ECOLOGICAL PATTERN OF MICROALGAL COMMUNITIES AND ASSOCIATED RISKS IN COASTAL ECOSYSTEMS

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Ecological Pattern of Microalgal Communities and Associated Risks in Coastal Ecosystems

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______________________(Signed)

___Zhang Li___________(Name of student)

Abstract

The occurrence of Harmful algal blooms (HABs) is a prominent environmental issue that pose significant threats to marine ecosystems, seafood safety, and human health. Over recent decades, the increasing frequency, intensity, and global distribution of HABs have underscored the urgency of understanding their ecological dynamics and associated risks. Beyond natural seawater, human-induced substrates such as plastics also provide a novel habitat, “the plastisphere” (a microecosystem with plastics as the matrix) for microalgal communities in the coastal ecosystem. However, the ecological dynamics and associated risks of microalgal communities in both seawater and plastisphere, as well as the associations between these two habitats, remain largely unexplored. Moreover, the absence of a specific and comprehensive sequence database for harmful and toxic microalgae has hindered the accurate identification and monitoring of these species. To address these gaps, this study developed the harmful and toxic microalgae database (HTMaDB) to reveal the ecological dynamics and microalgae-associated risks in the coastal ecosystem.

We constructed the HTMaDB, a comprehensive resource that consolidates 1,346 18S full-length reference sequences from public repositories. A total of 79 harmful and toxic species were identified in the typical coastal city Hong Kong surface seawaters with the application of curated database. The results revealed that dinoflagellates and diatoms constitute most of the toxic and harmful taxa, respectively. Seasonal variations in algal

community structures were observed. Specifically, temperature was found to be the primary factor shaping seasonal patterns of toxic algal communities, with increased toxic species abundance during the dry season. The dominance of causative taxa in this period was consistent with the higher prevalence of algal toxins, supporting the reliability of the database. These findings highlight the potential for escalating risks associated with toxic microalgae under a warming climate, as differential responses of specific species to temperature fluctuations contribute to the complexity of HAB occurrences. Species such as *Alexandrium* spp., *Dinophysis* spp., *Prorocentrum* spp., and *Karenia* spp. were identified as the primary toxin producers, underscoring the critical need for targeted management strategies to mitigate their ecological and health impacts.

In addition to exploring the ecological patterns of algal communities in the surface seawater, this study further investigated the ecological dynamics and associated risks of microalgal communities within the plastisphere. Plastic pollution has become a global environmental challenge, with millions of tonnes of plastic waste entering the oceans annually. The plastisphere provides a durable and hydrophobic surface that facilitates the colonization and transport of microorganisms, including harmful and toxic algae. By analyzing 92 paired samples of plastic debris and ambient water collected from coastal ecosystems, this research revealed that the plastisphere selectively harbors distinct algal communities compared to the surrounding waters. The relative abundance of Chlorophyta increased significantly, while that of Dinoflagellata decreased within the plastisphere. Furthermore, the plastisphere exhibited significantly higher alpha diversity, indicating its potential to shelter unique or alien microalgal taxa transported from upstream systems. These results suggest that the plastisphere serves as a microhabitat that enables the selective assembly, enrichment, and transport of harmful and toxic algae across ecosystems.

The study also found that harmful and toxic diatoms, such as *Pseudo-nitzschia cuspidata*, *Chaetoceros socialis*, and *Skeletonema marinoi*, thrived within the plastisphere. Some harmful algal taxa were exclusively detected on plastic debris but absent from the surrounding water, highlighting the potential of plastics to act as vectors for the transport of harmful algae. Environmental factors such as temperature and salinity were positively associated with the abundance of risk-associated microalgae, whereas pH exhibited a negative correlation. These findings demonstrate that plastic pollution not only alters the composition and diversity of microalgal communities but also amplifies the ecological risks associated with HABs by facilitating the spread and enrichment of harmful algae and their toxins. The potential for plastics to carry harmful algal species across marine ecosystems poses significant challenges for managing HAB risks in the context of increasing plastic pollution.

This integrated study bridges critical knowledge gaps by systematically investigating the pelagic microalgal communities in the coastal ecosystem. By developing HTMaDB, this research provides a valuable resource for improving the accuracy and efficiency of

HAB monitoring and identification. The findings highlight the role of environmental factors, particularly temperature, in driving the seasonal dynamics of toxic algal communities and emphasize the impact of climate change on HAB risks. Additionally, the investigation into the plastisphere offers novel insights into how plastic debris assembled a distinct microalgal community compared to the seawater community and increased the risks associated with harmful and toxic algae. These findings contribute to a comprehensive ecological view of pelagic microalgal communities in the coastal ecosystem.

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As I stand at this juncture where this protracted academic journey approaches its terminus, retrospection unveils the perplexities encountered in literature reviews, the uncertainties faced with datasets, now interwoven with this moment of clarity and gratitude, coalesce into heartfelt appreciation to the numerous individuals who illuminated my path.

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Abbreviations

Abbreviations	**Full names**
ASP	Amnesic shellfish poisoning
AST	Amnesic shellfish toxins
ASVs	Amplicon sequence variants
AZA-1	Azaspiracid-1
AZA-2	Azaspiracid-1
AZP	Azaspiracid poisoning
CE	Collisions energies
CEP	Collision cell entrance potentials
CP	Ciguatera poisoning
DA	Domoic acid
DDBJ	DNA Data Bank of Japan
DO	Dissolved oxygen
DOC	Dissolved organic carbon
DP	Declustering potentials
DSP	Diarrhetic shellfish poisoning
DST	Diarrhetic shellfish toxins
DTX-1	Dinophysistoxin-1
DTX-2	Dinophysistoxin-2
EMBL	European molecular biology laboratory
EP	Entrance potentials
EPS	Extracellular polymeric substances
GYM	Gymnodium
HABs	Harmful algal blooms
HAEDAT	Harmful algal event database
HTMaDB	Harmful and toxic microalgae database
HTS	High-throughput sequencing
INSDC	International nucleotide sequence database collaboration
LAT(s)	Lipophilic algal toxin(s)
LOD	Limits of detection
LOQ	Limit of quantification

LSU	Large subunit
MST	Modified stochasticity ratio
NCBI	National center for biotechnology information
NSP	Neurotoxic shellfish poisoning
NST	Normalized stochasticity ratio
OA	Okadaic acid
PCoA	Principal coordinate analysis
PERMANOVA	Permutational Multivariate Analysis of Variance
POPs	Persistent organic pollutants
PP	Polypropylene
PR2	Protist ribosomal reference database
PSP	Paralytic shellfish poisoning
PSTs	Paralytic shellfish toxins
PTX-2	Pectenotoxin-2
PTXs	Pectenotoxins
RDA	Redundancy analysis
rRNA	Ribosomal RNA
SD	Standard deviation
SPM	Suspended particulate matters
SSU	Small subunit
VPA	Variation partitioning analysis
YTX	Yessotoxin

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Chapter 1 Introduction

1.1 Background

The global range, regional intensity, and frequency of harmful algal blooms (HABs) have increased over the last few decades in coastal areas (Dai et al. 2023a). Some of HABs-forming species can release toxins leading to fish death, shellfish poisoning, and even human illnesses after consuming contaminated seafood (Berdalet et al. 2016). To date, over 300 phycotoxins and Furthermore, a number of seafood poisoning cases caused by algal toxins have been reported worldwide (Holmes & Teo 2002; Hossen et al. 2011; Jiang et al. 2017; Kim et al. 2010; Mackenzie 2019; Mafra et al. 2019; Visciano et al. 2016). These seafood toxins accounted for nearly half of total HAB events, and over the past three decades, an increase in the global frequency of causative organisms, such as *Dinophysis* spp., *Alexandrium* spp., and *Pseudo-nitzschia* spp. was observed according to the global HAB status report 2021. Some nontoxic microalgae form high biomass blooms and cause mortality of aquatic organisms by clogging gills or triggering hypoxia/anoxia conditions in the ambient water (Anderson et al. 2021a). This global ecological phenomenon has resulted in remarkable socioeconomic losses due to massive fish kills and fishery closure (Boyce et al. 2017).

Microalgae are not only found in natural water bodies, growing attention has been paid to the colonization in artificial or human-disturbed niches, such as the "plastisphere" (microbial habitat with plastic as the matrix) (Amaral-Zettler et al. 2020; Zettler et al.

2013). These non-traditional niches also participate in the dynamics of pelagic communities and have an important impact on their structure and function. The buoyancy, durability, and hydrophobic properties of plastics enable them to act as vectors for the transport and enrichment of harmful species like disease-causing microorganisms and antibiotic resistant bacteria (Bergmann et al. 2022; Bhagwat et al. 2021; Dey et al. 2022). These studies on plastisphere microbiology and associated risks mainly focus on bacteria, with comparatively less attention given to eukaryotes. Other life forms, such as microalgae, a key component of aquatic ecosystems, are poorly understood in the plastisphere. Uncovering the full picture of this novel, unique habitat generated in the Anthropocene and the associated potential ecological threats will help to achieve a more comprehensive understanding of plastic pollution risks and the influence of human activities on the Earth's microbiome (Li et al. 2024b; Rillig et al. 2024a). A previous investigation shows that one square centimeter of the plastic surface can harbor more than 80,000 diatom cells, pinpointing that marine plastispheres act as a suitable habitat for microalgae containing substantial microalgal biomass (Casabianca et al. 2019). However, the compositional dynamics and associated ecological risks of microalgal communities within distinct habitats, namely, the seawater and the plastisphere, remain poorly understood. Furthermore, the potential interactions, convergences, or divergences between these two ecological niches have not been thoroughly investigated, leaving a critical gap in our understanding of how microalgal populations function and evolve in anthropogenically influenced marine environments.

Metabarcoding monitoring efforts are highly beneficial for early HAB species detection and risk assessment due to robust sensitivity and specificity when compared to traditional time-consuming, labor-intensive morphology-based approach (Feist & Lance 2021). Many microalgal species with small sizes are difficult to distinguish via their morphology (Huang et al. 2021; Pearson et al. 2021). The accuracy of DNA metabarcoding will fluctuate depending on the reference database, however, there is no specific harmful and toxic microalgae sequence database till now.

Collectively, this PhD thesis provides significant contributions to the field of marine ecology by establishing a comprehensive database of harmful and toxic microalgae, exploring the ecological dynamics and risks of pelagic microalgae communities including surface seawater and plastisphere, and the interactions between these two habitats in the coastal ecosystem. Moreover, the exploration of the plastisphere reveals new insights into the role of plastic debris in altering microalgal community composition, thereby increasing the risks associated with harmful and toxic algae. The findings advance our understanding of how environmental and anthropogenic factors influence algal blooms and their ecological consequences. This work not only enhances our ability to monitor and manage HABs effectively but also underscores the emerging environmental challenge posed by plastic debris in marine ecosystems. Continued research and adaptive management strategies are essential to mitigate these ecological threats and protect marine biodiversity.

1.2 Research objectives

This thesis aims at conducting an in-depth examination of the ecological pattern of microalgal communities and the associated risks in coastal ecosystems. The specific objectives of this study are as follows:

a) To develop and apply a comprehensive database (HTMaDB) containing taxonomic information on harmful and toxic microalgae, thereby enabling accurate identification and effective monitoring of HAB species;

b) To analyze the spatiotemporal distribution patterns of harmful and toxic algae associated with key algal toxins in coastal surface seawater, in order to validate the reliability and applicability of the newly constructed database;

c) To investigate the characteristics of microalgal communities within the plastisphere compared to the seawater microalgal community, with a particular focus on the enrichment of HAB species and their implications for marine ecosystem; and

d) To determine what are the key environmental factors governing HAB community dynamics and the potential implications of climate change on the HAB community.

1.3 Organization

This thesis is structured into seven chapters, including “Introduction,” “Literature Review,” “Methodology,” two results and discussion chapters, and a concluding chapter with “Conclusions and Recommendations.” Chapter 1 introduces the background of the study, focusing on HABs and their ecological and economic impacts, as well as the emerging challenges of plastic pollution and the plastisphere. Furthermore, the thesis structure is outlined as guidelines for the reader, and the research objectives are set out. Chapter 2 summarizes existing knowledge on phytoplankton communities in coastal ecosystems regarding their ecological impacts and environmental drivers. Several monitoring and detection techniques, traditional and DNA-based, molecular and HAB-specific database development, are discussed. The chapter then looks at the plastisphere as a new microhabitat, how it forms, the ecological risks associated with living in it, and the emerging issue of the proliferation of HAB species within this microhabitat. Chapter 3 details the methodologies employed in the thesis. It includes the construction of the database (HTMaDB), covering the collection, taxonomic, and diversity of HAB species. It also describes marine sampling campaigns, including sampling strategies, environmental parameter measurements, DNA extraction, and sequencing techniques. Statistical analyses to quantify algal community patterns and chemical analyses for LATs are also described. In chapter 4 HTMaDB is applied to analyze distribution dynamics of microalgal communities in coastal seawater to validate the reliability of the dataset. Specifically, it maps harmful and toxic microalgae and evaluates environmental factors, such as temperature, shape toxic algal communities. It further explores the linkage among environmental parameters, non-toxic species interactions, and toxic algal community variations, identifying distribution pattern of potential causative taxa linked with lipophilic algal toxins (LATs). Chapter 5 examines the microalgal communities and associated risks in the plastisphere in coastal ecosystems, focusing on ecological shifts induced by plastic debris. It reveals how plastics selectively enrich HAB species, their interactions with the environmental factors, as well as the potential risks posing to marine biodiversity and ecosystem dynamics. Finally, Chapter 6 summarizes the major findings and limitations of the current research, as well as provides a future perspective on advancing the study of microalgal communities and their associated risks in coastal ecosystems.

Chapter 2 Literature Review

Given the growing ecological threats posed by HABs and plastic pollution in coastal ecosystems, this chapter provides a comprehensive review of the interactions between HABs, plastic debris, and microalgal communities under a climate change world. The review focuses on understanding the ecological impacts and potential risks associated with these environmental challenges. From an ecological and environmental health perspective, this review emphasizes the role of toxigenic microalgae and how plastic pollution may influence the spread and dynamics of harmful algal species. It further explores the mechanisms driving the formation of HABs and plastisphere communities, their spatiotemporal variations, sources, and risk assessments, highlighting critical research gaps and guiding future studies toward effective monitoring and management strategies.

2.1 The phytoplankton in the coastal ecosystems

2.1.1 HABs and ecological impact

HABs, consisting of over-proliferation of algae in both marine and freshwater systems, represent a critical and escalating global environmental challenge. The frequency, regional intensity, and geographic distribution of HABs have increased over the last few decades in coastal areas, posing threats to ecosystems and human health (Anderson et al. 2021b; Dai et al. 2023b; McKenzie et al. 2021; Yu et al. 2023b). Of the nearly 5,000 documented marine phytoplankton species inhabiting global waters, researchers have identified more than 100 distinct variants that endanger human populations by generating harmful toxins. These bioactive compounds compromise both food safety through contaminated marine harvests and public health via direct exposure risks (Hallegraeff et al. 2021a,b). The poisonous compounds directly impact aquatic ecosystems by triggering mass mortality events in both natural and farmed fish populations. Their presence disrupts coastal recreational activities and inflicts substantial financial damage on marine industries. Even non-toxic algal species contribute to harmful blooms when excessive growth leads to visible water discoloration, oxygen depletion, or sticky mucus production - all capable of severely disrupting ecological balance and coastal livelihoods. The Harmful Algal Event Database (HAEDAT) serves as the sole global repository documenting toxic bloom incidents across marine and freshwater systems, with significant disparities in regional reporting accuracy. Its records categorize algae-related phenomena that trigger regulatory interventions, incur financial losses, or alter ecosystem dynamics. These incidents encompass four operational definitions: water surface anomalies like colored patches or foam linked to socioeconomic disruptions from algal presence (toxic or benign); seafood contamination exceeding human safety thresholds from accumulated biotoxins; precautionary closures of fisheries or recreational areas due to algal overgrowth risks; and any algae-driven impacts on organisms, regardless of direct human health implications. Seafood biotoxin incidents (48%.) accounted for nearly half of total HAEDAT events across the globe. Among all events associated with seafood poisoning syndromes, Paralytic Shellfish Toxins (PST) contributed 35%, Diarrhetic Shellfish Toxins (DST) 30%, Ciguatera Poisoning (CP) and toxins from marine and brackish water cyanobacteria each accounted for 9%, Amnesic Shellfish Toxins (AST) represented 7%, and other toxins made up the remaining 10%. (Fig.1) (Hallegraeff et al. 2021b).

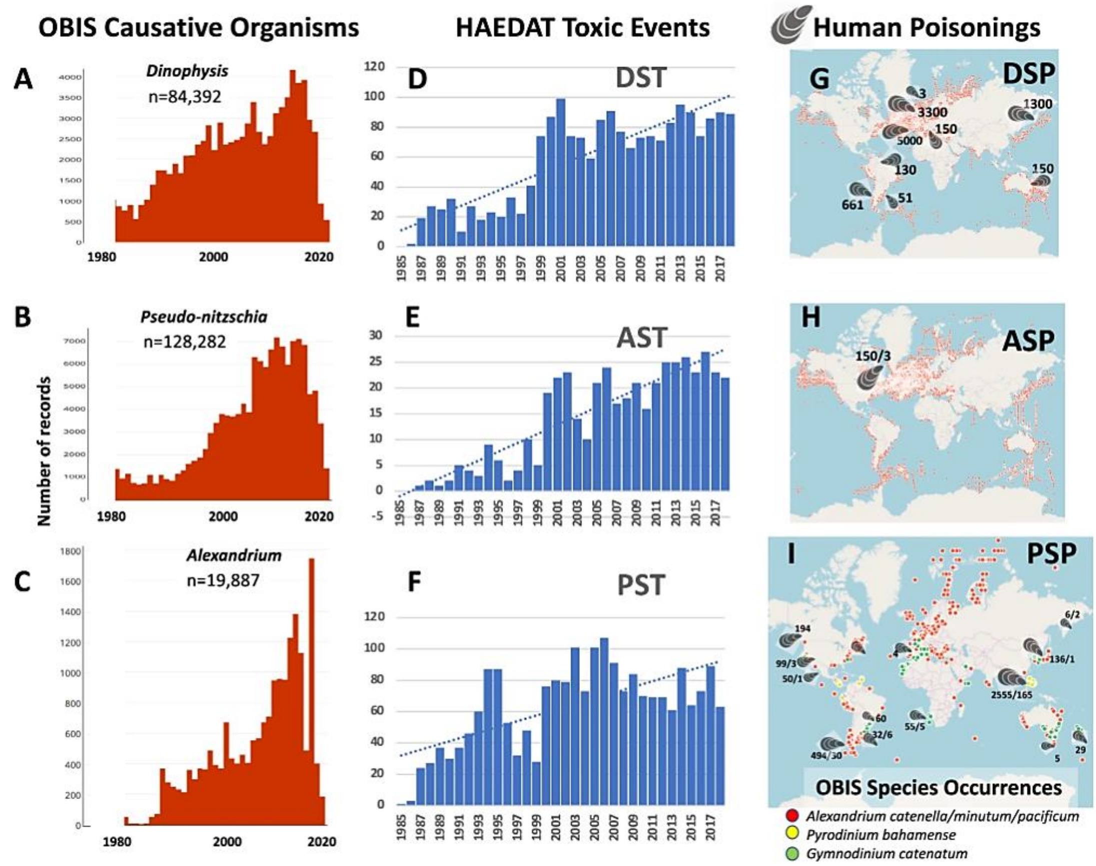


Figure 2-1 An increases global trend of HAB associated organisms, poisoning events and distributions of the toxin syndromes between 1985 and 2018. (A-C document the total number of global observations of causative microalgal organisms of *Dinophysis spp., Pseudo-nitzschia spp. and Alexandrium spp.*; D-F provid the number of records of HAEDAT database regarding toxic events of DST, AST and PST.; G–I show the distribution maps as of 2018 of *Dinophysis spp*. (DSP), *Pseudo-nitzschia spp*. (ASP) and *Alexandrium, Pyrodinium*, *Gymnodinium catenatum* (PSP) with red dots across the

globe. Toxic incidents that have led to human poisoning are represented on the map with shellfish icons, whose sizes correspond to the severity of the events. The first number shows the number of poisonings, the second number indicates fatalities. Specifically, for ASP, the notation 150/3 denotes 150 clinical cases with three fatalities) (Hallegraeff et al. 2021b).

The ecological impacts of HABs are profound and multifaceted. Toxins produced by harmful algae can bioaccumulate in marine organisms, such as fish, shellfish, and other invertebrates, leading to mass mortalities in marine life (Karlson et al. 2021). These toxins can also be transferred through the food web, impacting top predators, including marine mammals, seabirds, and even humans (Turner et al. 2021). Ingesting contaminated seafood can lead to a variety of shellfish poisoning illnesses. These conditions can lead to severe health complications and even death in some cases. Furthermore, some HABs are associated with aerosolized toxins that can be inhaled by people, causing respiratory issues, particularly in coastal communities (Patterson et al. 2016). For example, *Karenia brevis*, the species responsible for red tides in the Gulf of Mexico, can release toxic aerosols that cause respiratory irritation and exacerbate conditions like asthma in people living near affected areas (Jang et al. 2025). The socio-economic consequences of HABs are staggering. In regions heavily dependent on fisheries and aquaculture, HABs can result in massive losses. The red tide event along U.S. West Coast in 2015 led to an estimated $48.3 million losses (Anderson et al. 2021c).

Similarly, in Asia, coastal communities rely on shellfish harvesting and aquaculture, which can be severely impacted by HABs. The presence of toxins in seafood can lead to closures of fisheries, tourist beach restrictions, and the contamination of commercial seafood, all of which result in significant economic losses.

2.1.2 Environmental drivers of HABs

Microalgal communities in marine and coastal ecosystems are highly sensitive to environmental changes, with temperature, salinity, and nutrient availability being the most influential factors shaping their structure, diversity, and functionality. These factors not only regulate the growth and composition of microalgal populations but also play a pivotal role in the formation and intensity of HABs. Understanding how these environmental variables interact with microalgal communities is critical for predicting ecosystem responses to natural and anthropogenic disturbances, including climate change and nutrient pollution.

Temperature is one of the most significant environmental drivers of microalgal dynamics. In general, temperature significantly influences the physiology and metabolism of phytoplankton (Falkowski et al. 2004). Various species of microalgae thrive at specific temperatures. For instance, widely cultivated algal species like *Chlorella*, *Scenedesmus*, *Chlorella vulgaris*, *Navicula*, *Chlamydomonas*, *Haematococcus*, and *Monoraphidium* typically flourish in temperatures between 15 and

35°C (Singh & Singh 2015). Microalgal communities react differently to specific temperatures based on their strain's optimal temperature, exhibiting negative, neutral, or positive responses (Kholssi et al. 2023). Rising water temperatures are expected to enhance both the abundance and diversity of *Gambierdiscus* and *Fukuyoa* species in the Gulf of Mexico and along the southeastern U.S. Atlantic coast. In contrast, species adapted to lower temperatures in the Caribbean Sea would likely decline in prevalence. However, their distribution is projected to extend further north into the Gulf of Mexico and potentially reach the western Atlantic (Kibler et al. 2015). Elevated temperatures can also disrupt predator-prey relationships, reduce grazing pressure on microalgae, and shift competitive advantages among species, thereby altering community dynamics (Anderson et al., 2002). Additionally, warmer temperatures often lead to stronger water column stratification, reducing vertical mixing and nutrient exchange, which can further stimulate harmful algal species that are adapted to low-nutrient conditions.

Temperature and salinity are two environmental factors which are closely related to climate change. With the increase of seawater temperature, the salinity changes accordingly (Frame & Stone 2013). Salinity significantly influences the distribution and composition of microalgal communities, especially in estuarine and coastal regions where freshwater and seawater interact. Changes in salinity can create osmotic stress, limiting the growth of some species while promoting the dominance of halotolerant or halophilic species. For example, *Prorocentrum minimum* and *Karlodinium veneficum* are known to tolerate wide salinity ranges, enabling them to bloom in estuarine environments (Ajani et al. 2018; Zhang et al. 2008). Fluctuations in salinity caused by heavy rainfall, river discharge, or drought conditions can disrupt existing microalgal assemblages and facilitate the introduction and establishment of invasive or harmful species (Lazrak et al. 2024; Röthig et al. 2023).

