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Editorial: Deep-sea chemosynthetic ecosystems: Living in extreme environments

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Editorial on the Research Topic

Deep-sea chemosynthetic ecosystems: Living in extreme environments

Occurring in different geological settings, cold seep and hydrothermal vent systems are energy hotspots on the deep-sea seafloor, supporting the distribution and an abundance of chemosynthetic microorganisms and megafauna. With the advance in deep-sea exploration technology, we are now recognizing the greater habitat complexity and biodiversity of chemosynthetic ecosystems. We also recognize that the contribution of chemosynthetic production on the global carbon cycle may have been underestimated. Deep-sea chemosynthetic ecosystems in seeps and vents therefore are ideal system to study the interactions among the geosphere, hydrosphere and biosphere enabling a continued support of in chemosynthetic ecosystems. In Research Topic “*Deep-sea chemosynthetic ecosystems: living in the extreme environments*”, we have presented updated information on the chemosynthetic ecosystems from cold seeps of South China Sea, and its role in the global biosphere with the help of state-of-the-art geochemical and molecular technologies.

Among the unsolved questions on deep-sea chemosynthetic ecosystems, how the systems have originated, evolved and supported the biota communities is fundamental to further our knowledge on the physical and chemical principles that sustain deep-sea chemosynthetic ecosystems and their thriving biological communities. A series of studies have been conducted on the biogeochemistry of deep-sea chemosynthetic ecosystems to answer these questions. It is now widely acknowledged that the high concentrations of reduced chemicals such as methane, sulfur, hydrogen, ammonia and even reduced metals could sustain distinct chemosynthetic microbiomes such as methanotrophs and thiotrophs. Meanwhile, heterotrophic communities such as hydrocarbon degraders are also divergent and

prosperous in some cold seep and hydrothermal vent fields, demanding high concentrations of dissolved organic carbon (DOC) as their nutrition. Reports showed that the DOC concentrations in seep sediments are higher than non-seep deep-sea sediments. Although methane-derived DOC could play important roles in the deep ocean carbon cycle, information on the reactivity of these seep DOC is yet quite limited. Here, with biogeochemical analysis, [Hu et al.](#) confirmed the significant contribution of methane-derived DOC at the seep cores and characterized the enhanced production of relatively labile dissolved organic matter (DOM) by anaerobic oxidation of methane (AOM) process in seep sediments. Their study suggested the lower degradation degree of these labile DOM, highlighting the indispensable role of methane derived DOC in supporting the heterotrophic microbial communities of deep-sea.

Though the deep-sea chemosynthetic ecosystems are featured by high concentrations of reduced chemicals, local environmental conditions of these ecosystems are also known to be dynamic in both time and space. The heterogeneity of deep-sea environments is recognized as a vital challenge and decisive factor for deep-sea organisms, shaping their community distribution and driving their environmental adaptations. Using cultivation dependent and independent methods, previous studies have investigated the diversity, adaptation and ecological significance of microorganisms in deep-sea chemosynthetic ecosystems. Corresponding to the environmental heterogeneity, [Zhai et al.](#) have observed both horizontal and vertical heterogeneity in microbial community in the cold seep sediments. Their results indicated that sulfate and methane were the main factors that structured the microbial community. While the microbial compositions from different sampling sites and depths were distinct, the microbial community cooperated closely to promote the overall community productivity. In addition, [Zhang et al.](#) has cultured a representative of *Lentisphaerae* bacteria from cold seep sediments, which is able to utilize polysaccharides for growth. Interestingly, the *Lentisphaerae* bacteria could significantly increase the environmental microbial diversity by metabolizing polysaccharides or other substances, demonstrating their unique physiological characterizations and ecological roles in the deep-sea habitats.

Besides the diverse microbial communities, a variety of megafauna inhabit in deep-sea chemosynthetic ecosystems. While continuous efforts are still being made to characterize novel megafauna species (e.g. the polyplacophoran *Thermochiton xui* by [Wang et al.](#), and the amphipods *Cyphocaris lubrica* and *Cyphocaris formosa* by [Wang et al.](#)), focuses on physiological novelty and diversity of megafauna are also growing. More so as for the case of mollusks, crustaceans and polychaetes, which are known to form symbiotic relationships with chemosynthetic bacteria that provide most of the organic carbon needed for the animal host's nutrition.

However, knowledge on the molecular basis of chemosynthetic symbiosis is yet still limited. Moreover, the reproductive strategies and the dispersal and connectivity of megafauna in deep-sea ecosystem are also of interest. In this Research Topic, [Guan et al.](#) investigated the lipid inventories of seep-dwelling bivalves and identified several lipids biomarkers reflecting symbiont types and local environments of bivalve hosts. The information derived from lipid biomarkers could also help interpret data from the rock record, providing valuable tools to investigate the nutrition strategies of

ancestor chemosymbiotic hosts. Similarly, [Wang et al.](#) characterized the different nitrogen sources that fuel symbiotic mussels at cold seeps. This multifaceted study has provided important evidence on the mechanism of nitrogen acquisition in symbiotic mussels and a broad perspective for carbon and nitrogen transformations in cold seep systems. Diverged from their ancestors a few hundred million years ago, the deep-sea mussels have evolved an unique lifestyle that is distinct from their non-symbiotic relatives. How these deep-sea mussels reproduce and whether they share the same sex determination/differentiation mechanisms with non-symbiotic mussels are less investigated. Here, resorting to transcriptome and whole-genome DNA methylation analyses, [Zhong et al.](#) have characterized hundreds of genes that may participate in the sex determination of deep-sea mussel, and concluded that the sex determination mechanisms are conserved in mussels from different habitats. These studies have substantially advanced our knowledge on the chemosymbiotic molluscan hosts.

Although widely recognized as oases of life over the last four decades, deep-sea chemosynthetic ecosystems are still mysterious, with many hidden secrets awaiting discovery. Besides studies covered by our current Research Topic, more efforts are still needed to unravel the unique biological diversity, structure and ecological processes in these deep-sea chemosynthetic ecosystems. For instance, there is limited information about temporal and spatial changes of free-living chemosynthetic microbial community, let alone the individual/population changes of deep-sea megafauna in response to environmental changes and human activities ([Wang et al.](#)). Finally, interdisciplinary efforts and the application of state-of-the-art methods (such as single-cell sequencing [[Li et al.](#)], spatial transcriptomics, mass spectrometry imaging, *in situ* experiments and *in situ* detection) are also needed to reveal the adaptations of these deep-sea organisms. We expect to see more exciting discoveries in the years to come.

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Conflict of interest

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