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Editorial

The Impact of Changes in the Marine Environment on Marine Organisms

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The ocean is a critical element of human well-being and livelihood, providing a home for a diverse range of creatures that inhabit both coastal and pelagic ecosystems, from microbes to marine mammals. However, in recent decades, numerous significant changes have been observed in our oceans, including pollution, rising seawater temperatures, acidification, altered nutrient loads, overfishing, loss of coastal habitats, and changes in ocean circulation. These changes have had profound impacts on marine primary productivity, biodiversity, ecological habits, and physiological functions of marine organisms, affecting multiple trophic levels and resulting in the potential collapse of the marine ecosystem.

To further explore the impact of these changes, this Special Issue, entitled "The Impact of Changes in the Marine Environment on Marine Organisms," features seven contributions from the period 2022–2023. The primary aim of this Special Issue is to gather studies on the impact of environmental changes on marine organisms, caused by either natural or anthropogenic effects.

Kenting National Park in southern Taiwan is a popular destination for both domestic and international tourists seeking a retreat. However, the increasing numbers of visitors have the potential to overburden the coastal ecosystems. To gain a better understanding of human impacts on the area, Chen et al. (2022) [1] initiated a long-term ecological research program in 2001 to monitor water quality at 14 coral reef-abutting sites throughout the park. Analysis of the data collected over the 20-year survey period indicated that during the summer rainy season, there was an increase in nutrient levels, coupled with a decrease in salinity due to freshwater inputs from both land and rainfall. This phenomenon had the most significant impact on the coral reef ecosystem in Kenting. Cluster analysis further identified that the nutrient influx was mainly attributed to the discharge outlets from the dense concentration of villages and hotels upstream. As a result, more efforts are necessary to control tourist numbers, treat wastewater discharge, and strengthen land protection facilities to mitigate the impact of human activities on the local ecosystem.

Seagrass beds play a crucial role as carbon sinks, and increasing their quantity and quality may help to mitigate global climate change. To achieve this, it is necessary to improve our understanding of seagrass bed metabolism and document how these ecosystems are affected by climate change-associated factors, such as ocean acidification and warming. Liu et al. (2022) [2] investigated the response of the tropical seagrass species *Thalassia hemprichii* to elevated CO_2 levels using a mesocosm-based approach to simulate ocean acidification and increasing temperature. After 12 weeks of exposure, high CO_2 levels led to increased underground biomass and root C:N ratios, but decreased root nitrogen content. On the other hand, rising temperatures increased photosystem II yield, productivity, leaf

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growth rate, decomposition rate, and carbon sequestration but reduced shoot density and carbon content in the leaves. These findings suggest that warming alone does not enhance the short-term carbon sink capacity of this seagrass species. However, under high CO_2 and the highest temperature used in the study, the seagrass exhibited its highest productivity, photosystem II yield, leaf growth rate, and carbon sequestration. Overall, it seems that high CO_2 levels counteract the negative effects of high temperatures on this seagrass species.

As the decline of coral reefs continues globally, there is a pressing need to understand how corals respond to local environmental stressors. Coral-associated bacterial communities have been suggested to have a rapid response to environmental pollutants. Hussien et al. (2022) [3] investigated the variation in bacterial communities present in the mucus of two coral species, *Pocillopora damicornis* and *Stylophora pistillata*, as well as the coral-surrounding seawater, from three areas exposed to contamination along the Jordanian coast of the Gulf of Aqaba (Red Sea). Additionally, they explored the antibacterial activity of these bacteria. The researchers collected corals from three contaminated zones along the coast and quantified and identified the bacteria present using conventional morphological and biochemical tests, as well as 16S rRNA gene sequencing. The average number of bacteria varied significantly among the coral mucus in the sampling zones and between the coral mucus and the surrounding seawater. The bacterial community associated with the mucus of *P. damicornis* was dominated by members of the classes Gammaproteobacteria, Cytophagia, and Actinomycetia, while the mucus of *S. pistillata* exhibited higher bacterial diversity, with the dominance of the bacterial classes Gammaproteobacteria, Actinomycetia, Alphaproteobacteria, and Bacilli. The effects of local anthropogenic impacts on coral mucus bacterial communities were reflected in the increased abundance of bacterial species related to coral diseases. Furthermore, the results demonstrated the presence of bacterial isolates with antibacterial activity that may act as a first line of defense to protect and maintain the coral host against pathogens. The dynamics of coral-associated microbial communities highlight the importance of comprehensive studies that focus on microbial interactions throughout the coral reef ecosystem.