Nutrient enrichment is another critical factor regulating microalgal community structure. Key nutrients, particularly nitrogen (N) and phosphorus (P), serve as essential resources for microalgal growth. Coastal eutrophication, often driven by agricultural runoff, wastewater discharge, and urbanization, can lead to excessive nutrient loading in aquatic ecosystems (Lie et al. 2011). The form and ratio of nutrients (e.g., N:P ratio) also influence species composition, with certain species favoring either nitrate- or ammonium-rich conditions (Lagus et al. 2004; Nhu Y et al. 2019). Moreover, nutrient limitation or imbalance can trigger toxin production in certain species such as *Prorocentrum hoffmannianum*, further elevating ecological and health risks (Accoroni et al. 2018).

The combined effects of temperature, salinity, and nutrients often interact in complex ways, amplifying their influence on microalgal community dynamics. Warming temperatures can intensify nutrient-driven eutrophication effects by accelerating nutrient cycling and stimulating harmful algal species adapted to high nutrient and warm conditions. Similarly, altered precipitation patterns due to climate change can modify salinity regimes and nutrient inputs, creating conditions conducive to HAB outbreaks. Therefore, it is essential to consider the synergistic effects of these environmental factors when assessing microalgal community responses.

2.1.3 Assembly process in shaping the algal community

Understanding the relative contribution of different assembly processes in shaping microalgal communities over spatiotemporal scales is crucial for understanding how these communities respond to local, regional, and global changes (Skouroliakou et al. 2022). Deterministic and stochastic processes explain the assembly of microbial communities (Nemergut et al. 2013; Zhou & Ning 2017). Deterministic processes generally refer to factors that affect community structure through environmental selection and species interactions (Chesson 2000; Fargione et al. 2003). Environmental filtering plays a key role in deterministic processes by emphasizing how environmental factors like temperature, salinity, light, and nutrient availability influence the distribution of species. Water temperature directly affects the growth and reproduction of algal species (Matula et al. 2022). While some algae species are thermally sensitive, thermotolerant algae (cyanobacteria, green algae, certain species of dinoflagellates, etc.) can prevail in communities, especially in warmer waters (Rossi et al. 2023). Being more tolerant to high temperatures than other algae, they tend to increase reproduction at higher temperatures, which modulates the composition of the community. The distribution of different species also depends on salinity variations; some species of algae perform better under low salinity while others are adapted to high salinity (Mo et al. 2021). Nutrient concentration is another critical environmental factor directly affecting algal growth rates and community composition, especially the concentrations of nitrogen and phosphorus, which often determine the prosperity of certain algal populations. In addition to environmental factors, species interactions are also a significant component of deterministic processes (Zhou & Ning 2017). The community structure is often affected by competitive, predatory, and symbiotic interactions among species (Solomon et al. 2022). Certain algal species may dominate specific ecological niches through competitive advantages, inhibiting the growth of other species. Some algae enhance their survivability through symbiotic relationships with microbial communities, obtaining nutrients. Additionally, predatory pressures can alter algal community structures, especially when planktonic predators consume algae (Behrenfeld et al. 2021; Thompson et al. 2024).

Stochastic ecological processes including dispersal, speciation, and ecological drift, which typically drive species composition and diversity (Chase & Myers 2011; Stegen et al. 2012). Dispersal refers to the movement of species across different areas, while speciation describes the generation of new genetic variation. Ecological drift, on the other hand, is the random fluctuations in the abundance of species over time, driven by stochastic processes (Fodelianakis et al. 2021). Fluctuations in the abundance of some species within such communities may take place without any reference to environmental selection, and, hence, be purely due to random factors, when communities are in dynamic equilibrium. For instance, some algal species might rapidly occupy ecological niches due to initial accidental advantages (such as fewer predators or higher initial biomass), becoming dominant in the community, a phenomenon known as the priority effect (Debray et al. 2022; Reijenga et al. 2021). Gene flow is also part of stochastic processes, especially when there is genetic exchange between multiple communities (Arnold et al. 2022). Genetic diversity among species can be promoted by gene flow, and thus community structure and function (Irwin et al. 2022). Additionally, dispersal events are an important part of stochastic processes, particularly in open waters or large water bodies, where species dispersal is often unpredictable (Albright & Martiny 2018). Some algae may enter new habitats due to random dispersal events, profoundly impacting community structure. Deterministic and stochastic processes are not independent of each other but are intertwined and complementary (Skouroliakou et al. 2022). Environmental selection and species interactions usually collaborate with stochastic processes in shaping community structures in most ecosystems (Li et al. 2022b; Menéndez-Serra et al. 2023). For example, in ecosystems with stable environmental conditions, such as temperature and salinity, deterministic processes might be the dominant force, but in dynamic, fast-changing ecosystems, stochastic processes might play a larger role. In community succession, During community succession, deterministic and stochastic processes might gradually transition over time (Hanusch et al. 2022; Mården et al. 2017). During the early stages of a community, stochastic processes may be the principal dynamic processes due to high species diversity and unstable environmental conditions. However, as the community reaches a stable phase, deterministic processes may become the dominating force as the impact of environmental factors on species selection becomes more pronounced. At this stage, the competitive and cooperative relationships among species will determine the final form of the community structure.

2.2 Advances in monitoring and detection techniques for HABs species

2.2.1 Traditional morphological identification

The identification and monitoring of microalgal species, particularly in the context of HABs, have historically relied on traditional morphological methods. Traditional morphological identification is based on the microscopic examination of physical and structural characteristics of algal cells (Manoylov 2014). Current taxonomy and ecology of algae have been based on this approach, for the most important information of species diversity and ecological functions. However, the efficacy of this method is limited by several factors. Firstly, the morphological features of many microalgae can be highly variable, depending on environmental conditions, which can lead to misidentification (Fawley & Fawley 2020). Moreover, some algal species exhibit minimal morphological variations, which complicates the identification of closely related species or different life stages within the same species (Krivina & Temraleeva 2020). Furthermore, traditional microscopy is labor intensive, requiring taxonomic expertise, and can be time-consuming, which is impractical during urgent assessments of HABs where rapid response is critical.

2.2.2 DNA-based molecular techniques

Advances in molecular techniques have significantly transformed the landscape of algal research, offering new insights and overcoming many limitations inherent in traditional methods. The application of DNA barcoding as a tool for species identification has become routine use across the biological fields including phycology (Kowalska et al. 2019; Steinhagen et al. 2023). DNA barcoding refers to sequencing a short, standard length of DNA from a sample and matching it against reference sequences in a database (Antil et al. 2023). This technique allows for precise species identification, regardless of the life stage or condition of the organism, thereby addressing some of the key challenges of morphological methods. In microalgal research, commonly targeted genes for barcoding include the 16S rRNA for prokaryotic cyanobacteria and the 18S rRNA gene for eukaryotic algae (Karlusich et al. 2022).

Metabarcoding extends the principles of DNA barcoding to community-level assessments, enabling the identification of multiple species within environmental samples simultaneously (Jiménez-García et al. 2023) . This technique combines high-throughput sequencing with specific molecular markers to identify and quantify the diversity of microbial communities. High-throughput sequencing (HTS) techniques, including metabarcoding, offer significant advantages for the early detection and monitoring of HABs (Zaytsev et al. 2024). HTS can process numerous samples quickly and provide data on species composition and abundance at a much finer scale than traditional methods (Lopes Dos Santos et al. 2022). This rapid processing capability is crucial for the timely management of HABs, allowing for early warning and mitigation measures to be implemented before blooms reach harmful levels. Moreover, HTS can detect low-abundance species that might be overlooked by microscopy, providing an early indication of a potential bloom (Wang et al. 2022). The development of comprehensive, curated databases containing reference sequences is critical for the success of metabarcoding. Such databases allow researchers to assign taxonomy to the vast amounts of sequence data generated, facilitating rapid assessments of biodiversity and community structure. Databases such as the SILVA (ribosomal RNA sequences) and the Protist Ribosomal Reference database (PR2) have been instrumental in storing and providing access to reference sequences that enhance the accuracy and efficiency of species identification (Quast et al. 2013; Guillou et al. 2013).

In addition to 18S amplicon sequencing, metagenomic sequencing and metatranscriptome sequencing have also become essential molecular tools for analyzing the structural and functional characteristics of microalgal communities. 18S amplicon sequencing achieves high-throughput analysis of microalgae diversity and community composition in environmental samples by specifically amplifying the conserved region of the small subunit ribosomal RNA gene. This technology has advantages of low cost, simple operation process and the ability to process large-scale samples, and is suitable for ecological monitoring, geographical distribution pattern analysis and time series research. However, limited by the species resolution of the 18S rRNA gene, some microalgae groups with similar systematic classification positions or highly conserved gene sequences are difficult to accurately distinguish by this method. In addition, the bias in the PCR amplification process may lead to bias in population abundance estimation, and this technology only provides "existence" information and cannot reveal the functional characteristics of microalgae. In contrast, metagenomic sequencing directly extracts the total DNA of all organisms in environmental samples without the need for specific primer amplification, thereby reducing amplification bias and being able to comprehensively depict the population composition of microalgae and their associated microorganisms, while analyzing their potential functional genomic characteristics (Aplakidou et al. 2024). Metagenomic data allows researchers to reconstruct partial or complete microalgae genomes (i.e., MAGs), and then conduct in-depth studies on metabolic pathways, environmental adaptation mechanisms, and microbial interaction networks. However, since environmental samples usually have extremely high biological complexity, especially in microalgae communities accompanied by a large number of bacteria, fungi, and viruses, the assembly and directional binning process of metagenomic data is extremely complex, and the coverage of low-abundance microalgae populations is often insufficient, resulting in the risk of information loss in subsequent analysis (Navgire et al. 2022). At the same time, the high cost of metagenomic sequencing also limits its application in large-scale sample screening. In contrast, metatranscriptome sequencing starts with total RNA, and high-throughput sequencing is performed after rRNA removal or mRNA enrichment, which can capture the active expression profiles of microalgae and related microorganisms in the environment under specific spatiotemporal conditions (Wahl et al. 2022). Metatranscriptome data not only reveals the level of "who is active", but also provides dynamic information at the functional level, which helps to analyze the transcriptional response of microalgae to environmental changes (such as light, temperature, salinity, nutrient changes, etc.), as well as the symbiotic, parasitic, or competitive relationship between microalgae and other microorganisms (Berman et al. 2020). However, since mRNA is easily degraded, metatranscriptomics have extremely high requirements for sample collection, preservation, and RNA extraction and purification. At the same time, there are still a large number of rRNA residues in environmental transcriptome data, resulting in a limited proportion of effective information. In addition, changes in gene expression levels may be due to environmental induction or fluctuations in community structure, which adds additional complexity to data interpretation. Therefore, in actual research design, the three technologies are often used in a reasonable combination according to research objectives and resource conditions: if the main focus is on the species diversity and community structure changes of microalgae, 18S amplicon sequencing is still the first choice with high cost performance; if the research focus is on the genomic characteristics and metabolic potential of microalgae and their associated microorganisms, metagenomic sequencing is more suitable; if it is necessary to reveal the functional dynamics of microalgae under environmental stress or ecological interaction, metatranscriptome sequencing is indispensable. It is worth noting that with the development of sequencing technology and the continuous improvement of multi-omics joint analysis methods, future microalgae research will tend to integrate and analyze amplicon, metagenomic and metatranscriptome data to build a panoramic understanding from community structure to functional dynamics.

2.2.3 The database construction of HAB species

The downstream interpretation of molecular surveys relies heavily on the accuracy and completeness of the reference databases used for classifying taxonomy (Leray et al. 2022). The construction of comprehensive reference databases for harmful and toxigenic microalgae has emerged as a critical component in the effective monitoring and management of HABs. These databases not only facilitate accurate species identification but also enhance our understanding of the ecological impacts associated with algae. A comprehensive and accurate database should contain well-curated, vetted sequences that cover a wide range of known microalgal species, including those that are less common but potentially harmful. The quality of the database entries, including the correctness of the sequence data and the taxonomic resolution, directly impacts the success of molecular identification techniques such as DNA barcoding and metabarcoding. Mistakes in sequence annotation or the inclusion of poorly resolved sequences can lead to erroneous species identification, which in turn affects ecological studies and management decisions.

Databases enable researchers to quickly identify the presence of harmful or toxic microalgae in water samples using molecular techniques. This capability is crucial for the early detection of HABs, allowing for timely interventions and mitigation strategies that can prevent ecological and economic damage. By providing detailed taxonomic and genetic information, these databases facilitate ecological studies that explore the distribution, diversity, and dynamics of algal populations. Understanding the impact of environmental changes on algal biodiversity requires robust baseline data, which well-maintained databases can provide. Consequently, the development and application of databases for harmful and toxic microalgae are of great significance in addressing the global challenge posed by HABs. While there are significant challenges in achieving accurate species identification, the development of reliable and comprehensive databases is a critical step forward. These databases not only support effective monitoring and management but also enhance our scientific understanding of algal biology and ecology. As molecular techniques continue to advance, the importance of these databases will only grow, underscoring the need for ongoing investment in their development and maintenance.

2.3 Plastisphere: a novel microhabitat in coastal ecosystems

The pervasive presence of plastics poses a threat to various ecosystems around the world. Their widespread presence is attributed to their ability to travel long distances by ocean currents or wind, reaching even the most remote areas of the planet. Plastic debris colonized by biofilm-forming microbial communities are known as the “plastisphere”. The revelation that this unique substrate can aid microbial dispersal has piqued interest in the ground of microbial ecology.

2.3.1 Global plastic pollution and the formation of the plastisphere

The relentless accumulation of plastic waste in the world’s oceans represents one of the most pressing environmental challenges of the 21st century (Geyer et al. 2017; Law 2017). Plastics have become the most common form of marine litter, with increasing amounts of post-consumer plastic waste inevitably entering the oceans from recycling and waste streams (MacLeod et al. 2021; Stubbins et al. 2021; Weiss et al. 2021; Li et al. 2021b). Plastic pollution is pervasive across all marine environments, from the poles to the equator and from the sea surface to the deep sea sediments (Kanhai et al. 2019). Plastic debris ranges in size from large, visible items to microplastics less than 5 millimeters in diameter. These plastics originate from both land-based and marine sources, including consumer and industrial waste that escapes waste management and treatment processes. Ocean currents carry these plastics across vast distances, leading to their accumulation in remote areas far from their original source and often converging in subtropical gyres where they form large floating “garbage patches” (Lebreton 2022). Currently, over 400 million tonnes of plastic waste are produced globally each year. As estimated, approximately 5-13 million tonnes of plastic waste enter the ocean from coastal land annually (Jambeck et al. 2015). This causes more than 170 trillion pieces weighted approximately 2 million tonnes floating in the world's ocean (Eriksen et al. 2023). If no effective action, the plastic stock in the ocean could triple by 2040 (Lau et al. 2020).

The buoyancy, hydrophobic, organic, and durable surface of plastics in the environment provide a unique niche for microorganisms, resulting microecosystems with plastic as the matrix, termed "the plastisphere" (Amaral-Zettler et al. 2020; Zettler et al. 2013).. The huge stock of plastic waste in the environment, combined with the ongoing emission, indicates that the plastisphere is a habitat with a vast and expanding total area (Li et al. 2024a,c). It consists of a variety of microorganisms, including bacteria, algae, fungi, and small invertebrates (Wang et al. 2021a). These organisms colonize plastics in a biofilm, a robust layer of cells and extracellular matrix, adhering to the plastic surface. The formation of the plastisphere begins almost immediately after the plastic enters the water, with pioneer species attaching to the surface, followed by a succession of other organisms that form a complex, multi-species community. The community structure of the plastisphere is distinct from surrounding water column biota, often harboring species not commonly found in other marine environments (Pang et al. 2023). Growing evidence shows that the plastisphere may pose critical threats to the ecosystem function and biological health by enriching biogeochemical process-involved microorganisms as well as harmful species like disease-causing microorganisms and antibiotic resistant bacteria (Bergmann et al. 2022; Bhagwat et al. 2021; Dey et al. 2022). The unique conditions of the plastisphere, including the availability of new niche spaces and the presence of plastic additives, might encourage the evolution of novel biochemical pathways (Yu et al. 2023a). The durability of synthetic polymers, the building blocks of plastics, ensures that they persist in the marine environment for decades or even centuries. Unlike natural materials, plastics do not biodegrade but instead photodegrade under sunlight, breaking down into smaller and smaller pieces while never completely disappearing. This slow degradation process leads to the continuous accumulation of microplastics, which are ingested by marine organisms and can enter the food chain, leading to broader ecological consequences.

2.3.2 Potential ecological risks of the plastisphere

The ecological implications of the plastisphere are profound and multifaceted. Plastics, due to their durable and persistent nature, provide a unique substrate for microbial colonization in marine environments. These communities differ significantly from those found on natural substrates, partly due to the distinct chemical composition of plastics and their ability to persist and accumulate in marine environments. As the prevalence of plastic debris continues to increase globally, understanding the ecological implications of the plastisphere becomes critically important.

One of the primary ecological risks of the plastisphere is acting as a vector for invasive species. Plastics can travel long distances across oceans, carrying with them a wide range of colonizing organisms, which may not naturally occur in the habitats they reach. Habitat alterations can occur when non-native introduced species either compete with or displace indigenes marine life leading to the reduction of biodiversity and interference of local community structures. Moreover, animal, plant, and human pathogens are enriched in the plastisphere indicate that the plastisphere presents a significant biosecurity risk and a potential threat to human health (Li et al. 2024a). Pathogens harbored on plastic debris can infect animals, particularly aquatic species through filter feeding, adversely impacting their growth, behavior, and dietary habits (Jacob et al. 2020; Li et al. 2021a). There is evidence that even microplastics can be ingested and accumulate in terrestrial plants (Li et al. 2020). The exposure of plants to pathogens associated with the plastisphere could be a key factor behind reports of diminished crop yields(Zhang et al. 2020). Furthermore, reduced plant biomass has been linked to the presence of plastic contaminants (Zhang et al. 2022). The prevalence of pathogens in the plastisphere underscores an elevated risk of disease transmission. Plastics are known to absorb and concentrate persistent organic pollutants (POPs) from the marine environment, including PCBs, DDT, and PAHs (Koelmans et al. 2013; Wang et al. 2021b). Harmful compounds such as the phthalate plasticizers, bisphenol A, and metal additives such as zinc, copper, and nickel, can be released during plastic degrades process (Hahladakis et al. 2018). These chemicals can become part of the plastisphere and enter the food web through microorganisms that colonize plastics. This incorporation leads to bioaccumulation and potentially biomagnification as toxins move up the food chain, reaching higher trophic levels and posing significant risks to marine wildlife. These pathogens and POPs might not only affect marine organisms but could also impact coastal communities and industries, such as fisheries and aquaculture, leading to economic losses and public health concerns. The complex interaction highlights the extensive impact of plastic pollution on ecosystem and human health (Li et al. 2024a).

Microbial communities within the plastisphere can significantly impact biogeochemical processes, particularly those related to carbon, nitrogen, and phosphorus cycling. The metabolic activities of these microorganisms can alter the rates of biogeochemical transformations in marine environments, potentially impacting nutrient availability, primary productivity, and overall ecosystem function. Regions with high plastic contamination tend to exhibit greater plastic biodegradation potential. Additionally, the accumulation of plastic residues has been shown to negatively impact soil organic matter in agricultural lands (Zhang et al. 2020). Another noteworthy discovery is that the higher degradation rates within the plastisphere may contribute to the release of greenhouse gases such as CO_2 and CH_4, which are by-products of plastic decomposition. The plastisphere also demonstrates enhanced potential for nitrogen-related processes, including denitrification, nitrogen respiration, and nitrate reduction, particularly within freshwater ecosystems (Li et al. 2024a). These processes increase the likelihood of producing a potent greenhouse gas with a global warming potential, like N_2O (Kuypers et al. 2018; Repo et al. 2009). The metabolites released from the plastisphere into the surrounding environment disrupt the natural nutrient cycles. The potential for plastic to alter the metabolism of organic compounds, along with its significant influence on the nitrogen cycle, indicates that the plastisphere could disrupt biogeochemical processes and potentially exacerbate climate change (Bhagwat et al. 2021; Su et al. 2022). Beyond its ecological impacts, the accumulation of plastic waste and the ensuing formation of the plastisphere can also degrade the natural beauty of marine environments, potentially impacting tourism and recreational activities. Beaches and coastal areas littered with plastic waste are less appealing to tourists, which can result in significant economic losses for communities that rely on tourism revenue.

2.3.3 The HAB species in the plastisphere: emerging concerns

Previous studies on plastisphere microbiology and associated risks mainly focus on bacteria, with comparatively less attention given to fungi. Other life forms, such as microalgae, a key component of aquatic ecosystems, are poorly understood in the plastisphere. The convergence of two significant environmental issues, HABs and plastic pollution, presents new challenges for marine ecosystems globally. The plastisphere, a complex microbial community that colonizes floating plastic debris, provides a unique habitat that can facilitate the spread of harmful algal species and their toxins. In 2003, marine microplastics were recognized for the first time as potential migration vectors for potential harmful dinoflagellates such as *Ostreopsis* sp. and *Coolia* sp. under macroscopic observation (Mercedes et al. 2003). One square centimeter of the plastic surface can harbor more than 80,000 diatom cells, pinpointing that marine plastispheres act as a suitable habitat for microalgae containing substantial microalgal biomass (Casabianca et al. 2019). The stable and durable nature of plastics offers a persistent platform for these algae, potentially allowing them to thrive and proliferate outside their usual geographic and temporal boundaries. The long-distance mobility of plastics across oceanic regions enables them to serve as carriers, transporting HAB species to previously unaffected areas, where these species may establish new outbreaks (Do Prado Leite et al. 2022). This capability is particularly concerning for regions previously unaffected by specific types of HABs, as it could lead to the introduction of new ecological threats to those ecosystems. Another critical concern is the accumulation of algal toxins on plastics. Studies have shown that plastics can adsorb and concentrate not only chemical pollutants but also biotoxins produced by toxic algae (Pires et al. 2025). This adsorption process can lead to higher concentrations of toxins on plastic surfaces than in surrounding waters, posing significant risks to marine life that ingest plastic debris. The ingestion of these toxin-loaded plastics by marine organisms can lead to bioaccumulation and biomagnification of toxins through the food web, impacting species up to and including humans. The risk is compounded by the potential for these toxins to be released into environments where they were previously absent, carried over vast distances by floating plastics. This scenario not only spreads the geographic impact of HABs but also complicates efforts to manage and mitigate their effects. Moreover, climate change adds a new dimension to this complex interaction. Global climate change exacerbates the uncertainty of marine environments, potentially altering basic environmental parameters such as ocean temperature, salinity, and circulation patterns, which in turn indirectly or directly affect the distribution and impact of plastic pollution and harmful algal blooms.

Chapter 3 Methodology

This section provides general information of database construction, sample collection, and detailed descriptions of the biological, statistical analyses and chemical applied in this study.

3.1 Construction of HTMaDB

3.1.1 Collection of HAB species

At the Fourth Session of the IOC Intergovernmental Panel on Harmful Algal Blooms, Vigo, Spain, 30 June-2 July 1997, it was decided to establish a Task Team on Algal Taxonomy with the aim of providing an agreed reference list of harmful algal species, including correct citation of the author(s), date of valid publication, and a list of synonyms. IOC-UNESCO Taxonomic Reference List of Harmful Micro Algae provides a reference for the use of names and information on each species of toxic microalgae. The list contains at the moment species producing toxins or toxic effects, and a few species suspected to form toxins. Note that a toxic species may not produce toxins everywhere it occurs. However, the reference list does not include species that cause harm due to high biomass. To include the harmful bloom-forming but not toxic species, we conducted literature review by searching publications with keywords “harmful microalgae” OR “toxic microalgae” OR “HAB species” OR “harmful and toxic algae” in Web of Science citation database Core Collection. After manually checking the collected 197 publications (Appendix 1), we further added 101 non-toxic but bloom causing species to the database. The detailed collected HAB species was provided in

Table 3-1.

3.1.2 18S sequence database construction for HAB species

3.1.2.1 Introduction of public databases

The International Nucleotide Sequence Database Collaboration (INSDC) is a global collaboration of independent governmental or non-profit organisations that manage nucleotide sequence databases capturing and preserving nucleotide sequence information and annotations to create a comprehensive collection that preserves the scientific record and enables broad sharing of such data (International Nucleotide Sequence Database Collaboration). INSDC Participating Databases including European Molecular Biology Laboratory (EMBL)-Bank, National Center for Biotechnology Information (NCBI)-GenBank, and DNA Data Bank of Japan (DDBJ). These three organizations exchange data on a daily basis. Although the three databases provide a wide range of sequence data, specialized databases such as SILVA and PR2 offer more in-depth and specialized resources in specific fields.

