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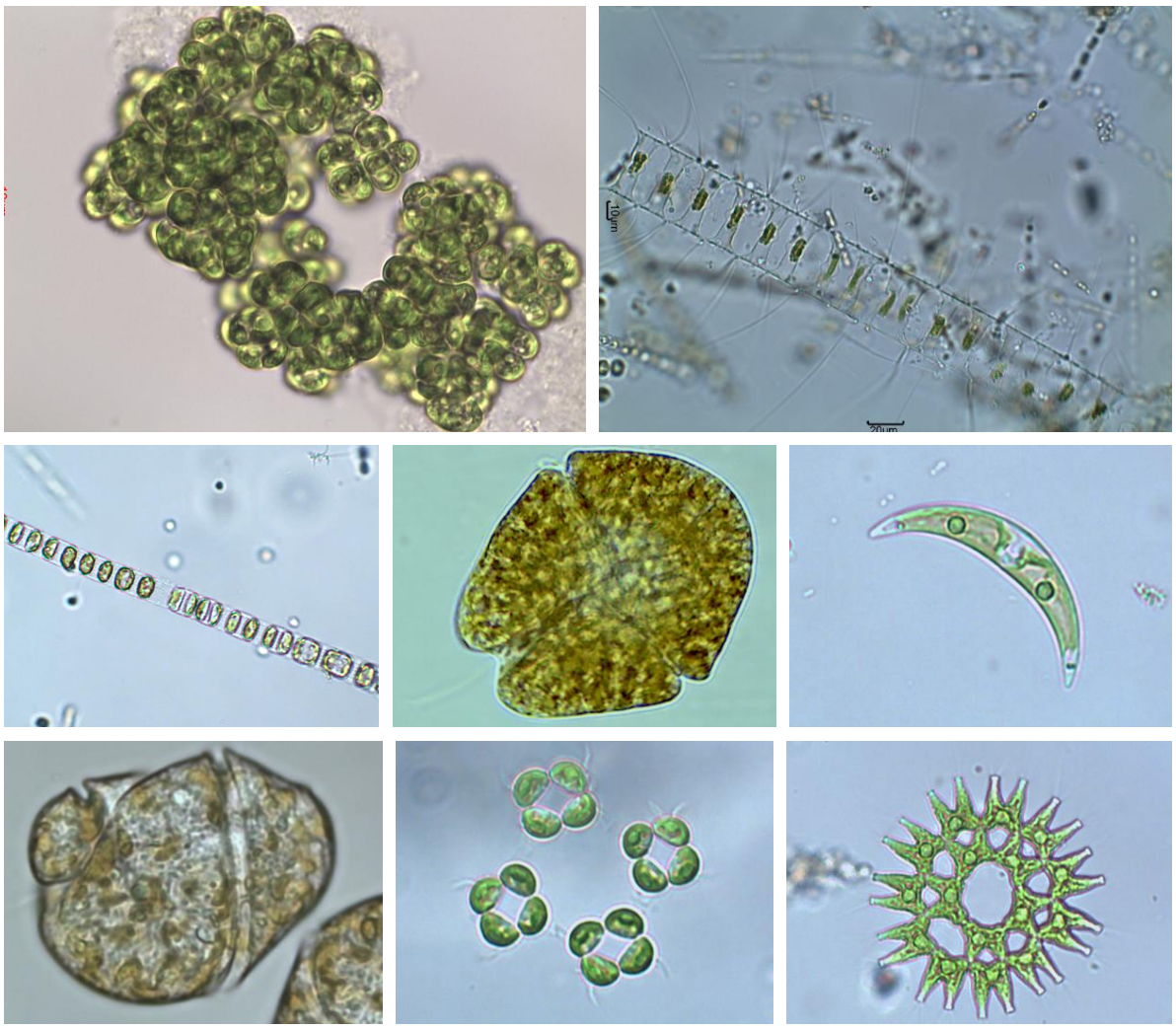
CONFERENCE ABSTRACT BOOK



International Conference on Algal Research, Application and Management

22-24 Aug 2023
Hong Kong

About the Conference

Algae, also referred to phytoplankton or planktonic algae, are photosynthetic organisms usually found in both freshwater and marine environments. They serve as primary producers in aquatic food webs and are the irreplaceable foundation in many ecological systems. Algae are food of filter-feeding bivalve shellfish such as oysters, mussels and clams, as well as the larvae of commercially important crustaceans and finfish. Some algae even have long history served as human food source. They can also be applied in pollution control including wastewater treatment and carbon sequestration. In recent years, algae are re-defined as a sustainable resource for a wide range of applications such as biofuel, soil modifier, colourant, oil and protein food sources and supplements. Today, algae and their related products is one of the fast-growing markets of global economy. However, not all algae are beneficial to us. Some algal species are responsible for causing harmful algal blooms (HABs; formerly red tide) that can cause massive contamination and even death of aquatic lives leading to substantial economic losses in fishery industry in Hong Kong and other parts of the world. Studies on HABs for establishing effective control and management policy are necessary to sustain fishery industry and safeguard human health.

This international conference is funded by The Croucher Foundation. Hong Kong Metropolitan University has a long and excellent track record in environmental science research, especially in harmful algal blooms (HABs) and applications of microalgae. This conference aims at encouraging exchanges and collaborations among experts, scientists, practitioners and research students from governmental authorities, institutions, universities, algae industry and fishery industry in Hong Kong, Mainland China, South-East Asia and overseas on research, applications and management of algae.

Themes

- Advances in biology of algae
- Algae cultivation, maintenance and advanced applications
- Algal biomass production technologies and commercialization
- Prevention, monitoring, management and policies for controlling harmful algae blooms

Organizing Committee

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International Conference on Algal Research, Application and Management

School of Science and Technology, Hong Kong Metropolitan University

22 - 24 August 2023

Programme

22 August 2023 (Day 1)

Time	Activity
14:00 – 17:30	Registration
18:30 – 20:30	Organizing Committee Meeting
– End of Day 1 –	

23 August 2023 (Day 2)

Time	Activity
08:15 – 08:45	Registration
08:45 – 09:00	Opening Ceremony **Welcome Remarks: Prof. Fred Wang-Fat LEE** Associate Dean, School of Science & Technology, Hong Kong Metropolitan University, Hong Kong SAR, China **Opening Speech: Prof. Yu-Zao QI** Jinan University, Guangzhou, China President, The Association on Harmful Algal Bloom in the South China Sea
Section 1: Conference Speech Chairman: Prof. Ya-Hui GAO Xiamen University, Xiamen, China	
09:00 – 09:30	Prof. Tian YAN Institute of Oceanology, Chinese Academy of Sciences, Qingdao, China **Title**: Harmful Algae and Algal Toxins in Coastal Waters of China: Investigation and Database
09:30 – 10:00	Prof. Hong-bin LIU The Hong Kong University of Science and Technology, Hong Kong SAR, China **Title**: Effect of Nutrient Limitation on Thermal Sensitivity of Marine Phytoplankton
10:00 – 10:30	Prof. Rhodora AZANZA National Academy of Science and Technology, Philippines **Title**: Philippine Harmful Algal Blooms : Research and Management Needs Aligned with Climate Change Impacts
10:30 – 10:45	Tea Break

23 August 2023 (Day 2)

Time	Activity
Section 2: Conference Speech Chairman: Dr. Steven Jing-Liang XU Hong Kong Metropolitan University, Hong Kong SAR, China	
10:45 – 11:15	Prof. Song-Hui LU Jinan University, Guangzhou, China **Title**: Biodiversity of Dinoflagellates and the Importance in Harmful Algal Studies
11:15 – 11:45	Prof. Po-Teen LIM Institute of Ocean and Earth Sciences, University of Malaya, Malaysia **Title**: Assessing the Diversity and Dynamics of Harmful Microalgae by Using a Metabarcoding Approach
11:45 – 12:15	Dr. Satoshi NAGAI Japan Fisheries Research and Education Agency, Japan **Title**: Population Genetic Studies of Worldwide Populations in the Toxic Dinoflagellate Alexandrium catenella and A. pacificum
12:15 – 14:30	Lunch
Section 3: Conference Speech Chairman: Dr. Sidney Man-Ngai CHAN Hong Kong Metropolitan University, Hong Kong SAR, China	
14:30 – 14:50	Prof. Kin Chung HO Shanghai Ocean University, Shanghai, China **Title**: From HAB (harmful algal blooms) to PAB (profitable algal blooms): the Hong Kong case
14:50 – 15:10	Prof. Jun-Rong LIANG Xiamen University, Xiamen, China **Title**: Understanding the Mechanisms Related to Diatom Resting Cells Formation and Survival
15:10 – 15:30	Prof. Fred Wang-Fat LEE Hong Kong Metropolitan University, Hong Kong SAR, China **Title**: Advancing the Establishment of Bacterial - free Karenia mikimotoi Cultures: A promising Methodology and Characterization of an Algicidal Bacterial Strain isolated from a K. mikimotoi Bloom in Hong Kong
15:30 – 15:45	Tea break
Section 4: Conference Speech Chairman: Dr. Sidney Man-Ngai CHAN Hong Kong Metropolitan University, Hong Kong SAR, China	
15:45 – 16:05	Prof. Yi TAO Tsinghua Shenzhen International Graduate School, Shenzhen, China **Title**: Induction of Programmed Cell Death in Cyanobacteria: Growth Suppression Effects and Death Features

23 August 2023 (Day 2)

Time	Activity
16:05 – 16:25	Prof. Chang-Ping CHEN Xiamen University, Xiamen, China **Title**: Unexpected Diversity of Diatom Species on Coastal Beaches in Southern China
16:25 – 16:45	Prof. Yang LI South China Normal University, Guangzhou, China **Title**: Exploring Pseudo-nitzschia Diversity and Tracing Domoic Acid Producers in the Taiwan Strait using a Metabarcoding Approach
16:45 – 17:05	Dr. Xin LIN Xiamen University, Xiamen, China **Title**: Ocean Acidification has a Strong Effect on Communities Living on Plastic in Mesocosms
Section 5: Sharing by Algal Industrial Representatives and e-Poster Presentation Chairman: Dr. Charles Chi-Hung TANG Hong Kong Metropolitan University, Hong Kong SAR, China	
17:05 – 17:15	Shanghai Guangyu Biological Technology Co., Ltd., China
17:15 – 17:25	Polar Chain Biotechnology Limited, Hong Kong
17:25 – 17:35	AlGreen Limited, Hong Kong **Title**: The Revolution of Carbon Capture & Utilisation with Algae Photobioreactor
17:35 – 17:45	biochrome., Hong Kong **Title**: Regenerative Potential of Microalgae: Addressing Sustainability Challenges in Cities
17:45 – 17:50	**Closing Remarks** Prof. Fred Wang-Fat LEE Associate Dean, School of Science & Technology, Hong Kong Metropolitan University, Hong Kong SAR, China
18:30 – 21:30	Conference Banquet (for invited guests only)
– End of Day 2 –	

