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EDITED AND REVIEWED BY
Eva Sintes,
Spanish Institute of Oceanography (IEO), Spain

*CORRESPONDENCE
Zhangxi Hu
huzx@gdou.edu.cn
Aifeng Li
lafouc@ouc.edu.cn
Zhun Li
lizhun@kribb.re.kr
Margaret R. Mulholland
mmulholl@odu.edu

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Editorial: The impacts of anthropogenic activity and climate change on the formation of harmful algal blooms (HABs) and its ecological consequence

Zhangxi Hu[1]*, Aifeng Li[2]*, Zhun Li[3]* and Margaret R. Mulholland[4]*

[1]College of Fisheries, Guangdong Ocean University, Zhanjiang, China, [2]Key Laboratory of Marine Environment and Ecology, Ocean University of China, Ministry of Education, Qingdao, China, [3]Biological Resource Center/Korean Collection for Type Cultures (KCTC), Korea Research Institute of Bioscience and Biotechnology, Jeongeup, Republic of Korea, [4]Department of Ocean and Earth Sciences, Old Dominion University, Norfolk, VA, United States

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Editorial on the Research Topic
The impacts of anthropogenic activity and climate change on the formation of harmful algal blooms (HABs) and its ecological consequence

Recent decades have witnessed a marked increase in the intensity of human activities, including agriculture, aquaculture, and manufacturing, leading to significant environmental repercussions (Smith and Schindler, 2009; Lu et al., 2021; Priya et al., 2023). These activities have resulted in the excessive discharge of nutrients, notably nitrogen (N) and phosphorus (P), into riverine systems, which subsequently transport these nutrients to estuaries and coastal seas (Seitzinger and Sanders, 1997; Liu et al., 2020; Voss et al., 2021; Yu et al., 2021; Beusen et al., 2022). The resultant nutrient composition shift towards a dominance of organic over inorganic nutrients has significant implications for aquatic ecosystems (Hébert et al., 2023). Eutrophication in estuarine and coastal waters has been exacerbated by an excess of nutrient runoff, a situation that is predicted to worsen (Sinha et al., 2017). Concurrently, climate change, characterized by increased atmospheric and aquatic CO_2 levels and rising temperatures, has had profound impacts on biological processes within marine ecosystems, further complicating the challenges posed by eutrophication (Brierley and Kingsford, 2009; Boyd et al., 2013; Brandenburg et al., 2019; Fu et al., 2024).

The frequency, severity, and duration of harmful algal blooms (HABs) in coastal and estuarine waters worldwide has shown a troubling increase, and is responsible for negative wildlife and human health effects, ecological disasters, and significant economic losses (Anderson et al., 2021; Sakamoto et al., 2021; Yu et al., 2023). Understanding the causative mechanisms and the ecological consequences of HABs is crucial due to the considerable ecological, economic, and societal ramifications (Anderson et al., 2021; Yu et al., 2023). Alterations in nutrient content, notably the increase in organic nutrient loads, coupled with climate change, significantly affects the growth, species composition, toxin production, and toxicity of HAB-forming species (Gobler et al., 2017; Brandenburg et al., 2019; Gobler, 2020; Raven et al., 2020). The persistence of HABs in an anthropogenically altered marine environment necessitates a comprehensive understanding of phytoplankton diversity, growth, physiology, allelochemicals, toxins, and toxicity of harmful algae, alongside the exploration of mitigation strategies.

Seven studies in our Research Topic focused on the diversity of resting cysts and phytoplankton in both marine and freshwater environments. Wang et al. investigated dinoflagellate cysts, particularly the distributions of toxic and harmful species along the Qingdao coast of the Yellow Sea, China, and analyzed the relationship between contents of biogenic elements and cysts. They identified a total of 32 cyst taxa, including 23 autotrophic and 9 heterotrophic taxa, among them, 17 of the cyst types identified were formed by HAB-causing species. The redundancy analysis demonstrated the influence of biogenic elements on cyst assemblages, and explained why the three sea areas examined, each with different degrees of human disturbance, showed different dinocyst assemblages and abundance. Roche et al. used amplification of the *Pseudo-nitzschia*-specific 18S-5.8S rDNA internal transcribed spacer region 1 (ITS1) in plankton samples and high throughput sequencing to characterize *Pseudo-nitzschia* species composition over a decade in Narragansett Bay, including eight years before the 2016–17 fisheries closures and two years following, and found that several species now recur as year-round residents in Narragansett Bay (*P. pungens* var. *pungens*, *P. americana*, *P. multiseries*, and *P. calliantha*). Various other species increased in frequency after 2015, and some appeared for the first time during the closure period. *Pseudo-nitzschia australis*, a species prevalent along the US West Coast and known for high domoic acid (DA) production, was not observed in Narragansett Bay until the 2017 closure but has been present in several years since the closures. Annual differences in *Pseudo-nitzschia* community composition were correlated with physical and chemical conditions, predominantly water temperature. Sun et al. investigated the phytoplankton community and its association with physicochemical properties in coastal waters of the northern Yellow Sea in 2016. These authors identified 39 taxa belonging to 4 phyla and 24 genera. Diatoms and dinoflagellates were the dominant groups. An algal bloom dominated by *Thalassiosira pacifica* occurred in March, effecting a shift in diatom-dinoflagellate dominance; notably dinoflagellates dominated throughout the summer but switched to diatom dominance again in September. Hypoxic zones (<2 mg·L^{-1}) developed in bottom waters in August, with minimum dissolved oxygen (DO) of 1.30 mg·L^{-1}, as a result of the diatom bloom in March. The effects of algal blooms on phytoplankton composition and hypoxia could have a cascading effect on fisheries sustainability and aquaculture in nearshore waters of the northern Yellow Sea. Xin et al. identified eight major marine phytoplankton assemblages, cryptophytes, pelagophytes, prymnesiophytes, diatoms, and chlorophytes using CHEMTAX analyses, and 149 species belonging to 96 genera of 6 major groups (diatoms, prymnesiophytes, pelagophytes, chlorophytes, cryptophytes, and dinoflagellates) by metabarcoding sequencing in the Western Subarctic Gyre during the summer of 2021.Sixteen out of the 97 identified species were annotated as potentially harmful algal species, e.g., *Heterocapsa rotundata*, *Karlodinium veneficum*, *Aureococcus anophagefferens*, etc. Nutrient concentrations were more important in shaping the phytoplankton community than temperature and salinity.

