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Editorial: Microbial ecology of the Arabian/Persian Gulf

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Editorial on the Research Topic
Microbial ecology of the Arabian/Persian Gulf

The Arabian/Persian Gulf is a naturally stressed, semi-enclosed sea characterized by one of the highest reported surface temperatures of any water body on the planet (Riegl and Purkis, 2012). The relatively high-latitude location of this subtropical sea (Figure 1) creates significant seasonal temperature fluctuations ranging from 16°C to 35°C due to seasonal differences of intense solar radiation and the cold winds from the nearby highlands (Chao et al., 1992; Alsayed et al., 2023). The high evaporation rates combined with low annual precipitation increase salinity levels in most Gulf water from an average oceanic value of 35 psu to > 40 psu (Chao et al., 1992). The large fluctuations in temperature and high salinity create an extreme environment that makes the Arabian/Persian Gulf relatively selective for biota that can flourish and survive. Furthermore, extensive urbanization of the Gulf coasts has resulted in permanent coastline alteration and marine habitat loss, which exacerbate stressors on the indigenous species of the Gulf (Sheppard et al., 2010). Large areas of the Gulf coasts are frequently exposed to heavy pollution from crude oil, microplastics, endocrine-disrupting chemicals, and/or heavy metals (Sheppard et al., 2010; Abayomi et al., 2017; Mirzaei et al., 2020). Despite the above mentioned factors, changes in the Gulf species composition along spatial gradients are significant, suggesting adaptation to local disturbances. Recent research has shown this to be true for higher organisms (D'angelo et al., 2015; Howells et al., 2016; Smith et al., 2022; Torquato et al., 2022); however, little is known about how microorganisms respond to these significant and abrupt environmental changes. Marine microbial ecology research in the region began almost 50 years ago following the flourishing of the oil industry and the modernization of the countries bordering the Gulf banks.

Despite the research already published on the Gulf environment, there are large gaps in knowledge on microbial diversity, activity, and dynamics. For instance, little is known about the ecophysiology of marine bacteria, viruses, archaea, algae, and fungi, as well as their adaptability to harsh Gulf conditions. Furthermore, information about the functional roles of various marine microbes in the food chain and recycling of nutrients, minerals,

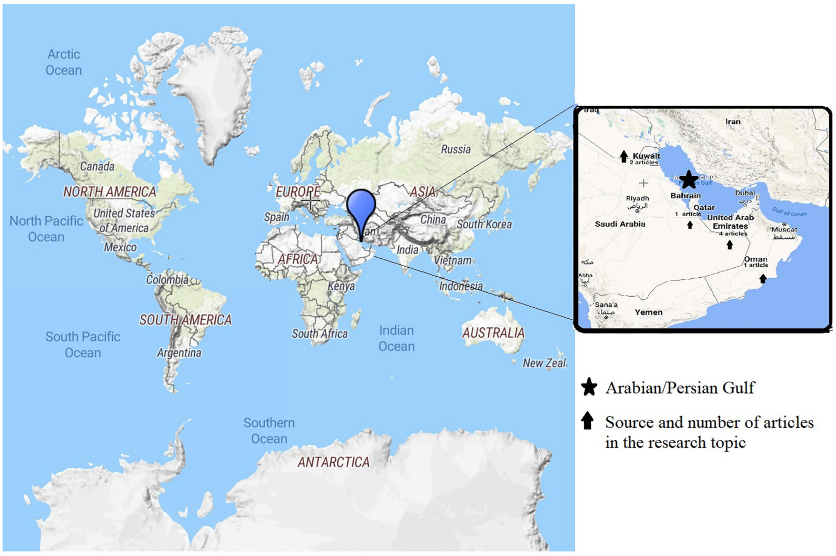

FIGURE 1
Arabian/Persian Gulf map generated using Scribblemap.com. Location of the Gulf on the world map; inset: the arrows show the source and number of articles published in the Research Topic.

