, with many populations being present in more than four sites. Nonetheless, most of these populations differed in abundance across locations, and the composition of viral communities was influenced by the bacterial composition of the samples and by temperature, oxygen and nutrient availability, and ocean currents. The authors propose that the composition of viral communities in the upper ocean is consistent with a seed-bank hypothesis: local environmental conditions directly determine the bacterial composition at specific locations, which indirectly influences the dominant viral communities at these sites; and these dominant viral populations are then passively transported by ocean currents to seed neighbouring locations, where different environmental conditions dictate the structure of the local viral community.

Villar *et al.* studied the plankton composition of Agulhas rings, which are large water rings that circulate from the Indo-Pacific ocean to the Atlantic ocean. The authors found that vertical mixing between ocean layers occurs within these rings,

which drives nitrogen cycling and promotes phytoplankton blooms, particularly the expansion of cyanobacteria that carry genes involved in nitrogen metabolism.

The Tara Oceans consortium also analysed the composition of eukaryotic ocean plankton. de Vargas *et al.* examined 18S rDNA sequences from unicellular and multicellular small eukaryotes and found that the smaller organisms, particularly poorly characterized heterotrophic protists, were responsible for the majority of the taxonomic diversity observed in the upper layers of the ocean.

Finally, Lima-Mendez *et al.* created a species interaction network that includes prokaryotes, viruses and eukaryotes, which revealed that environmental conditions are insufficient for predicting the composition of ocean communities. The authors suggest that biological interactions, such as symbiosis and phage–bacteria interactions, have an important role in determining community structure.

Collectively, these studies expand our knowledge of the community composition and functions of the global oceans and provide important insights into the ecological factors that govern community structure in these ecosystems.

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ORIGINAL RESEARCH PAPERS Sunagawa, S. *et al.* Structure and function of the global ocean microbiome. *Science* **348**, 1261359 (2015) | Brum, J. R. *et al.* Patterns and ecological drivers of ocean viral communities. *Science* **348**, 1261498 (2015) | Villar, E. *et al.* Environmental characteristics of Agulhas rings affect interoceanic plankton transport. *Science* **348**, 1261447 (2015) | de Vargas, C. *et al.* Eukaryotic plankton diversity in the sunlit ocean. *Science* **348**, 1261605 (2015) | Lima-Mendez, G. *et al.* Determinants of community structure in the global plankton interactome. *Science* **348**, 1262073 (2015)