Two more works focused on freshwater ecosystems. Jiang et al. investigated the species composition and spatial distribution with respect to environmental factors in Lake Longhu, China, in July of 2020. They identified a total of 68 phytoplankton species belonging to 7 phyla, in which Chlorophyta, Bacillariophyta and Cyanophyta contributed more to the total cell density, while Chlorophyta and Cryptophyta contributed more to the total biomass. The parameters including pH, water temperature, nitrate, nitrite, and chemical oxygen demand were the main environmental factors affecting the composition of phytoplankton communities in Lake Longhu. Li et al. investigated the phytoplankton community in the Ashi River Basin (ASRB), Harbin, China, between April and October 2019, and identified 137 phytoplankton species belonging to seven phyla. They selected five critical ecological indices (Shannon-Wiener index, total biomass, percentage of motile diatoms, percentage of stipitate diatom, and diatom quotient) to evaluate the biological integrity of phytoplankton in the Ashi River Basin, and concluded that P-IBI (Phytoplankton Index of Biological Integrity) was a reliable tool to assess the relationship between phytoplankton communities and habitat and environmental conditions in that system. Their findings contribute to the ecological monitoring and protection of rivers impacted by anthropogenic pollution.

Four studies made significant contributions to our understanding of HAB physiology: one characterized the transcriptome of a species known to form HABs; another investigated the growth physiology of four harmful raphidophyte species; a third examined the interactions between bacteria and algae; and the fourth reviewed existing research on the impact of picophytoplankton on the carbon (C) and silicon (Si) cycles. Chen et al. used single-molecule real-time (SMRT) sequencing technology to characterize the full-length transcript in *Akashiwo sanguinea*, a harmful algal species commonly observed in estuarine and coastal waters around the world. In total, 83.03 Gb SMRT sequencing clean reads were generated, 983,960 circular consensus sequences (CCS) with average lengths of 3,061 bp were obtained, and 81.71% (804,016) of CCS were full-length non-chimeric reads (FLNC). Furthermore, 26,461 contigs were obtained after being corrected with Illumina library sequencing, with 20,037 (75.72%) successfully annotated in the five public databases. This work provides a sizable insight into gene sequence characteristics of *A. sanguinea*, and provides an important reference resource for *A. sanguinea* draft genome annotation. Lum et al. compared the growth responses to temperature and salinity for four harmful raphidophyte species that coexist in the tropical waters, *Chattonella malayana*, *C. marina*, *C. subsalsa*, and *C. tenuiplastida*, using unialgal cultures grown at ten temperatures (ranging 13.0–35.5°C) and five salinities (ranging 15–35) to better understand how these factors might regulate their distribution in the environment. They found that their growth rates with respect to optimal temperature were 28.0, 30.5, 25.5, and 30.5°