SILVA (from Latin silva, forest) database provides comprehensive, quality checked and regularly updated datasets of aligned small (16S/18S, SSU) and large subunit (23S/28S, LSU) ribosomal RNA (rRNA) sequences, which are widely used in microbial classification and ecological research (Quast et al. 2013). The SILVA databases are made available as releases, rather than being updated continuously, to enhance the comparability of the studies employing these databases. Each release is numbered according to the EMBL-Bank release from which the sequence data were extracted and is permanently available for download via the SILVA website. The dataset encompasses a broad range of biological groups, including bacteria, archaea, and eukaryotes. The SILVA database includes taxonomic information, sequence data, and relevant functional annotations, facilitating users in conducting diversity analyses and phylogenetic studies.

The Protist Ribosomal Reference database (PR2) reference sequence database was initiated in 2010 in the frame of the BioMarks project from work that had developed in the previous ten years in the Plankton Group of the Station Biologique of Roscoff. The PR2 provides a unique access to eukaryotic small sub-unit (SSU) ribosomal RNA and DNA sequences, with curated taxonomy (Guillou et al. 2013). The database mainly consists of nuclear-encoded protistan sequences. However, metazoans, land plants, macrosporic fungi and eukaryotic organelles (mitochondrion, plastid and others) are also included because they are useful for the analysis of high-throughput sequencing data sets. Introns and putative chimeric sequences have been also carefully checked. Taxonomic assignation of sequences consists of nine unique taxonomic fields (from domain to species).

3.1.2.2 Collection of 18S full length from public databases

Advances in HTS have led to unprecedented growth in the amount of available sequencing data. Owing to existing reference databases such as SILVA and PR2, while widely used, exhibit notable limitations when it comes to the accurate identification and comprehensive coverage of harmful and toxic microalgae. Several key species known to be associated with HABs are entirely absent from these repositories. As a result, sequence alignment and taxonomic assignment using these databases may lead to incomplete characterization of harmful/toxic microalgal communities. To facilitate HAB research and related studies, we have developed the HTMaDB, comprehensive yet specific coverage of harmful and toxic algae taxa extracting from SILVA and PR2, which provides access to users for searching, downloading, aligning eukaryotic algal sequencing data. It offers enhanced taxonomic resolution and improved specificity for HAB-related organisms, thereby minimizing the risk of misidentification. The HTMaDB represents the first 18S full length sequence database for HAB species. Based on the scientific accepted species name, we extracted the full-length 18S sequences of the collected harmful and toxic taxa from eukaryotic microorganism databases (Silva 138.1 SSU and PR2 5.0.0 SSU Ref database). A total of 1346 sequences were obtained. We reorganized the taxonomic classification of the collected taxa by referring to AlgaeBase since inconsistent classification methods in different databases (M.D. Guiry & Guiry, G.M. 2024). The collected 18S full length sequences consist of 238 eukaryotic HAB species. The construction procedure was provided in Figure 3-1.

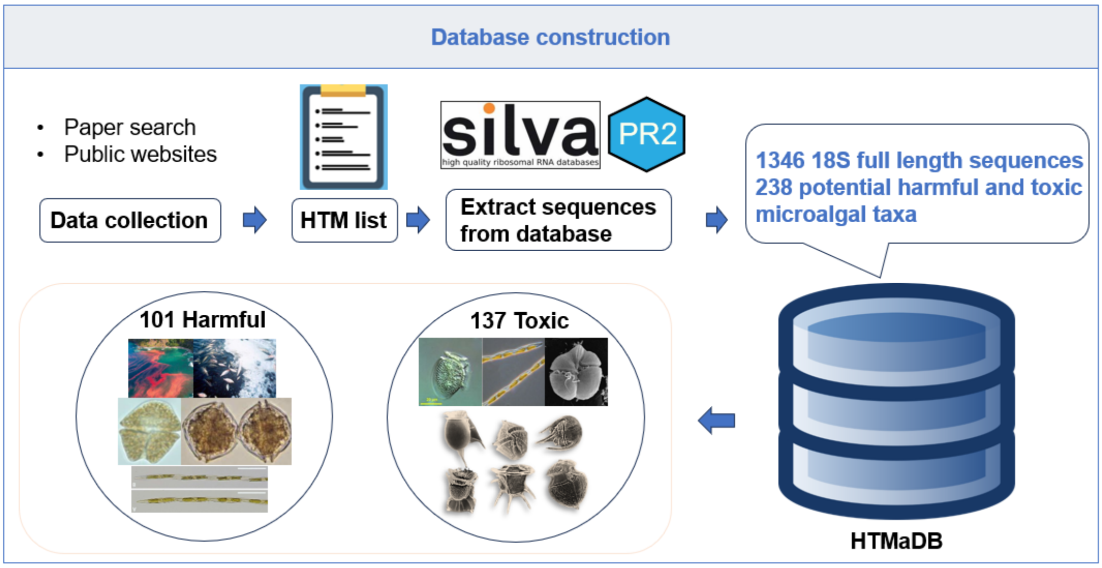


Figure 3-1 Flowchart of 18S sequence database construction of HTMaDB.

Table 3-1 The HAB species in the HTMaDB.

Type	Species				
Toxic	*Akashiwo sanguinea*	*Coolia malayensis*	*Gambierdiscus toxicus*	*Prorocentrum concavum*	*Pseudo-nitzschia caciantha*
	Alexandrium affine	*Dinophysis acuminata*	*Gonyaulax bohaiensis*	*Prorocentrum cordatum*	*Pseudo-nitzschia calliantha*
	Alexandrium andersonii	*Dinophysis acuta*	*Gonyaulax spinifera*	*Prorocentrum emarginatum*	*Pseudo-nitzschia cuspidata*
	Alexandrium australiense	*Dinophysis caudata*	*Gymnodinium catenatum*	*Prorocentrum hoffmannianum*	*Pseudo-nitzschia delicatissima*
	Alexandrium catenella	*Dinophysis fortii*	*Heterocapsa bohaiensis*	*Prorocentrum leve*	*Pseudo-nitzschia fraudulenta*
	Alexandrium fragae	*Dinophysis infundibulum*	*Heterocapsa borneoensis*	*Prorocentrum lima*	*Pseudo-nitzschia fukuyoi*
	Alexandrium hiranoi	*Dinophysis miles*	*Heterocapsa circularisquama*	*Prorocentrum mexicanum*	*Pseudo-nitzschia galaxiae*
	Alexandrium leei	*Dinophysis norvegica*	*Heterocapsa horiguchii*	*Prorocentrum panamense*	*Pseudo-nitzschia granii*
	Alexandrium limii	*Dinophysis tripos*	*Heterocapsa niei*	*Prorocentrum rhathymum*	*Pseudo-nitzschia kodamae*
	Alexandrium minutum	*Fukuyoa paulensis*	*Heterocapsa pygmaea*	*Prorocentrum texanum*	*Pseudo-nitzschia lundholmiae*
	Alexandrium monilatum	*Fukuyoa ruetzleri*	*Karenia bicuneiformis*	*Protoceratium reticulatum*	*Pseudo-nitzschia multiseries*
	Alexandrium ogatae	*Fukuyoa yasumotoi*	*Karenia brevis*	*Protoperidinium crassipes*	*Pseudo-nitzschia pseudodelicatissima*
	Alexandrium ostenfeldii	*Gambierdiscus australes*	*Karenia mikimotoi*	*Pyrodinium bahamense*	*Pseudo-nitzschia pungens*
	Alexandrium pacificum	*Gambierdiscus balechii*	*Karenia papilionacea*	*Pyrodinium bahamense var. compressum*	*Pseudo-nitzschia seriata*
	Alexandrium pseudogonyaulax	*Gambierdiscus belizeanus*	*Karenia selliformis*	*Takayama acrotrocha*	*Pseudo-nitzschia simulans*
	Alexandrium tamarense	*Gambierdiscus caribaeus*	*Karlodinium veneficum*	*Vicicitus globosus*	*Pseudo-nitzschia subcurvata*
	Alexandrium tamiyavanichii	*Gambierdiscus carolinianus*	*Lingulodinium polyedra*	*Chattonella marina*	*Pseudo-nitzschia turgidula*
	Alexandrium taylorii	*Gambierdiscus carpenteri*	*Margalefidinium fulvescens*	*Chattonella marina var. antiqua*	*Chrysochromulina leadbeateri*
	Amphidinium carterae	*Gambierdiscus cheloniae*	*Margalefidinium polykrikoides*	*Chattonella marina var. ovata*	*Phaeocystis globosa*
	Amphidinium gibbosum	*Gambierdiscus excentricus*	*Ostreopsis ovata*	*Chattonella subsalsa*	*Phaeocystis pouchetii*

	Amphidinium klebsii	*Gambierdiscus holmesii*	*Ostreopsis rhodesiae*	*Fibrocapsa japonica*	*Prymnesium calathiferum*
	Amphidinium operculatum	*Gambierdiscus honu*	*Ostreopsis siamensis*	*Heterosigma akashiwo*	*Prymnesium faveolatum*
	Amphidoma languida	*Gambierdiscus lapillus*	*Pfiesteria piscicida*	*Nitzschia bizertensis*	*Prymnesium parvum*
	Azadinium dexteroporum	*Gambierdiscus lewisii*	*Pfiesteria shumwayae*	*Pseudochattonella farcimen*	*Prymnesium polylepis*
	Azadinium poporum	*Gambierdiscus pacificus*	*Phalacroma mitra*	*Pseudochattonella verruculosa*	*Prymnesium zebrinum*
	Azadinium spinosum	*Gambierdiscus polynesiensis*	*Phalacroma rotundatum*	*Pseudo-nitzschia australis*	
	Centrodinium punctatum	*Gambierdiscus scabrosus*	*Polykrikos hartmannii*	*Pseudo-nitzschia batesiana*	
	Coolia canariensis	*Gambierdiscus silvae*	*Prorocentrum cassubicum*	*Pseudo-nitzschia brasiliana*	
Harmful	*Alexandrium cohorticula*	*Chaetoceros tenuissimus*	*Gymnodinium aureolum*	*Proboscia alata*	*Thalassiosira curviseriata*
	Alexandrium margalefii	*Chaetoceros throndsenii*	*Gymnodinium impudicum*	*Prorocentrum donghaiense*	*Thalassiosira rotula*
	Alexandrium insuetum	*Chaetoceros tortissimus*	*Protodinium simplex*	*Prorocentrum micans*	*Thalassiosira lundiana*
	Asterionellopsis glacialis	*Chaetoceros lorenzianus*	*Guinardia delicatula*	*Prorocentrum triestinum*	*Thalassiosira mala*
	Aureococcus anophagefferens	*Chaetoceros wighamii*	*Guinardia flaccida*	*Prorocentrum dentatum*	*Thalassiosira minima*
	Aureoumbra lagunensis	*Coscinodiscus radiatus*	*Halamphora coffeiformis*	*Prorocentrum redfieldii*	*Thalassiosira minuscula*
	Blixaea quinquecornis	*Coolia monotis*	*Heterocapsa triquetra*	*Prorocentrum gracile*	*Thalassiosira punctigera*
	Chaetoceros affinis	*Cylindrotheca closterium*	*Heterocapsa rotundata*	*Pseudocochlodinium profundisulcus*	*Thalassiosira weissflogii*
	Chaetoceros atlanticus	*Cyclotella meneghiniana*	*Heterocapsa pygmaea*	*Pyrophacus steinii*	*Thalassiosira pseudonana*
	Chaetoceros constrictus	*Dictyocha fibula*	*Lauderia annulata*	*Scrippsiella acuminata*	*Thalassiosira gravida*
	Chaetoceros convolutus	*Dictyocha speculum*	*Lepidodinium chlorophorum*	*Scrippsiella trochoidea*	*Thalassionema nitzschioides*
	Chaetoceros curvisetus	*Dinophysis hastata*	*Leptocylindrus danicus*	*Skeletonema tropicum*	*Tripos dens*
	Chaetoceros danicus	*Phalacroma rapa*	*Leptocylindrus minimus*	*Skeletonema costatum*	*Tripos furca*
	Chaetoceros debilis	*Diplopsalis lenticula*	*Levanderina fissa*	*Skeletonema marinoi*	*Tripos fusus*
	Chaetoceros decipiens	*Dunaliella salina*	*Lithodesmioides polymorpha*	*Skeletonema menzelii*	*Tripos lineatus*
	Chaetoceros diadema	*Eucampia zodiacus*	*Noctiluca scintillans*	*Skeletonema pseudocostatum*	*Tripos muelleri*
	Chaetoceros laevisporus	*Eutreptiella gymnastica*	*Nitzschia longissima*	*Takayama pulchella*	*Tryblionella compressa*
	Chaetoceros pseudocurvisetus	*Euglena viridis*	*Ostreopsis lenticularis*	*Takayama xiamenensis*	

Chaetoceros rostratus
Chaetoceros socialis
Chaetoceros simplex
Gonyaulax polygramma
Gonyaulax verior
Gonyaulax digitale
Paralia sulcata
Plagioselmis prolonga
Plagioselmis nannoplanctica
Teleaulax acuta
Tenuicylindrus belgicus
Thalassiosira allenii

3.1.3 Taxonomic composition and diversity of the HTMaDB

Among 238 eukaryotic HAB species. 137 toxic microalgae encompass Dinoflagellates (99), Ochrophyta (30), and Haptophyta (8) with, whereas 101 harmful microalgae consist of Dinoflagellates (37), Ochrophyta (56), Cryptophyta (3), Chlorophyta (1), and Euglenozoa (2) at phylum level (Fig.3-2a). This indicates that dinoflagellates are the dominant contributor of toxins, whereas harmful algal blooms are primarily caused by Ochrophyta.

Among the toxic and harmful genera in the database, *Alexandrium* is the most abundant, with an obvious higher sequence count than others (Fig.3-2b). This well-known toxic genus is associated with PSTs, posing severe risks to marine organisms such as shellfish and fish, as well as to human health. *Gambierdiscus*, ranking second in abundance, is linked to ciguatoxins, which are major contributors to food chain contamination, particularly in tropical and subtropical marine ecosystems. *Skeletonema* and *Prorocentrum*, ranked third and fourth, respectively, have distinct ecological impacts. While *Skeletonema*, primarily a diatom, can contribute to eutrophication in high concentrations, *Prorocentrum* is frequently associated with the production of algal toxins. *Thalassiosira* and *Heterosigma* also exhibit strong presence in the database. *Thalassiosira*, a diatom, generally does not produce toxins but can exacerbate eutrophication when overabundant, whereas *Heterosigma* is a known toxic genus capable of producing substances lethal to fish. Genera with lower abundance, such as *Margalefidinium*, *Pfiesteria*, and *Cyclotella*, are less frequent but still noteworthy. For instance, *Pfiesteria* is associated with neurotoxin production, posing a significant threat to aquatic life, especially fish. This comprehensive assessment highlights the varying ecological and toxicological roles of these genera, emphasizing the importance of monitoring and managing their presence in marine ecosystems to mitigate potential risks.

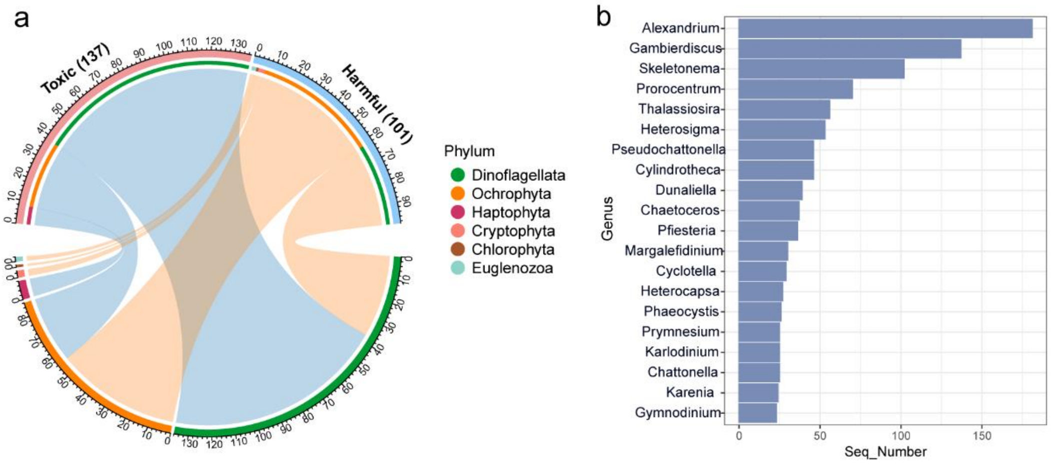


Figure 3-2 Taxonomic composition at phylum level (a) and top 20 genera based on sequence number (b) in constructed HTMaDB.

3.2 Marine sampling campaign

3.2.1 General information of the region studied

Hong Kong, a vibrant and densely populated coastal city in southern China, is known for its diverse marine ecosystems and thriving aquaculture industry. Its geographical location is at the mouth of the Pearl River in southern China, bordered by the South China Sea to the east and the Pearl River to the west, creating a diverse coastline that spans over 1,600 kilometers and includes various types such as bays, estuaries, beaches, and rocky shores. This supports a rich biological diversity, housing numerous species of fish, crustaceans, shellfish, and seaweed, making it an essential marine ecosystem.

Hong Kong located in the subtropical zone, significantly influenced by monsoon climate, with seasonal changes impacting the marine ecology and hydrological features.

3.2.2 Samling strategy

In this study, sample collection was first conducted in multiple sites under different areas during wet and dry seasons, to investigate the spatiotemporal distribution patterns and underlying mechanisms of the toxic algal community along Hong Kong's coastal waters using metabarcoding techniques. We collected seawater from 36 sampling sites of Hong Kong coastal ecosystems in wet and dry seasons (Figure 3-3 and Table 3-2). Surface seawater samples were collected using stainless-steel buckets and were transferred to 1-L polypropylene (PP) bottles. The bottles were covered with foil and kept in a portable icy incubator below 4°C during transportation to the laboratory. At each sampling location, a total of 5 L seawater samples were collected for the analysis of LATs (1 L), nutrients (1 L), phytoplankton density (1 L), and phytoplankton communities (2 L). Three bottles of Milli-Q water were also transported from the laboratory to the field site and then returned to the laboratory. These bottles served as field blanks to ensure negligible contamination. The samples were stored in a 4°C fridge and all samples were analyzed within 1 month. Detailed sampling information is provided in Appendix 2.

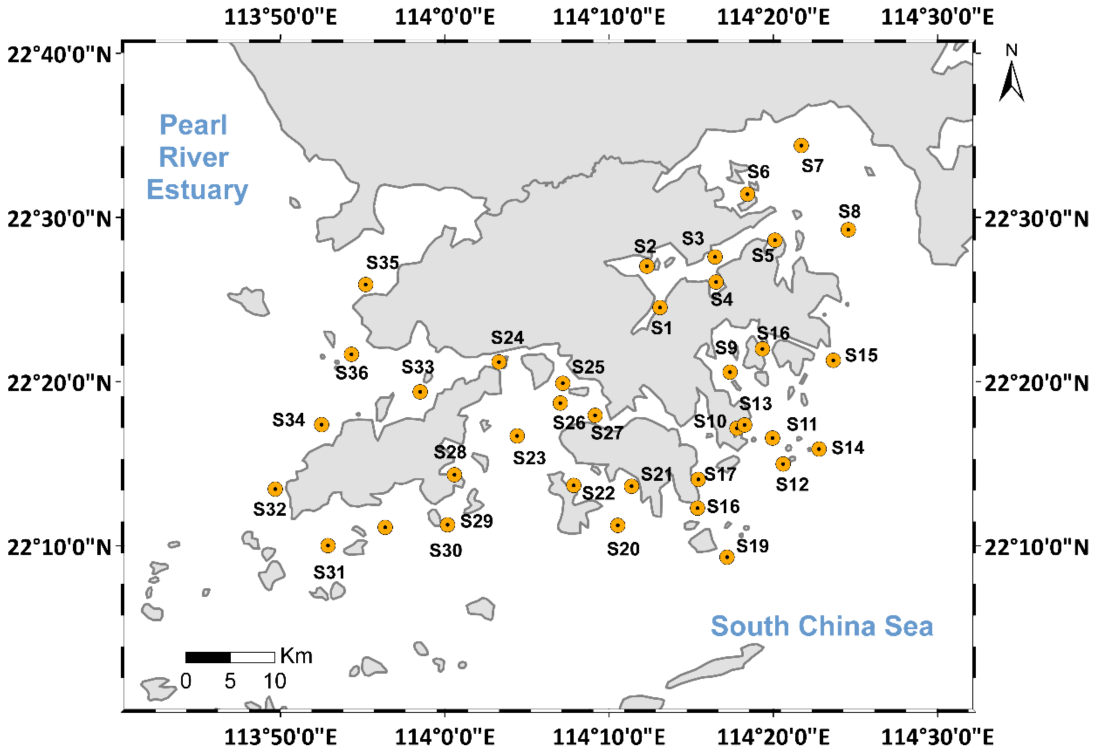


Figure 3-3 Sampling locations of surface seawater along the coastline of Hong Kong.

Table 3-2 Sampling period and number of samples in this study.

Location	Sampling period	Sample sites	Sample size
Eastern Waters	Wet season (August 2022)	S1-S15	30
	Dry season (February 2023)		
Southern Waters	Wet season (August 2022)	S16-S31	32
	Dry season (February 2023)		
Western Waters	Wet season (August 2022)	S32-S36	10
	Dry season (February 2023)		

To reveal the ecological impacts of microalgae in coastal plastisphere, plastic debris and its ambient seawater samples were paired collected from coastal areas of Qingdao and Hong Kong, China, in August 2021 and February 2022. A Manta trawl (mesh size = 333 µm) was employed to collect plastic debris. A plastic sample was retrieved every

30 minutes of trawling. The collected plastic debris from the trawl was transferred into a 50-mL centrifuge tube. Simultaneously, 2 L of surface seawater was collected in a sterile glass bottle. All the samples were immediately stored in a 4 °C ice box. A total of 92 plastic samples and 92 ambient seawater samples were obtained during the field sampling. Samling information is listed in Table 3-3. Detailed information can be found in Appendix 2.

Table 3-3 Sampling period and number of samples in this study.

Location	Sampling period	Sample type	Sample size
Hong Kong	Wet season (August 2021) Dry season (February 2022)	Plastic	38
	Wet season (August 2021) Dry season (February 2022)	Ambient	38
Qingdao	Wet season (August 2021) Dry season (February 2022)	Plastic	54
	Wet season (August 2021) Dry season (February 2022)	Ambient	54

We visually confirmed that all collected debris pieces were plastic. To verify this objectively, we randomly selected a subset of debris for polymer identification via Midinfrared photothermal (MIP) microscopy, also called optical photothermal infrared (O-PTIR) microscopy, an emerging tool for bond-selective chemical imaging of living biological and material samples. O-PTIR spectroscopy is utilized to identify plastic polymer types through spectral analysis. Potential plastic samples are collected and mounted onto a glass slide without cleaning or peroxide treatment. A laser, set to 48% IR power and 4.4% probe power, induces photothermal effects to generate an infrared spectrum based on absorption characteristics. Spectra are recorded across 941–3007

cm^{-1}, including diagnostic bands such as C-H stretching (2900 cm^{-1}) and aromatic C-H bending (700 cm^{-1}). Polymer identification is performed by comparing spectral peaks to the KnowItAll library (Wiley). This method provides a non-destructive approach for identifying plastic polymers, enabling rapid characterization of samples. All tested pieces were confirmed as plastic (Appendix 3). According to our previous study, we propose a novel, conceptual framework of the "microplastome", encompassing the entirety of plastic particles and their associated entities, such as chemicals and microbes, within a given sample, along with their collective environmental and toxicological (Li et al. 2024b). In this study, we extracted DNA from all collected plastic samples, followed by sequencing, in order to provide an integrated perspective to capture the real-world ecology of plastics.

3.2.3 Determination of environmental parameters

Salinity, temperature, pH, and dissolved oxygen (DO)of seawater in each sampling site were measured *in situ* using the YSI Professional Plus Quatro water quality meter (YSI Incorporated, Yellow Springs, OH, USA). Dissolved organic carbon (DOC) was measured using a total organic carbon analyser (Elementar Acquray TOC cube, Frankfurt, Germany). Dissolved organic carbon (DOC) was measured using a total organic carbon analyser (Elementar Acquray TOC cube, Frankfurt, Germany). The concentrations of nutrients, including NH_4^+, NO_2^-, NO_3^- SiO_3^{2-}, and PO_4^{3-} were determined in the laboratory by a continuous flow autoanalyser (Scalars San++, Skylar Analytical B.V., Breda, The Netherlands).