The purpose of environmental impact assessments is to prevent and reduce negative effects on the environment caused by economic development activities. These assessments are critical to providing decision-makers with sufficient information to evaluate environmental impacts prior to initiating new projects. However, there have been few studies examining the verification of environmental impact assessments, despite their importance in public policy. Chou et al. (2022) [4] utilized principal component analysis (PCA) to identify the primary sources of influence on the coastal waters surrounding a major tourist attraction, an aquarium, in southern Taiwan. They then constructed a structural equation model (SEM) to determine the direct and indirect impacts of abiotic factors on phytoplankton and zooplankton density and diversity. The results revealed that river input, suspended matter, and seasonal changes were the primary factors affecting the coastal area. The SEM indicated that phytoplankton density and diversity were directly affected by seasonal changes and suspended matter, but only indirectly by river input due to its effect on suspended matter. Conversely, the SEM indicated that zooplankton density and diversity were directly affected by seasonal changes, but indirectly by both river input and suspended matter due to their effects on phytoplankton density and diversity. Despite Q2 being the season with the highest number of visitors to the aquarium, none of the abiotic or biotic parameters exhibited significant differences, indicating that variations in those parameters in the adjacent coastal waters were not related to visitors. They recommended the use of PCA and SEM in future studies to validate environmental impact assessments in different contexts.

The marine food chain is affected by the bioaccumulation of persistent organic pollutants in zooplankton. The Gaoping waters in southwestern Taiwan are exposed to large quantities of polybrominated diphenyl ethers (PBDEs) due to various anthropogenic activities. However, information on the levels of these contaminants in zooplankton in this area is limited. To address this gap, Hsieh et al. (2022) [5] analyzed PBDE concentrations in

36 zooplankton samples collected from the Gaoping waters, and they found a high variation in the total PBDE concentrations in zooplankton, ranging from not detected to 1415 ng g^{-1} dry weight. The highest PBDE levels were found near the entrance of Kaohsiung Harbor (KH), with significantly higher levels observed in the KH transect compared to the Gaoping River estuary (GR) and Fengshan Township (FS) transects. This indicated that PBDE inputs originate from ocean sewage outfalls. The predominant PBDE congeners in the zooplankton were BDE-15 (43%) and BDE-209 (16%). The results suggest that anthropogenic activities may significantly contribute to high PBDE concentrations that can pose a risk to higher trophic levels of marine organisms since the Gaoping waters serve as essential nurseries and spawning grounds for invertebrates and fishes in the area.

Cyanobacteria have a diverse range of ecological functions in coral reefs, including primary carbon and nitrogen fixation, calcification, nutrient cycling, and oxygen production. However, they can also contribute to coral reef degradation through skeletal biocorrosion and polymicrobial diseases. Kang et al. (2022) [6] investigated the diversity of cyanobacteria in sediment, water, and coral tissues in relation to the health status of coral reefs at Weizhou Island in the South China Sea. The coral health status was categorized as slightly, moderately, or severely damaged. Both microscopy and 16S rRNA gene metabarcoding were used to identify cyanobacterial genera. The metabarcoding approach was found to be more efficient than universal prokaryotic 16S rRNA gene primers in identifying cyanobacterial genera. Culture-based methods were also found to be useful in identifying cyanobacterial strains that could not be detected using molecular methods. There was a clear difference in the composition of cyanobacterial assemblages between healthy and degraded reefs, with degraded reefs exhibiting approximately a 1.25-fold increase in species compared to healthy habitats. Potentially toxic cyanobacteria, such as *Nostoc* and *Lyngbya*, were found to be spreading in the degraded reef, suggesting a possible link to reef degradation. This study highlights the importance of using metabarcoding as an effective tool for revealing cyanobacterial diversity patterns, which can provide critical information for the management of coral reef ecosystems.

Hanafi et al. (2023) [7] reviewed the *Johnius* genus in Taiwanese waters and discovered a new species, *Johnius taiwanesis*. A comprehensive approach was used that involved field samples, museum specimens, and a review of the scientific literature. Based on gill raker length, tip of upper and lower jaws to mouth hinge length, and second spine length of the anal fin, seven valid *Johnius* species were identified and distinguished. The phylogenetic tree constructed using cytochrome oxidase subunit I (COI) showed high interspecific genetic diversity, forming a monophyletic group. The *Johnius* species in Taiwan are mainly found in the latitude range from 22.4° N to 24.8° N, with *J. taiwanensis*, *J. distinctus*, and *J. belangerii* being the most caught throughout the year. *Johnius amblycephalus* and *J. borneensis* were only caught in the summer, while *J. trewavasae* was rarely caught. In conclusion, a dichotomous key for the *Johnius* genus in Taiwanese waters is provided.

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

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