



# Global ocean microbiome catalogue: A gateway to unlock marine microbial resources and ecosystem functions

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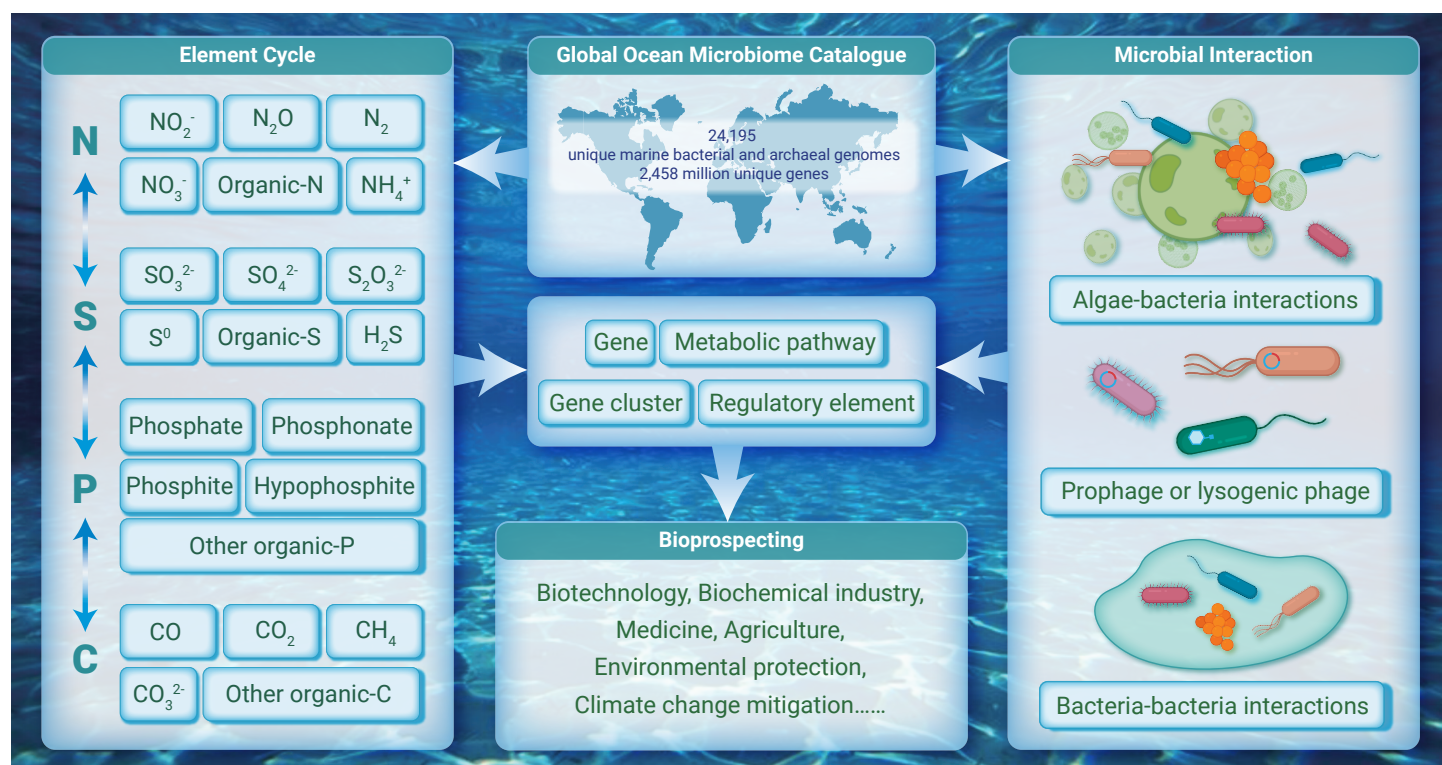
Received: September 23, 2024; Accepted: October 23, 2024; Published Online: October 30, 2024; <https://doi.org/10.59717/j.xinn-life.2024.100099>

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Citation: Zhang Z., Jiao N., and Zhang Y. (2024). Global ocean microbiome catalogue: A gateway to unlock marine microbial resources and ecosystem functions. *The Innovation Life* 2(4): 100099.