3.3 DNA extraction, sequencing and bioinformatic analysis

This section presents a comprehensive description of the molecular biological analyses employed in this study, containing the pretreatment of surface seawater samples, DNA extraction, library generation, 18S amplicon sequencing and (Figure 3-3).

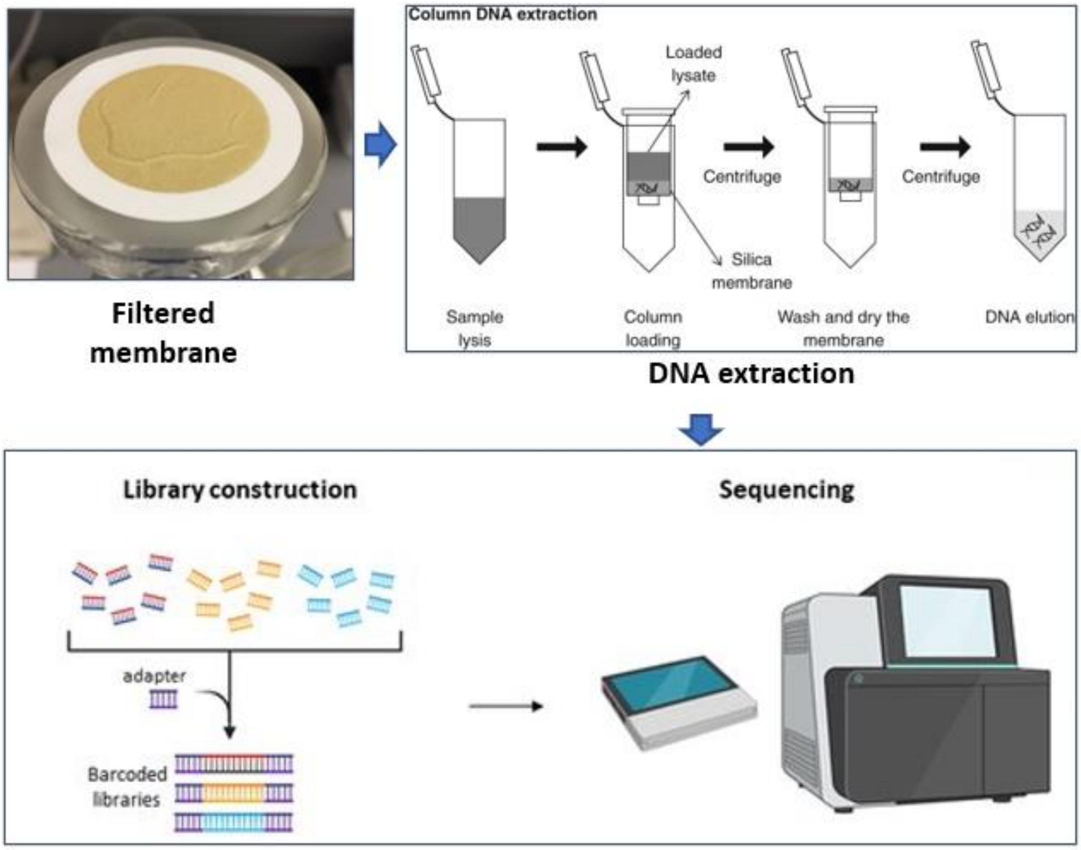


Figure 3-4 Flow chart of molecular biological analyses.

3.3.1 DNA extraction

For the extraction of total algal DNA, the seawater was filtered through a 0.45 µm MCE membrane. All filters were then stored at -80 °C until DNA extraction. The total DNA was extracted from the filters using FastSpinKit for soil (MP Biomedicals, Santa Ana, CA) following the manufacturer’s instructions. Briefly, the membranes were cut with sterile scissors and transferred to a lysing matrix E tube. Homogenize with the FastPrep instrument for 40 seconds at a speed setting of 6.0 m s^{-1} with 978 µL sodium phosphate buffer and 122 µL MT buffer in it to mechanical disruption of algal cell walls and releasing nucleic acids into the protective buffer. The supernatant was transferred to a clean 2 mL microcentrifuge tube after centrifuge to pellet debris. Two hundred 50 µL of protein precipitation solution was added to separate the solubilized nucleic acids from the cellular debris and lysing matrix. The supernatant was transferred to a clean 15 mL tube after centrifuge to pellet precipitate for removal of flocculated proteins. Binding matrix solution (1 mL) was added for binding nucleic acids. The DNA solution was transferred to a spin filter tube and empty catch tube. The prepared SEWS-M solution was added to wash the spin filter for removing impurities by centrifuging through the filter while the purified DNA is still bound to the silica. The binding matrix in spin filter was resuspended in 100 µL elution buffer after the spin filter had been air dried for 5 minutes at room temperature for removal of residual ethanol. Purified DNA solution was ready after centrifuge. The concentration of DNA was measured using a NanoDrop One Microvolume UV-Vis Spectrophotometer (Thermo Fisher Scientific, Waltman, MA, USA).

3.3.2 18S amplicon sequencing and bioinformatic analysis

The *18S rDNA V9* region was amplified using the universal primers: 1380F (5′-CCCTGCCHTTTGTACACAC-3′) and 1510R (5′-CCTTCYGCAGGTTCACCTAC-3′) (Cheung et al. 2010; Zimmermann et al. 2011). The amplicons were paired-end sequenced using an DNBSEQ-G400 platform. Paired-end sequences were merged using USEARCH v10.0.240 (Edgar & Bateman 2010). Primer-cut from merged reads and quality control was performed using “fastx_filter” command by VSEARCH v2.15 (Rognes et al. 2016). The quality-filtered reads of each sample were dereplicated using the “derep_fulllength” command, and less than 8 reads were removed from all samples as the potential sequence errors. The amplicon sequence variants (ASVs) were generated by denoising with unoise3 in USEARCH (Labouyrie et al. 2023; Li et al. 2022a). Taxonomic information of ASVs was annotated based on the SILVA database (Quast et al. 2013). Phytoplankton taxonomic assignment of ASVs was classified against the Silva Database (Release 123) (Liu et al. 2020). The harmful and toxic taxa in our samples were identified by aligning our sequences to the HTMaDB with a threshold of 0.8 using VSEARCH. Rarefaction curves were generated to assess the degree of sample saturation using picante and vegan function packages of R4.2.1 (Figure 3-4 and Figure 3-5).

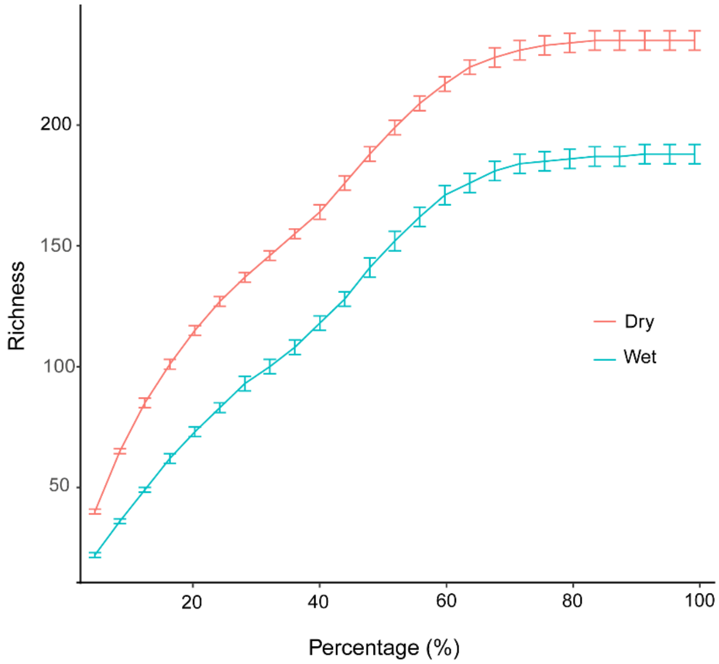


Figure 3-5 Rarefaction curves of the richness in the wet and dry seasons reach the

saturation stage with means and standard errors under 1% - 100%, indicating that the number of samples in our study is sufficient to capture most microorganisms in each season.

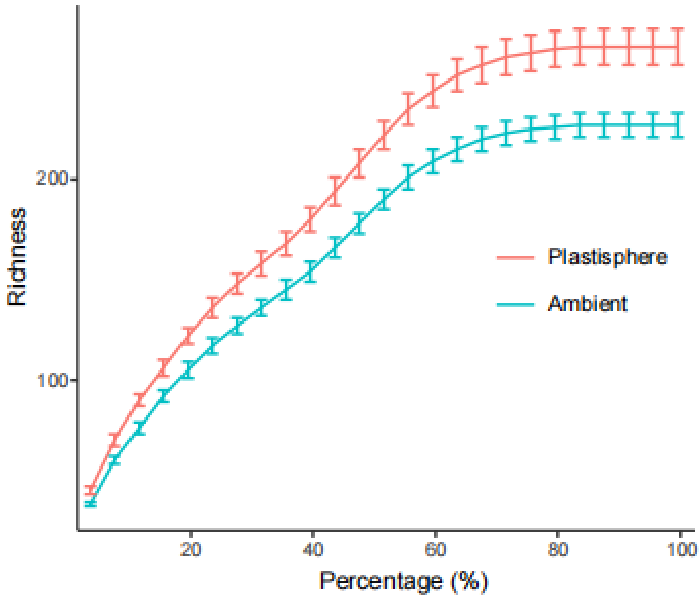


Figure 3-6 Rarefaction curves of detected phytoplankton richness from the plastisphere and the ambient environment in coastal ecosystem reach saturation stage with increasing sequencing depth.

3.4 Statistical analyses

3.4.1 The difference of the phytoplankton community in Hong Kong coastal seawater and plastisphere

Principal coordinate analysis (PCoA) based on Bray-Curtis dissimilarity was performed to evaluate the spatiotemporal pattern of phytoplankton community structure in Hong Kong coastal seawater. Permutational multivariate analysis of variance (PERMANOVA) was used to investigate differences in phytoplankton communities between sampling seasons. Similarly, PCoA was utilized to illustrate the compositional difference between the plastisphere microalgal community and the ambient community, with the PERMANOVA used to test the statistical significance. The richness and Shannon indexes were calculated using the “vegan” package to reflect the alpha diversity of microalgal communities. Furthermore, Bray-Curtis distances between each two samples in each group were calculated to reflect the beta diversity of the communities with the “vegan” package. Differences in the abundances of ASVs between the plastisphere and the ambient microalgal community were analyzed using the “edgeR” package and were depicted in a Manhattan plot. For the identified harmful and toxic algal taxa, the differences of their abundances in the plastisphere community and the ambient community were assessed using the Wilcoxon rank-sum test.

3.4.2 Quantifying ecological stochasticity and niche breadth in the microalgal community

Understanding the community assembly mechanisms controlling biodiversity patterns is a central issue in ecology. An index, normalized stochasticity ratio (NST) was developed to quantify ecological stochasticity under different situations by considering abiotic filtering, competition, environmental noise, and spatial scales (Ning et al. 2019). Accuracy and precision of stochasticity estimation decreased when application to a global scale. Modified Stochasticity Ratio (MST) is a special form of NST, making it more general (Liang et al. 2020). Niche breadth is an important indicator of species adaptability to the environment within a community (von Meijenfeldt et al. 2023). Ecological niche breadth was calculated the Levins’ niche breadth index (Levins 1968).

$$B_i = \frac{1}{\sum_{j=1}^{r}(P_{ij})^2}$$

Equation 3-1

In the above equation, Bi refers to the niche breadth of species i. Pij means the proportion of species i at a given location j. r is the number of locations. If a species has a higher B value, it indicates that the species has a greater niche breadth, with a wider, more even, and larger distribution. Conversely, a lower B value for a species suggests that its distribution is less frequent and more uneven (Pandit et al. 2009).

The MST and habitat niche breadth were estimated to reveal the underlying community assembly mechanisms of microalgal community using “NST” package. The MST model is typically applied to quantify the relative importance of stochasticity and determinism in the community assembly process. The values of MST range from 0 to 1, with 0.5 as the boundary defining deterministic (MST < 0.5) or stochastic (MST > 0.5) dominated assembly processes (Ning et al. 2019). To uncover the patterns of assembly process and their influence on microalgal communities across different habitats, we further calculated the niche breadth index of each species in the community. The habitat niche breadth was estimated based on the average niche width across all species within a community (Jiao et al. 2020; Richard 1968; Wu et al. 2018a). The analysis was conducted using the “niche.width” function in “spaa” package in R.

3.4.3 Identification of specialist algal taxa

Specificity refers to the average abundance of species (*S*) in the samples of a group (*H*);

and occupancy represents the relative frequency of occurrence of S in the samples of H (See Equation 3-2). Nindividual$_{S,H}$ represents the average number number of individual species S across all samples in group H, while Nindividual$_S$ is the total mean number of individual S across all groups; Nsites$_{S,H}$ refers to the count of samples in H where S is present, whereas Nsites$_H$ refers to the total number of samples in H (Dufrêne & Legendre 1997; Gweon et al. 2021).

$$\text{Specificity} = \frac{\text{Nindividuals}_{S,H}}{\text{Nindividuals}_S}$$

$$\text{Occupancy} = \frac{\text{Nsites}_{S,H}}{\text{Nsites}_H}$$

Equation 3-2

In our study, we calculated the specificity and occupancy of each toxic species across seasons to identify specialist taxa. Specificity is defined as the mean abundance of a species in the samples of a season, while occupancy is characterized as the relative frequency with which species occur within the same season. Species with specificity and occupancy of 0.7 or higher were classified as specialist species, indicating their preference for a particular season (Kang et al. 2024).

3.4.4 Associations between environmental factors and microalgal community

The correlation between toxic taxa and environmental factors in Hong Kong coastal seawater was demonstrated based on the spearman test. Redundancy analysis (RDA) was employed to identify potential environmental driving factors of the plastisphere microalgal community and its ambient community. The Mantel test was carried out to investigate the potential driving environmental factors of plastisphere microalgal communities. Linear regression models were employed to determine relationships between the plastisphere microalgal risk and environmental factors. Procrustes analysis was performed to analyze the associations between the plastisphere community and the ambient community.

3.4.5 Quantifying the relative contribution of biotic and abiotic factors to microalgal community

Variation Partitioning Analysis (VPA) is a statistical technique used in ecology to assess the contribution of various environmental factors to the variability in biological data (Figure 3-10). Variation partitioning analysis results are typically shown using a Venn diagram, displaying the variance percentage explained by each data set. In a case where we are partitioning the variation among two explanatory matrices, the result could be represented as Figure 3-11. Fraction [a + b + c] represents the explained variance by both $X1$ and $X2$, calculated through an RDA of Y with both $X1 + X2$. Fraction [d] indicates the unexplained variance by $X1$ and $X2$, derived from the same RDA. Fraction [a] represents the explained variance by $X1$ alone, calculated through a partial RDA of Y by $X1|X2$ (controlling for $X2$). Fraction [c] represents the explained variance by $X2$ alone, calculated using a partial RDA of Y by $X2|X1$ (controlling for $X1$). Fraction [b] is determined by subtraction: b= [a + b] + [b + c]- [a + b + c]. Because [b] is not the result of an RDA, it cannot be tested for significance. It can also be negative, which indicates that the response matrix is better explained by the combination of $X1$ and $X2$ than by either matrix on its own (Peres-Neto et al. 2006; Tedersoo et al. 2016; Lai et al. 2022). Here we employed VPA to explain the contribution of the community variations to co-occurring species interaction and environmental factors using the 'vegan' package in R (Labouyrie et al. 2023; Tedersoo et al. 2016).

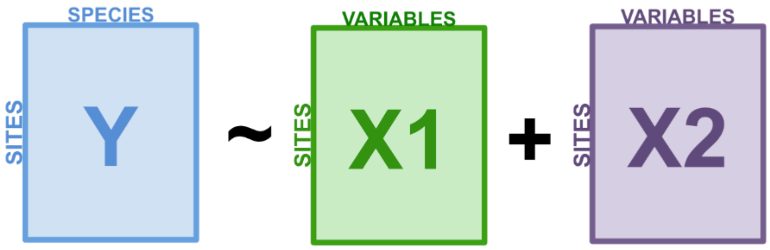


Figure 3-7 The basic structure of variation partitioning.

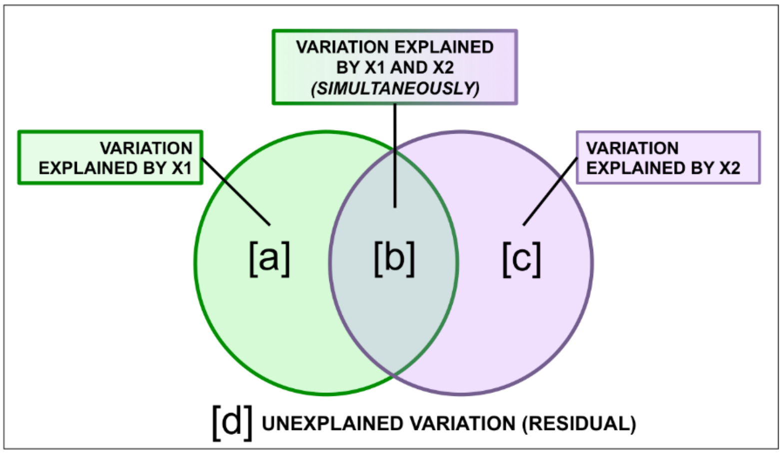
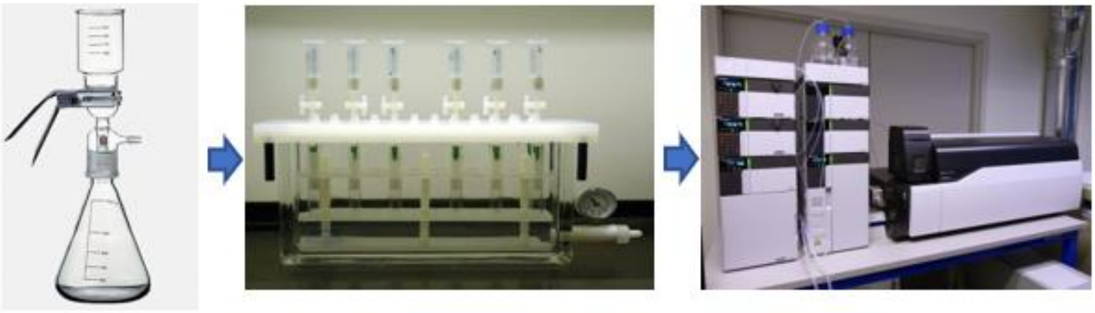


Figure 3-8 Representing variation partitioning results.

3.5 Chemical analysis

3.5.1 Methods for extracting LATs

For LATs extraction, seawater samples were filtered through 0.45 µm glass microfiber filters (GF/A, Whatman Schleicher & Schuell, Maidstone, England) to remove visible particulate matter and algal cells. SPE was performed using Oasis HLB cartridges (200 mg, 6 mL, Waters, Medford, MA, USA), following the procedure outlined in a previous study (Li et al. 2014). The cartridges were pre-conditioned with 4 mL of ammonium hydroxide/methanol (3:1000, v:v), followed by 4 mL of methanol and 4 mL of deionized water. Then, 250 mL of seawater samples were passed through each cartridge at a flow rate of 1 mL·min-1. Afterward, the cartridges were rinsed with 4 mL of methanol/water (15:85, v:v) and dried by centrifugation at 3500 rpm for 2 minutes. The extracts were obtained by eluting the cartridge three times with 3 mL of ammonium hydroxide/methanol (3:1000, v:v). The extracts were then evaporated until dry under a gentle nitrogen stream at 40℃, reconstituted with 100 μL of methanol, centrifuged at 3500 rpm for 3 minutes, and transferred to an analysis vial. For extraction of SPM, each filter loaded with suspended particulate matter was cut off in pieces and placed in 50 mL centrifuges. Samples were extracted with 8 mL 26 mM Ammonia-MeOH by 30 mins ultrasonication. The liquid from the centrifuge tube was transferred to a 5 mL syringe, filtered through a PTFE filter membrane (0.22μm) into a centrifuge tube (15 mL). Conduct other 2 extractions with 5 mL 26 mM Ammonia-MeOH separately. The extract was dried under a gentle nitrogen stream, reconstituted with 100 μL of methanol, and filtered through a 0.22 μm PTFE filter before being transferred to an analysis vial. The samples were then stored at -20°C until further analysis.



Seawater filtration

Solid phase extraction

Chemical analysis

Figure 3-9 Surface seawater treatment for algal toxins.

The standards of gymnodium (GYM), okadaic acid (OA), pectenotoxin-2 (PTX-2), dinophysistoxin-1 and -2 (DTX-1 and -2), and azaspiracid-1 and -2 (AZA-1 and -2) were purchased from the National Research Council, Institute for Marine Biosciences (Halifax, Nova Scotia, Canada). The properties of algal toxins were shown in Table 3-4. The standards were stored at -20°C. Acetonitrile and methanol of gradient grade were purchased from Merck (Darmstadt, Germany). Ammonium hydroxide (≥ 25%) of MS grade was purchased from SUPELCO (Bellefonte, PA, USA). Ultrapure water was obtained from a Milli-Q water-purification system (Millipore, Billerica, MA, USA).

Table 3-4 Molecular weight, molecular formula, and octanol-water partition coefficient of the LATs.

Compound	**CAS number**	**Molecular Weight ($g·mol^{-1}$)**	**Molecular Formula**	**Log K_{ow}** (Takahashi et al. 2007)
OA	78111-17-8	805.0	$C_{44}H_{68}O_{13}$	5.05
DTX-1	81720-10-7	819.0	$C_{45}H_{70}O_{13}$	6.88
DTX-2	139933-46-3	805.0	$C_{44}H_{68}O_{13}$	5.61
PTX-2	97564-91-5	857.0	$C_{47}H_{70}O_{14}$	6.47
GYM	173792-58-0	507.7	$C_{32}H_{45}NO_4$	6.64
AZA-1	214899-21-5	842.1	$C_{47}H_{71}NO_{12}$	7.54
AZA-2	265996-92-7	856.1	$C_{48}H_{73}NO_{12}$	8.18

3.5.2 Instrumental analysis of LATs

Separation of the seven LATs in seawater samples was conducted on an ExionLC UHPLC system (Sciex, Foster City, CA, USA) with an ACQUITY UPLC BEH C18 Column (2.1 mm × 50 mm, 1.7 μm particles, Waters, Medford, MA, USA), maintained at 40°C. The gradient condition began with 5% solvent B, increasing to 45% at 3.5 minutes, followed by a linear rise to 55% at 6.5 minutes, and finally reaching 100% at 7.5 minutes. After 1 minute, the gradient returned to the initial conditions at 9.5 minutes and was held for 2 minutes. The total run time was 11.5 minutes, with 10 μL injected for each sample. During analysis, the autosampler's sample illumination was turned off.

The MS method was developed and optimized for maximum sensitivity using the 6500+ QTRAP (García-Altares et al. 2013). Instrumental data were acquired and processed with Analyst 1.6.3 software (Sciex, Foster City, CA, USA). Chromatographic analysis employed dual fragment ions derived from parent ions for compound verification, with quantification based on the higher-intensity transition. Retention time alignment combined with parent-fragment ion transitions provided three-dimensional confirmation of chromatographic peaks. Seawater analyte concentrations were determined using external calibration curves matching established reference standards. Detailed parameters can be found in Table 3-5 and Table 3-6. The QA/QC measures included evaluating for method limits of detection (LODs), quantification (LOQs), calibration curves, procedure blanks. Each sample was extracted and analyzed in duplicate, and for every batch of real samples, procedural blank (n = 2), and blank-spiked recoveries (n = 2) were also included.

Table 3-5 Source parameters in negative mode and positive mode.