24 August 2023 (Day 3)

Time	Activity
09:30 – 11:30	Workshop/Seminar sharing of algal research **Venue**: E0712
14:00 – 17:00	Technical visit to a local algal company **Venue**: biochrome.
– End of Day 3 –	

List of Abstracts

Harmful Algae and Algal Toxins in Coastal Waters of China: Investigation and Database

Tian Yan

CAS Key Laboratory of Marine Ecology and Environmental Sciences, Institute of Oceanology, Chinese Academy of Sciences, Qingdao 266071, China

Abstract

The "Harmful Algae and Algal Toxins in Coastal Waters of China: Investigation and Database" project (HAATC) intends to determine the overall distribution of marine harmful microalgae and macroalgae, and marine algal toxins (in phytoplankton and shellfish) through a large-scale investigation in the coastal waters of China. Continuous investigation have been carried out more than three years in seven key sea areas, which are HAB&farming zones from south to north coast. Biotic and abiotic processes were observed during harmful red tides and green tides events. It also aims to establish an open database and query platform of harmful algal blooms in China for understanding the long-term evolution of HAB occurrence under the influence of intensified human activity and global change. It is funded (US$2.3 million) by the Ministry of Science and Technology of China for 5 years starting on the 1st Jan 2019. This HAATC research consortium, led by chief scientist Prof. Tian YAN, includes approximately 100 scientists and students. More than 4 years of work have shown the increased distribution of HAB species (including cysts) and algal toxins in coastal waters of China, the increased occurrence of macro-algae blooms (mainly by *Ulva prolifera* and *Sargassum horneri*) in the Southern Yellow Sea, increased amount of causative species being identified, and new records of algal toxins such as azaspiracid, cycloimines and neurotoxins β-N-methylamino-l-alanine have been detected. Eventually, the project will provide systematic basic data and techniques for the rapid and accurate identification of harmful algae species to support the research, monitoring, and control of harmful algal blooms, as well as seafood safety management in China.

Keywords: harmful algae, algal toxins, coastal waters of China, database

* Supported by the Science and Technology Basic Resources Investigation Program of China (No. 2018FY100200).

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Effect of Nutrient Limitation on Thermal Sensitivity of Marine Phytoplankton

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Abstract

Understanding how marine phytoplankton and their primary consumer (i.e., microzooplankton) will respond to projected warming is critical for enhancing our ability to predict the response of marine planktonic ecosystems to climate changes. This is also critical to our ability to predict the capacity of the ocean in absorbing and storing anthropogenic CO_2. To gain more in-depth insights into the response of marine plankton community to warming, we conducted a series of experiments to evaluate their temperature sensitivity through activation energy (*Ea*) based on the framework of Metabolic Theory of Ecology (MTE). However, the growth of phytoplankton in different parts of ocean is limited by nutrient availability, such as nitrogen, phosphorus and iron. How resource availability affects phytoplankton thermal sensitivities is still not well studied. I will present a few case studies conducted by my team in recent years. Results from these studies provide new insights into the complex nature of trait specific thermal response of plankton and its implication to global carbon cycling in a warming ocean.

Philippine Harmful Algal Blooms : Research and Management Needs Aligned with Climate Change Impacts

Rhodora V. Azanza

The Marine Science Institute, University of the Philippines

Abstract

Harmful Algal Blooms (HABs) previously referred to in general as "red tides", have been reported in the Philippines since 1983 when Samar-Leyte and Sorsogon marine waters were affected by the bloom of *Pyrodinium bahamense*, a Paralytic Shellfish Poisoning (PSP) causative dinoflagellate species . The 1983 event resulted to almost a thousand cases of human poisoning and since then, monitoring and research have continued with the detection of persistent HAB causative organisms and identification of novel HAB species.

This report/paper is a review of the status of HAB research and monitoring in the Philippines in relation to the management of their hazards and risks. Among others, it is recommended that a thorough review of the monitoring and management of HABs in the Philippines be undertaken by relevant inter-agency committee considering the increase in the number of areas regularly affected by HABs and the apparent effects of climate change on this phenomenon. It should be noted that the general scheme of Philippine "Red Tide " monitoring and management was developed almost three (3) decades ago. A number of specific suggestions to enhance HAB research, monitoring and management to address their continuing and emerging hazards and risks are included.

Biodiversity of Dinoflagellates and the Importance in Harmful Algal Studies

Songhui Lu

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Abstract

So far more than 300 species has been reported responsible for algal blooms. A statistics from Intergovernmental Oceanographic Commission (IOC) reported that about 173 species can produce algal toxins or other toxic substances. The majority of those toxic species in marine are dinoflagellates.

Cells of dinoflagellates are nano- to micro-sized, some of them are unarmored. The fragile and high similarities in cell morphology among species make it difficult to be distinguished. The accurate identification of species is the basis of harmful algal bloom (HAB) studies, e.g. in diagnosis of toxic or non-toxic, in decision options of early warning, in operation measures of prevention.

The most toxic dinoflagellates in China, which made human intoxication or aquaculture losses, are species of *Karenia*, *Alexandrium*, as well as some benthic species. The total of 5 species of *Karenia* has been reported so far in Chinese waters, i.e. *Karenia mikimotoi*, *K. brevis*, *K. longicanalis*, *K. papilionacea*, and *K. selliformis*. *Karenia mikimotoi* is the most notorious harmful species off the South and East China Sea, which have caused more than 100 bloom events from 1998 to 2018. In most cases, the causative species of a *Karenia* bloom was not a single dominant species, but coexistence of species in the genus *Karenia* or other genus of family Kareniaceae. It might be the explanation that some of the blooms were toxic, but others were not.

Five morphotypes of benthic *Prorocentrum lima* has been identified from the southern Chinese waters. The results from ecophysiological and toxicological studies revealed that there are differences among the morphotypes within the species.

* This work was supported by the Nature Science Foundation of China (42276157, 42076144)

Assessing the Diversity and Dynamics of Harmful Microalgae by Using a Metabarcoding Approach

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Abstract

Harmful Algal Blooms (HABs) occur due to the proliferation of harmful microalgae in the aquatic environments. Often, HAB causes deleterious effects on the coastal ecosystem. This included the contamination of commercially important shellfish, massive mortality of farmed or wild finfish, and damaging the socioeconomic value of the marine ecosystem. The increasing impacts of HAB on socioeconomic and public health are tremendous, affecting regionally and globally, partly because of the emergence of new HAB events in areas with no prior record and involving novel toxic species. Rapidly growing aquaculture industries in the country has been hindered by frequent occurrence of fish kill and shellfish toxicity events. In this presentation, the emergence of HAB events due to new and unrecorded harmful species in Malaysia will be shared. To allow better assessment of the risk of HABs to the rapid growing aquacultures, studies have been taken to detect the potential harmful species using both advanced microscopy and molecular methods. Dynamic of phytoplankton communities and its related environmental factors in Johor strait, an important aquaculture area, will be elaborated further. This presentation emphasizes on the use of DNA metabarcoding to detect HAB species at different spatial scales covering the South China Sea and Straits of Malacca, and how this approach aids in the inventory of species distribution for monitoring, risk assessment, and early detection of HAB outbreaks. The challenges of this approach and its future perspective in assessing long-term coastal ecosystem changes will be further elaborated.

Keywords: Harmful Algal Blooms, DNA metabarcoding

Population Genetic Studies of Worldwide Populations in the Toxic Dinoflagellate *Alexandrium catenella* and *A. pacificum*

Satoshi Nagai

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Abstract

The geographic range of *Alexandiurm catenella* poisoning appears to be increasing on both regional and global scales. The molecular ecological study of genetic relationships using highly polymorphic genetic markers may reveal the dispersal mechanism of this species. In this study, MIG (multiplexed ISSR Genotyping)-seq was employed to reveal the genetic relatedness among Pacific Rim populations. Loci which were detected in >70% individuals and isolates in which >50% loci were detected were chosen for the further analysis, resulting in detecting 349 SNPs in 165 samples isolated from Akkeshi (eastern Hokkaido), Sendai, Osaka, Hiroshima Bays (Japan), Jinhae Bay (Korea), Bering Sea, Chukchi Sea, Puget sounds (USA) and Chile. Pairwise Fst values showed significant differences among most of the pairwise samples except for between Osaka & Jinhae Bay and Osaka & Hiroshima Bay. In the principal coordination analysis, the samples from Japan and Korea, the Bering Sea, and the Chukchi Sea (7 samples) were positioned closely, but Puget sounds and Chilean samples were plotted quite far away. Also, results of the bar plot analysis by STRUCTURE suggested when K = 3, each cluster was grouped as 1) Japan and Korean except for Akkeshi Bay, 2) Akkeshi Bay and the Bering/Chukchi Sea, 3) Puget sounds and Chilean samples. These data suggested the presence of a large genetic break between the Bering Sea and Puget sounds populations and genetic connectivity between Akkeshi Bay and the Bering/Chukchi Sea populations.

The distribution of *Alexandrium pacificum* has been increasingly documented worldwide during the last decades. To examine the genetic relatedness of global populations, we conducted a genetic study using a haplotype marker and 7 microsatellite markers. Seawaters or sediment samples were collected from 11 different localities (17 samples) along 10 Japanese, 3 Chinese, 2 Mediterranean Sea, 2 New Zealand coastal waters and 839 clonal strains (temperate Asian clade) were analyzed. The haplotype marker showed high resolution to discriminate the difference of the geological origin in the populations. We could obtain the sequences from 673 clonal isolates. Two haplotypes were predominant of 85 haplotypes. The first one "*Haplo01*" (n = 316 isolates) and the second one "*Haplo02*" (n = 122) were predominated by Japanese isolates and Chinese isolates, respectively. Some Japanese isolates also belonged to *haplo2*. Interestingly, the Sea of Japan population had unique and highly diversified haplotypes derived from *haplo2*. New Zealand populations were mainly divided into three groups, i.e. the first one belonged to *Haplo2*, the second one derived from *Haplo1*, and the third one positioned in the middle of *Haplo1* and *Haplo2* groups. The half of Mediterranean Sea isolates belonged to *Haplo1* and other half isolates had unique haplotypes derived from *Haplo2*. Microsatellite analysis data showed the significant population differentiation among most of the pairwise populations except for several Japanese pairwise populations. Results of the haplotype analysis well supported those at microsatellites analyses.

