

Editorial

Diversity and Dynamics of Microbial Communities in Marine Ecosystems

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The ecological and scientific significance of microbial communities in marine ecosystems is underscored by their diverse and dynamic nature. In marine ecosystems, microbes play a pivotal role, actively contributing to a range of biogeochemical cycles, nutrient cycling, and the overall functioning of the ecosystem. Marine ecosystems boast an astounding array of diversity, a richness mirrored within the intricate microbial realm. These ecosystems host a myriad of microorganisms, encompassing bacteria, archaea, viruses, fungi, and protists [1]. Each group plays distinct roles vital to the ecosystem's balance.

Spanning the water column, from the surface ocean to the deep sea and sediments, microbial communities adapt to diverse physical and chemical conditions, shaping their composition and diversity [2]. Microorganisms play a vital role in the cycling of nutrients within marine ecosystems [3]. Their functions include decomposing organic matter, nitrogen fixation, carbon conversion, and nutrient recycling, all contributing to the overall vitality and productivity of the ecosystem [4]. Over time and space, microbial communities undergo dynamic shifts influenced by factors like temperature, nutrient availability, and predation. Seasonal variations and short-term perturbations exert significant impacts on these communities [5].

The revolutionary strides in DNA sequencing and metagenomics have transformed the study of marine microbial communities. Researchers can now unravel the identities and functions of microbes without the need for cultivation, unveiling deeper insights into these complex ecosystems [6–8]. Climate change and ocean warming further add layers of complexity, affecting the composition and distribution of microbial communities. These changes ripple through the entire ecosystem, influencing fisheries and nutrient cycling [9,10]. Remarkably, extreme environments like hydrothermal vents and deep-sea trenches host specialized microbial communities adapted to harsh conditions, offering profound insights into the boundaries of life on Earth [11,12]. A comprehensive understanding of microbial community diversity and dynamics is imperative for effective conservation and sustainable management of marine ecosystems. Conserving microbial diversity is integral for sustaining the health and resilience of aquatic ecosystems.

This Editorial pertains to the Special Issue “Diversity and Dynamics of Microbial Communities in Marine Ecosystems”, emphasizing novel opportunities and challenges in marine microbial communities. The Special Issue specifically addresses the diversity, dynamics, and potential carbon contributions of marine microbes and the interactions between microbial communities, sewage, and aquatic organisms.

Employing Illumina 16S rRNA sequencing, Zhou et al. (2022) study explored the bacterial community composition within the ecosystem of sea cucumber *Apostichopus japonicus* culture ponds and its association with overall community structures. The key findings reveal Proteobacteria as the dominant bacterial community across various media, accounting for a substantial portion of the bacterial community structure, followed by Bacteroidetes and Verrucomicrobia. Striking similarities in bacterial community structures were observed across



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multiple media in different regions, providing evidence for deterministic natural evolution. The specific functions of the multiple media within the ecosystem serve as the primary driving force behind the formation of other bacterial communities. This work demonstrates that bacterial communities emerge from natural evolution within the ecosystem, driven by adaptation to the prevailing environment. The principal conclusions highlight the dominant bacterial community as a significant contributor to the overall bacterial community structure, reflecting the ecosystem's overall function. Simultaneously, the pivotal ecological processes driven by bacteria lead to the formation of specific bacterial communities within multiple media in the ecosystem. Environmental functions among media were found to correlate with their bacterial community structure, with specific bacterial communities exhibiting differential expressions across regions within media.

Wang et al. (2022) delved into the dynamics of abundance and community structure of Labyrinthulomycetes within the surface waters of plume, offshore, and pelagic habitats in the South China Sea. The highest and lowest abundance of Labyrinthulomycetes were observed in the waters of plume and pelagic habitats, respectively. The findings revealed that the genus *Aplanochytrium* dominated Labyrinthulomycete communities in offshore and pelagic habitats, while *Aurantiochytrium* and *Ulkenia* were prevalent in the plume. The physiological and metabolic characteristics of these genera indicated that the ecological functions of Labyrinthulomycetes also exhibited significant variation along this salinity gradient. This study comprehensively characterized the abundance, diversity, and community structure of Labyrinthulomycete protists, an essential group of unicellular heterotrophic eukaryotes, along a plume-to-pelagic gradient in the South China Sea. The salinity gradient was found to influence diversity levels and exert control over their community structure. Contrary to expectations, the diversity in the plume was substantially lower compared to offshore and pelagic habitats. Further analysis of the composition of dominant amplicon sequence variants in each habitat revealed distinct patterns in the dominant genera composition between plume and oceanic habitats. These findings shed new light on their potential functional shifts along the salinity gradient.

