



Editorial: Microbial Communities of Coastal Eutrophic Systems

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Editorial on the Research Topic

Microbial Communities of Coastal Eutrophic Systems

Although climate change influences all life, microbes are generally not considered when discussing climate change impacts. We must explore not just how microorganisms affect climate change, including production and consumption of greenhouse gases, but also how they will be affected by climate change and other human activities (Cavicchioli et al., 2019). Indeed, coastal systems worldwide are in high risk of significant anthropogenic modifications as part of urbanization and global warming leading to increased eutrophication phenomena (Rabalais et al., 2009). Especially in these systems, where land-air-sea interactions are greater than at the open sea (Genitsaris et al., 2011), the first responders of high nutrient inputs and therefore biological indicators of the environmental status of these habitats are microbial communities. Coastal microbes, through their diverse morphology, functions, ecological strategies, and genetic content, play crucial roles in biogeochemical cycles, and food webs, which directly or indirectly affect human activities (Smith, 2003). This topic explores the responses of coastal microbial communities to environmental pressures of eutrophication and describes the complex processes that shape coastal system properties.

Coastal and estuarine sediments are drawing attention in recent years as systems highly threatened by multiple anthropogenic stressors that influence microbial populations of the benthos. Species that spend part of their life cycles in sediments, often reappear in the water column *via* resuspension of their resting stages, can rapidly increase in abundance under favorable growth conditions and influence planktonic food webs and biogeochemical cycles. Yi et al. reported that seasonality in bacterial assemblages of intertidal sediments in a subtropical river estuary affected by wastewaters, is related to rainfall and the monsoon climate; but spatial differences are attributed to pH variability and skewed nutrient inputs in the different sampling locations. Furthermore, RNA sequencing of sediment samples revealed higher expression patterns of multiple genes involved in bacterial stress responses far from localized anthropogenic stressors in well-flushed estuarine channels in Sydney Harbor, suggesting that bacterial communities might be more tolerant to urbanized eutrophication (Birrner et al.). Both studies suggest that several of the identified taxa with unique spatial distributions in the sediments of the sampled areas can be used as contaminant bioindicators in estuarine sediments. Complementing these contributions, Wallenius et al. reviewed the recent literature on anthropogenic and environmental constraints on the microbial methane cycle in coastal sediments. Although large amounts of methane are produced in hypoxic sediments of eutrophic coastal areas by methanogenic archaea, favored by global warming, the involvement of specific groups in methanogenesis is unclear. Furthermore, methane can be oxidized by aerobic methanotrophs in the upper sediment layers or in the water column, albeit the pathways involved, the key players and the factors controlling these processes

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is yet to be determined. Integration of the knowledge on microbial and geochemical processes is necessary to produce accurate predictions of methane emissions from coastal zones.

Contributions in this topic included studies on the roles of protease-producing bacteria in aquacultures, and the impacts of oyster aquaculture on nitrogen removal via bacterial processes in sediments. Protease-producing bacteria participate in the degradation processes of organic matter in aquaculture systems. Wei et al. found that protease-producing bacteria were more diverse and abundant in the sediment of tropical aquaculture systems than in the water column. Dissolved oxygen, chemical oxygen demand and salinity were the main factors with positive effects on the dominant assemblages. These findings lay the basis for the development of protease-producing bacterial agents for wastewater purification and the construction of an environment-friendly tropical aquaculture model. In parallel, Mara et al. compared three of the most common oyster aquaculture methods and their potential to enhance microbial nitrogen removal from coastal systems, through oyster biomass and particulate export to underlying sediments. All three methods enhanced nitrogen removal, albeit with different rates depending on the season, choice of gear and approach, indicating that monitoring for these shifts is essential for making decisions about siting and size of aquaculture sites from year to year.

Moving on from sediment microbes, Quéménéur et al. examined the prokaryotic diversity along environmental gradients in the water column of a Mediterranean site (Tunisian coast) for the first time. Their results support further investigation on the role of bacterioplankton in the biogeochemical cycles of the region. Knowledge on bacterial community composition and structure in the water column was considered the first step to further investigate the coupling of bacterio- and phyto-plankton in coastal areas. The resource competition between these two interdependent compartments of plankton, and how this is affecting the productivity of eutrophic sites was examined at the molecular expression level during a summer bloom in the Baltic Sea (Sörenson et al.). The expression of selected pathways of carbon, nitrogen and phosphorus metabolism varied over time, independently, for both phytoplankton and bacterioplankton, indicating partitioning

of the available resources and functional flexibility, which are deemed necessary to maintain phytoplankton-bacterioplankton interactions at stable environmental conditions.

Unicellular eukaryotes were examined at the taxonomic and functional levels in the last two contributions in this topic. Wang et al. explored pico- and nano-eukaryotic diversity in coastal surface waters of northern China, and the influence of environmental factors. They concluded that taxonomic composition is related to dissolved oxygen, but functional composition is shaped by limiting nutrient gradients in a regional scale. In addition, Breton et al. applied a trait-based approach to explore the mechanisms of the seasonal species succession of diatoms and copepods in a nutrient-enriched coastal system marked by recurrent spring *Phaeocystis* blooms. Results suggest that the trade-off between the competition advantages and the costs of defense mechanisms played important roles in promoting species richness and in triggering *Phaeocystis* blooms in the meso-eutrophic Eastern English Channel. The seasonal maximum of the defense trait that is the start of *Phaeocystis* single cells transformation into mucilaginous colonies and the timing of the bloom initiation of *Phaeocystis* were synchronized. Copepod assemblage homogenization coincided with the harmful, foam producing *Phaeocystis* bloom, confirming that eutrophication favors biotic homogenization which leads to blooms of inedible species, such as *Phaeocystis*.

The advances in high-throughput sequencing accompanied by the technological innovations of classical microscopy have provided the researchers contributing to the topic the tools to address questions on the diverse and complex marine microbial communities of eutrophic coastal areas. These contributions highlight the magnitude of the unexplored microbial diversity, the complex responses of marine microbes to cultural eutrophication in terms of community structure and roles, and offer insights on the who, when, where, and how they are affecting ecosystem function and biogeochemical cycles.

AUTHOR CONTRIBUTIONS

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

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