From HAB (harmful algal blooms) to PAB (profitable algal blooms): the Hong Kong Case

HO Kin Chung

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Department of Geography, HKU

AIT (Hong Kong) Co. Ltd

Abstract

After reviewing the water quality and marine ecological data in Hong Kong from 1975-2020, it is interesting to find that harmful algal blooms (HAB) often generate incidental clean-up of marine environmental conditions in enclosed embankments such as Tolo Harbour. Further analyses showed that the causative organisms of HAB could take up the excessive nutrients such as carbonates, nitrogenous compounds and inorganic phosphate in water bodies that helps to improve water quality. Applying these natural phenomenon in environmental engineering, a research plant in Yuen Long Sewage Treatment Plant was established to study the capability of microalgae in treating wastewater with satisfactory results for industrialization of relevant process. The project was subsequently subsidized by a fund in the Greater Bay Area for cleansing of fish ponds and polluted watercourses. By modification of cultivation tanks, new receipts of seeded algae and enhanced industrial control of production systems, research team found that various challenges in the algal industry including cost-economic issues, environmental shocks of the system and marketing of algal products could be overcome comfortably, that attracts stronger interest from investors. The future of the 'profitable algal blooms' is further brightened by recent urges for carbon-capturing and green finance because of ESG and global climate change.

Understanding the Mechanisms Related to Diatom Resting Cells Formation and Survival

Jun-Rong Liang, Guang-Ning Wang, Lu Huang, Meng-Yuan Hao, Shan-Shan Zhuang, Fan Hang, Qian-Qian Huang, Chang-Ping Chen, Xue-Song Li, Lin Sun, Ya-Hui Gao

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Abstract

Diatoms are well known to produce resting cells when they sink to deeper waters or sediment to endure prolonged periods of unfavorable environmental conditions. Once resting cells return to euphotic layers, they can rejuvenate quickly, functioning as “seed banks” to initiate a new seasonal bloom, which is considered the cornerstone of the ecological success of diatoms. Despite their significance for the survival of diatoms and their contribution to carbon export from surface oceans, the mechanisms of resting cells formation and survive remain elusive. Here, we have applied an integrative analysis based on histology, physiology, biochemistry, and transcriptome profiling to shed light on processes involved in resting-cell formation in the model diatom *Thalassiosira pseudonana*. Our results have revealed that the formation of RCs in *T. pseudonana* is characterised by histological changes of organelles and by a marked acidification of the cytoplasm. These physico-chemical changes were accompanied by the catabolism of storage compounds probably required for the development of RCs. The genes expressions associated with antioxidant defenses, DNA/protein repairs, autophagy, and specific transcription factors were enhanced to increase stress resistance and support resting cells survival. Thus, our results suggest that the formation of resting cells in *T. pseudonana* requires storage compounds and protons, both of which likely contributing to metabolism in quiescence essential to cope with conditions unfavorable for diatom growth in the marine system.

Advancing the Establishment of Bacterial – free *Karenia mikimotoi* Cultures: A promising Methodology and Characterization of an Algicidal Bacterial Strain isolated from a *K. mikimotoi* Bloom in Hong Kong

Thomas Chun-Hung Lee, Steven Jingliang Xu, Fred Wang-Fat Lee*

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Abstract

Karenia mikimotoi is a well-known and highly damaging species of harmful algal bloom (HAB)-causing dinoflagellate. Algal blooms caused by this species are widespread and often result in significant fish and shellfish mortality. Extensive research has been conducted on algicidal bacteria targeting HAB species, which could serve as a promising method for HAB control. In this study, we characterized a bacterial strain that exhibited potent algicidal activity against a *K. mikimotoi* strain. We employed an in-house developed methodology for establishing axenic *K. mikimotoi* cell cultures. Both the bacterial strain and *K. mikimotoi* cells were isolated from a *K. mikimotoi* bloom that occurred in Yim Tin Tsai, Hong Kong in 2016.

Developing axenic cultures for HAB species presents challenges. Although various methods have been reported for establishing axenic cultures of microalgae, there is no universally accepted approach. Many of the reported methods are ineffective and time-consuming. Generating an axenic culture of *K. mikimotoi* is particularly difficult due to the fragile structure of their unarmed outermost cell surface. Our developed methodology combines three key techniques: Percoll density gradient centrifugation, antibiotic treatment, and serial dilution. Generally, over 99% of the associated bacteria from the *K. mikimotoi* cell culture can be eliminated through physical separation via density gradient centrifugation and bactericidal action via antibiotic treatment. Instead of focusing on removing the remaining 1% of bacteria from the culture, our objective was to identify and isolate axenic clones of algal cells through serial dilution. The axenic status of the cell culture established from these axenic clones can be sustainably maintained for many generations (at least 50 generations in our study) without the use of antibiotics.

Axenic *K. mikimotoi* cells were employed to assess the algicidal activity of a novel strain of algicidal bacteria, *Maribacter dokdonensis*, isolated from a *K. mikimotoi*-induced HAB. Our results demonstrated that this *M. dokdonensis* strain exhibits efficient indirect algicidal action against *K. mikimotoi*. Both the bacterial culture and its supernatant (spent medium) completely lysed all algal cells within 48 hours. However, the algicidal effect of bacterial cells (residues after centrifugation) was negligible. At a 25% v/v dose, the algicidal efficiency of *M. dokdonensis* was 55% and 100% at 24 hours and 48 hours, respectively. The algicidal efficiency of *M. dokdonensis* against *K. mikimotoi* in the stationary phase was considerably higher than that in the log growth phase. This suggests that *K. mikimotoi* cells in the log phase display greater tolerance to the algicidal effect. Interestingly, the bacterial culture of *M. dokdonensis* exhibited a higher algicidal efficiency (~90%) against xenic *K. mikimotoi* than against axenic *K. mikimotoi* (~50%) after 24 hours of incubation. The enhanced algicidal effect could be attributed to the presence of associated bacteria in the algal culture. Further research is required to unravel the underlying algicidal mechanism of *M. dokdonensis* against *K. mikimotoi*.

Induction of Programmed Cell Death in Cyanobacteria: Growth Suppression Effects and Death Features

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Abstract

The occurrence of harmful cyanobacterial blooms (HCBs) has accelerated and intensified due to the global warming. It is of great significance to explore and investigate green, economical and highly efficient strategies to control the development of HCBs. Programmed cell death (PCD) is a form of suicide that is strictly regulated by gene expressions when cells are exposed to environmental stresses. Induction of cyanobacterial PCD is conducive to suppressing biomass as well as reducing risks of toxin biosynthesis and release. In this study, *Microcystis aeruginosa* FACHB-905 was exposed to different stresses, including UV irradiation, β-cyclocitral (BCC) and hydrogen peroxide (H_2O_2). Electron microscopy, flow cytometry and transcriptomics were employed to investigate the growth suppression and PCD forms in *M. aeruginosa* cells at cellular, molecular and transcriptomic levels, respectively. The aim of this study was to illustrate the suppression efficacy and features of different PCD forms induced by the applied strategies. Results demonstrated that different PCD forms were induced by different stresses imposed on *M. aeruginosa* cells. Moderate dosages of H_2O_2 and BCC induced cells into apoptosis characterized by cell shrinkage and lysis. By contrast, higher H_2O_2 and BCC concentrations led to ferroptosis and *mazEF*-mediated PCD characterized by membrane rupture and perforation, respectively. Both strategies resulted in ghost cells whose cell structure remained. UV irradiation also resulted in the *mazEF*-mediated PCD. The identification of different PCD forms in *Microcystis aeruginosa* cells inspires the combined induction of these PCD forms for highly efficient HCB control.

Keywords: *cyanobacteria, programmed cell death, apoptosis-like death, mazEF, ferroptosis*

Unexpected Diversity of Diatom Species on Coastal Beaches in Southern China

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Abstract

Sandy beaches are common in coastal areas, usually with unstable substrates, low nutrients, unfavourable environment and low biodiversity. However, diatoms are well adapted to sandy beaches. In this study, the morphological characteristics and species diversity of epipsammic diatoms in sandy environments along the coast of South China were studied, and 3 new genera, 21 new species, 6 new recorded genera and 40 new recorded species were published, which comprehensively and objectively reflect the diversity and ecological roles of the diatoms in sandy coasts. The study is the first to carry out epipsammic diatom biodiversity research in China, and finds that diatoms are abundant in sandy coasts, changing the views that "sandy ecosystems are low in biodiversity", and providing a basis for the protection and utilization of marine diatom biological resources. We found a biraphid diatom species with flexed frustules in beach environment on Weizhou Island, Beihai City, Guangxi Zhuang Autonomous Region, China. *Yuzaoea sinensis* gen. et sp. nov. CH Li, HH Liu, YH Gao & CP Chen (Bacillariophyceae) was described, which was characterized by heterogeneous frustule and complete raphe on both valves. Phylogenetic analyses based on SSU rRNA and *rbc*L showed that the genus *Yuzaoea* was the sister group to the clade of *Rhoicosphenia* (Bootstrap values = 100%), and the clade "*Yuzaoea+Rhoicosphenia*" was sister to the clade of monoraphid diatoms, in which the genus *Achnanthidium*, *Planothidium* and some *Cocconeis* (Bs = 100%). Morphologically, the genus *Yuzaoea* shares many morphological features with monoraphid diatoms like genera *Achnanthidium* and *Planothidium* and the members within the Rhoicospheniaceae. Therefore, based on a combined morphological studies and phylogenetic results we suggested that this branch may represent the evolution of one kind monoraphid diatoms, from biraphid diatoms (genus *Yuzaoea*), to incompleted biraphid diatoms (e.g. genera *Rhoicosphenia*, *Campylopyxis*), to monoraphid diatoms (e.g. genera *Achnanthidium* and *Planothidium*).

This study was financially supported by the National Natural Science Foundation of China (Nos. 42076114, 41776124) and the Natural Science Foundation of Xiamen (3502Z20227173).

