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Editorial: Interaction between marine invertebrates and symbiotic microbes in a changing environment: Community structure and ecological functions

Jie Li[1]*, Yang Zhang[1], Jin Sun[2], Fabiano Thompson[3] and Yanying Zhang[4]

[1]CAS Key Laboratory of Tropical Marine Bio-resources and Ecology, South China Sea Institute of Oceanology, Chinese Academy of Sciences, Guangzhou, China, [2]Institute of Evolution & Marine Biodiversity, Ocean University of China, Qingdao, China, [3]Institute of Biology and COPPE, Federal University of Rio de Janeiro, Rio de Janeiro, Brazil, [4]School of Ocean, Yantai University, Yantai, China

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M Pilar Francino,
Fundación para el Fomento de la Investigación Sanitaria y Biomédica de la Comunitat Valenciana (FISABIO), Spain

*CORRESPONDENCE
Jie Li
✉ lijietaren@scsio.ac.cn

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Editorial on the Research Topic
Interaction between marine invertebrates and symbiotic microbes in a changing environment: Community structure and ecological functions

Symbiotic associations between marine invertebrates and microbes have been found in various ecosystems ranging from coral reefs (Figure 1) in shallow coastal waters to hydrothermal vents and cold seeps in the deep sea. Marine organisms surviving in diverse environments depend to a large extent or completely on symbiotic microbes (Dubilier et al., 2008). Symbiotic relationships between microorganisms and their marine invertebrate hosts are continuously formed and co-evolved with a long-term history that impacts morphology, behavior, development, metabolism, and even evolution (McFall-Ngai et al., 2013; Gould et al., 2018). In addition to organismal adaptation and evolution, symbioses between marine invertebrates and microbes underpin the health of marine ecosystems, especially the most threatened ecosystems (Wilkins et al., 2019). In the face of global climate change and the Anthropocene, it is essential to understand the interaction between marine invertebrates and symbiotic microbes in a changing environment to predict whether symbiosis will allow marine life to cope with future threats to the biosphere (Li et al., 2022). Given the significance of symbiosis between marine invertebrates and microbes, this Research Topic aims to contribute to a better understanding of the community structure and function of marine invertebrate-associated microbes and the interaction between marine invertebrates and their symbiotic microbes in a changing environment.

Dynamic marine invertebrate-associated microbial communities have been largely observed in response to environmental disturbance as well as the physiological and developmental status of their hosts (Webster and Taylor, 2012; Apprill; van Oppen and

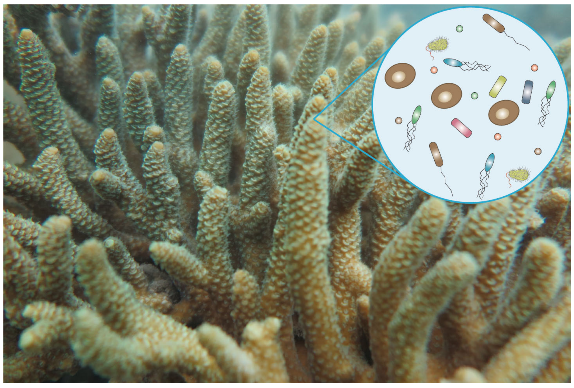

FIGURE 1
A typical case of symbioses between marine invertebrates and microbes: Coral and its associated microorganisms.

Blackall, 2019; Carrier and Bosch, 2022). The flexibility of symbioses between marine invertebrates and microbes has been considered to be crucial for host health and fitness (Reshef et al., 2006; Apprill, 2020). To explore how plastic coral-associated microbial communities are in response to environmental variation, Haydon et al. reciprocally transplanted the coral *Pocillopora acuta* between a mangrove lagoon and an adjacent reef crest-slope on the northern Great Barrier Reef and investigated the bacterial and Symbiodiniaceae communities associated with the transplanted coral specimens. The results demonstrated obvious changes in the bacterial communities. These shifts were distinct between the reef-to-mangrove and mangrove-to-reef transplanted corals. The Symbiodiniaceae communities remain highly stable. Scleractinian corals, whose food source mainly comes from the photosynthesis of algal symbionts, are principal coral reef-builders. Scientists recently found that sponges are the major reef epifauna in a newly recognized biogenic reef system, the Great Amazon Reef System, which stays under a plume layer (Moura et al., 2016; Francini-Filho et al.; de Menezes et al., 2022). Pinto et al. found that plume-associated dissolved and particulate organic carbon (originating from the Amazon forest) and the heterotrophic microbiota associated with sponges may support host survival in an environment with attenuated light availability.