Marine microbes dominate oceanic life and play critical roles in driving biogeochemical cycling and regulating global climate. Moreover, the immense genetic and functional diversity of marine microbes highlight their important potential for application. These microbes offer transformative opportunities in biotechnology, medicine, and environmental management. For instance, marine microbes are increasingly recognized for their ability to produce novel bioactive compounds, enhance bioremediation processes, and contribute to innovative bioengineering solutions. Large-scale initiatives such as the Global Ocean Sampling (GOS) and the Tara Oceans Expedition have

significantly expanded our understanding of marine microbial diversity and their functional roles. However, the full potential of marine microbes remains underexplored, largely due to difficulties in translating genomic discoveries into practical applications. A comprehensive, unified catalogue is crucial for addressing this challenge by enabling researchers from diverse fields to efficiently search, compare, and analyze genomic data, facilitating practical applications. The recent publication of the Global Ocean Microbiome Catalogue (GOMC) by Chen et al. in *Nature* marks a significant advancement in bridging this gap.<sup>1</sup>



**Figure 1. The Global Ocean Microbiome Catalogue (GOMC): A vital gateway to marine microbial diversity and ecosystem functions, with substantial potential for bioprospecting.** GOMC can be further expanded and integrated with various factors, such as elemental cycling and microbial interactions, enabling the discovery of novel genes, gene clusters, or metabolic pathways that can promote more effective bioprospecting outcomes.

Chen et al. presented a comprehensive integration of 24,195 species-level genomes from marine samples collected across a wide range of environments. This extensive catalogue, further enriched by the global ocean microbiome protein catalogue (GOPC), offered an invaluable resource for detailed exploration of marine microbial diversity and functionality, marking a significant advancement in marine microbiology. One of its notable features was the broad geographical scope, spanning polar regions, tropical waters, and deep-sea zones, providing a more comprehensive understanding of marine microbial diversity than prior studies. The identification of functional elements further underscored the versatile characteristics of marine microbes. For instance, the discovery of a novel CRISPR-Cas9 system expanded the reper-

toire of genetic tools for precision genome editing. Additionally, the identification of novel antimicrobial peptides (AMPs) was useful to address the pressing need for alternative therapeutic strategies to combat resistant pathogens. Another breakthrough was the discovery of plastic-degrading enzymes like PETases, which opened up new avenues for bioremediation of synthetic polymers and mitigation of plastic pollution. The GOMC also holds significant value for synthetic biology, offering extensive genomic and proteomic datasets that enhance our understanding of microbial functionality. Researchers can identify more key metabolic pathways and genetic determinants that underpin specific microbial traits. This knowledge facilitates the engineering of microbes for improved functional efficiency and wider applica-

tions in biomaterial, medicine, energy production, and other fields.

Indeed, microbes are inextricably intertwined with their biotic and abiotic environments and studying them in isolation often yields incomplete understanding. The GOMC offers a comprehensive spectrum of microbial genomic diversity, along with background environmental parameters, providing crucial insights into the complex interactions between microbes and their biotic and abiotic environments. These aspects are essential for accurately understanding microbial functions, the latent conditions required for specific functions, and their ecological significance (Figure 1). For instance, in the euphotic layer of the ocean, algae and microbes interact closely, with algae being the major primary producers. Algae and microbes exhibit species-specific associations, where certain algae tend to enrich specific groups of microbes and some bacteria confer environmental competitive advantages to algae.<sup>2</sup> Notably, living algal cells have also been identified in the dark, deep-sea environment, where co-existing bacteria may be associated with algal-derived organic matter or potentially contribute to algal survival under extreme conditions. Additionally, emerging microbial classifications from the GOMC could shed light on metabolic auxotrophies in certain bacteria and algae, such as dependencies on vitamin B<sub>12</sub> and peroxidases, illuminating novel ecological roles and interdependencies. Chen et al. reported that certain bacteria with large genomes belong to Planctomycetota. This bacterial phylum is often present in algal environments, where some members possess multiple carbohydrate hydrolases and sulfatases. They prefer to utilize sulfur-containing polysaccharides from the algae.<sup>3</sup> The association implies their co-evolution or influence. Another critical and currently fascinating aspect is the intricate interactions between microbes and viruses (i.e., phages). GOMC provides a vast repository of species-specific genomes, making it an ideal resource for identifying prophages within microbial communities. Prophages have gained significant attention due to their diverse yet distinct characteristics compared to lytic phages, highlighting their often-overlooked importance.<sup>4</sup> Understanding the roles of prophages in regulating microbial metabolism, facilitating gene transfer, and shaping evolutionary trajectories may reveal previously unknown genetic tools, therapeutic agents, or innovative biotechnological platforms, with the CRISPR-CAS system exemplifying this potential. A deeper exploration of the diversity and functional implications of prophages could unveil novel pathways for manipulating microbial systems. Furthermore, interactions among microbes in the same environments are common, particularly within biofilms and transparent extracellular polymers, where they can engage in co-degradation of polysaccharides, cross-feeding, or sequential synthesis of compounds such as vitamin B<sub>12</sub>. Researchers can use GOMC to generate specialized datasets focused on key biosynthetic pathways, such as algal growth regulators like indole-3-acetic acid and inhibitory substances like tetrabromo biphenyldiol. These datasets are essential for deepening our understanding of algae-bacteria interactions in marine ecosystems. Additionally, the platform supports the development of prophage datasets and gene subsets related to quorum sensing and vesicle synthesis, providing deeper insights into microbial communication and co-evolution.