Keywords: Bacillariophyceae, diversity, marine, new genus, sandy beaches

Exploring *Pseudo-nitzschia* Diversity and Tracing Domoic Acid Producers in the Taiwan Strait using a Metabarcoding Approach

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Abstract

Pseudo-nitzschia is a cosmopolitan phytoplankton genus that can form blooms and produce a neurotoxin called domoic acid (DA). Identification of *Pseudo-nitzschia* is generally based on field material or strains followed by morphological and/or molecular characterization, which are time-consuming and laborious. *Pseudo-nitzschia* taxa with low abundance in the field or potentially unavailable for culturing may easily be overlooked. To understand the complete profile of the *Pseudo-nitzschia* community, a metabarcoding approach using annotated amplicon sequence variants (ASV) was applied based on a carefully-calibrated reference sequence database for *Pseudo-nitzschia* and newly designed primers targeting the ITS1 rDNA domain. This approach was used in the Taiwan Strait of the East China Sea during the two cruises in spring and summer 2019. In total, 48 *Pseudo-nitzschia* taxa/phylotypes including 36 known and 12 novel were recovered, verified by divergence analyses and haplotype networks. The most frequent species were *P. multiseries* and *P. multistriata* in spring, and *P. calliantha* in summer. Redundancy analyses revealed that temperature was a key factor affecting the *Pseudo-nitzschia* community. Significantly positive correlation was present between particulate DA (pDA) and presence of *P. cuspidata* Clade III in summer, whereas no correlation was found between pDA and the other *Pseudo-nitzschia* species in summer, nor in spring. PDA was detected in four strains of *P. cuspidata* Clade III in summer, implying *P. cuspidata* Clade III as the main pDA producer. This comprehensive analysis gave new insights into the diversity of *Pseudo-nitzschia* in the natural environment.

Ocean Acidification has a Strong Effect on Communities Living on Plastic in Mesocosms

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Abstract

Plastic waste in the ocean is an urgent environmental concern and has given rise to a novel habitat, known as the "plastisphere." Under ocean acidification (OA), changes in plastisphere community composition may alter plastic degradation, deposition, and passage through food webs, but these have not been studied yet. This is the first study about the effects of simulated high CO_2 on the plastisphere using a mesocosm. We discovered that after 1 month the beta diversity of prokaryotic communities living on single-use plastic drinking bottles was significantly different under different carbon dioxide concentrations, with more pathogens at high CO_2. Based on function prediction analysis, the relative abundance of bacterial taxa involved in nitrogen and nitrate respiration and ureolysis was significantly higher under simulated high CO_2. We conclude that OA has significant effects on the plastisphere and its predicted functions.We conducted a mesocosm experiment to examine how ocean acidification (OA) affects communities of prokaryotes and eukaryotes growing on single-use drinking bottles in subtropical eutrophic waters of the East China Sea. Based on 16S rDNA gene sequencing, simulated high CO_2 significantly altered the prokaryotic community, with the relative abundance of the phylum Planctomycetota increasing by 49%. Under high CO_2, prokaryotes in the plastisphere had enhanced nitrogen dissimilation and ureolysis, raising the possibility that OA may modify nutrient cycling in subtropical eutrophic waters. The relative abundance of pathogenic and animal parasite bacteria also increased under simulated high CO_2. Our results show that elevated CO_2 levels significantly affected several animal taxa based on 18S rDNA gene sequencing. For example, Mayorella amoebae were highly resistant, whereas Labyrinthula were sensitive to OA. Thus, OA may alter plastisphere food chains in subtropical eutrophic waters.

Shanghai Guangyu Biological Technology Co. Ltd., China

Poster presentation is available HERE.

Polar Chain Biotechnology Limited, Hong Kong

Poster presentation is available HERE.

The Revolution of Carbon Capture & Utilisation with Algae Photobioreactor

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Abstract

Algae-based carbon capture and utilization (CCU) is a promising technology for mitigating greenhouse gas emissions from industrial and power plant sources. Algae photobioreactors, which use artificial light and controlled environmental conditions to cultivate algae and support their growth, are a key technology in this field. Our research focuses on optimizing the design of photobioreactors to enhance algae growth and lipid production. We utilize advanced cultivation techniques to control cultivation conditions, such as light intensity, temperature, and CO2 concentration, and thereby optimize carbon sequestration in the biomass. Our closed-loop system minimizes contamination and maximizes resource efficiency, making it an ideal technology for scalable algae cultivation.

Our research also focuses on the development of environmentally friendly solvents and low-energy-intensive methods for effective cell wall breakage. Incorporating pretreatment techniques, such as ultrasound or microwave, enhances the extraction of microalgal lipids to improve the yield of algal oil. Our lab-scale production capacity currently yields 0.8L of algal crude oil per week, which has a high calorific value and can be used for various applications, including biodiesel.

Microalgae are increasingly recognized as the primary feedstock for third-generation biofuels due to their ability to grow rapidly and convert solar energy to chemical energy via CO2 fixation. Biodiesel, one of the most commonly used biofuels, is considered an ideal recyclable energy carrier and a potential primary energy source. Algae biomass can also be used as a feedstock for producing fertilizers, such as nitrogen, phosphorous, and potassium (NPK), while simultaneously sequestering CO2 by burying biomass in sediment.

Our research on algae photobioreactors, algae cultivation, physical cell description, and algae lipid extraction aims to advance the development of algae-based CCU systems and promote the utilization of algae biomass in fertilizer and biodiesel production. The application of algae-based fertilizers has shown promising results in enhancing crop yields and improving soil health. Additionally, algae-based biodiesel has the potential to reduce reliance on fossil fuels and mitigate greenhouse gas emissions. We believe that algae technology has the potential to revolutionize carbon capture and utilization and play a critical role in the transition to a sustainable future.

Poster presentation is available HERE.

Regenerative Potential of Microalgae: Addressing Sustainability Challenges in Cities

Jane C.Y. Wong

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Abstract

The concept of circularity is increasingly gaining prominence in the realm of sustainability, necessitating a profound reevaluation of our production systems. The traditional "take-make-dispose" linear model is proving to be unsustainable. This model relies heavily on readily available resources and energy, produces substantial waste, and, over time, contributes to environmental degradation. This approach favors efficiency over sustainability, thereby exposing a critical flaw in our design philosophy. However, an abrupt transition to complete circularity isn't always feasible. Microalgae can serve as a valuable intermediary in the product cycle, capturing waste that would otherwise be discarded and reintegrating it into the production chain through nutrient recovery. Our technology finds its inspiration in corals, where microalgae are encapsulated to perform key tasks such as carbon capture and wastewater treatment. The biomass generated from this process can be harvested and potentially used in various sectors like agriculture, animal feed production, and the manufacture of high-value bioproducts. As interest in and applications for microalgae continue to emerge, we will demonstrate examples of how microalgae can function as an essential element in circular production systems.

Structure and Diversity of Epimicroplastic Microalgae Community and Influencing Factors in the Southeast Coast of China

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Abstract

Epimicroplastic microalgae (EMP-MA) refer to these microalgae attached on microplastics (MPs), which consist mainly of diatom and dinoflagellates. In this study, a total of 172, 120 and 56 algal species were identified from MPs samples collected form Quanzhou Bay, Dongshan Bay, and Luoyuan Bay, respectively. Diatoms and dinoflagellates were the two most abundant groups, accounting for 76.3%-95.6% and 0.0%-11.3% of the total number of algal species in EMP-MA communities, respectively. In addition, Chlorophyta, Cyanophyta, and Xanthophyta were also found in EMP-MA communities. In diatom group, 85.51%-93.80% of the diatom species belonging to pennatae in EMP-MA communities, these proportions were significantly higher than that in planktonic microalgae (PM) communities (62.22%-84.62%) ($p < 0.05$). Almost all the dominant species in EMP-MA communities belonged to pennatae, *Navicula* and *Nitzschia* were the two most common genera. The results of PCA showed that there were significant difference in community structures between EMP-MA and PM communities ($p < 0.05$). Based on the results of CCA, temperature, salinity, ammonium and phosphate had significant effects on EMP-MA community ($p < 0.05$). Some algal species belonging to *Navicula*, *Nitzschia* and *Cymbella* showed negative correlation with temperature and salinity but positive correlation with phosphate, ammonium, nitrate and nitrite. It is worth noting that a total of 17 harmful algal species were found in EMP-MA communities, which may drift with MPs and increase the risks of harmful algal blooms (HABs). This study is helpful to reveal the dispersal mechanism of HABs and potential impacts of EMP-MA on marine ecosystem.

The Anti-fouling Application and Algicidal Mechanism of Rare Earth Compounds

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Abstract

Marine biofouling is a severe problem on ships and offshore drilling platforms due to its detrimental effects on the economy and ecosystem. Diatoms play a crucial role in the formation process of marine fouling. Therefore, it is imperative to develop efficient and environmentally friendly compounds for diatom removal in marine fouling. In the present study, rare earth compounds (RECs) were synthesized as novel antifoulants that demonstrate high efficacy while being environmentally friendly. Meanwhile, physiological analysis and transcriptomic approach were employed to elucidate the algaecide mechanism of RECs on diatoms. The results showed significant inhibitory effects of RECs with growth inhibition rates at 24 hours reaching 89.65% for *Thalassiosira pseudonana* and 56.65% for *Amphora* sp., respectively. In the transcriptome analysis, the up-regulation of genes associated with photosynthesis, DNA replication, glycolipid synthesis, and inositol metabolism was observed. Conversely, the expression levels of genes related to antioxidant enzymes, glycolysis, the tricarboxylic acid (TCA) cycle, the pentose phosphate pathway, fatty acid synthesis, and calcium ion binding/ion transport processes were down-regulated. Our findings provide insights into the transcriptome-level algicidal mechanism of RECs and highlights their significance in marine environmental protection and antifouling applications.

The Ecological Advantages of Resting Cells in *Thalassiosira pseudonana*

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Abstract

Diatoms are characterized by their distinctive silica cell walls known as frustules and utilize resting cells as a unique dormant life stage in response to environmental stress. However, the ecological benefits provided by resting cells have not been fully elucidated. In this study, a comprehensive approach including morphological observations physiological assessments, and ecological analyses was employed to investigate the ecological advantages of resting cells in *Thalassiosira pseudonana*. The results demonstrated that resting cells possess enhanced defense mechanisms against bacterial attacks and marine pollutant BaP due to the reinforcement provided by their frustules. The findings shed light on diatom survival strategies and provide valuable insights into the critical role played by diatom resting cells as a "seed bank".