Salinity is one of the important drivers of microbial distribution (Lozupone and Knight, 2007). To explore the effects of changes in salinity on host-protected microbiomes, Kivistik et al. investigated the bacterial communities within the gastrointestinal tract of *Ampullaceana balthica* in different salinities. The results showed a high mortality rate of *A. balthica* after a shift from freshwater to salinity 6, along with altered gastrointestinal bacterial communities. There was a substantial difference between the bacterial communities in aquaria and *in situ* at salinity 6. Kivistik et al. further suggested that the intestinal microbiome needs long-term adaptation to higher salinity. Microbiomes associated with aquatic animals have received increasing attention. Haditomo et al. found alterations in the gut bacterial composition of sea urchins *Mesocentrotus nudus* and *Strongylocentrotus intermedius* after rearing in an aquarium with circulating and running water. In addition, the results of the transplanting experiment further revealed that these gut microbiota were affected by diet rather than rearing environment and host species. Furthermore, Haditomo et al. proposed that the gut microbiome reduces nitrates to ammonium to promote sea urchin growth. Increasing evidence supports the importance of pioneer microbes in early life stages in host biology (Korpela and de Vos, 2018; Fallet et al., 2022). To understand the pioneer microbiota of sea cucumber, Yu et al. investigated the bacterial communities in the early life stages of *Apostichopus japonicus*. The results demonstrated significant changes in the microbiota in the late auricularia stage and possible first colonizers in the gut affiliated with *Rhodobacterales* and *Flavobacterales*. On the basis of the dynamic changes in the bacterial community alongside the developmental stages and feeding time, Yu et al. suggested that organogenesis and feeding are major drivers of variation in early life microbiota in sea cucumber.

Exploring the evolution of the physiological and genomic properties of microbes associated with marine invertebrates is helpful for understanding their roles in symbioses. Jiang et al. compared the genomes of type strains of Halioticoli clade species in Vibrionaceae with different lifestyles and found more carbohydrate metabolism-related genes in the genome of free-living *Vibrio ishigakensis* compared to host-associated lineages. Guo et al. demonstrated a more complex antagonistic network among coral-associated bacteria at 32°C than at 25°C and proposed that the trade-off between antagonism and resource exploitation shifted in the antagonistic interactions under varied environmental temperatures.

A phylosymbiotic signal, i.e., the degree of similarity between microbial communities reflecting the evolutionary history of their hosts, has been observed in many hosts and their symbiotic microbiomes (Lim and Bordenstein, 2020). On the basis of the differential bacterial communities associated with two *Aurelia* polyp species, Li et al. proposed a correlation between the symbiotic microbial community and their host genetic background though they did not refer to the concept of phylosymbiosis. Co-evolutionary patterns may be affected by both horizontally and vertically transmitted microbes. Wale et al. summarized the vertical and horizontal transmission of the microbiome in crab larval stages and speculated that symbiotic microbiomes facilitate the transition of crabs from living in water to land. The authors further proposed that the integration of the early life history stages of crabs and their microbiomes is a crucial paradigm for the evolution of terrestrialization in crabs.

This Research Topic provides a glimpse of host-microbe interactions and possible examples of co-evolution that demonstrate the immense potential of the global marine biodiversity for discoveries. In addition, studies have shown the dynamic microbiomes associated with the developmental stages of marine invertebrates, e.g., in the case of the sea cucumber *A. japonicus* and its associated microbiome. Moreover, the impacts of altered environments because of both local and global changes are possibly altering microbial communities associated with marine invertebrates and the potential functions of microbial symbionts. We advocate that the phylosymbiosis and co-evolution of marine invertebrate hosts and their symbiotic microbiome are worth further investigation. Currently, we know much about the community compositions of microbial symbionts under various environmental conditions. However, we know far less regarding the mechanistic connections between the microbiome and its host at micro-spatial and short-term time scales, as well as *in situ* microbial activities and interactions within holobionts. Approaches that combine imaging technologies with metabolic activity detection and single-cell and (meta)genomic/transcriptomic sequencing will facilitate addressing these questions in the not-too-distant future.

Author contributions

JL drafted the editorial. All authors reviewed and edited the editorial. All authors contributed to the article and approved the submitted version.

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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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