Parameters	**Negative mode**	**Positive mode**
Curtain Gas	25	25
Collision Gas	Low	Low
Voltage (V)	-4500	5000
Temperature (°C)	550	550
Gas 1 (psi)	60	60
Gas 2 (psi)	60	60

Table 3-6 Optimized mass spectrometry parameters for LATs detection: Transitions monitored, dwell times, declustering potentials (DP), entrance potentials (EP), collision cell entrance potentials (CEP) and collisions energies (CE)

Compound	**Transitions (m/z)**	**Time (ms)**	**DP (V)**	**EP (V)**	**CE (V)**	**CXP (V)**	**Precursor ion**
OA	803.1>255.1	40	140	-10	-60	-20	$[M\text{-}H]^-$
	803.1>563.1	40	140	-10	-58	-25	
DTX-2	803.5>255.2	40	140	-10	-60	-38	$[M\text{-}H]^-$
	803.5>563.2	40	140	-10	-58	-17	
DTX-1	817.6>255.2	40	140	-10	-60	-15	$[M\text{-}H]^-$
	817.6>563.2	40	140	-10	-58	-30	
YTX	570.4>467.2	40	140	-10	-40	-28	$[M\text{-}2H]^{2-}$
	570.4>501.8	40	140	-10	-31	-30	
GYM	508.3>490.3	40	140	10	32	26	$[M+H]^+$
	508.3>392.3	40	140	10	46	30	
	508.3>202.4	40	140	10	50	10	
PTX-2	876.6>823.3	40	140	10	34	20	$[M+NH_4]^+$
	876.6>805.3	40	140	10	37	20	

AZA-1	842.5>824.6	40	140	10	43	27	$[M+H]^+$
	842.5>806.2	40	140	10	46	35	
AZA-2	856.7>838.4	40	140	10	41	38	$[M+H]^+$
	856.7>820.5	40	140	10	49	40	

To determine the LODs and LOQs for LATs, we conducted the same extraction procedure with real environment samples on 11 blank samples. The standard deviation (SD) of the signals was calculated, LOD and LOQ can be estimated to 3 times and 10 times of the standard deviation respectively (Table 3-7). Calibration curves for the seven LATs had concentrations (seven data points) with correlation coefficients ranging from 0.9977 to 0.9999. Recoveries of the 7 LATs varied from 52.9% to 92.5% in seawater and from 89.3% to 116.3% in suspended particulate matters (SPM) samples (Figure 3-10). Importantly, none of the 7 target LATs were found in procedure blanks. The reported LATs concentrations were not surrogate recovery corrected.

Table 3-7 Limits of detection, limits of quantification, correlation coefficients of the external calibration (r^2), and recoveries of the targeted LATs.

LATs	LOD ($pg\ L^{-1}$)	LOQ ($pg\ L^{-1}$)	r^2	Recovery Mean (SW)	Recovery Mean (SPM)
PTX-2	2.83	9.43	0.9977	81.2%	116%
AZA-2	0.58	1.94	0.9988	52.9%	91.2%
GYM	1.15	3.83	0.9993	66.3%	89.3%
AZA-1	0.66	2.20	0.9999	56.3%	101%
OA	9.60	32.0	0.9984	84.7%	105%
DTX-1	3.12	10.4	0.9988	63.0%	96.9%
DTX-2	2.54	8.46	0.9980	92.5%	108%

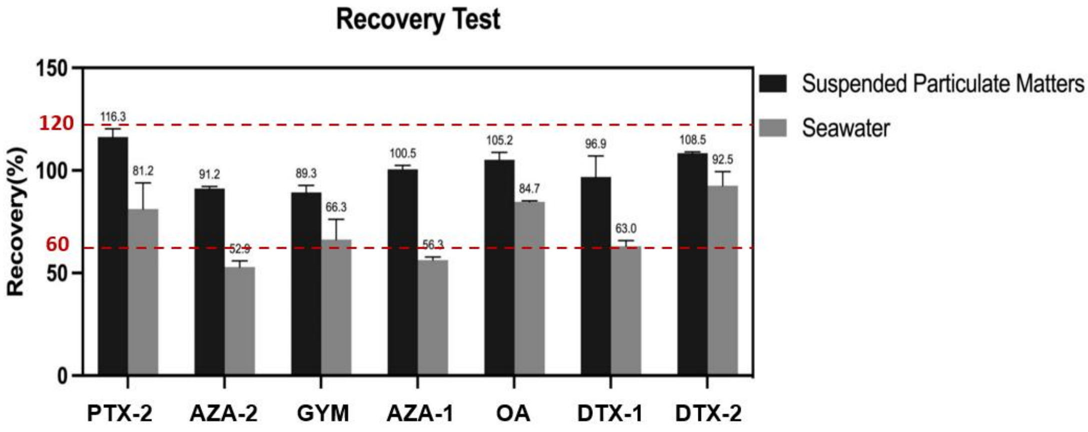


Figure 3-10 Recovery of targeted LATs.

Chapter 4 Ecological pattern of microalgal communities in coastal ecosystems – An application of HTMaDB in Hong Kong

For better identification of harmful and toxic microalgae, we constructed a HTMaDB, which contained 1346 18S full-length reference sequences. With marine field sampling campaign, the spatiotemporal variations in microalgal communities were investigated along Hong Kong coastal zone during wet (August 2022) and dry seasons (February 2023). The phytoplankton community was far more affected by seasonal change compared with spatial distribution. Based on the application of HTMaDB, we revealed the driving factors of toxic algal community and potential causative organisms of targeted toxins.

4.1 Distinct seasonal pattern of phytoplankton community across Hong Kong coastal seawater

A total of 1,649 ASVs were identified as eukaryotic microalgae based on amplicon data. PCoA and PERMANOVA was conducted to discern disparities in spatiotemporal distribution of the structure of the eukaryotic phytoplankton community in Hong Kong coastal surface seawater (Figure 3-1a). Our results unveiled a notable differentiation in taxonomic compositions among two sampling seasons compared to different regions, suggesting a greater influence of seasonality over spatial factors on a small localize scale ($R^2_{\text{season}} = 0.3164 > R^2_{\text{region}} = 0.057$). Given this seasonal variation, we further characterized taxonomic richness across the two sampling seasons. An increase was observed in taxonomic richness in dry season compared to wet season (Figure 4-1b).

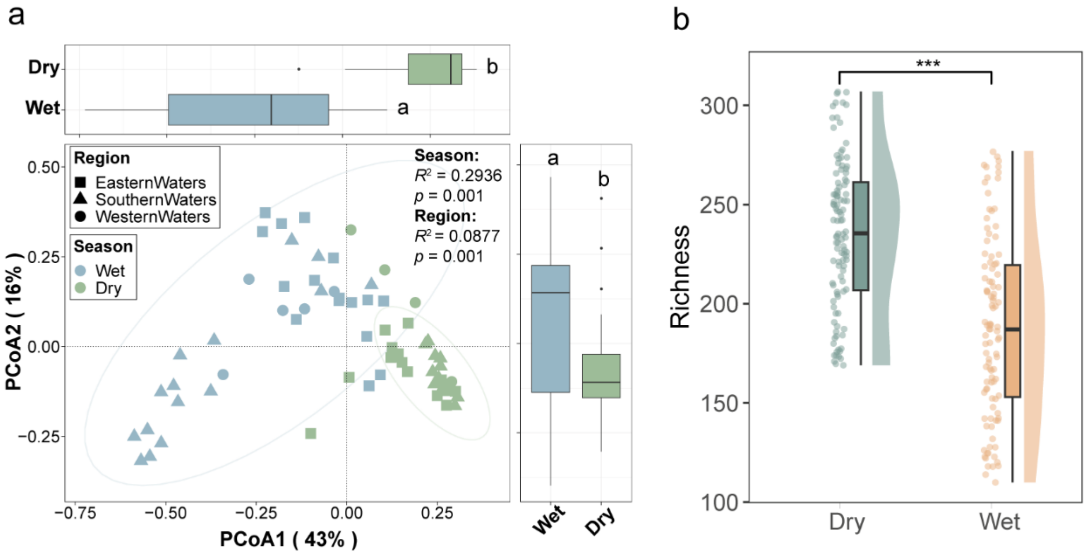


Figure 4-1 Significant seasonal pattern of community structure. **a**, Unconstrained principal coordinate analysis (PCoA) with permutational multivariate analysis of variance (PERMANOVA) showing a significant compositional difference between the wet and dry seasons. **b**, Differences in the Richness index between the wet and dry seasons (***$p < 0.001$; Wilcoxon rank-sum test).

Distinct patterns in phytoplankton composition during different seasons (Figure 4-2). The eukaryotic phytoplankton were categorized into 7 phyla (Dinoflagellata, Ochrophyta, Chlorophyta, Haptophyta, Cryptophyta, Rhodophyta, and Cercozoa). Dinoflagellates and Ochrophyta predominated in taxonomic composition, accounting for more than 70% in both seasons. The relative abundance of dinoflagellates was highest in the dry season, whereas Ochrophyta peaked in the wet season.

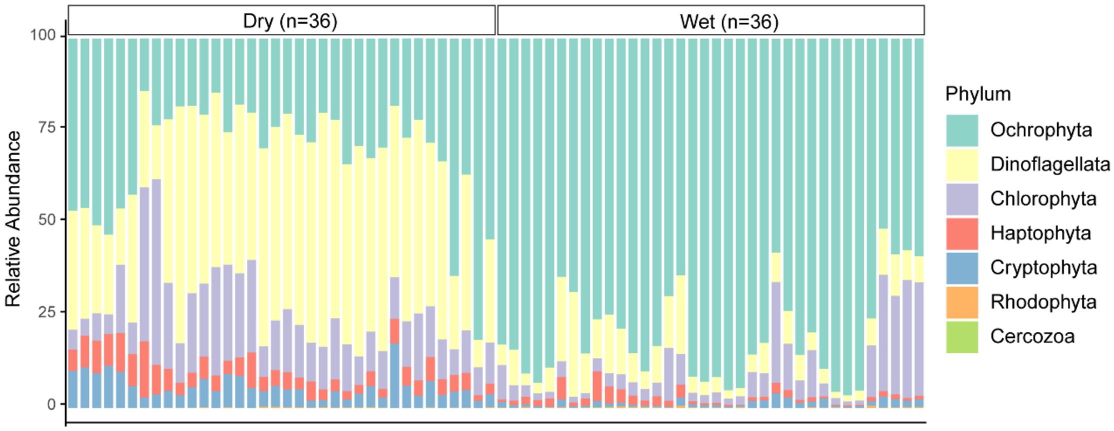


Figure 4-2 Taxonomic composition of phytoplankton community.

4.2 The deterministic process shaping phytoplankton community

Community assembly describes how different ecological processes shape microbial community composition and structure. Modified Stochasticity Ratio (MST) was calculated based on the null model to assess the relative importance of deterministic and stochastic processes. The importance of phytoplankton communities was shaped by different assembly processes during two sampling periods (Figure 4-3).

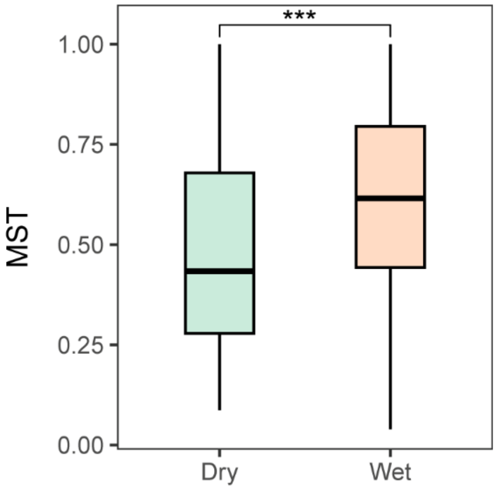


Figure 4-3 Assembly process based on modified stochasticity ratio (MST). The MST index has a boundary of 50% to distinguish between more deterministic (<50%) and more stochastic (>50%) assembly (***$p < 0.001$; Wilcoxon rank-sum test).

4.2 Mapping harmful and toxic microalgae using HTMaDB

Out of 1,649 ASVs, a total of 403 were identified as eukaryotic harmful and toxic microalgae in Hong Kong coastal seawater, belonging to the 9 class Dinophyceae, Diatomea, Coccolithophyceae, Raphidophyceae, Prymnesiophyceae, Chlorophyceae, Cryptophyceae, Pelagophyceae, and Dictyochophyceae (Figure 4-4a). Dinophyceae and Diatomea were the dominant class of toxic and harmful taxa, respectively. In the case of toxic ASVs, Coccolithophyceae represented a significant proportion as well. For harmful ASVs, both Chlorophyceae and Cryptophyceae also constituted considerable proportions. The relative abundance of 192 toxic ASVs and 211 harmful ASVs displayed different seasonal patterns. Toxic algae were prevalent in the dry season, whereas harmful taxa were relatively stable across seasons (Figure 4-4b).

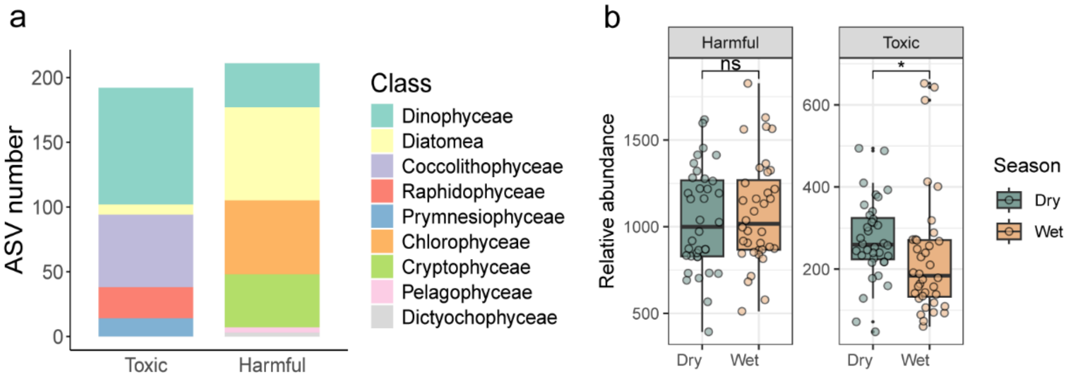


Figure 4-4 The composition and relative abundance of identified harmful and toxic ASVs using HTMaDB. The proportion of classified ASV numbers at class level (a), significantly higher relative abundance of all toxic taxa in dry season (b).

The abundance of 22 harmful and toxic algal genera in wet and dry seasons was showed in Figure 4-5. Among HAB algal taxa, the diatom in the genus of *Pseudo-nitzschia* displayed the highest absolute abundance, indicating the potential of bloom forming and toxin contamination of DA especially in the wet season. A higher number of dinoflagellates were identified for the genera of *Alexandrium*, *Dinophysis, Gymnodinium*, and *Prorocentrum*. Additionally, the genera of *Chrysochromulina*, *Phaeocystis*, and *Prymnesium* in Haptophyta were also detected. These harmful and toxic algal taxa result in varied harmful effects on marine ecosystems. The occurrence of water discolorations and oxygen depletion owed to harmful bloom-forming species, for example, most diatom taxa and some of the dinoflagellates.

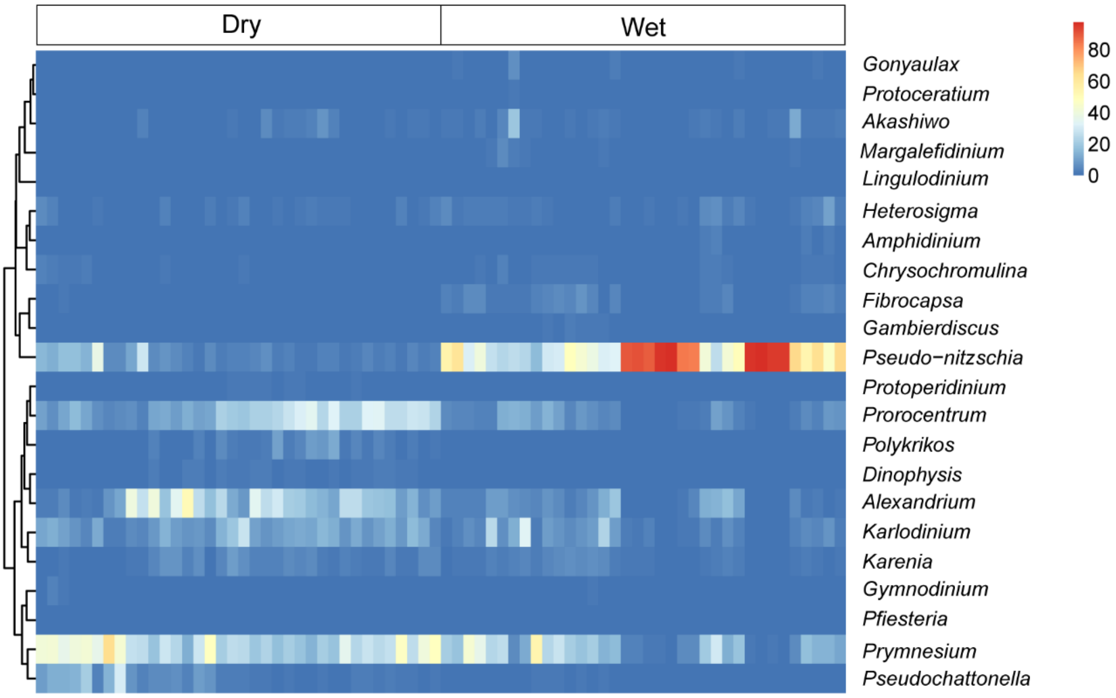


Figure 4-5 Temporal distribution of harmful and toxic taxa at genus level in two seasons.

The identified 22 HAB genera belonged to the 30 toxic and 49 harmful algal species (Table 4-1). Toxic algal taxa pose a threat to fish and shellfish and may cause mass mortality in aquaculture organisms, such as ichthyotoxic dinoflagellates

Margalefidinium polykrikoides and *M. fulvescens* (previously known as *Cochlodinium polykrikoides* and *C. fulvescens*) (Hofmann et al. 2021). *Alexandrium* spp. are the major producers of PSP toxin (Valbi et al. 2019). A total of twenty-six ASVs were attributed to five species of *Alxandrium*, all of them (including *A. andersonii*, *A. hiranoi*, *A. leei*, *A. ostenfeldii*, and *A. tamarense*) were proven to be PSP producers (Lassus et al. 2016). *Pseudo-nitzschia* spp., the only producers of domoic acid (DA), such as *Pseudo-nitzschia australis* and *P. pungens*, can lead to ASP (Wang et al. 2023). *Dinophysis* spp. and *Prorocentrum* spp. are source organisms of PTX-2, OA and its derivatives DTX-1, which are responsible for DSP (Marzidovšek et al. 2024). *Azadinium.* spp were associated with AZP. *Karenia mikimotoi* can produce the brevetoxins, which cause NSP (Li et al. 2024d). Diverse yessotoxin (YTX) producers, including *Gonyaulax spinifera* and *Protoceratium reticulatum*, were identified in coastal waters. The widespread species *Prymnesium parvum*, primarily in coastal waters, but also found in rivers and marine environments, have been reported with large-scale fish mortality events globally (Wagstaff et al. 2021). Furthermore, recent study indicates that prymnesins, rather than organic micropollutants, possess strong in vitro neurotoxic effects (Escher et al. 2024). A total of 49 harmful algal taxa were identified, most of them are diatoms.

Table 4-1 The identified HAB species in coastal seawater.

Phylum	Species	Impacts	Phylum	Species	Impacts
Dinophyta	*Akashiwo sanguinea*	Toxic	Ochrophyta	*Heterosigma akashiwo*	Toxic
	Alexandrium andersonii	Toxic		*Fibrocapsa japonica*	Toxic
	Alexandrium hiranoi	Toxic		*Pseudo-nitzschia australis*	Toxic
	Alexandrium leei	Toxic		*Pseudo-nitzschia cuspidata*	Toxic
	Amphidinium klebsii	Toxic		*Pseudo-nitzschia delicatissima*	Toxic
	Alexandrium ostenfeldii	Toxic		*Pseudochattonella verruculosa*	Toxic
	Alexandrium tamarense	Toxic		*Asterionellopsis glacialis*	Harmful
	Amphidinium klebsii	Toxic		*Aureococcus anophagefferens*	Harmful
	Dinophysis acuminata	Toxic		*Chaetoceros affinis*	Harmful
	Dinophysis miles	Toxic		*Chaetoceros debilis*	Harmful
	Gambierdiscus scabrosus	Toxic		*Chaetoceros diadema*	Harmful
	Gonyaulax spinifera	Toxic		*Chaetoceros lorenzianus*	Harmful
	Gymnodinium catenatum	Toxic		*Chaetoceros pseudocurvisetus*	Harmful
	Karenia mikimotoi	Toxic		*Chaetoceros rostratus*	Harmful
	Karlodinium veneficum	Toxic		*Chaetoceros simplex*	Harmful
	Lingulodinium polyedra	Toxic		*Chaetoceros socialis*	Harmful
	Margalefidinium fulvescens	Toxic		*Chaetoceros tenuissimus*	Harmful
	Margalefidinium polykrikoides	Toxic		*Chaetoceros throndsenii*	Harmful

	Pfiesteria piscicida	Toxic
	Polykrikos hartmannii	Toxic
	Prorocentrum cordatum	Toxic
	Prorocentrum rhathymum	Toxic
	Protoceratium reticulatum	Toxic
	Protoperidinium crassipes	Toxic
	Gonyaulax polygramma	Harmful
	Gymnodinium impudicum	Harmful
	Heterocapsa rotundata	Harmful
	Heterocapsa triquetra	Harmful
	Noctiluca scintillans	Harmful
	Pseudocochlodinium profundisulcus	Harmful
	Prorocentrum triestinum	Harmful
	Protodinium simplex	Harmful
	Pyrophacus steinii	Harmful
	Tripos furca	Harmful
Haptophyta	*Prymnesium parvum*	Toxic
	Chrysochromulina leadbeateri	Toxic
	Prymnesium polylepis	Toxic
Cryptophyta	*Plagioselmis prolonga*	Harmful
	Coscinodiscus radiatus	Harmful
	Cyclotella meneghiniana	Harmful
	Cylindrotheca closterium	Harmful
	Guinardia flaccida	Harmful
	Lepidodinium chlorophorum	Harmful
	Levanderina fissa	Harmful
	Dictyocha fibula	Harmful
	Eucampia zodiacus	Harmful
	Lauderia annulata	Harmful
	Leptocylindrus danicus	Harmful
	Nitzschia longissima	Harmful
	Paralia sulcata	Harmful
	Proboscia alata	Harmful
	Skeletonema marinoi	Harmful
	Tenuicylindrus belgicus	Harmful
	Thalassiosira allenii	Harmful
	Thalassiosira curviseriata	Harmful
	Thalassiosira mala	Harmful
	Thalassiosira pseudonana	Harmful
	Thalassiosira punctigera	Harmful

	Teleaulax acuta	Harmful		*Thalassiosira weissflogii*	Harmful
Chlorophyta	*Dunaliella salina*	Harmful			

4.3 Deterministic processes driven by temperature shaping toxic algal communities

To explore the complexities of toxic algal communities and the assembly processes shaping them, it is crucial to delve deeper into how these processes are modulated by environmental stress, particularly temperature fluctuations. Deterministic processes are pivotal in defining the community structure of phytoplankton by favoring species that can adapt to prevailing conditions, thus reducing community stochasticity and increasing predictability in species composition.

4.3.1 The deterministic process shaping toxic algal community

As mentioned above, toxic algae displayed a significant seasonal difference in sampling period. The proportion of deterministic process increased with increasing abundance of toxic microalgae from wet season to dry season (Figure 4-3). The difference in toxic microalgae abundance was significantly negatively correlated with stochasticity for the toxic algal community ($R^2 < 0.01$, $p = 0.025$), suggesting the importance of deterministic process increased with the toxic microalgae stress, which align with the theoretical framework of deterministic assembly increases as stress increases (Figure 4-6) (Ning et al. 2024). High stress usually imposes strong selective pressure. As stress increases, many species will be more suppressed, but those with higher tolerance or adaptation to the stressor(s) will thrive, leading to more deterministic community assembly. Determinism indicates that selection is the primary force that shapes microbiomes, including environmental filtering and species interactions (Kang et al. 2024).

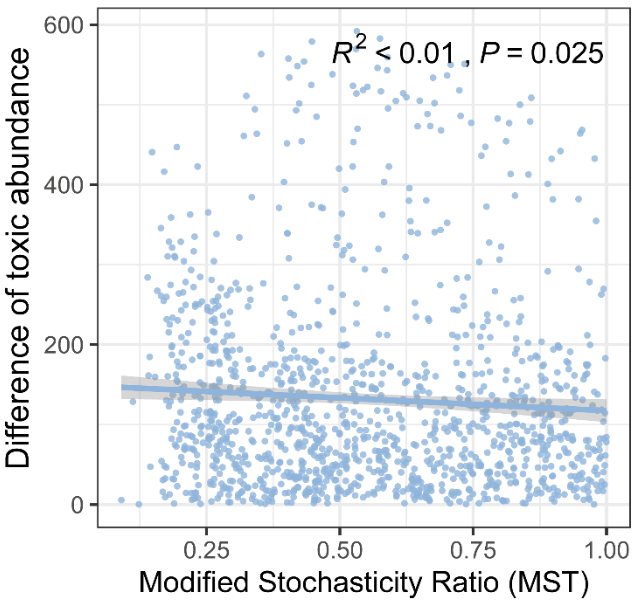


Figure 4-6 Relationships of the stochasticity and the difference of toxic algal abundance.