A New Marine Epizoic Diatom, *Halamphora yundangensis* var. nov. *foramina* (Bacillariophyceae), from Xiaodeng Island, Southeast Coast of China

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Abstract

Diatoms (Bacillariophyta) are diverse and abundant mircoalgae, with many of them found in marine intertidal environments and with great ecological importance in intertidal area. Here, we present a new variety of diatom *Halamphora yundangensis* var. nov. *foramina*, epizoic on the hermit crab, from Xiaodeng Island, Fujian Province, China. Morphological differences were found among our strains of *H. yundangensis* var. nov. *foramina* and *H. yundangensis* with respect to the poroids on the ventral side. These differences were examined using both light microscopy and scanning electron microscopy. *H. yundangensis* is characterized by dorsiventral, semi-lanceolate valves with a convex dorsal margin, straight ventral margin, and distinctly protracted and capitate valve ends. Externally, a prominent marginal ridge creates a broad hyaline area. Internally, the dorsal striae are regularly arranged in a biseriate pattern, and a row of areolae is observed along the raphe. *H. yundangensis* var. nov. *foramina* differs from *H. yundangensis* by the presence of a uniseriate row of small pores on the ventral side of its frustule. In this study, the new variety is compared with other similar species. This comprehensive analysis aids in differentiating the new variety from closely related species.

This study was supported by the Natural Science Foundation of China under contract (Nos: 42076114), and the National Key Research and Development Program of China (No. 2022YFC31054004).

Keywords: Diatom, new variety, morphology, epizoic

Impacts of a cosmopolitan dinoflagellate *Amphidinium carterae* (genotype 2) exposing to a worldwide spread pharmaceutical antibiotic macrolide Clarithromycin

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Abstract

Amphidinium carterae (Genotype 2) is a cosmopolitan benthic dinoflagellate that can be found on various substrates in the marine environment. Ecologically, it is one of the vital primary producers in the marine ecosystem. It is the producer of bioactive compounds like Amphidinolides, a compound of macrolide, and Amphidinols. They have properties like antitumor, antibacterial, antifungal, and anti-diabetes, making it potentially important to pharmaceutical industry. Clarithromycin (CLM) is one of the widely used pharmaceuticals macrolide antibiotic. High demand of this antibiotic and the waste causing accumulation of CLM in the marine environment. CLM was found to be harmful to microalgae. There is a lack of knowledge of CLM effects on a benthic dinoflagellate *A. carterae* especially their survival and their production of bioactive compound productions. This study aims to investigate the effects of *A.carterae* exposing CLM at various environmental concentrations over a long-term exposure with 3 generations. This is the first report on the effect of CLM on a Hong Kong isolated benthic dinoflagellate *A. carterae*. *A. carterae* strain SKLMP_Ve021, genotype 2, was exposed to six concentrations of CLM (0.01 to 1000 ng/L) and the controls for three generations. Each generation was collected at exponential phase. Endpoints of morphological and physiological changes, analysis of antioxidant responses, the changes in CLM concentrations in algal culture medium, as well as intracellular portions of A. carterae were examined in each generation. Production of bioactive compounds will be determined in A. carterae cultures after exposures. The highest CLM concentration, 100 and 1000 ng/L were only last 2 generations due to the depleting cell number, only 5-8 % (n=4) at day 14 of generation 2 of total cell density compared to the control group. With increasing of CLM, decreasing of maximum photosynthetic efficiency and changes of the analysis of antioxidant responses were observed. *A. carterae* could potentially absorb CLM intracellularly. Further results of the above-mentioned data will be further obtained and analyzed. Our result provides a better understanding of the effects of CLM on cosmopolitan benthic dinoflagellate *A. carterae* over three generations. The data obtained can be used to evaluate the benthic microalgae with the long-term effects of marine environmental macrolide antibiotic pollutants.

Effects of Nutrient Depletion and Changes of Light Intensity on the Growth of a *Karenia mikimotoi S*train *I*solated from Hong Kong

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Abstract

Karenia mikimotoi (KM) is a fish-killing harmful algal blooming (HAB) causative species and the blooms caused by this species can lead to massive death of fish and shellfish over the world. Algal blooms cause by KM have been found frequently in both Mainland China and Hong Kong. For instance, blooms of KM caused massive mortalities of abalones in Fujian, China in 2012. Such blooms resulting in economic losses estimated at no less than USD $300 million. In 2016, several Hong Kong fish farming zones were severe damaged by KM blooms, leading to deaths of over 200 tons of fish. Abiotic factors were found to influence growth of harmful algal bloom species. However, the study of the effect of various abiotic factors on the growth of KM is very limited.

We had successfully established a monoculture of KM cells from such algal blooms and the culture is denoted as KMHK. In this study, we investigated the effects of nutrient deficiency and changes of light intensity on the growth of KMHK. Cell densities of KMHK growing under different growth phases (lag, log and stationary growth phases) with various nutrient levels and light intensities were determined. Our findings revealed that cell densities of normal growing KMHK cells (initial 1000 cells ml^{-1}) at the three growth phases were 5.51 x 10^3, 18.0 x 10^3, and 23.4 x 10^3 cells ml^{-1} respectively. However, the cell densities dropped dramatically to less than 100 cells ml^{-1} when the cells were growing under N-deplete or P-deplete conditions. On the other hand, KMHK cells with initial density of 1000 cells ml^{-1} growing in various growth phases under 4 light intensities (2600, 3900, 6000 and 10800 lux) were investigated. KMHK cells growing under 3900 lux achieved the highest cell densities (lag phase: 5.51 x 10^3 cells ml^{-1}, log phase: 18.0x 10^3 cells ml^{-1}, and stationary phase: 23.4 x 10^3 cells ml^{-1}). When the light intensity was reduced to 2600 lux, the cell densities of KMHK has reduced 37% in lag phase, 13% in log phase, and 41% in stationary phase respectively. The growth of the cells would be greatly inhibited and maintained at around 1.4 – 1.8 x 10^3 cells ml^{-1} throughout different growth phases when they were growing under extremely high light intensity (10800 lux). No significant differences were observed between cells growing at 6000 lux and 3900 lux in both lag and log phases. Interestingly, significant drop to 16.0 x 10^3 cells ml^{-1} was observed in the stationary phase of KMHK under 6000 lux (a 1.5-fold decrease when compared to the cells growing at 3900 lux, i.e 23.4 x 10^3 cells ml^{-1}). Our preliminary data demonstrated that the growth of KMHK is greatly affected by the changes of nitrogen, phosphate and light intensity and the effects could be growth-phase dependent. However, more research is needed to reveal the role of these abiotic factors in KMHK bloom dynamics.

Time Dependent Interactions and Effects of nanoCuO to *Microcystis aeruginosa*

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Abstract

The wide application and concomitant increase of environmental concentrations of copper oxide nanoparticles (nanoCuO) raised concerns about its effects in the aquatic environment. Despite existing literature showing the possible detrimental effects of high nanoCuO concentrations to aquatic biota, the temporal aspects of the expression of biological responses, however, are not well understood. The aim of this study was to quantify the toxicity of nanoCuO on *Microcystis aeruginosa* during a relatively long-term exposure. The time course of the interactions in system containing nanoCuO and algae was investigated over a time of 42 days. The emphasis is on (i) the algal growth inhibition, photosynthesis activity, cellular ROS generation and lipid peroxidation in the presence of nanoCuO; (ii) nanoCuO stability and sedimentation kinetics; (iii) nanoCuO adsorption and availability kinetics by *M. aeruginosa* in terms of adsorbed and intracellular Cu; (iv) Microcystin production by *M. aeruginosa* in the presence of nanoCuO. Results showed that increasing concentrations of nanoCuO inhibited algal growth, photosynthesis activity and induced oxidative stress and membrane damage. The observed toxic effect of nanoCuO appeared much earlier for the materials with higher concentration. Besides, the toxicity mechanism may different between nanoCuO at low and high concentration. Further research is ongoing to understand nanoCuO adsorption and uptake by algae. The results highlighted the need for improved understanding of the toxicity effects of contaminants under a relative long-term exposure.

Keywords: *nanoCuO; cyanobacteria; bioavailability; toxicity*

Contribution of Benthic Microalgae to Carbon Flux in Coastal Intertidal Zone from Unvegetated Beach

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Abstract

The unvegetated beach is an important ecological environment in the intertidal zone ecosystem. Among them, benthic microalgae play a crucial role in the carbon flux of the beach ecosystem. By collecting sediment samples from the unvegetated beach, we measured the content of chlorophyll a in the sediment to characterize the biomass of benthic microalgae, analyzed their photosynthetic activity, and measured the amount of organic carbon fixed and released by benthic microalgae. Through measuring the carbon flux of greenhouse gases in the sediment, we explored the relationship between benthic microalgae and the greenhouse gas fluxes. At the same time, surface sediments and interstitial water were collected for the determination of environmental factors such as nutrient salts, organic carbon, total nitrogen, grain size, EC, EH, and pH, which were used to analyze key influencing factors. Combined with 18S amplification sequencing analysis, we further understood the structure and diversity of benthic microbial communities. This helped us better understand the relationship between benthic microalgae and greenhouse gas fluxes in the environment and their functions and roles. The results showed that benthic microalgae play an important role in coastal carbon fluxes. First, benthic microalgae are rich and diverse, and the results of their biomass and chlorophyll content show that they are widely distributed in the beach area and have high photosynthetic activity. Second, there is a negative correlation between benthic microalgae and greenhouse gases. Benthic microalgae convert a large amount of carbon dioxide into organic carbon through photosynthesis and immobilize it in their bodies, indicating that the presence of benthic microalgae may inhibit greenhouse gas emissions. The biological activities of benthic microalgae may be achieved by absorbing carbon dioxide greenhouse gases. These research results are significant for understanding the carbon flux process of intertidal zone beaches ecosystems and global carbon cycling. In summary, benthic microalgae play an important role in coastal carbon fluxes, making important contributions to the health and carbon balance of coastal ecosystems and providing important guidance for beach ecological protection and management.

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Keywords: intertidal zone, benthic microalgae, carbon flux, greenhouse gases

Seasonal Variation of Benthic Microbial Food Web Structure in Intertidal Zone

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Abstract

The intertidal zone is the typical nearshore marine ecosystem with extremely high biodiversity and biomass, and the environmental change is very intense and cyclical, in which the microbial food web contributes an important role in material cycle and energy flow. This study investigated the seasonal variations of the microbial food web structure in the surface sediments of the typical sandy intertidal zone in four successive seasons of Quanzhou, Fujian Province, China, paying special attention to the multi-trophic relationships and the potential role of benthic microorganisms in nutrient cycles. Environmental DNA (eDNA) method was used to bridge the molecular taxonomy of bacteria with micro-eukaryotic communities, allowing investigation of the potential interactions between different trophic-levels of the microbial food web. Our results revealed the discontinuity in bacterial and eukaryotic community composition, functional group proportion, as well as α-diversity due to fragmentation. It is proposed that the cycles of carbon, nitrogen, phosphorus and silicon are influenced by multi-trophic groups through autotrophic and heterotrophic processes, predator–prey relationships, as well as the release of nutrients mainly by microfauna. The seasonal variation of food web structure of benthic microorganisms in sandy intertidal zone was analyzed and discussed.