pollutants, and their contribution to the biogeochemistry of the Gulf, is rather limited. Most of the information available so far was generated for intertidal areas (Abed et al., 2007; Al-Sarawi et al., 2008), but very little from the pelagic and benthic regions. Therefore, more research at the microbial level involving holistic multidisciplinary studies is required to reveal the unique diversity, adaptability, and spatial variation. These studies should involve the Gulf as a whole, rather than fragmented studies that focus on specific areas of the Gulf. Only holistic studies can provide a comprehensive picture of how variations in the Gulf environment affect marine microbes. The significance of this work is that it can be extended to fully understand how the Gulf system influences adjacent water bodies such as the Gulf of Oman, the Arabian Sea, and the Indian Ocean. Some of the holistic investigations include looking into benthic and planktonic microbial community structure and variance across the Gulf, similar to the studies done across the Atlantic (Bracher et al., 2020).

Little research has also been conducted to exploit the Gulf extremophilic microbes for biotechnology and industry, where studies on the biotechnological potential of the Gulf microbiome are sporadic and biased toward the bioremediation of hydrocarbon pollutants (Radwan et al., 1999; Radwan et al., 2010). Most available microbiological data was generated by conventional approaches such as culturing techniques (Radwan et al., 1999; Mahmoud and Kalendar, 2016); whereas data generated using more robust approaches like omics is scarce (Abed et al., 2020; Habibi et al., 2023). Finally, no research has been conducted to leverage the evolutionary adaptation of microbes in the Gulf to higher salinity and temperature and lower pH and their relevance to the wider ocean in light of climate change.

Because of the growing international interest in the Arabian/Persian Gulf's environment and biodiversity, the Research Topic attempted to better understand its microbial ecology. The current Gulf ecosystem is predicted to dominate the world's oceans by the end of the century, sparking this interest. The Research Topic compiles interdisciplinary fundamental and applied research on several aspects of microbial ecology. It includes one review and seven research articles.

The review article by Al-Thani and Yasseen discussed the microbial ecology in the main habitats of the State of Qatar. The microorganisms found within Qatari habitats have shown potential in bioremediation, phytoremediation, and various aspects of human life, including health, agriculture, and wildlife. The review addressed the essential principles for successful ecological restoration and future perspectives on using biological approaches to solve many problems.

Two articles on microbial community structural and functional diversity were published. Ismail and Almutairi investigated the bacterioplankton community profile of Kuwaiti surface water. Their results provided in-depth insights into the temporal and spatial variations of bacterioplankton dynamics in Kuwait waters using next-generation sequencing methods. Their findings highlighted the strong seasonal influence of natural and anthropogenic stressors on the bacterioplankton composition and predicted functional capabilities. For the first time, the geographical, temporal, and functional potential of bacterioplankton communities in the Kuwaiti Sea was assessed. The data revealed a core bacterioplankton population as well as significant seasonal changes in bacterioplankton community organization. Temperature, nitrogen levels, and total petroleum hydrocarbon have all been identified as important environmental factors affecting the bacterial community structure. The study findings highlight the importance of niche specialization and resource partitioning in the surrounding habitat in supporting the existence and abundance of different phylotypes in local waters.

On the other hand, Abbas and Mahmoud identified sponge-associated bacteria from the coast of Kuwait and studied their potential biotechnological applications. Using amplicon next-generation sequencing, the study expanded our understanding of sponges at the Arabian Gulf's northwest coast and their associated microbiomes. This technique identified more than 25 bacterial phyla linked to new sponge species. In addition, 315 bacterial isolates associated with *Haliclona* sp. 1Kl were identified using culturing techniques, and selected bacterial strains from the genera *Vibrio*, *Bacillus*, *Pseudovibrio*, and *Shewanella* caused the formation of various forms of calcium carbonate crystals. The study was the first to demonstrate the isolation of sponge-associated calcifying bacteria and to harvest calcium carbonate crystals.