Environmental factors such as temperature and light directly influence the growth and metabolic activities of algae (Deutsch et al. 2008; Liao 2024). When environmental conditions shift to favor the growth of specific toxic algae, these organisms can rapidly proliferate, thereby increasing their abundance within the community. For instance, toxic algae, such as *Dinophysis* spp., flourish in warm water conditions (Fiorendino et al. 2020). Nutrient conditions also exert significant selective pressure. An increase in specific nutrients, such as phosphates and nitrates, can enhance the growth of certain toxic algae, which may be more sensitive to or capable of more effectively utilizing resources (Bonilla 2023). When referring to the species interaction, toxic algae reduce the risk of predation by producing toxins, a defensive mechanism that can decrease predator pressure and allow toxic algae to occupy a larger proportion within the community (Borrell 2010).

Moreover, some toxic algae engage in symbiotic relationships with other microorganisms, such as bacteria (Higashi et al. 2016). These relationships are mutually beneficial, as the associated microorganisms can assist the algae in more efficiently utilizing available nutrients or even provide other survival benefits (Fei et al. 2025; Gajardo et al. 2023). Such symbiotic interactions not only help toxic algae thrive in their existing environments but also enhance their adaptability to changing ecological conditions, thereby reinforcing their presence in the ecosystem.

4.3.2 The relationship between environmental factors and toxic algal community

Network correlation test was applied to further elucidate the major influencing environmental variables, including salinity, pH, temperature, DO, NO_2^-, NO_3^-, SiO_3^{2-}, PO_4^{3-}, and NH_4^+. Significant correlations were identified linking toxic algal taxa with temperature, salinity, pH, and concentrations of PO_4^{3-} and SiO_3^{2-} (Figure 4-7a). Responses to environmental drivers varied among different algal taxa.

Temperature emerged as the most influential factor among all the environmental parameters evaluated, with 5 toxic algal taxa, including the genera *Dinophysis*, *Fibrocapsa*, *Herterosigma*, *Protoperidinium*, and *Pseudo-nitzschia*, primarily displaying a positive correlation with temperature except for the *Dinophysis*. The genus of dinoflagellates, *Dinophysis*, were more abundant at the cooler temperatures observed during the dry season (18–20°C) may owing to their optimal growth at temperatures ranging from 18 to 24°C (Fiorendino et al. 2020).

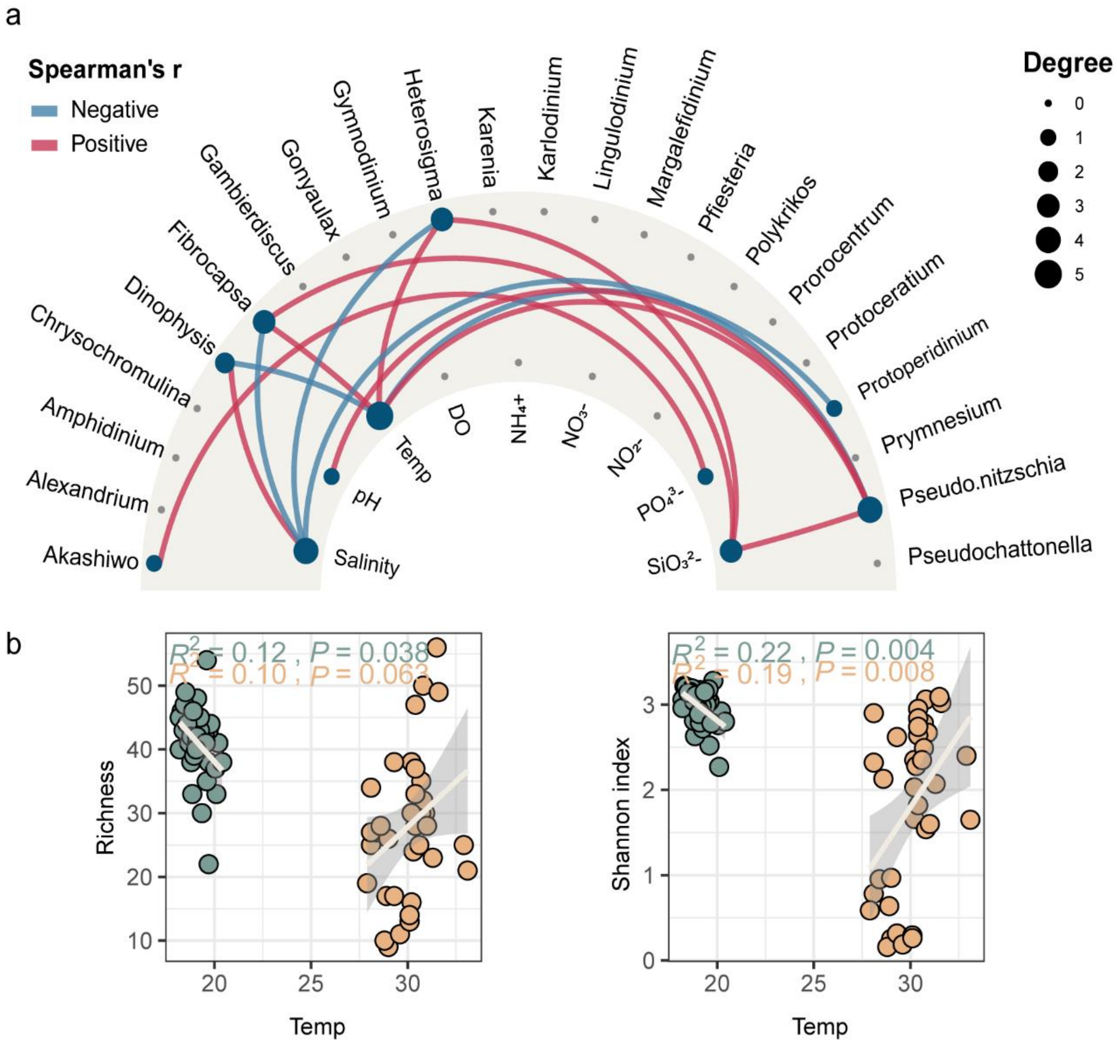


Figure 4-7 Major driving environmental factors shaping toxic community. (a) Relationships between identified communities and environmental factors. When p<0.05, a significant correlation is represented by a line. Different colors are used to distinguish between positive and negative correlations (red: positive; blue: negative). (b) The size of the circles represents magnitude of the correlation coefficient, with larger circles indicating a greater impact. Relationships between temperature and toxic algal community alpha diversity.

Growth responses towards temperature change were very variable and remained inconsistent across the different algal groups, species and strains, reflecting evolutionary constraints and past adaptations to its environmental regime (Boyd et al. 2013; Brandenburg et al. 2019). Species that thrive at higher optimal growth temperatures typically exhibit faster growth under favorable conditions compared to those with lower optimal temperatures (Suzuki & Takahashi). When the temperature exceeds a species' optimal range, growth rates tend to decline sharply (García et al. 2018). However, evolution surveys have demonstrated that phytoplankton species can rapidly adapt to higher temperatures. Diatom species have increased their temperature optima by 1 °C, with adjust their metabolic pathways to optimize resource utilization at different temperatures (Hattich et al. 2024). This adaptation driven by evolutionary changes in baseline gene expression, a process known as transcriptional investment or divestment (Liang et al. 2019).

Linear regression analysis also confirmed that temperature significantly affected the alpha diversity of the toxic algal community (Figure 4-7b). Under elevated temperature stress, both species richness and Shannon diversity index of toxic algal community displayed a significant positive correlation. This suggests that increasing environmental stress fosters toxic algal assemblages, potentially due to the enhanced selection for thermotolerant and opportunistic species that thrive under changing conditions. The negative correlations between 3 algal taxa with salinity levels were observed, suggesting the possibility of presence of salinity stress. The growth of diatoms (*Pseudo-nitzschia*), Dinoflagellate (*Akashiwo*), and Heterokontophyta (*Herterosigma*) were promoted with increasing nutrients of PO_4^{3-} and SiO_3^{2-} on a limited scale. The risk of HABs and toxin contamination could be more severe by eutrophication of coastal zones.

Biotic filtering processes such as species competition, facilitation and predation, and abiotic filtering where functional differences between individual species play a central role (Yuan et al. 2021). The occupancy and specificity analysis revealed that the numbers of keystone toxic species in dry and wet season were 25 and 7, respectively (Figure 4-8 and Table 4-2). Specialist species in the dry season were mostly dinoflagellates, including *Alexandrium*, *Dinophysis*, *Karlodinium*, *Polykrikos*, and *Prorocentrum*, whereas *Pseudo-nitzschia*, belonging to diatoms accounted for nearly half of specialist species in the wet season. The increasing abundance of toxic algal community in the dry season could be attributed to these characteristic dinoflagellate species.

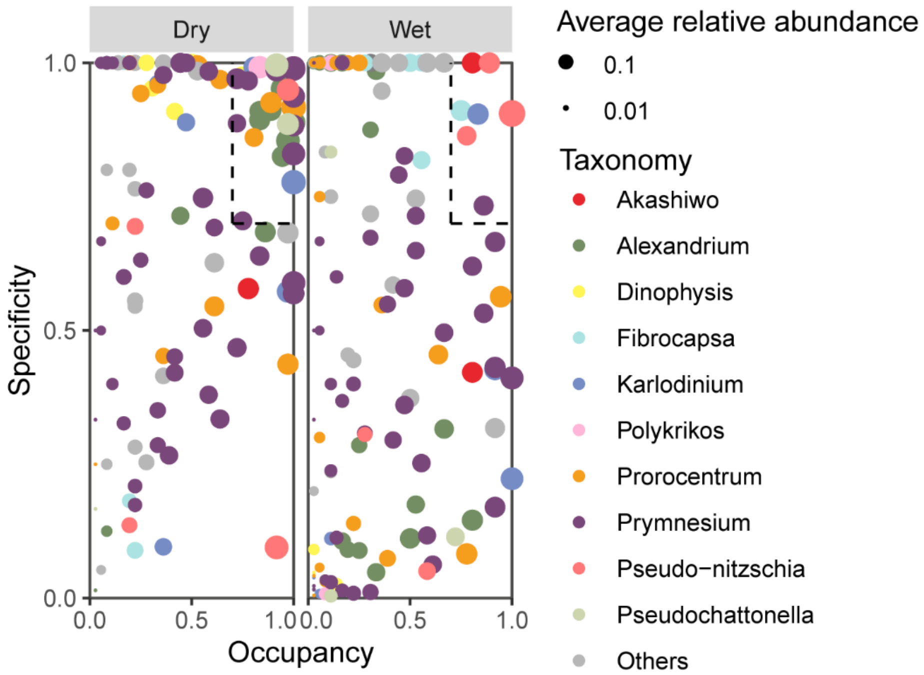


Figure 4-8 The specificity-occupancy plot shows the distribution and specificity of the abundant toxic species with a mean relative abundance higher than 0.01% in each season. Species with specificity and occupancy greater or equal to 0.7 are specialist

species.

Table 4-2 Specialist species in the dry and wet seasons.

NO.	Season	OTU	Specificity	Occupancy	Species
1	Wet	ASV_342	1	0.805555556	*Akashiwo sanguinea*
2	Wet	ASV_1576	0.910852713	0.75	*Fibrocapsa japonica*
3	Wet	ASV_292	0.904225352	0.833333333	*Karlodinium veneficum*
4	Wet	ASV_438	0.733333333	0.861111111	*Prymnesium parvum*
5	Wet	ASV_337	1	0.888888889	*Pseudo-nitzschia cuspidata*
6	Wet	ASV_641	0.863829787	0.777777778	*Pseudo-nitzschia cuspidata*
7	Wet	ASV_13	0.905371556	1	*Pseudo-nitzschia delicatissima*
8	Dry	ASV_209	0.951785714	0.944444444	*Alexandrium andersonii*
9	Dry	ASV_634	0.911111111	0.888888889	*Alexandrium andersonii*
10	Dry	ASV_115	0.854388635	0.972222222	*Alexandrium hiranoi*
11	Dry	ASV_153	0.888530928	1	*Alexandrium tamarense*
12	Dry	ASV_525	0.825174825	0.944444444	*Alexandrium tamarense*
13	Dry	ASV_574	0.909482759	0.833333333	*Alexandrium tamarense*
14	Dry	ASV_431	0.893548387	0.833333333	*Alexandrium tamarense*
15	Dry	ASV_726	0.974358974	0.75	*Dinophysis miles*
16	Dry	ASV_701	0.991836735	0.805555556	*Karenia mikimotoi*
17	Dry	ASV_290	0.776990649	1	*Karlodinium veneficum*
18	Dry	ASV_460	0.992025518	0.833333333	*Polykrikos hartmannii*
19	Dry	ASV_503	0.925816024	0.888888889	*Prorocentrum cordatum*
20	Dry	ASV_989	0.860606061	0.805555556	*Prorocentrum cordatum*
21	Dry	ASV_70	0.917433538	1	*Prorocentrum rhathymum*
22	Dry	ASV_117	0.830131827	1	*Prymnesium parvum*
23	Dry	ASV_163	0.937427578	1	*Prymnesium parvum*
24	Dry	ASV_111	0.988690476	1	*Prymnesium parvum*
25	Dry	ASV_353	0.985887097	0.916666667	*Prymnesium parvum*
26	Dry	ASV_173	0.990983607	1	*Prymnesium parvum*
27	Dry	ASV_451	0.882926829	1	*Prymnesium parvum*
28	Dry	ASV_763	0.966292135	0.777777778	*Prymnesium parvum*
29	Dry	ASV_881	0.704761905	0.75	*Prymnesium parvum*
30	Dry	ASV_1178	0.887096774	0.722222222	*Prymnesium parvum*
31	Dry	ASV_308	0.970260223	0.722222222	*Prymnesium polylepis*

32	Dry	ASV_225	0.949579832	0.972222222	*Pseudo-nitzschia australis*
33	Dry	ASV_105	0.995830438	0.916666667	*Pseudochattonella verruculosa*
34	Dry	ASV_254	0.88558952	0.972222222	*Pseudochattonella verruculosa*

4.3.2 The contribution of environmental factors and non-toxic species interactions to toxic algal community variation.

VPA was used to further quantify the contribution of environmental factors and non-toxic species interactions to toxic algal community variation. A combined 47% of the variation in toxic algal community could be explained, with non-toxic algal taxa accounting for 12%, environmental factors for 2%, together for 33%; the remaining 53% of variation was unexplained (Figure 4-9). The unaccounted variability in toxic algal distribution, as indicated by the VPA, might also be influenced by complex interactions between viruses, bacteria, and algae. Symbiotic relationships between *Planctomycetaceae* bacteria and diatoms can play a significant role in the resurgence of algal blooms (Ma et al. 2022). These bacteria not only provide essential nutrients that aid algal growth but may also indirectly affect algae by modifying environmental conditions through changes in bacterial physiological traits (Seymour et al. 2017). Therefore, a more thorough investigation into the myriad interactions that impact toxic taxa is essential. To effectively protect marine ecosystems and ensure public health and safety, a comprehensive understanding of the composition, ecological dynamics, and toxin production mechanisms of harmful algae, as well as the pathways through which they spread, is crucial.

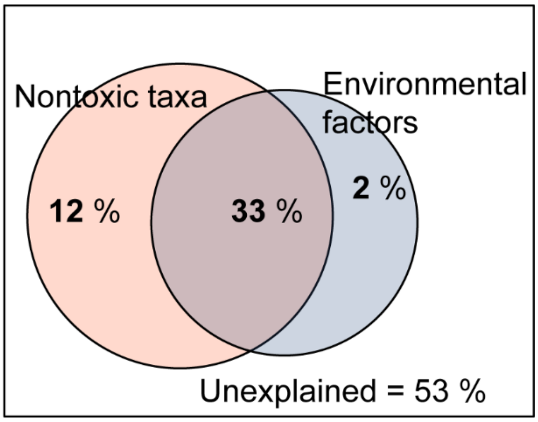


Figure 4-9 Variation partitioning showed the effects (%) of co-occurring nontoxic algal taxa and environmental factors (temperature, salinity, pH, DO, and nutrients) on the spatiotemporal distribution of toxic community.

4.4 Potential causative taxa of targeted LATs

Toxic algal taxa exhibited the same seasonal pattern as targeted LATs (Figure 4-10). LATs are of high priority due to their bioaccumulation effects. We further investigated the levels of typical LATs in surface seawaters of Hong Kong. Out of the seven targeted LATs, PTX-2, OA, GYM, and DTX-1 were present in Hong Kong waters. In contrast, DTX-2, AZA-1, and AZA-2 were undetected at all sampling sites (Appendix 3). The majority of LATs were detected in the dissolved seawater phase, with the only exception of PTX-2, which was more prevalent in SPM during the dry season. Within the dissolved phase, PTX-2 and OA emerged as the dominant toxins, collectively accounting for approximately 80% of the total concentrations of the detected LATs. These patterns mirror those found in the nearby waters of the Pearl River Estuary (Liu et al. 2020) and the northern South China Sea (Li et al. 2022a). Notably, PTX-2 and OA concentrations surged during the dry season compared to the wet season. DTX-1 was observed exclusively in the dry season. GYM concentrations remained no significant seasonal fluctuation. Notably, *Dinophysis* spp. are the sole known producers of PTX-2, and they exhibit optimal growth at temperatures ranging from 18 to 24°C, which could explain the higher concentrations of PTX-2 observed during the dry season. In contrast, OA and DTX-1 maintain stability in seawater, resulting in less pronounced seasonal variations in their distribution when compared to the distribution pattern of PTX-2 (García-Altares et al. 2016).

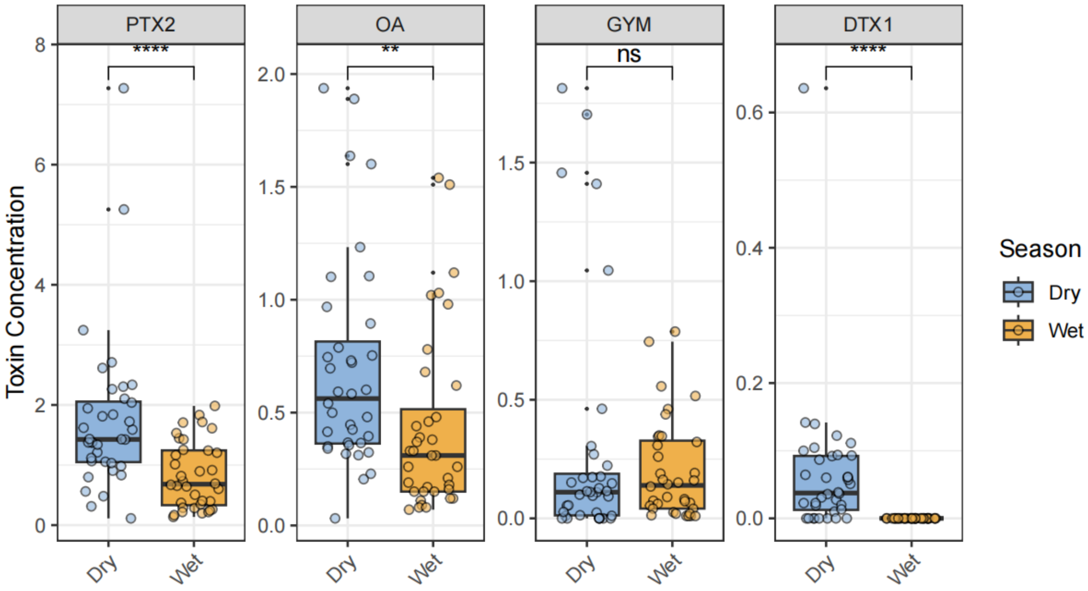


Figure 4-10 Seasonal patterns of targeted LATs.

PTXs are synthesized by toxic *Dinophysis* species, which are also capable of producing OA and DTXs (Reguera et al. 2012). Six ASVs related to *Dinophysis* spp. were identified as *D. acuminata* and *D. mils*. PTX-2, in particular, has been linked to *D. acuminata* and *D. mils*. These potential producers have been observed in Hong Kong waters, their toxin profiles are not yet fully understood (Lu & Hodgkiss 2004). OA and DTX-1 are primarily produced by *Dinophysis* spp., and epibenthic dinoflagellates *Prorocentrum* (Lee et al. 2020). ASVs linked to *Prorocentrum* species in this study, including *P. cordatum* and *P. rhathymum*, *P. rhathymum* have been reported to produce

OA. GYM toxins are associated with *Karenia mikimotoi* (formerly *Gymnodinium mikimotoi*) and *Alexandrium ostenfeldii* in our study (Molgó et al. 2017). Toxic algae related to detected toxins were summarized in Table 4-3. The relative abundance of toxic algal species was significantly higher in the dry season, sharing the same seasonal pattern with corresponding LATs (Figure 4-11). Accordingly, these can be assumed as potential causative organisms of LATs in Hong Kong coastal waters.

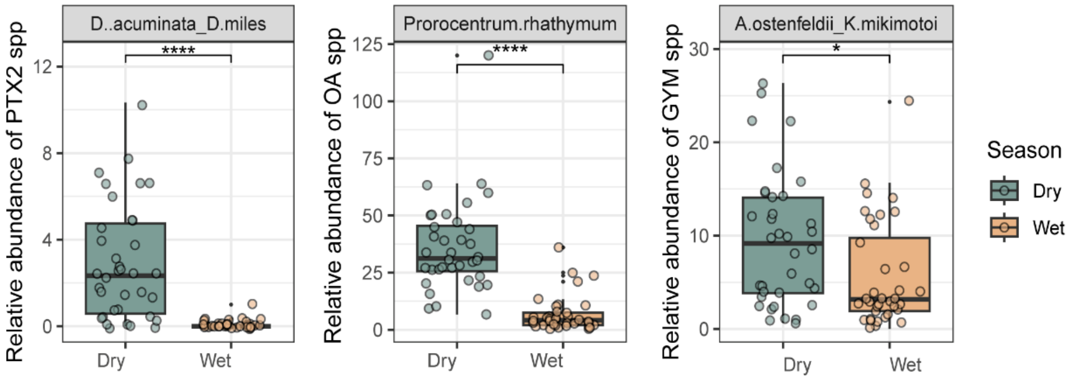


Figure 4-11 Seasonal patterns of potential producers.

Beyond the primary focus on specific LATs and their direct producers, it is imperative to also consider the broader influence of other harmful algal species present in Hong Kong's marine waters. For example, species within the *Prorocentrum* group have been linked to fish mortality events, causing hypoxia or anoxia that can lead to massive fish kills (Lu & Hodgkiss 2004). Equally concerning is the production of ciguatoxins by *Gambierdiscus scabrosus*, which are notable for their bioaccumulation through the marine food web-from herbivorous to carnivorous reef fish-and the consequent health risks they pose to humans upon consumption of contaminated fish (Pisapia et al. 2017). Further research is necessary to identify the toxin profiles of the prevailing algal species in the region.

Table 4-3 Toxic algae related to detected toxins.