This study was supported by the National Key Research and Development Program of China (No. 2022YFC31054004), the Natural Science Foundation of Xiamen (No.3502220227173) and the Natural Science Foundation of China under contract Nos: 41776124, 42076114.

Keywords: intertidal zone, benthic microbial food web, seasonal variation

Effects of four traditional Chinese Medicine, namely *Astragali Radix, Coptidis Rhizom*a, *Lonicera Japonica Flos,* and *Poria,* on the growth of *Heterosigma akashiwo*

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Abstract

The marine fishery is an important industry in Hong Kong. However, the occurrence of harmful algal blooms may cause a great number of fish deaths, leading to significant economic losses in fish farming. Recently, researchers have started investigating the inhibitory effects of traditional Chinese medicine on the growth of algae. In this project, the effect of four selected traditional Chinese medicines, including *Astragali Radix*, *Coptidis Rhizom*a, *Lonicera Japonica Flos,* and *Poria,* on the growth of harmful algae, *Heterosigma akashiwo,* was explored.

The four selected Chinese medicines were mashed into powder using a blender and separately passed through a 60-mesh strainer. Each species of the Chinese medicine powder was mixed with L1 medium at a ratio of 1 gram of Chinese medicine per 10 mL of L1 medium, resulting in a concentration of 100 mg/mL. The mixtures were then soaked for 5 hours at 25°C and filtered with a 0.2 μm sterilized syringe filter. Concentrations of 100 mg/mL and 10 mg/mL were prepared and the filtered Chinese medicine extracts were kept at 4°C before use.

The algal cultures of *Heterosigma akashiwo*, strain GY-H24, were grown in L1 medium prepared with sterile-filtered seawater. The algae were incubated at 25°C, with 12-hour light-dark cycle in an illuminating incubator at 3,000 lux. After the algal cell density reached about 10,000 cells/mL, the algal cells were seeded into a 24-well plate, with each well containing 2 ml of algal culture. The cells were then treated with either 0, 1, or 10 mg/mL of each of the selected Chinese medicine for 6 hours or 24 hours, respectively. After the incubation, the density of algal cells was counted using a Sedgewick Rafter Counting Chamber under a light microscope.

For the 24-hour treatment, *Astragali Radix* (LC_{50} = 0.78 mg/mL), and *Lonicera Japonica Flos* (LC_{50} = 1.11 mg/mL) showed prominent inhibitory effects on the growth of *Heterosigma akashiwo* at concentrations 1 and 10 mg/mL while *Coptidis Rhizoma* exerted significant inhibitory effects at 10 mg/mL only (LC_{50} = 7.17 mg/mL). For the 6-hour treatment, *Astragali Radix, Coptidis Rhizoma* and *Lonicera Japonica Flos* exerted significant inhibitory effects at 10 mg/mL while promoting effects were found in treatment with *Astragali Radix* and *Coptidis Rhizoma* at 1 mg/mL. *Poria* had significant promoting effects at 10 mg/mL in both 24- and 6-hour treatments. Further studies were suggested for investigating the underlying mechanisms for the effects of Chinese medicines on the growth of *Heterosigma akashiwo.*

Effect of Benthic and Planktonic Phytoplankton on the Commercial Red Macroalga *Pyropia haitanensis*

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Abstract

This study aims to investigate the effect of two different types of microalgae on the growth and biochemical composition of economically important red macroalga *Pyropia haitanensis*. In this study, *P. haitanensis* were co-cultured with planktonic microalga *Skeletonema costatum* and benthic microalga *Navicula climacospheniae*. We investigated microalgal cell density, macroalgal growth, nutrient variation during experiments, photosynthetic pigments, total carbohydrate, and total protein concentration. Our results revealed that *P. haitanensis* growth was inhibited significantly with benthic microalgae, whereas planktonic microalgae do not significantly affect growth. During co-culture, macroalga *P. haitanensis* inhibited the growth of planktonic microalgae with increasing time but could not affect the benthic microalgal growth. The photosynthetic pigments of *P. haitanensis,* except chlorophyll, were higher than the control, which clearly shows that macroalgal thalli were under stress when inoculated with planktonic and benthic microalgae. Microscopic images of macroalgae show the dense attachments of benthic microalgae on thalli, which could cause severe stress on macroalgal thalli with respect to light availability and EPS secretion. Furthermore, the total carbohydrate of *P. haitanensis* was slightly less than the control in both microalgal treatments but not significantly affected, whereas total protein concentration was significantly reduced with higher initial cell densities of attached microalgae. Based on the results, benthic microalgal attachments significantly affect *P. haitanensis* growth, photosynthetic pigments, and total protein concentration. Hence, this study provides valuable findings of benthic and planktonic microalgae interaction on economic red macroalga *P. haitanensis*.

Keywords: Algal interaction; *Pyropia haitanensis*; Diatoms, Growth inhibition, Photosynthetic pigments, Total protein

Phytoplankton Community Structure and Environmental Factors during the Outbreak of Crown-of-Thorns Starfish in Xisha Islands, South China Sea

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Abstract

The "larval starvation hypothesis" proposed that the growing frequency of Crown-of-Thorns Starfish (CoTS) outbreaks could be attributed to increased availability of phytoplankton. However, comprehensive field investigation on the living environment of CoTS larvae and the availability of phytoplankton are still lacking. A cruise was conducted in June 2022 in Xisha Islands, South China Sea, to study the interaction between environmental conditions and phytoplankton communities during CoTS outbreak period. The average concentrations of dissolved inorganic phosphorus (0.05 ± 0.01 μmol·L^{-1}), dissolved inorganic nitrogen (0.66 ± 0.8μmol·L^{-1}) and chlorophyll *a* (0.05 ± 0.05 μg·L^{-1}) suggested that phytoplankton may be limited for CoTS larvae in Xisha Islands. Microscopic observation and high-throughput sequencing were used to study the composition and structure of the phytoplankton communities. Bacillariophyta predominated in phytoplankton communities with the highest abundance and species richness. 29 dominant species, including 4 species with size-range preferred by CoTS larvae, were identified in Xisha Islands. The diversity index of all stations indicated a species-rich and structure-stable phytoplankton community in Xisha Islands during the period of CoTS outbreak, which may contribute to CoTS outbreak. These findings revealed the structure of phytoplankton community and environmental factors in the study area during CoTS outbreak, providing the groundwork for future research into the causes and processes of CoTS outbreak.

Selection and Characterization of DNA Aptamers Binding to *Phaeocystis globosa*- A Harmful Algae with Recurrent Outbreaks of Blooms in Beibu Gulf, China

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Abstract

In recent years, the frequency, range and species of harmful algae blooms (HABs) showed an increasing trend by time in northern Beibu Gulf, among which, *Phaeocystis globosa* is a typical HAB species in this gulf. Researches showed that *P. globosa* blooms generally develop from increasing of solitary cells. However, the solitary cells are too tiny (3-7 μm) to be identified by morphological observation. Therefore, it is of great significance to explore new methods for rapid detection of *P. globosa* cells for early warning of HABs. Aptamer is a novel molecular probe with high specificity obtained by Systematic Evolution of Ligands by Exponential Enrichment (SELEX). The aptamers of *P. globosa* were obtained based on SELEX technique, and the characteristics including specificity, affinity, stability and sensitivity of these aptamers were studied in this study. Results showed that four aptamers with high specific binding ability to *P. globosa* solitary cells was obtained based on SELEX, including PgGx9, PgGx12, PgGx16 and PgGx20. These four sequences had similar stem ring structure, and the equilibrium dissociation constants (Kd) were 394.3 nmol/L, 76.0 nmol/L, 51.7 nmol/L and 330.0 nmol/L, respectively, suggesting high affinity for binding *P. globosa* cells; The aptamer probes screened can stably recognize *P. globosa* cells in the temperature range of 4-28 ℃, and with high sensitivity. Therefore, aptamer can be used in the development of convenient and sensitive detection kit for the rapid detection of nano- and pico- algae, so as to realize the real-time monitoring and early warning of HABs caused by these algae.

Visualization on the Formation of Resting Spores of *Chaetoceros pseudocurvisetus*

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Abstract

Some marine diatoms form resting spores under unfavorable conditions, and this process is usually related to the concentration of nutrients in the environment. Ecophysiological characteristics of resting spores produced from vegetative cells of the marine diatom *Chaetoceros pseudocurvisetus* under nitrogen depletion were investigated in this study. A variety of morphological and cytological changes during the formation of resting spores of *C. pseudocurvisetus* have been observed, such as valve deposition, neutral lipid accumulation, and glucose accumulation in reserved polysaccharides. This study aimed to visualize the process of remodeling and thickening of siliceous frustule and dynamic changes of neutral lipid and carbohydrate accumulation during the formation of resting spores using time-lapse microscopy and confocal laser scanning microscopy (CLSM) with different fluorochromes. The fluorochrome PDMPO, binds to the newly deposited silica, showed the formation process of siliceous frustule. Microscopic analysis of BODIPY and aniline blue stained cells reveals neutral lipid and carbohydrate accumulation, respectively.

This study was financially supported by the National Natural Science Foundation of China (Nos. 42076114, 41876146, 41776124) and the National Key Research and Development Program of China (No. 2022YFC31054004)

Keywords: *Chaetoceros pseudocurvisetus*, resting spores, ecophysiological characteristics, time-lapse microscopy, CLSM

Presence of Possible Harmful Algal Bloom Forming Micro-phytoplankton Genera in Four HAB-prone Bays in the Philippines

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Abstract

Harmful algal blooms (HABs) have long devastated the Philippines since its first report in 1983. HABs occur when single or several species of phytoplankton dominate the community producing negative or deleterious effects on other organisms present in the area. The mechanisms in which HABs produce harm to others may include (1) the production of toxic substances, (2) the depletion of oxygen in the area, or (3) the induction of mechanical injuries to other organisms. The determination of possible HAB-forming genera in coastal waters is crucial in understanding the phytoplankton dynamics occurring in that bay. Knowing which HAB-forming genera are present in specific bays would also give us insights into HAB events that might occur in the future.

Four HAB-prone areas in the Philippines were selected for this study namely, (1) Sorsogon Bay, Sorosogon, (2) Milagros Bay, Masbate, (3) Cancabato Bay, Tacloban City, and (4) Dauis-Tagbilaran, Bohol. Sampling was done during the dry season from March to April 2022. Five stations for each bay were established, and samples for the determination of the phytoplankton community were collected. Micro-phytoplankton was counted and identified up to the genus level using light microscopy. Water-physicochemical parameters including intracellular PST toxin content, nitrogen and phosphorous content, temperature, pH, and DO were also collected per station.

