

 MARINE MICROBIOLOGY

Deep sequencing of the global oceans

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. 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. Brum *et al.* determined the viral composition of 43 samples from 26 sites, mostly from the epipelagic layers of different oceans, and found that viral populations were rarely endemic to a location, with many populations being present in more than four sites. 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. 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.

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 interocean 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)