C, respectively, and that growth rate maxima with respect to salinity were similar for *C. subsalsa* and *C. malayana* (30), and for *C. marina* and *C. tenuiplastida* (25). The high adaptability of *C. subsalsa* to a wide range of temperatures and salinities suggests it is highly competitive in a range of environments. The ability of *C. marina* to thrive in colder waters compared to other species likely contributes to its wide distribution in the temperate Asian waters. The narrow and warmer temperature window in which *C. malayana* and *C. tenuiplastida* grew well suggests they are well suited and growth and distribution are more limited. This study provides a physiological basis for the relative occurrences and bloom potential of *Chattonella* spp. in Asia. Tang et al. isolated and identified a cultivable bacterium (*Alteromonas* sp.) coexisting with *Levanderina fissa* by the gradient dilution method and investigated the characteristics of the bacterial interactions with three diatom species (*Chaetoceros curvisetus*, *Skeletonema dohrnii*, and *Phaeodactylum tricornutum*) and three dinoflagellate species (*Scrippsiella acuminata*, *Karenia mikimotoi*, and the host alga), and found that *Alteromonas* sp. had significant inhibitory effects on the growth of all the algal species except its host (*L. fissa*). However, all the algal species tested, especially their natural hosts, showed significant stimulatory effects on the growth of *Alteromonas* sp. This study implies a highly complicated and variable interaction between phycosphere bacteria and their host alga. Picophytoplankton have been found to have significant silica (Si) accumulation, a finding which provides a new insight into the interaction of the marine carbon (C) and Si cycles and questions whether large diatoms (>2 μm) dominate the Si cycle. Wei and Sun found there were few studies on the physiology and ecology of picophytoplankton, especially regarding their potential roles in the biogeochemical Si cycle. These authors extensively reviewed past studies regarding the influence of picophytoplankton on the C and Si cycles, used this as the basis for conducting targeted studies on the picophytoplankton Si pool and its regulation. This work also provides a theoretical framework for further study of the role of small cells in the global ocean Si cycle and the coupling of C and Si cycles.

Two studies focused on the effects of algal toxin(s) and allelochemical(s) on other organisms. Yang et al. investigated the ability of 10 strains of *Margalefidinium polykrikoides* with different geographic origins and ribotypes to cause mortality in two strains of the dinoflagellate, *Akashiwo sanguinea* (allelopathy), and the sheepshead minnow, *Cyprinodon variegatus* (toxicity). Results showed that the potency of allelopathy against both strains of *A. sanguinea* and toxicity to the fish were significantly correlated across strains of *M. polykrikoides*. They concluded that the major allelochemicals and toxins of *M. polykrikoides* are identical chemicals, an ecological strategy that may be more energetically efficient than the separate synthesis of toxins and allelochemicals as has been reported for other HABs. Fu et al. investigated the effects of neurotoxin β-N-methylamino-L-alanine (BMAA) on the early development of embryos of mussel *Mytilus galloprovincialis*, oyster *Magallana gigas*, and marine medaka *Oryzias melastigma*. Results demonstrated that the embryonic development of mussels and oysters were significantly inhibited when BMAA concentrations were above 0.65 μM and 5.18 μM, respectively. The shell growth of mussel embryos was also markedly inhibited by BMAA at concentrations ≥ 0.65 μM. A sustained and dose-dependent decrease in heart rate was apparent in marine medaka embryos at 9-days post fertilization following BMAA exposure. This study contributes to our knowledge regarding the sublethal effects of BMAA on early embryonic development of marine bivalves and medaka.

Lastly, three studies explored the biological and chemical methods for controlling species that cause HABs. Wang et al. isolated a strain of algicidal bacterium *Pseudoalteromonas* sp. strain LD-B6 with high efficiency against *Noctiluca scintillans*, the highest algicidal activity reached 90.5%, and the algicidal activity of *Pseudoalteromonas* sp. was influenced by the density of *N. scintillans*. This bacterium could also lyse other algal species. This work provides a candidate algicidal bacterium against *N. scintillans* blooms. Chi et al. introduced a modified clay (MC) method to regulate the nutrients and phytoplankton community in *Litopenaeus vannamei* ponds. Compared to the control, they found that in the MC-regulated pond, there were reduced concentrations of both organic and inorganic nutrients and a distinct change in the phytoplankton community composition, with green algae becoming the most abundant phytoplankton species. This study provides new insights into an effective treatment for managing water quality and maintaining sustainable mariculture. Liu et al. compared the removal capacity of polydimethyl diallyl ammonium chloride (PDMDAAC) modified clay (MP) and hexadecyl trimethyl ammonium bromide (HDTMA) modified clay (MH) on the HAB-forming species *Prorocentrum donghaiense*. They found that PDMDAAC could remove microalgae at a low dose (2 mg/L) and quickly clarify the water by significantly enhancing the flocculation of algae onto the clay. This study provides support for the development of organic-modified clay.

In summary, the papers in this Research Topic contribute new insights into the effects of anthropogenic activities and climate change on the composition of phytoplankton communities in marine and freshwater ecosystems. They delve into the ecological physiology of species that form harmful algal blooms (HABs), the roles of allelochemicals, and the toxins and toxicity produced by harmful algae, as well as exploring methods for controlling HABs through both biological and chemical strategies. These studies offer valuable contributions to our understanding of ecosystem complexities and the impact of human activities on HAB-forming species. Moreover, this topic highlights the urgent need for further research on HAB species and their adverse effects on various trophic levels within aquatic ecosystems, alongside mitigation strategies for these impacts in both marine and freshwater environments.

Author contributions

ZH: Writing – review & editing, Writing – original draft, Funding acquisition, Conceptualization. AL: Writing – review & editing, Validation. ZL: Writing – review & editing, Validation. MM: Writing – review & editing, Validation.

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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.

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