Several genera with toxin-producing members were observed in the bays. Three genera with possible paralytic shellfish toxin-producing members were recorded namely, *Gymnodinium* sp., *Pyrodinium* sp., and *Alexandrium* sp. This is supported by the detection of PSTs in the four bays, with high levels detected in Dauis-Tagbilaran, Bohol. Furthermore, the identity of the PST-producing dinoflagellate that has long devastated Milagros Bay, Masbate is suggested to be *Alexandrium* sp through the results of the study. Several members of the genus *Dinophysis* sp., which might be capable of inducing diarrhetic shellfish poisoning were also detected. The two diatom genera *Nitzschia* sp. and *Pseudo-nitzschia* sp., which might produce amnesic shellfish poisoning were also identified. The okadaic acid-producing genus, *Prorocentrum sp.*, was also observed. Other known HAB-forming genera that were found in the bays include *Chatonella* sp., *Noctiluca* sp., and *Scripsiella* sp.

The data generated from this study provides information on HAB-prone areas that can be used for developing prediction models necessary to establish coordinated efforts and aid in policymaking to mitigate the impacts of HABs. Data regarding specific community composition and the presence of possible HAB-forming micro-phytoplankton in the area would allow us to devise appropriate and specific mitigation tools. The complexity of the production of PST toxin in *Pyrodinium* sp. cells and the environmental factors that affect them warrant a more frequent and thorough analysis of our coastal bays.

Exploring Low-Cost Strategies for Sustainable Microalgae Cultivation and Harvesting using Wastewater and Chitosan Flocculation

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Abstract

Microalgae are being used in a variety of commercial applications due to their high nutritional value and value-added products such as nutraceuticals, aquaculture feed, feedstock for biodiesels. They play a crucial role in the circular economy, remediating waste and turning available nutrients into biomass to generate value-added goods. The extensive application of microalgae is hindered by its production cost. One way to lower the cost is to use wastewater, such as food waste leachate, rather than culture medium as nutrients for supporting the growth of microalgae. Harvesting the microalgae from liquid culture is another expensive process in microalgal biomass production using traditional approach such as centrifugation and filtration. In this study, anaerobic digestate from the treatment of food and sewage waste was examined as an alternative source growth medium for cultivating *Chlorella sp*., a local isolate. After 14 days, the microalgae biomass cultivated in diluted anaerobic digestate (AD, 10%) demonstrating comparable biomass productivity when compared to BG11 medium. The protein content of AD-grown microalgae showed a dose-dependent relationship, with the protein content increasing from 15.3% to 30% of biomass from 10% to 75% AD. Chitosan flocculation was employed to harvest *Chlorella sp.* cultivated in AD at larger scales. The optimal initial dosage of chitosan was found to be 52.8 mg per g dry algal biomass, and the biomass retrieval efficiency reached 98.7% as determined gravimetrically. This study provides a low-cost manner in cultivating and harvesting microalgae which can be used in large scale, sustainable and economical applications.

The work was supported by the grant from the Research Grants Council of the Hong Kong Special Administrative Region, China (UGC/FDS16/M09/20).

Microplastics Ingestion by the Heterotrophic Dinoflagellate Species *Noctiluca scintillans*

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Abstract

Microplastics (MPs) are solid wastes in the size of <5 µm that are found in the terrestrial and aquatic environments. Prolonged existence of microplastics in the environments has increased the exposure risks of different life forms at multiple trophic levels. Previous eco-toxicity studies have been focusing on larger planktonic consumers such as crustacean larvae, soft-bodied invertebrates and fish larvae, the effects of microplastic ingestion on smaller unicellular grazers, the primary consumers of producers, are poorly understood. The heterotrophic dinoflagellate species *Noctiluca scintillans*, one of the red-tide forming species, is of cosmopolitan distribution in coastal waters worldwide. The aim of this study was to determine the effects of microplastic ingestion on the growth and *per capita* algal ingestion rates of *N. scintillans*. Fluorescent microspheres of 10 µm diameter were used as surrogates for microplastic wastes in the aquatic environment for the investigation. Exposure experiments were conducted with *N. scintillans* and its algal prey species, *Dunaliella tertiolecta*, in cultures. The functional and numerical responses of *N. scintillans* feeding on *D. tertiolecta* were determined. In addition, in two different scenarios of microplastic abundance (i.e., at prey:MP ratios of 500:1 and 5000:1), the dinoflagellate *N. scintillans* ingested more prey cells in treatments with the addition of fluorescent microspheres than those without the addition of the microspheres. This finding suggested that microplastic particles in the seawater could have altered the feeding of this heterotrophic dinoflagellate species. The ecological implication of the results could be substantial as the microplastic pollution problem is expected to worsen in the aquatic environments.

Bioprospecting Potential of Seaweed Resources from Rocky Shores of Coastal Karnataka in Peninsular India

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Abstract

Growing interest in the discovery of natural products for use, is attributed to different ecosystem exploration. Marine algae in particular being the oldest family and ancestors of modern-day plants on earth got noteworthy qualities of being flexible, prolific, tenacious and are a cheap source in the preparation of new chemicals and contribute to the wealth of novel bioactive compounds. Diversity and exploration field is never be saturated and ever active. Thus, in the present study, exploration was done to collect seaweeds from coastal Karnataka in peninsular India during October 2022 to April 2023. 62 sites from 10 talukas of 3 coastal districts namely Uttara Kannada, Udupi and Dakshina Kannada were visited, and seaweeds were collected from intertidal rocky pools by random pick method and were identified using authenticated sources. Collected seaweeds were preserved by means of wet, dry methods and photographic formats as per the requirements. Totally 11 species belong to 2 families of green algae, 14 species belong to the 7 families of red algae, and 11 species belong to the 2 families of brown algae were identified. Genera like *Ulva*, *Hyphnea*, *Sargassum*, and *Gracilaria* were observed as dominant, which are of high economic value. Some new additions were observed from this work to the checklist of seaweeds of Karnataka (*Sebdenia flabellata*, *Turbineria conoides* and *Sargassum cristaefolium*). The number of species during the collection is less compared to previous reports that may be attributed to seasonal variation, environment factors and sampling sites. Since these bioresources have lot of applications in food, medicine and industrial sector, there is a much scope on the bioprospecting of these locally and abundantly available seaweed genetic resources.

Limited Toxicity of $nTiO_2$ on Freshwater Cyanobacteria (*Microcystis aeruginosa*)

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Abstract

For decades, engineered nanomaterials have been mass-produced and widely applied for the requirements of diverse technologies, which caused the massive input of engineered nanomaterials to the aquatic environment from sewage effluent and runoff. Besides, the increasing anthropogenic sources of engineered nanomaterials may pose a risk to phytoplankton. Hence, in the present study, the most used engineered nanomaterial TiO_2 ($nTiO_2$) of three sizes was selected to investigate their effects on growth, photosynthesis and reactive oxygen species (ROS) generation in *Microcystis aeruginosa*. There was no significant effect of three kinds of differently sized $nTiO_2$ on the growth of *Microcystis aeruginosa* during 5 days of exposure ($p>0.05$). However, compared to the control, rates of effective quantum production of *Microcystis aeruginosa* significantly decreased when exposed to $nTiO_2$ with sizes of 5 nm and 30 nm rather than 100 nm ($p<0.05$). Besides, there were no significant differences in ROS content between the control and $nTiO_2$ treatment ($p>0.05$) though lower GSH contents were observed in 5 nm and 30 nm $nTiO_2$ treatments ($p<0.05$). Overall, the toxicity of $nTiO_2$ on *Microcystis aeruginosa* is limited. Besides, $nTiO_2$ of smaller sizes (5 nm and 30 nm) exhibited greater effects on *Microcystis aeruginosa* than that of the larger size (100 nm).

Keywords: *Engineered nanomaterial, $nTiO_2$, cyanobacteria, toxicity, ROS*

The Effect of Microplastics on Different Microalgae Focusing on their Growth and Bio-adsorption Responses

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Abstract

Microalgae are essential components of aquatic ecosystems where they serve as the primary producer of food web, a food source of some aquatic lives and maintain the balance of the global carbon cycle. Despite their ecological significance, microalgae are threatened by the pervasive presence of microplastics, a tenacious pollutant pervading aquatic environments. Microplastics present an insidious risk as they are readily adsorbed by microalgae, thereby enabling their transfer and accumulation throughout the food chain. In this study, five microalgae species including *Scenedesmus quadricauda*, *Scenedesmus dimorphus*, *Scenedesmus obtusus*, *Characiochloris sp.* and *Coelastrella sp.* were exposed to microplastics for 10 days to monitor their growth and microplastics bio-adsorption responses. Different microalgae manifested vary growth responses to the microplastics exposure, with *S. quadricauda* and *Characiochloris sp.* exhibited growth enhancement of up to +43.90% in cell density compared to the control, whereas *S. dimorphus* and *Coelastrella sp.* showed growth inhibition with a decrease in cell density of up to -45.85% compared to the control. *S. obtusus*, however, showed no effect on growth. The study also identified chlorophyll *a* content as an essential factor affecting microalgae growth, with a significant positive correlation (r = 0.5810 – 0.9226) between cell density and chlorophyll *a* content demonstrated across all species. Additionally, there was a similar trend in the bio-adsorption rates of microplastics by microalgae, with smaller microplastics exhibiting higher bio-adsorption rate (average 3.11% for 10 µm, 16.85% for 1 µm and 46.20% for 0.08 µm). Overall, these findings suggest that microplastics can affect microalgae growth varies widely and smaller microplastics demonstrate higher potential for bio-adsorption and subsequent transfer into the food chain posing significant risks to aquatic ecosystems.

The work was supported by the grant from the Research Grants Council of the Hong Kong Special Administrative Region, China (UGC/FDS16/M07/19).

Cell Surface Proteomic Research: New Insight into the Identification of Toxic Dinoflagellates

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Abstract

Harmful algal blooms (HABs) caused by toxin-producing dinoflagellates have serious negative impacts on the aquaculture sector. However, traditional methods for toxic dinoflagellate identification, such as morphological analysis and DNA sequencing, are either subjective or time-consuming. Rapid and accurate identification methods are therefore required to mitigate the impacts promptly. To provide a basis for the development of quick and reliable antibody-based detection methods, this study aims to identify species-specific surface protein biomarkers of toxic dinoflagellates by comparative analysis of cell surface proteomes.