Beyond microbial interactions, GOMC offers a unique perspective on the roles of marine microbes in driving elemental cycles and ensuring the stability of marine ecosystems. Microbiomics has facilitated the identification of novel pathways for methane generation, nitrogen cycling, and carbon fixation, suggesting previously unknown processes driven by marine microbes. Researchers can employ GOMC to develop specialized datasets for microbial species engaged in crucial functional processes, including nitrogen fixation, methane production, methane oxidation, and carbon fixation. By integrating these datasets with *in situ* environmental parameters, researchers can effectively identify new taxa and explore ecological niches that may express these essential functions. In addition, oceans are crucial in absorbing and sequestering atmospheric CO<sub>2</sub>, with marine microbes playing a vital role in these

processes. As vast carbon reservoirs, oceans position marine microbes at the forefront of global climate regulation.<sup>5</sup> The microbial carbon pump (MCP) is a key mechanism that transforms labile dissolved organic carbon into recalcitrant forms sequestered in the ocean for thousands of years. Despite its ecological significance, the underlying mechanisms governing the MCP remain poorly understood, partly due to the lack of comprehensive microbial metabolic functional gene sets, metabolome databases, and environmental organic carbon molecular libraries, as well as their integration. GOMC offers a unique resource for exploring the molecular and genetic pathways underlying the MCP. Integrating the GOMC dataset, which encompasses detailed genetic signatures and functional traits of marine microbes, with high-resolution organic carbon molecular fingerprinting and advanced artificial intelligence, may help elucidate the complex networks between microbial genomes and chemical molecules. This approach sheds light on the critical role of marine microbes in modulating long-term carbon sequestration pathways. These resulting discoveries will enhance our understanding of the ocean's future carbon sequestration capacity and guide strategies to optimize this natural process, ultimately supporting global climate change mitigation efforts.

In conclusion, the GOMC constitutes a substantial step forward in our understanding of marine microbial diversity and its far-reaching implications. By integrating comprehensive genomic data with functional insights, this study opens new avenues for exploring the ecological and biotechnological potential of marine microbes. As research progresses, the critical role of marine microbes in addressing global challenges, such as antimicrobial resistance, plastic pollution and climate change, will likely become increasingly apparent. Future studies should leverage the GOMC findings to further elucidate the intricate interactions within microbial communities and between them and their environment, ultimately further enhancing our capacity to tap the broader application value of marine microbes.

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## FUNDING AND ACKNOWLEDGMENTS

This work was supported by the National Key Research and Development Program of China (2020YFA0607603, 2020YFA0608304), the projects of the Natural Science Foundation of China (No. 42276105, 42476115), the Youth Innovation Promotion Association of the CAS (2023220), and the Ocean Negative Carbon Emissions (ONCE) program. The funders had no role in study design, data collection and analysis, decision to publish or preparation of the manuscript.

## AUTHOR CONTRIBUTIONS

Yongyu Zhang conceived the original idea and provided critical revisions. Zenghu Zhang wrote the manuscript and designed the figures. Nianzhi Jiao and Yongyu Zhang reviewed and revised the manuscript.

## DECLARATION OF INTERESTS

The authors declare no competing interests.