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Understanding the ocean metagenome

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An Editorial on the Frontiers in Science Lead Article

Metagenomic probing toward an atlas of the taxonomic and metabolic foundations of the global ocean genome

Key points

- We have only scratched the surface of understanding the diversity and function of microbes in the ocean.
- New metagenomic tools allow us to accelerate our knowledge of the ocean microbiome in a way that was unthinkable just a couple of decades ago.
- The applications of new knowledge of ocean microbial genes have enormous potential for human health and climate change mitigation.

The ocean comprises most of the living space in our biosphere, but if we had to write a catalog of what lives there, 99% of the pages would be blank. Our best estimate is that there are 2.2 million Eukaryote species in the ocean, yet only 10% of these have been cataloged (1). When it comes to knowing how many different types of microbes are in the ocean—such as the estimate of 2 million bacterial species (1)—we may well be off, especially because over two-thirds of the microbes live in the little-known dark depths of the ocean.

A liter of seawater contains about 1 billion bacteria and 10 billion viruses. A drop of seawater contains about 100 species of bacteria. Additionally, there are probably a billion times more viruses in the ocean than the number of stars in the known universe (at least before the launch of the James Webb telescope). This ignorance is remarkable since microbes—mainly bacteria and protists—account for about 70% of the total marine biomass (2).

But our knowledge of what all these microbes do is even slimmer. We know that microbes have a key role in the production of oxygen, nutrient cycling, carbon sequestration, and other global biogeochemical processes that make Earth habitable for us. But until we identify more ocean microbes we will not know what they specifically do, which genes allow them to do what they do, and whether we could benefit from the genes

and proteins they produce (for example, polymerases from bacteria living on hydrothermal vents are used in polymerase chain reaction [PCR] tests).

The good news is that modern techniques to sequence the genome of everything contained in a sample of seawater (metagenomic sequencing) have accelerated the identification of which species live in that sample (taxonomic diversity) and what they do (functional diversity).

To advance toward bridging this giant scientific gap, Laiolo et al. (3) present a novel synthesis of the global ocean genome using the KAUST Metagenome Analysis Platform (KMAP) Global Ocean Gene Catalogue 1.0, which contains over 2,000 metagenomic samples and ~305 million gene clusters. This is the largest ocean gene catalog of microbes living in different parts of the ocean, from the seafloor, across the water column, to the surface. The data show that shallower waters are greatly enriched with Eukaryota and viral genes, while depths below 200 m are relatively rich in unique Archaea genes. The seafloor (benthic realm) is highly enriched in Bacteria and Eukaryota gene clusters, the dark ocean is rich in both Archaea and Bacteria gene clusters, and the upper ocean presents the highest relative abundance of viral gene clusters. In addition, Laiolo and colleagues show that Fungi accounted for more than half the number of unique annotated gene clusters in the mesopelagic ocean zone.

Laiolo et al.'s study is, however, more than a catalog of genes; it also tells us how these microbes support vital metabolic processes. The analysis of the architecture of the ocean genome presented in the study allows us to match microbial taxonomy with biogeochemical cycling.

Global change and the ocean metagenome

Understanding the diversity and distribution of the metabolic capabilities of ocean microbes (and their link to taxonomic diversity) is essential for us to understand the role of microbes in, for instance, maintaining nutrient cycling and carbon sequestration. Microbes probably play an important role in mitigating the impact of global warming. We thus need to understand how human activities are changing the microbial ecosystem and, in turn, its ability to provide for us and the rest of life on the planet. We should see the ocean metagenome as a dynamic ecosystem across all scales, from a coral holobiont (bacteria, archaea, fungi, viruses, and zooxanthellae living in association with a coral polyp) to entire ocean realms (from the photic to hadal zones).

Functional metagenomics is a key tool to probe into the interactions between our activities and the functioning of microbial ecosystems. Much effort has been dedicated to the human microbiome, which has helped us better understand the role of nutrition in the structure and functioning of the gut microbiome and the link to our physical and mental health. Similarly, ocean microbiomes are affected by human activities. For example, there are 10 times fewer microbial cells and virus-like particles in the water column in pristine coral reefs than in inhabited ones. The microbes in pristine habitats are dominated by autotrophs, while the degraded habitats are dominated by heterotrophs, including a large percentage of potential pathogens (4). In the Line Islands, these differences were due mostly to changes in the coral reef food web owing to fishing and not to human pollution. Therefore, increased reef protection can restore the microbial ecosystem to a state that reduces the prevalence of coral and human disease.

What are we missing?

The ocean is vast, and the efforts to sequence its metagenome are relatively recent, chiefly because the technologies required to work economically at speed and scale have only been available in the last couple of decades. As massive as Laiolo et al.'s effort is, they acknowledge that "[o]ut of the 2,102 marine metagenomes analyzed, only 86 were sampled from benthic communities, accounting for less than 5% of the total metagenomes, while only 215 out of the 2016 pelagic metagenome samples (10.2%) were sampled from the dark ocean, the largest habitat on Earth." The study analyzed DNA but did not include RNA viruses.

Ocean metagenomic studies have focused primarily on the shallow open ocean, with samples easily obtained from research vessels. Deep sea studies are more costly, but there is no reason (other than available funding) why shallow benthic habitats should not be surveyed at a larger scale at a rapid pace. The habitat complexity provided by benthic habitats could increase the catalog of microbial diversity and function disproportionately to their area. The ocean metagenome is the last scientific frontier.

Genomic equity

Finally, data collection and analysis are not the endpoint of future work. As Laiolo and colleagues point out, the ownership of intellectual property derived from the exploration of the ocean genome will require the development of a just and equitable framework for benefit sharing. The Global Biodiversity Framework (5) approved in December 2022 at COP 15 of the United Nations (UN) Convention on Biological Diversity in Montreal stated that the benefits from the use of genetic resources and sequence information (e.g., the development of medical drugs) must be shared fairly and equitably in accordance with internationally agreed access and benefit-sharing instruments. This should not be an issue within the exclusive economic zones of countries, where any scientific research ought to be approved by the relevant government agencies, but Global South nations are wary of corporations benefitting silently from ocean genome discoveries in the high seas. A step in the right direction is the UN legal instrument for biodiversity beyond national jurisdiction (BBNJ), approved in 2023, which includes monetary benefit sharing associated with commercialization from the use of marine genetic resources and the associated digital sequence information. There is no reason why wealthy countries and pharmaceutical companies should be the only beneficiaries of the global commons. The irony is

that the ocean microbiome has already been providing benefits to our species for 200,000 years—for free.

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