Five toxic dinoflagellate species commonly found in Hong Kong coastal regions, including *Alexandrium minutum*, *A. lusitanicum*, *A. tamarense*, *Gymnodinium catenatum*, and *Karenia mikimotoi*, were investigated. With the help of intact-cell-compatible protein labelling technology (sulfo-NHS-ester biotinylation), together with liquid chromatography with tandem mass spectrometry (LC-MS/MS) and in-house constructed transcriptomic databases, potential species-specific surface protein biomarkers were identified and screened. Noticeably, compared to the whole cell lysates, more than 1000 protein identities were exclusively found in the theca extracts of the five dinoflagellate species studied. Around 20% of these identities are associated with the cell membrane or cell wall. Species-specific surface protein biomarkers were further screened from these identities and subjected to custom antibody production. These findings suggested that cell-surface proteome can provide valuable insight for new protein biomarkers discovery, which will facilitate the development of fast and reliable detection tools for toxic dinoflagellates.

Natural Diatom Frustules as a Biocarrier for Drug Delivery Applications

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Abstract

In the field of drug delivery, synthetic mesoporous materials have shown great potential for delivering hydrophobic drugs. However, their synthesis typically involves expensive and toxic chemicals, which limits their biomedical applications. As an alternative, naturally available diatoms with porous and biocompatible silica structures can be considered as substitutes for artificial mesoporous silica materials. This study aims to explore the use of porous frustules extracted from diatoms as carriers for poorly water-soluble drugs. To demonstrate this concept, the frustule of the diatom *Thalassiosira pseudonana* and indometacin (a model water-insoluble drug) were utilized and analyzed. The results indicate that *Thalassiosira pseudonana* frustules effectively encapsulated the drug with an encapsulation efficiency of 18.57±0.09 wt%. The similarity observed in FTIR spectra between bare *Thalassiosira pseudonana* frustules and indometacin-loaded ones suggests successful loading of indometacin into the pores. DSC curves obtained from indometacin-loaded *Thalassiosira pseudonana* frustules showed no melting peak, further confirming that the indometacin within the pores existed in an amorphous state. Moreover, compared to pure indometacin, significantly improved drug dissolution was observed in indometacin-loaded *Thalassiosira pseudonana* frustules based on their higher drug release profiles. These findings validate the successful application of natural material such as diatom frustules as carriers for poorly water-soluble drugs.

Long-term Changes of *Noctiluca scintillans* Blooms Along the Chinese Coast from 1933 to 2020

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Abstract

Noctiluca scintillans is one of the most common harmful algal species and widely known due to its bioluminescence. In this study, the spatial distribution, seasonal variations and long-term trends of *N. scintillans* blooms in China and the related drivers were analyzed and discussed. From 1933 to 2020, a total of 265 events of *N. scintillans* blooms were recorded in Chinese coastal waters, with a total duration of 1052 days. The first *N. scintillans* bloom occurred in Zhejiang in 1933, and only 3 events were recorded before 1980. From 1981 to 2020, *N. scintillans* caused harmful algal blooms (HABs) almost every year, both the average duration and the proportion of multiphase HABs showed an increasing trend. 1986-1992, 2002-2004 and 2009-2016 were the three peak periods with a frequency of no less than 5 events of *N. scintillans* blooms per year. In terms of spatial distribution, *N. scintillans* blooms spread from the Southeast China Sea to the Bohai Sea after 2000, Guangdong, Fujian, and Hebei were the three provinces with the highest numbers of recorded events of *N. scintillans* blooms. Moreover, 86.8% of the events of *N. scintillans* blooms occurred in spring (March, April and May) and summer (June, July and August). Among environmental factors, the dissolved inorganic phosphate (DIP), dissolved silicate (DSi) and chemical oxygen demand (COD) were significantly correlated with the cell density of *N. scintillans* during *N. scintillans* blooms, and most of *N. scintillans* blooms were recorded in the temperature range of 18.0-25.0 ℃. Precipitation, hydrodynamics, water temperature, and food availability might be the main factors affecting the spatial-temporal distribution of *N. scintillans* blooms along the Chinese coast.

Effect of Diatomite Dosing on the Structure and Wastewater Treatment Efficiency of Microalgal-bacteria Granular Sludge

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Abstract

Granular sludge is an attractive strategy in wastewater treatment due to its high biomass concentration, excellent settling properties, and the ability to perform both nitrification and denitrification. Microalgal-bacteria granular sludge combining microalgae and sludge granules develops new possibilities for nitrogen and phosphorus assimilation, resource recovery, pollution reduction and carbon fixation. However, during operation, hydraulic shear and sludge bulking may cause granules' poor settling, resulting in biomass loss and treatment efficiency declining. The addition of solid carrier can help to improve the stability of granular sludge. Diatomite is a good bio-carrier because of its high biocompatibility and large surface area, so this study used diatomite enhanced aerobic granular sludge (AGS) and microalgal-bacteria granular sludge (MBGS) to investigate its influence on granules' structure and wastewater treatment efficiency. It was found that diatomite treatment group decreased more than 71.4% suspending solid in effluents compared to the control group, strongly prevented biomass loss, causing diatomite MBGS group had a high biomass concentration of more than 5g/L. The diatomite MBGS group had higher treatment efficiency than control with 5% higher TN and DTN removal rate. From SEM photos, it was found that more EPS, especially polysaccharides, was secreted around cells in diatomite treating groups, causing better stability of biofilm. Moreover, species and functional genes identification results showed that diatomite dosing helped to increase the abundance of *Nitrospirota* in AGS and photoautotrophic microbes in MBGS, respectively, along with the growth of denitrification function gene abundance, and may contribute to higher TN removal.

Keywords: *microalgal-bacteria granular sludge, diatomite, granular structure, wastewater treatment*

Effects of Antibiotics at Environmental Concentration on MIB Synthesis and Release of *Pseudanabaena* sp.

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Abstract

With continuous economic development and living standards improvement, numerous new pollutants represented by antibiotics are frequently detected in the drinking water environment. Cyanobacteria bloom has become a potential target organism sensitive to antibiotics because of its prokaryotic cell structure similar to bacteria. As a typical olfactory cyanobacteria, environmental concentrations of antibiotics (<1μg/L) can promote the growth of *Pseudanabaena* sp. and the generation and release of 2-methylisoborneol (MIB), further exacerbating the ecological risk of cyanobacteria outbreaks, threatening drinking water safety and public health. The new national standard of drinking water includes MIB as a routine monitoring index, which has become a research hotspot in the field of ecological environment. In this study, the effects of environmental concentration antibiotics on the cell growth and MIB generation characteristics of *Pseudanabaena* sp. were studied. The results showed that antibiotics promoted growth and MIB generation of *Pseudanabaena* sp. at low concentrations (<1 μg/L), and inhibited growth and MIB generation at high concentrations (10 mg/L). The sensitivity of ciprofloxacin (CIP) to *Pseudanabaena* sp. during MIB production was significantly higher than that of sulfamethoxazole (SMX). Studies on phosphate conversion and changes in EPS composition under antibiotic stress showed that the environmental concentrations of antibiotics could accelerate the utilization of surrounding phosphates (the cell density of *Pseudanabaena* sp. and MIB production began to increase rapidly on the 7th day), and the antibiotics increased the protein proportion in algae EPS. Under the action of antibiotics, EPS accelerated the absorption of phosphate, and the phosphate in CIP and MIX group was higher than that in the CT group. However, the key pathways and mechanisms of the regulation of extracellular release of MIB influenced by environmental concentration antibiotics still need to be further studied.

Keywords: antibiotics, *Pseudoanabaena* sp., 2-methylisoborneol (MIB), extracellular polymeric substances, phosphate

Community Structure of Toxic and Harmful Microalgae and Their Relationship with Environmental Factors in the Mussel Breeding Area of Gouqi Island, China

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Abstract

Gouqi Island, located at Zhoushan city, Zhejiang Province, China, has an important mussel breeding area, which have been frequently affected by the toxic and harmful microalgae in recent years. To investigate the changes in the toxic and harmful microalgae community structure and their relationship with environmental factors, seasonal samples were collected and analyzed for three consecutive years from 2020 to 2023 in the mussel breeding area of Gouqi Island. A total of 74 genera and 201 species of phytoplankton were identified, and the dominant genera was *Thalassiosira* in spring, *Prorocentrum* in summer, *Navicula* in autumn and *Skeletonema* in winter; 21 genera and 39 species of toxic and harmful microalgae were identified, and *Prorocentrum donghaiense* was the dominant species in spring, summer and autumn, and *Paralia sulcata* in winter. The results of the NMDS showed that the species composition of phytoplankton and toxic and harmful microalgae in spring and summer was similar, and also in autumn and winter, but the differences were significant between the spring-summer and autumn-winter season. At the same time, higher species diversity was showed in spring and summer. Redundancy analyses showed that water temperature, NO_2^-, NO_3^- and DO were the main influencing factors on the distribution of toxic and harmful microalgae.

Keywords: mussel breeding; phytoplankton; toxic and harmful microalgae; environmental factors.

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H_2O_2 Catastrophe from the Inside: Intracellular Fenton Led to Ferroptosis in Cyanobacteria

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Abstract

Harmful cyanobacterial blooms, HCBs, are global ecological issues that can threaten human health. In recent years, climate change has intensified and accelerated the occurrence of HCBs, requiring green and fast-acting strategies to suppress cyanobacterial growth. Hydrogen peroxide (H_2O_2) has been considered environmentally friendly and utilized to control the growth of cyanobacteria both in lakes and reservoirs. However, research into where and how H_2O_2 acts to inactivate cyanobacterial cells is still lacking. Pinpointing the location and the mode by which H_2O_2 kills cyanobacteria can benefit the design of target-specific strategies. In this work, we investigated the lethal effects of different concentrations of H_2O_2 on typical bloom-forming *Microcystis aeruginosa* FACHB-905, from the perspective of its acting location and critical mediators. Using the aquaporin-specific inhibitor acetazolamide (AZA), we found that *M. aeruginosa* AQPs transported exogenously added H_2O_2 into cells and contributed to its lethality. With the help of intracellular free Fe^{2+} chelator deferasirox (DFX) and hydroxyl radical quencher thiourea, intracellular Fenton reactions and the generated hydroxyl radicals were responsible for *M. aeruginosa* sensitivity to exogenously added H_2O_2. Based on these facts, we evidenced that ferroptosis occurred in *M. aeruginosa* cells as the addition of the typical ferroptosis inhibitor successfully abrogated the lethality of H_2O_2.

Keywords: *cyanobacteria, hydrogen peroxide, aquaporin, intracellular Fenton, ferroptosis*