Phylum	Class	Order	Family	Genus	Species	Toxin	References
Dinoflagellate	Dinophyceae	Dinophysiales	Dinophysaceae	Dinophysis	D. acuta	OA, DTX-2, PTX-2, PYX-2sa	(Fux et al. 2010)
						OA, DTX-1	(Lee et al. 1989)
					D. acuminata	OA	(Lee et al. 1989)
						DTX-1, PTX-2	(Kamiyama & Suzuki 2009)
					D.caudate	OA, PTX-2, PTX-2sa	(Fernández et al. 2006)
					D. fortii	OA, DTX-1, PTX-2	(Lee et al. 1989)
					D. miles	OA, DTX-1	(Marasigan et al. 2001)
					D. sacculus	OA, DTX-1	(Giacobbe et al. 2000)
					D. norvegica	OA, DTX-1	(Lee et al. 1989)
						PTX-2	(Suzuki et al. 2009)
					D. mitra	DTX-1	(Lee et al. 1989)
					D. rotundata	DTX-1	(Lee et al. 1989)
					D. tripos	DTX-1	(Lee et al. 1989)
		Prorocentrales	Prorocentraceae	Prorocentrum	P. lima	OA	(Murakami et al. 1982)
						OA, DTX-1	(Lee et al. 1989)
					P. faustiae	OA, DTX-1	(Morton 1998)
					P. concavum	OA	(Zou et al. 2020)
					P. hoffmannianum	OA	(Accoroni et al. 2018)

			P. maculosum	OA	(Zhou & Fritz 1993)
			P. belizeanum	OA	(Cruz et al. 2006)
			P. porosum	OA	(Arteaga-Sogamoso et al. 2023)
			P. rhathymum	OA	(Luo et al. 2017)
Gymnodiniales	Kareniaceae	Karenia	K. selliformis	GYM	(Seki et al. 1995)
			(Gymnodinium selliforme,)	GYM, GYM-B	(Miles et al. 2000)
Gonyaulacales	Ostreopsidaceae	Alexandrium	A. ostenfeldii (A. peruvianum)	12-methyl GYM	(Wagoner et al. 2011)
				GYM, 12-methyl GYM	(Waal et al. 2015)

4.5 Summary

This chapter investigated the distribution dynamics of microalgae communities, mainly focused on harmful and toxic algal community in coastal seawater using the self-constructed HTMaDB to verify reliability. The major findings are as follows:

A total of 1,649 amplicon sequence variants (ASVs) representing eukaryotic microalgae were identified. Principal coordinate analysis (PCoA) revealed that seasonal variation (R^2season = 0.3164) played a greater role than spatial variation (R^2region = 0.057) in shaping the phytoplankton community structure. Taxonomic richness was significantly higher during the dry season than the wet season, with dinoflagellates and Ochrophyta dominating both seasons. Dinoflagellates were more abundant in the dry season, while Ochrophyta peaked during the wet season. The modified stochasticity ratio (MST) suggested that deterministic processes, such as environmental filtering, became more pronounced with increasing toxic algal abundance. Out of the 1,649 ASVs, 403 were identified as harmful and toxic microalgae, belonging to nine classes, including Dinophyceae and Diatomea as dominant classes. Toxic algae, such as *Pseudo-nitzschia* spp., *Alexandrium* spp., and *Dinophysis* spp., were more prevalent in the dry season, whereas harmful, non-toxic taxa were relatively stable across seasons. Species like *Pseudo-nitzschia australis*, *Alexandrium ostenfeldii*, and *Prorocentrum cordatum* were identified as major toxin producers, contributing to PSP, ASP, and DSP. These harmful and toxic taxa have significant ecological impacts, including hypoxia, anoxia, and fish mortality.

The abundance of toxic algae increased during the dry season, correlating with temperature-driven deterministic processes. Key environmental factors influencing the toxic algal community included temperature, salinity, pH, and nutrients such as phosphate (PO_4^{3-}) and silicate (SiO_3^{2-}). Temperature emerged as the most influential factor, with some toxic genera, such as *Dinophysis*, *Pseudo-nitzschia*, and *Fibrocapsa*, displaying positive correlations with temperature. Controlling inputs of nutrients like phosphates could effectively suppress the proliferation of harmful algae such as Akashiwo, reducing bloom risks. Monitoring salinity changes could aid in predicting the distribution of specific algal taxa. Regulating key environmental factors could mitigate threats posed by algal toxins to aquaculture and human health. Specialist species such as *Alexandrium* and *Prorocentrum* were more abundant in the dry season, driving the seasonal increase in toxic algal abundance. VPA showed that 47% of the variation in the toxic algal community could be attributed to environmental factors (2%) and non-toxic algal interactions (12%), with the remaining 53% unexplained, possibly due to complex interactions with bacteria and viruses.

The strong alignment between toxin profiles and the relative abundance of toxic taxa highlights the robustness and reliability of our curated dataset. Beyond the targeted toxins, other harmful species such as *Gambierdiscus scabrosus*, associated with ciguatoxins, and hypoxia-inducing diatoms and dinoflagellates were identified. These species can have cascading ecological impacts, including bioaccumulation through food webs and large-scale fish mortality events. Improved identification of harmful and toxic species (via HTMaDB) and understanding of their environmental triggers enable early warning systems, supporting the development of effective management and mitigation strategies to minimize their impacts on ecosystems and human health.

Chapter 5 Microalgae and associated risks in coastal plastisphere

With the application of our newly constructed database, we explored the spatiotemporal distribution pattern and major driving factors of toxic microalgal communities in coastal ecosystem in chapter 4. The continued input of plastic waste into the ocean can alter marine microalgal community. Microbial risks stemming from the plastisphere (a microecosystem with plastics as the matrix) intensify the complexity and danger of marine plastic pollution. To further explore the ecological pattern and risk of microalgal community in the plastisphere, we collected 92 paired samples from Hong Kong and an additional coastal city, Qingdao, providing insights into the role of plastic debris as a novel habitat for microalgae in this chapter. Based on the amplicon sequencing data, the contrast in microalgal community structure among plastisphere and ambient are discussed. Additionally, the interactions between environmental factors such as temperature, salinity, and nutrients, and their impact on the abundance and diversity of microalgae within the plastisphere, are explored. Furthermore, the potential ecological risks posed by the proliferation of toxic microalgae within the plastisphere are discussed considering climate change and rising plastic pollution. By highlighting the growing concerns over algal blooms in the plastisphere, this chapter aims to provide a deeper understanding of how plastic pollution may exacerbate HABs in coastal ecosystems and contribute to the broader ecological challenges in marine environments.

5.1 Characteristics of microalgal communities in plastispheres

Overall, the composition of the plastisphere microalgal community and its ambient community was significantly different (Figure 5-1a-b). Ochrophyta (64.3%, 61.3%), Dinoflagellata (10.3%, 21.0%), and Chlorophyta (18.8%, 11.6%) were the dominant phyla in both the plastisphere and the seawater. However, the abundances of Chlorophyta were significantly higher in the plastisphere, while the abundance of Dinoflagellata was notably lower. (Figure 5-1c-d). Among 1270 ASVs, 423 ASVs showed significant changes in abundance with 170 ASVs (40.2%) significantly enriched in the plastisphere after filtering for an average relative abundance below 0.01% (Figure 5-1e).

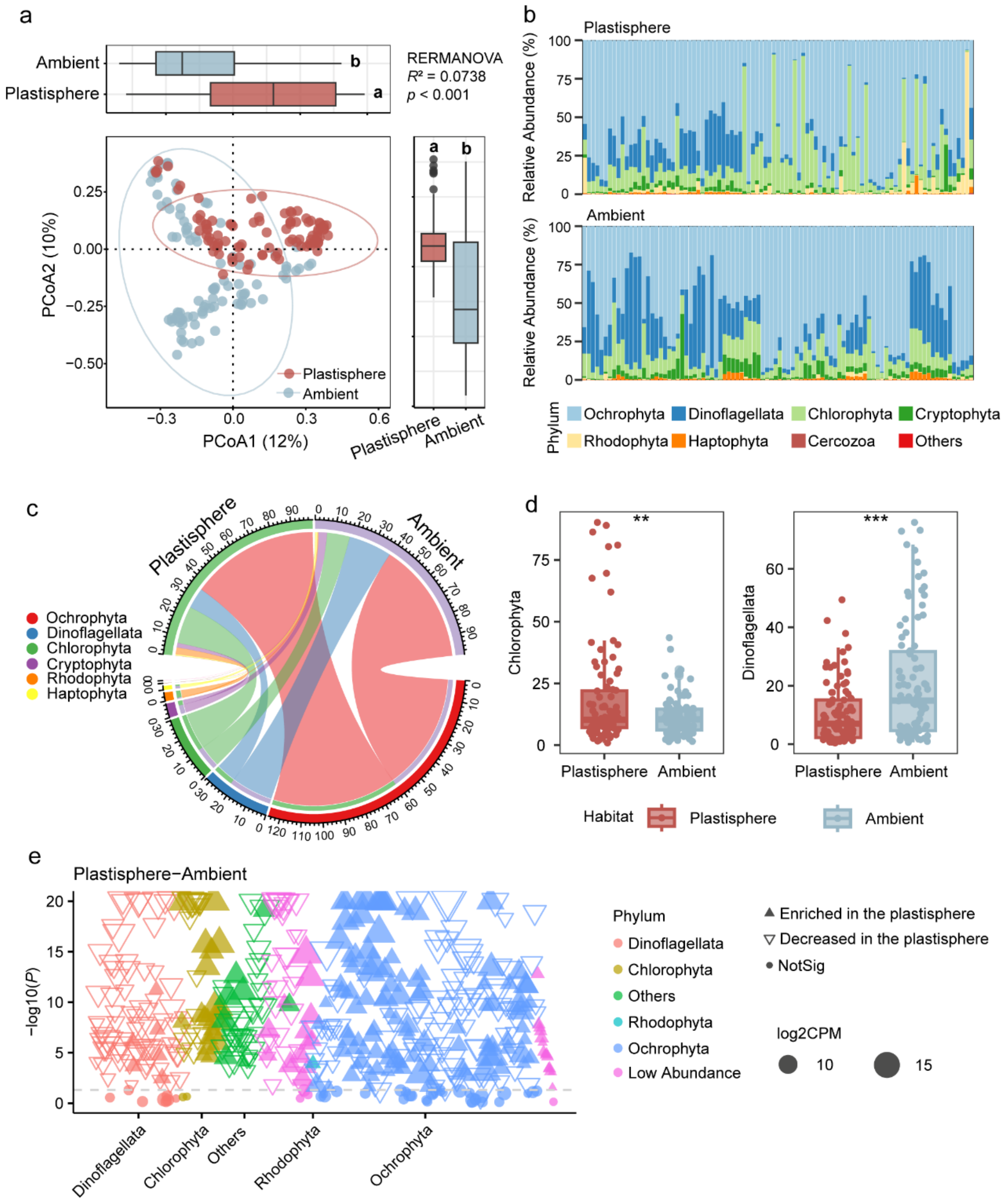


Figure 5-1 Characteristics of the plastisphere microalgal community. (a) Unconstrained principal coordinate analysis (PCoA) with permutational multivariate analysis of variance (PERMANOVA) showing a significant compositional difference between the plastisphere microalgal community and its ambient community. (b) The taxonomic composition at the phylum level of microalgal communities in each site in

the plastisphere and the ambient. (c) The taxonomic proportion of the microalgal community in the plastisphere and its ambient environment. (d) The difference of dominant phylum in the plastisphere and its ambient environment. (e) Manhattan plots showing differences in ASVs between the plastisphere and the ambient. Each circle or triangle represents a single ASV. An upward and filled triangle represents an ASV significantly enriched in the plastisphere, a downward and empty triangle represents an ASV significantly depleted in the plastisphere, while a circle represents an ASV with a nonsignificant difference between the two habitats ($*p < 0.05$; Wilcoxon rank-sum test). CPM, counts per million.

Both richness and Shannon indexes indicated that the plastisphere microalgal community, rather than its ambient community, exhibited a significantly higher level of alpha-diversity (Fig. 1d). Additionally, more unique ASVs were found in the plastisphere and a considerable proportion of ASVs was only detected in the plastisphere (Fig. 1e). These results suggest that the plastisphere could harbor alien microalgae from upstream systems into coastal ecosystems, potentially posing microalgal invasion risks. The plastisphere microalgal community also exhibited a significantly lower beta-diversity, suggesting that the plastisphere provides a shelter with less variations in environmental conditions for microalgae (Fig. 1f). The heightened microbial diversity observed within plastisphere communities cannot be attributed solely to passive accumulation of ambient microorganisms. This enrichment implies that plastic debris actively facilitates the transport and survival of non-indigenous species from upstream environments to new habitats, intensifying concerns over ecological colonization by foreign taxa. Notably, the presence of non-native algal species within plastispheres introduces critical ecological uncertainties. The prolonged retention and potential release of these algae into nutrient-rich coastal zones may induce localized HABs. Such proliferation events risk destabilizing native trophic networks through toxin-mediated species displacement and oxygen depletion, potentially triggering cascading disruptions across coastal ecosystems—from benthic community collapse to fisheries resource degradation.

Microalgae represent the primary productivity of marine ecosystems and regulate many biogeochemical cycling processes (Sommeria-Klein et al. 2021; De Vargas et al. 2015; Worden et al. 2015; Arrigo 2005). With the ever-increasing emission of plastic waste into the ocean, the density of plastisphere-associated microalgal communities with distinct compositions and higher taxonomic diversity will increase in the ocean. As a result, the overall structure and diversity of marine microalgal communities could be altered, and the associated ecological processes and biodiversity within marine ecosystems could be influenced.

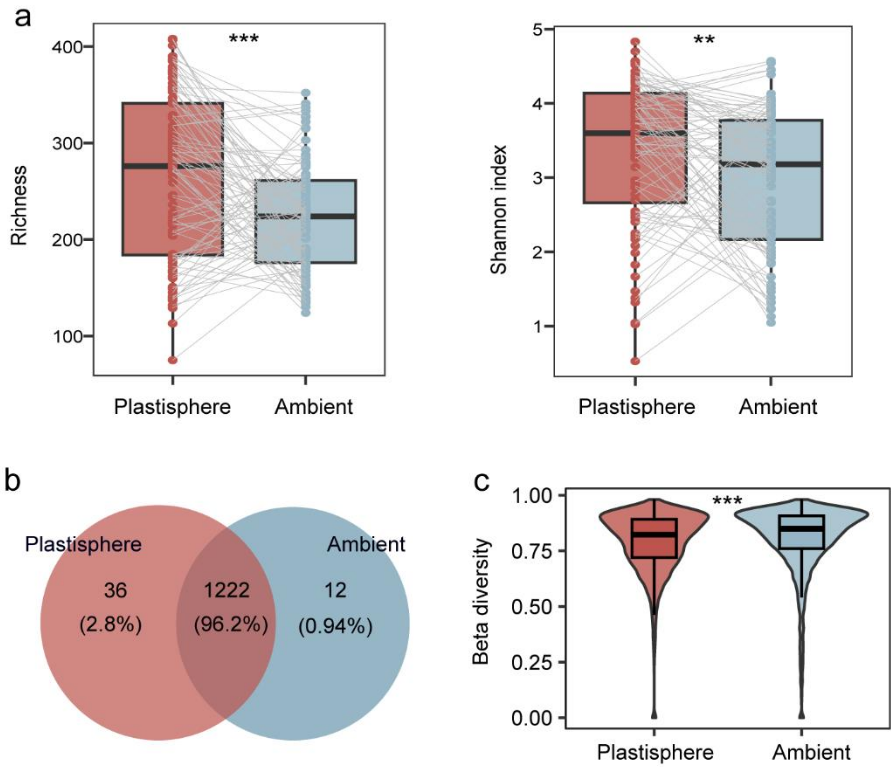


Figure 5-2 Taxonomic diversity in the plastisphere. (a) Differences in the alpha-diversity indexed by Richness and Shannon between the plastisphere microalgal community and its ambient community (**$p < 0.01$, **$p < 0.001$; Wilcoxon rank-sum test). (b) Overlap ASVs between plastisphere and ambient algal community. (c) Compositional dissimilarity between the plastisphere microalgal community and its ambient community based on Bray-Curtis distance.

5.2 The plastisphere provide a shelter to microalgal community

We then explored assembly mechanisms of the plastisphere microalgal community. The MST model showed that the assembly of both the plastisphere microalgal community and its ambient community was dominated by deterministic processes (MST < 0.5), but stochastic assembly played a more important role in the plastisphere community assembly than in the ambient community assembly (Figure 5-3a). Additionally, the habitat-level niche breadth was found to be significantly higher in the plastisphere (Figure 5-3b), suggesting that microalgae in the plastisphere might be less affected by environmental filtering (Li et al. 2021c; Wu et al. 2018b).

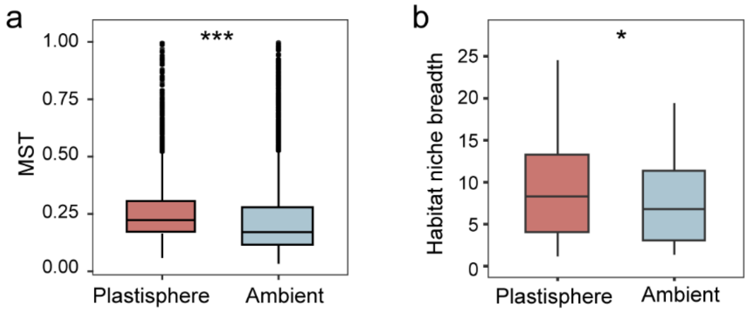


Figure 5-3 Community assembly mechanism of plastisphere microalgal community and its ambient community. (a) The modified stochasticity ratio (MST) model showing the relative importance of the stochastic process in the plastisphere and ambient microalgal community assembly (***$p < 0.001$; Wilcoxon rank-sum test). (b) Habitat niche breadth in the plastisphere and ambient microalgal community (*$p < 0.05$; Wilcoxon rank-sum test).

Procrustes analysis demonstrated that a significant correlation existed between the plastisphere microalgal community and its ambient community ($M^2 = 0.746$; $p < 0.001$; Figure 5-4a), indicating the plastisphere microalgal community was noteworthy shaped by surrounding community composition. The RDA result revealed that all detected physicochemical parameters were significantly associated with the microalgal community in seawater (Figure 5-4b). However, only pH, salinity, temperature, and phosphate concentration showed strong associations with the plastisphere microalgal community composition, while concentrations of nitrate and DOC did not (Figure 5-4c). The detected physicochemical factors explained 10.7% of variations in the plastisphere microalgal community, much less than the 19.6% explained in the ambient community. VPA was employed to further quantify the contribution of environmental factors and ambient species interactions to plastisphere algal community variation. A combined 25% of the variation in algal community could be explained, with non-toxic algal taxa accounting for 6%, environmental factors for 2%, and their combined effects for 17%; the remaining 75% of variation was unexplained (Figure 5-4d). The unexplained variability in the plastisphere algal community might also be influenced by intricate interactions among viruses, bacteria, and algae. These microbes not only supply crucial nutrients that promote algal growth but may also indirectly influence algae by altering environmental conditions through their physiological changes (Ma et al. 2022; Seymour et al. 2017).

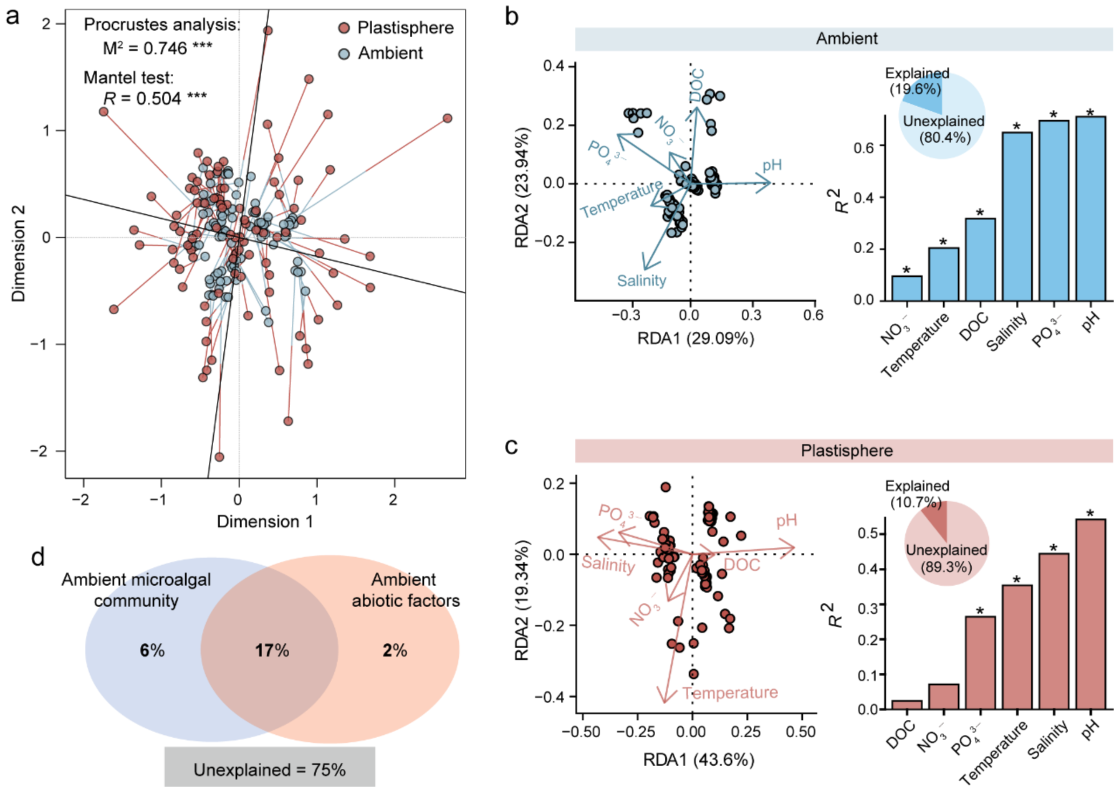


Figure 5-4 Potential driving factors shaping the plastisphere microalgal community and

its ambient community. (a) Significant correlation of microalgal community profile in the plastisphere with the ambient seawater based on Procrustes analysis (***$p < 0.001$). (b) Redundancy analysis between environmental variables and ambient algal communities (*$p < 0.05$). (c) Redundancy analysis between environmental variables and plastisphere algal communities (*$p < 0.05$). (d) Variation partition analysis showing the variations in the plastisphere microalgal community explained by ambient microalgal community and environmental factors.

The phenomenon of reduced environmental filtering effects on microalgae within the plastisphere is potentially due to the formation of biofilms by microalgae in conjunction with other microorganisms on plastic surfaces, which offer protective benefits, enhancing their resilience against adverse environmental conditions (Yan et al. 2024). The relatively stable microenvironments provided in the plastisphere can mitigate fluctuations in factors such as light, temperature, and water flow, facilitating easier adaptation and reproduction of microalgae, thereby further reducing the intensity of environmental filtering (Schaum 2019). Additionally, the adsorption and accumulation of organic matter from surrounding environmental media on plastic surfaces make the plastisphere a nutrient-rich environment (Bowley et al. 2021). This microenvironmental condition diminishes the reliance of microalgae on traditional environmental constraints, enabling them to survive and reproduce in relatively nutrient-poor marine ecosystems. This could explain why the microalgal community in the plastisphere was not affected by nitrate and DOC. The enhanced stochasticity and the reduced environmental filtering within the plastisphere reflect the unique and resource-rich growth environment provided by plastic surfaces. This environment facilitates the survival and reproduction of microalgae, particularly in nutrient-depleted marine ecosystems, thereby altering the dynamics and ecological functions of microbial communities. These findings provide crucial insights into understanding the impacts of plastic pollution on marine ecosystems and underscore the significance of the plastisphere as a new habitat influencing algal community structure.

5.3 Microalgal hazards harbored by plastispheres

Using our constructed database HTMaDB, a total of 373 ASVs among 1270 ASVs (29%) from our samples were identified as harmful/toxic microalgae. It is reasonable to expect that there are some taxa (2.4% ASVs) observed in the ambient community that were not detected in the plastisphere because some taxa may not have been exposed to or were not adapted to the plastisphere microenvironment. However, notably, 14 (3.8%) HAB ASVs were only detected in the plastisphere and were absent from the ambient community (Figure 5-5a). This result indicates that the plastisphere could harbor harmful/toxic microalgae from upstream environments entering coastal ecosystems, which may potentially trigger harmful algal blooms, thereby disturbing the balance and functioning of coastal ecosystems. The identified harmful/toxic ASVs attribute to 30 toxic and 44 harmful microalgal species (Figure 5-5b), primarily belonging to Diatomea (58.0%), Dinophyceae (28.3%), and Chlorophyceae (6.25%) (Figure 5-5c).