The study by He et al. (2022) sought to evaluate the variability in phytoplankton structure and its relationship with environmental drivers in the Qinhuangdao coastal area, China. The study area experiences a typical continental monsoon climate, and the sampling site was located in Jinmeng Bay, Qinhuangdao, Hebei Province, influenced by the Qiandaoxi River. Daily inshore water samples were collected from 10–22 July 2021, to analyze the phytoplankton community and environmental factors. The study revealed that the phytoplankton community in the Qinhuangdao coastal area underwent significant shifts during summer, with diatoms dominating in the early stage, followed by dinoflagellates and then cyanobacteria. Changes in environmental factors, including temperature, salinity, nutrients, and dissolved oxygen, were identified as the driving forces behind these shifts in the phytoplankton community. Additionally, the study found that diatoms and dinoflagellates were the primary causes of phytoplankton blooms in the Qinhuangdao coastal area, with the bloom period influenced by environmental factors such as temperature, nutrients, and dissolved oxygen. The study suggests that management strategies aimed at controlling algae blooms in coastal waters should consider the impact of these environmental factors. Overall, this study provides valuable insights into the changes in the phytoplankton community and the factors that drive these changes in the Qinhuangdao coastal area. The findings of this study contribute to our understanding of the impact of environmental changes on marine ecosystems and have implications for the management and conservation of marine resources in the Qinhuangdao coastal area.

The study by Ming et al. (2022) delves into the ramifications of a typhoon on both the microbial community structure and water quality of a marine bathing beach. Pre- and post-typhoon seawater and beach sand samples were systematically collected and subjected to analysis, focusing on fecal indicator bacteria (FIB) and specific taxa associated with fecal pollution. The investigation unveiled distinctive impacts of the typhoon on water quality, particularly concerning FIB of enterococci and fecal taxa. Notably, cultivable

enterococci exhibited an increase in seawater but experienced a significant reduction in dry sand post-typhoon. Interestingly, the abundance of total bacteria and cultivable enterococci contributed minimally to the variance in the bacterial community structure observed in beach sand. Furthermore, the study identified specific taxa of fecal pollution intricately linked with the typhoon event. This study underscores the critical importance of continuous water quality monitoring in coastal regions, particularly in the aftermath of natural disasters such as typhoons. The insights gleaned from this investigation provide valuable perspectives into the nuanced impact of hurricanes on marine ecosystems. Beyond its scientific contributions, the findings hold practical implications for informing disaster response strategies and shaping effective management approaches for coastal areas. Ultimately, this research contributes to the broader goal of promoting the sustainable development of marine resources in the face of environmental challenges.

The study by Su et al. (2022) aimed to investigate the prevalence and spatial distribution of antibiotic-resistant *Escherichia coli* (*E. coli*) in a popular urban coastal beach in China, aiming to assess potential risks linked to municipal sewage discharge. The researchers systematically collected water and sand samples from various locations on the beach and subjected them to analysis for the presence of *E. coli* and antibiotic-resistance genes. The study revealed a higher frequency of *E. coli* isolation in seawater than sand, with a noteworthy proportion of isolated *E. coli* strains exhibiting resistance to multiple antibiotics. Several antibiotic resistance genes, including *dfrA12*, *orfF*, *aadA2*, *linF*, and others, were identified within the *E. coli* strains. The findings strongly suggest that municipal sewage discharge may contribute to the dissemination of antibiotic-resistant bacteria in coastal areas. Consequently, the study advocates for more effective measures to mitigate the associated risks of recreational water use. Notably, the outcomes of this research hold significant implications for public health and environmental management, emphasizing the imperative for further investigation into the mechanisms governing the spread of bacterial resistance in coastal environments.

Liu et al. (2022) explored the dynamics of microbial communities and the carbon sink effect associated with upwelling in coastal ecosystems. Seawater samples were systematically collected from six stations along the east coast of Hainan Island in the South China Sea in June 2020. Three nearshore stations experienced coastal upwelling, while three offshore stations did not. High-throughput sequencing was employed to analyze the samples, revealing distinctive microbial community structures and interactions. The results underscored significant differences in microbial community structure and diversity between upwelling and non-upwelling stations. Notably, the study identified a close interaction between Cyanobacteria and microbial eukaryotes, suggesting a potential enhancement of carbon sequestration in coastal ecosystems. The findings advocate that upwelling plays a role in contributing to carbon sinks through the interactions of these microorganisms. This research holds notable implications for climate change mitigation strategies, emphasizing the pivotal role of coastal ecosystems in carbon sequestration. The study provides valuable insights by shedding light on the potential contribution of upwelling to carbon sequestration. Furthermore, it underscores the importance of comprehending microbial community dynamics in coastal ecosystems. Overall, this investigation contributes significantly to our understanding of the intricate processes governing carbon dynamics in these vital ecosystems.

The study by Song et al. (2022) revealed the diversity and community composition of Labyrinthulomycetes in the coastal zone of Hainan Island. The results showed that the abundance of these protists varied by location and depth, with the highest levels found in the middle layer offshore and the lowest in the bottom layer offshore. The middle layer had a higher abundance both inshore and offshore than the surface and bottom layers. Furthermore, the abundance significantly differed between the offshore surface and bottom layers. The genus *Aplanochytrium* dominated the community of Labyrinthulomycetes, and four different ecotypes were identified. Additionally, the genus *Aurantiochytrium* had different cooperative and competitive strategies with bac-

teria in different habitats. This study sheds light on the abundance and community structure of Labyrinthulomycetes in the coastal zone of Hainan Island, explores their potential interactions with bacterial populations, and raises questions about the possible differentiation of Labyrinthulomycete ecotypes.

Conflicts of Interest: The authors declare no conflict of interest.

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