In the research area of marine microbes' role in biotechnology, three articles reported the significance of endophytic and rhizospheric actinobacterial isolates promoting the growth of mangroves of the species *Avicennia marina* across the United Arab Emirates shores (UAE). The three articles, i.e., two by El-Tarabily et al. and one by Alkaabi et al., were the first to report culturable halotolerant, endophytes and rhizosphere-competent plant growth-promoting (PGP) actinobacteria inhabiting salty and arid ecosystems applied individually or in combination to promote mangrove growth under harsh conditions and inside greenhouses.

El-Tarabily et al. presented the first study on the use of polyamines-producing endophytic actinobacterial isolate *Streptomyces mutabilis* UAE1 to boost mangrove growth in a greenhouse setting. The strategy can be applied in the future to natural competitive nursery and/or field conditions and can be utilized to propagate marine plant species (e.g., mangrove) for reforestation in the Arabian Gulf coastal areas. In El-Tarabily et al. a list of actinobacterial species unique to mangrove habitats was provided and emphasized as rhizosphere-competent PGP species recovered from saline sediments in the UAE. Sowing mangrove propagules in sediments treated with four PGP Actinobacteria (PGPAs) is expected to produce strong, well-developed mangrove seedlings for permanent out planting in nurseries. The new work has the potential to develop marine agriculture technologies by applying seawater irrigation processes. As a result, this provides a comprehensive assessment of locally produced mangroves, as well as knowledge for future research that may aid conservation and management in hostile environments such as the Arabian Gulf.

On the other hand, Alkaabi et al. reported the outstanding influence of *Streptomyces tubercidicus* UAE1 [St] (an endophytic PGPA strain) and *Ascophyllum nodosum* (a commercial seaweed extract [SWE]-based biostimulant) on mangrove growth. This study showed that mangrove plants treated with St and SWE had higher levels of nutrients and endogenous plant growth regulators (PGRs) in plant tissues, resulting in enhanced growth of maritime plants (e.g., gray mangrove) in greenhouse and open-field nursery environments. As a result, this new combination can be commercially applied.

In the biofouling area, Muthukrishnan et al. investigated the monthly succession of biofouling communities and corresponding inter-taxa associations in the northwest (Kuwait coast) and southwest (Oman coast) of the Gulf. Spatio-temporal effects on the abundance and composition of micro- and macro-fouling communities were detected based on total biomass, bacterial and phototroph abundances, macrofouling coverage, and 16S rRNA amplicon sequencing. Biofouling communities developed from different locations had different succession patterns with strong co-occurrence between species indicative of unique ecological niches. The study provided insights into the underlying dynamics of biofouling processes in the continuously changing environment of the Gulf.

The climate change effect on Gulf coral reefs was addressed by Verneil et al. who investigated the summer oxygen dynamics and the recurrent hypoxia events in the Gulf. The study suggested that hypoxic phenomena represent a significant but underappreciated threat to the future of global coral reefs in the region. The data provided quantitative estimates of the oxygen fluxes produced by photosynthesis which is driven by macro and microalgae within the water column and coral framework, by respiration processes in the benthos, and from the atmosphere. The study concluded that biological oxygen production and consumption is a major player in oxygen flux, and any human induce-eutrophication to the Gulf marine environment can lead to deeper and longer hypoxia and anoxia events.

Many pressing issues in the field of Microbial Ecology can be studied in the Arabian/Persian Gulf. As a natural mesocosm, seasonal temperature extremes are a good way of studying the impact of climate change on marine life. We consider this Research Topic a significant addition to an ongoing effort to characterize and predict the contribution of microbes to the Gulf biogeochemistry. There is still work to be done to map out the microbial diversity across the Gulf, particularly during the hottest months. Studies of this type can promote our understanding of how global warming will affect microbial diversity in the future. More work is also needed to understand the role of phytoplankton, bacteria, archaea, viruses, and microeukaryotes in pelagic and benthic Gulf environments, the contribution of the microbial loop to carbon cycling, adaptation of various microbes to the extreme environment in the Gulf and how this knowledge can collectively inform our understanding of future changes in the oceans.

Author contributions

All authors listed have made a substantial, direct, and intellectual contribution to the work and approved it for publication.

Conflict of interest

The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

Publisher's note

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