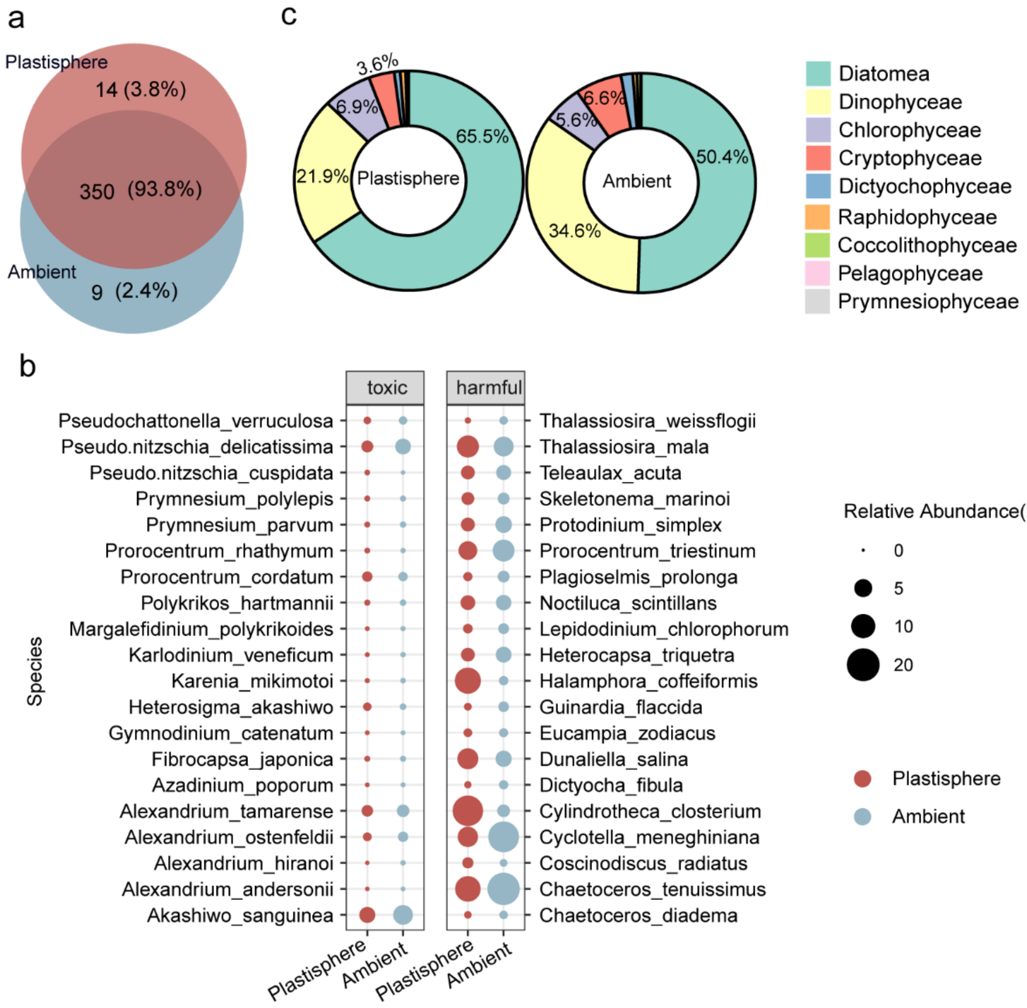


Figure 5-5 Harmful and toxic microalgal taxa. (a) The overlap of ASVs between the plastisphere and the bulk environment. (b) Top 20 relative abundance of harmful and toxic microalgae species in the two habitats. (c) The taxonomic composition of harmful and toxic algal community in the plastisphere and the ambient.

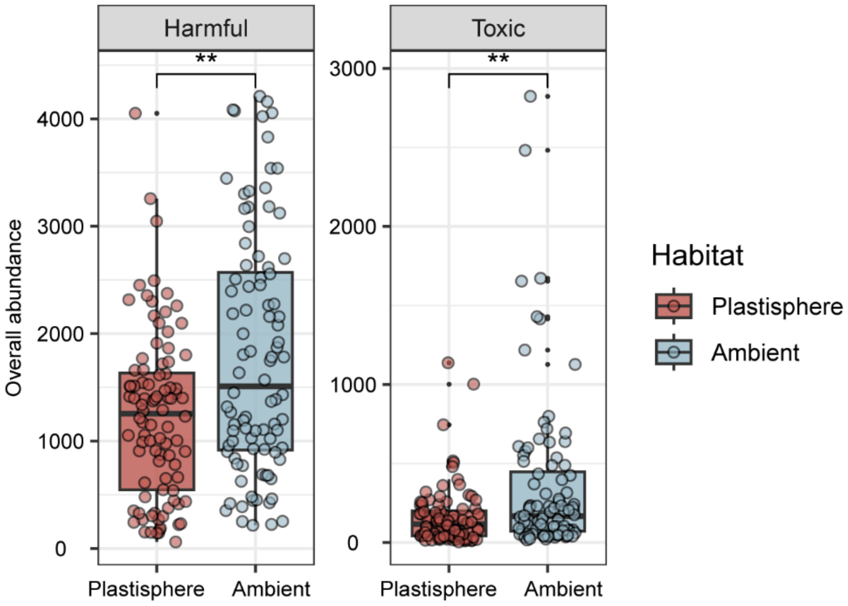


Figure 5-6 Comparison total abundance of HAB taxa in the two habitats.

Although the total abundance of these taxa was lower in the plastisphere (Figure 5-6), many harmful and toxic algal taxa were enriched in the plastisphere compared to the ambient community (Figure 5-7), The most abundant taxa were all diatoms in the plastisphere. Of the top 18 abundant harmful/toxic species, seven were enriched in the plastisphere, namely *Chaetoceros socialis*, *Cylindrotheca closterium*, *Halamphora coffeiformis*, *Nitzschia longissima*, *Skeletonema marinoi*, *Pseudo-nitzschia cuspidate* and *Thalassiosira allenii*. Notably, all these plastisphere-enriched harmful/toxic microalgae belong to diatoms. Most studies have reported that diatoms are common and primary residents of the plastisphere (Nava & Leoni 2021). A similar finding was observed for marine plastic debris collected from both pelagic and benthic environments along the Mediterranean coastal waters of Greece, Italy, and Spain, reporting that diatoms were present on nearly 100% of the plastic debris samples (Masó et al. 2016).In general, diatoms could be classified as centric (radial) or pennate (bilateral) according to their valve symmetry (Williams & Kociolek 2011). Pennate diatoms including *C. Closterium*, *H. coffeiiformis*, *N. longissimi* and *P. cuspidate* in our study were found to be abundant in both benthic and planktonic environment and capable of adhesion and motility on natural or artificial substrata. In contrast, centric diatoms are predominantly planktonic and are rarely observed in sediments or attached to various surfaces. However, a few centric diatom taxa, such as *C. socialis*, *S. marinoi*, and *T. allenii*, were found to be enriched within the plastisphere, suggesting that they can adapt to specialized habitats, such as the microenvironment provided by the plastisphere.

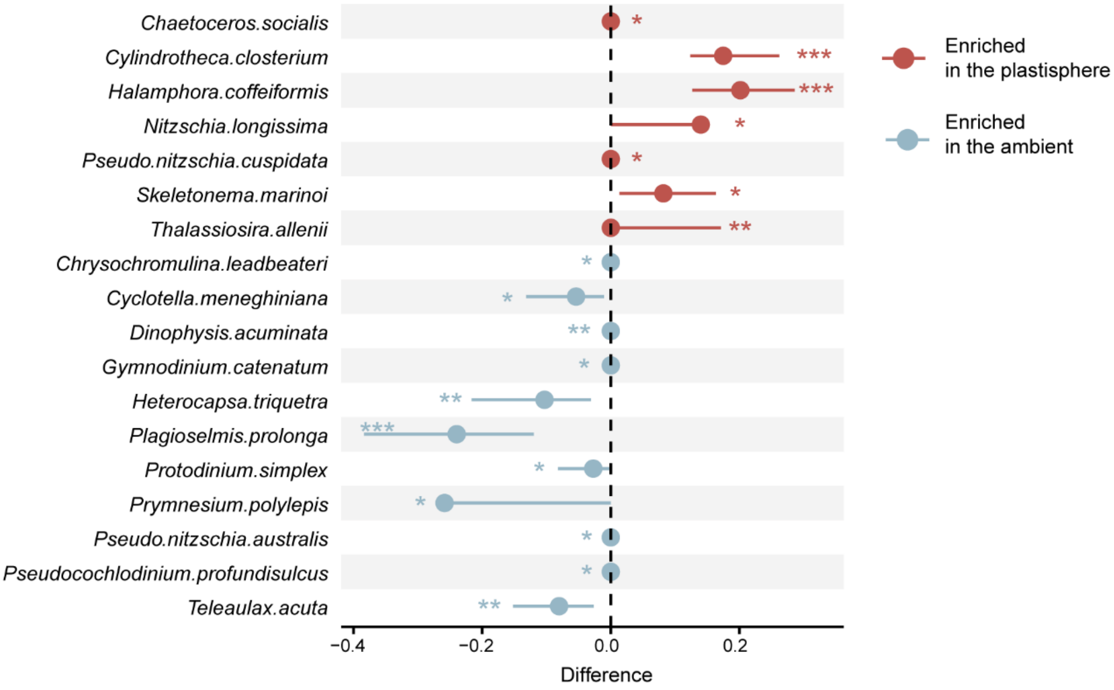


Figure 5-7 The enrichment of specific algal species in the plastisphere (*$p < 0.05$, **$p < 0.01$, ***$p < 0.001$; Wilcoxon rank-sum test).

The successful colonization of diatoms in the plastisphere is owing to their exceptional adhesion capabilities (Casabianca et al. 2019). Diatoms possess specialized structures, including a unique surface roughness from their nanoporous silica, which facilitates their attachment to various substrates, including plastic surfaces (Khan et al. 2020). The secretion of extracellular polymeric substances (EPS) by members of diatoms such as *Chaetoceros* and *Thalassiosira* during growth plays a crucial role in this process, creating a sticky matrix that allows diatoms to firmly anchor to the plastic (Vidal-Melgosa et al. 2021). This strong adhesion not only enables diatoms to resist detachment from the substrate but also promotes the formation of biofilms (Wright et al. 2020). Plastispheres are typically nutrient-rich environments, since they can sorb organic matter from the surrounding environment and leach organics from their interior (Rillig et al. 2024b; Sheridan et al. 2022), providing nutrient sources for diatoms (Christie-Oleza et al. 2017).

Diatoms typically exhibit rapid growth and reproduction rates, enabling them to occupy available ecological niches quickly (Inomura et al.; Taurozzi et al. 2024). This competitive advantage facilitates the establishment of dense populations on plastic surfaces. In contrast, dinoflagellates have slower growth rates and longer generation times, which may hinder their ability to compete effectively for resources in the dynamic environment of the plastisphere. The ability of diatoms to rapidly respond to environmental changes, such as fluctuations in light availability and nutrient concentration, enhances their competitiveness in these novel niches (Zhou et al. 2021).

Moreover, the interactions between diatoms and other microorganisms present in the plastisphere may further contribute their adaptation in the plastisphere. The ability of diatoms to form complex biofilms with bacteria enhances their nutrient acquisition and provides protection against predation (Flemming & Wingender 2010; Sun et al. 2023). These biofilms create a microenvironment that can stabilize nutrient availability, thereby supporting the growth of diatoms.

Together, the enhanced ability of diatoms to colonize the plastisphere can be attributed to their superior adhesion capabilities, rapid growth rates, efficient nutrient utilization, broad ecological adaptability, and beneficial interactions with other microorganisms. As plastic debris continues to accumulate in marine environments, the proliferation of diatoms in the plastisphere may have far-reaching implications for nutrient cycling, food web dynamics, and ecosystem health.

Coastal plastispheres enriched with harmful/toxic microalgae pose critical threats to biological health. For example, the plastisphere-enriched species *Pseudo-nitzschia cuspidate* is a producer of domoic acid (DA), a kind of neurotoxin that can cause animal seizures, disorientation, and even death (Cook et al. 2015). The widespread and long-distance transport of plastic debris facilitates the proliferation of toxic algal blooms. A High concentration of DA exposure have been linked to increased stranding events of California sea lions, with substantial impacts on their population dynamics (Scholin et al. 2000).

Beyond the enrichment of diatom species in the plastisphere, ichthyotoxic dinoflagellates such as *Margalefidinium polykrikoides* and *Prymnesium parvum* were also detected (Fig. S4) (Hofmann et al. 2021; Wagstaff et al. 2021). The presence of *Alexandrium* spp., *Dinophysis* spp., *Prorocentrum* spp., *Azadinium* spp., and *Karenia* spp. pose a threat to various shellfish poisoning (Lassus et al. 2016; Li et al. 2024d;

Marzidovšek et al. 2024; Valbi et al. 2019). A previous study has reported that the cultured *A. pacificum* strains isolated from plastic debris could produce paralytic shellfish toxins (Casabianca et al. 2019). The incidence of shellfish poisoning due to the consumption of contaminated seafood warrants attention, as it poses direct health risks to humans and further complicates the ecological ramifications of plastic pollution in marine ecosystems (Trainer et al. 2012). Additionally, many species of dinoflagellates such as *Alexandrium* spp. are able to form resting cysts (Dai et al. 2020), which are particularly relevant to survival and transport of these species on plastic debris. These interconnected issues underscore the urgency of addressing plastic debris and its role in the proliferation of harmful algal blooms, as well as the consequent effects on marine life and human health.

Monitoring data reveal that the frequency and intensity of harmful algal bloom events are increasing with human activities in the Anthropocene (Dai et al. 2023b). According to our findings, it is reasonable to hypothesize that the ever-increasing emission of plastic waste and its long-distance, cross-ecosystem transportable property may be an overlooked contributor to the increasing harmful algal bloom outbreaks. Further monitoring and more modeling evidence are needed to test this hypothesis. If confirmed, controlling plastic pollution will become a crucial strategy for managing and preventing algal bloom outbreaks in coastal ecosystems.

5.4 Risks associated with toxic and harmful communities under the background of climate change

We performed the Mantel test to investigate the major driving environmental drivers of the harmful and toxic algal community in the plastisphere. The result showed that harmful and toxic algal communities in both the plastisphere and its ambient seawater were significantly associated with temperature, pH, and salinity, with temperature showing the largest correlation coefficient (Figure 5-8a). Linear regression models were further applied to uncover how the total abundance of harmful and toxic microalgae responds to environmental factors (Figure 5-8b). The result indicated that the total abundance of harmful and toxic microalgae in both the plastisphere and its ambient was positively associated with temperature, while it was negatively associated with pH levels. In the future, the interwoven challenges of global changes, including climate warming leading to a warmer ocean, increasing CO_2 levels resulting in a more acidic ocean, and the ever-increasing trajectory of plastic emissions, may exacerbate the microalgal risk in coastal ecosystems (Simmer et al. 2023). Although current results provide valuable preliminary insights into the microalgal-associated risks with plastics, their application in risk assessment remains limited. Beyond species identification, future investigations should incorporate functional assessments, including toxin production, pathogenicity, and microbial viability analyses, to better understand the actual risk potential of these organisms. Ultimately, addressing the complex challenges posed by microplastic pollution and the associated biological risks will require interdisciplinary collaboration across microbiology, ecology, oceanography, toxicology, and public health sectors. Only through such concerted efforts can we better quantify risks and design targeted interventions to mitigate the impacts of plastic pollution on marine ecosystems.

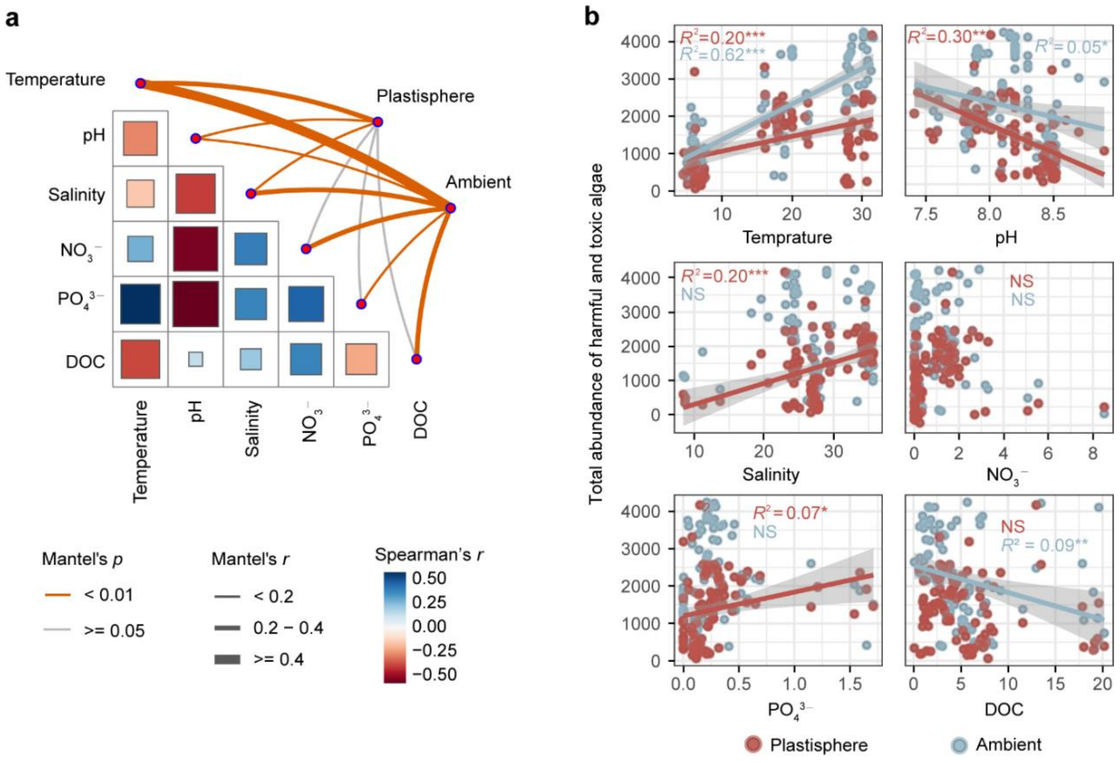


Figure 5-8 Associations between environmental factors and the microalgal risk. (a) Correlations of the plastisphere and ambient algal community with environmental factors using Mantel test. (b) Linear regression analysis between the driving environmental factors and total abundance of harmful and toxic microalgae in the plastisphere and ambient seawater. Environmental factors showing significant associations with harmful and toxic microalgal community structure in the Mantel test were all included in the linear regression models ($*p < 0.05$, $**p < 0.01$, $***p < 0.001$, NS = not significant).

5.5 Summary

This chapter investigated the composition, diversity, and ecological risks associated with microalgae in the coastal plastisphere, providing new insights into the potential impacts of plastic pollution on marine ecosystems. The study focused on the differentiation of microalgal communities between the plastisphere and ambient seawater, the environmental drivers influencing these communities, and the enrichment of harmful and toxic taxa in the plastisphere. Key findings are summarized below:

The microalgal community composition in the plastisphere was significantly different from that in ambient seawater. Ochrophyta, Dinoflagellata, and Chlorophyta were the dominant phyla in both environments; however, Chlorophyta were significantly enriched in the plastisphere, whereas Dinoflagellata were notably less abundant. Of the 1,270 ASVs identified, 423 showed significant abundance changes, with 170 ASVs enriched in the plastisphere. Both richness and Shannon indexes indicated higher alpha-diversity in the plastisphere, which also harbored unique ASVs not present in ambient seawater. These findings suggest that the plastisphere serves as a stable and nutrient-rich microhabitat capable of harboring alien microalgae, potentially introducing invasion risks into coastal ecosystems. The assembly of plastisphere microalgal communities was shaped by both deterministic and stochastic processes, with stochasticity playing a larger role compared to ambient seawater. The broader habitat-level niche breadth observed in the plastisphere indicated reduced environmental filtering effects, likely due to the stable microenvironment and biofilm formation on plastic surfaces. Procrustes analysis revealed a strong correlation between plastisphere and ambient microalgal communities, while RDA showed that pH, salinity, temperature, and phosphate concentrations were key factors influencing plastisphere community composition. However, the overall contribution of environmental factors to plastisphere community variation was much lower than that for ambient seawater, highlighting the unique ecological dynamics of the plastisphere.

Using the HTMaDB database, 373 harmful and toxic ASVs were identified, including 14 taxa exclusively detected in the plastisphere. Most harmful and toxic taxa belonged to diatoms, such as *Pseudo-nitzschia cuspidate*, *Chaetoceros socialis*, and *Skeletonema marinoi*. These species are known producers of toxins like DA, posing significant risks to marine ecosystems and human health. The enhanced colonization of diatoms in the plastisphere was attributed to their strong adhesion capabilities, rapid growth rates, and ability to form biofilms. In addition to diatoms, harmful dinoflagellates were also detected, raising concerns about the plastisphere's role in exacerbating HABs. The plastisphere's ability to enrich harmful and toxic microalgae poses significant ecological and health risks. The proliferation of toxin-producing algae in the plastisphere can disrupt nutrient cycling, food web dynamics, and ecosystem functions, potentially exacerbating the frequency and intensity of HABs. The presence of harmful algae, such as *Pseudo-nitzschia cuspidate*, in the plastisphere highlights its role in facilitating long-distance transport and proliferation of toxic algal blooms, which have been linked to mass mortality events in marine life and human shellfish poisoning incidents.

The Mantel test identified temperature, pH, and salinity as major environmental drivers of harmful and toxic algal communities in the plastisphere, with temperature showing the strongest correlation. Linear regression models further revealed that the abundance of harmful and toxic algae was positively associated with temperature and negatively associated with pH. These findings suggest that ongoing global changes, including ocean warming, acidification, and increasing plastic pollution, could amplify the risks posed by harmful algae in coastal ecosystems.

In summary, this chapter revealed significant compositional differences and higher diversity in plastisphere microalgal communities compared to ambient seawater. The plastisphere serves as a unique and nutrient-rich microhabitat that facilitates the survival, enrichment, and transport of harmful and toxic algae. The findings underscore the critical ecological risks posed by the plastisphere, particularly in exacerbating HABs and associated toxin production. The reduced environmental filtering effects and enhanced stochasticity within the plastisphere highlight its role as a novel ecological niche influencing marine microalgal dynamics. However, a large proportion of the observed variation in plastisphere algal communities remains unexplained, likely due to intricate interactions among algae, bacteria, and viruses. Future research should focus on these complex interactions and their implications for ecosystem health. Additionally, the role of the plastisphere in amplifying the impacts of climate change and plastic pollution on marine ecosystems warrants further investigation. Continued monitoring and management efforts are essential to mitigate the ecological and public health risks posed by the plastisphere and its associated harmful microalgae.

Chapter 6 Conclusions and Recommendations

6.1 Overall summary and major conclusions

This thesis undertook a comprehensive examination of the ecological patterns and driving mechanisms of microalgal community and associated risks in coastal ecosystems with our curated database. The research focused on understanding the dynamics and underlying mechanism of HAB species, as well as their colonization characteristic within the plastisphere-the unique ecological niche formed on the surfaces of plastic debris. This niche not only serves as a habitat for diverse microalgal communities but also significantly alters their composition and diversity. The main findings of the thesis are as follows:

1. Construction of a comprehensive 18S full length database: The utilization of the HTMaDB has significantly enhanced the capacity for accurately identifying and monitoring harmful and toxic microalgae. This tool is instrumental in assessing the diversity and distribution of algal species in affected marine regions, providing a crucial resource for researchers and policymakers aiming to mitigate the impacts of HABs.

2. Ecological impact of the plastisphere: The studies highlighted the plastisphere's role as a distinct ecological niche that selectively enriches and alters the composition of microalgal communities. Microalgal communities in the plastisphere were less constrained by ambient physicochemical factors, enabling the shelter role of the plastisphere for microalgae. Compared to its ambient community, the microalgal community in the plastisphere harbored a higher diversity of algal species,

including prevelance of harmful and toxic diatoms (e.g., *Pseudo-nitzschia cuspidate*, *Chaetoceros socialis*, and *Skeletonema marinoi*). The plastisphere could facilitate the proliferation of these species by providing a stable habitat that is somewhat insulated from environmental stressors typically present in the surrounding marine environment.

3. Influence of environmental factors: Temperature and salinity are identified as critical environmental factors that influence algal community dynamics. The findings underscore that these abiotic factors, especially temperature, drive the seasonal patterns of algal communities and enhance the prevalence of HABs during certain times of the year. This relationship suggests that changes in these environmental variables due to climate change could potentially exacerbate the occurrence and severity of HABs.

4. Potential for increased HAB occurrences: By providing a refuge and a means of transport, plastic debris may increase the frequency and geographic spread of HABs. The ability of the plastisphere to act as a vector for harmful algae and their toxins introduces new dynamics into marine ecosystems, potentially facilitating the spread of these organisms beyond their natural geographic boundaries and leading to new outbreaks of HABs in previously unaffected areas.

The findings highlight the need for a paradigm shift in managing harmful algal blooms (HABs) – moving from reactive suppression strategies to proactive measures addressing plastic pollution. One approach is to designate high-risk regions, such as the Pearl River estuaries, as "HAB-plastic control zones," where stringent regulations on plastic use and disposal would be enforced. Additionally, developing chitosan-based coatings to prevent diatom adhesion without contributing to microplastic pollution represents a promising solution. This work provides a scientific foundation for incorporating plastic pollution management as an integral part of HAB mitigation efforts, which is essential for advancing toward Sustainable Development Goal 14 (Life Below Water) in the face of escalating global environmental challenges.

6.2 Limitations of the current study and future perspectives

Although the research study provided significant contributions to the field of marine ecology by establishing a comprehensive database of harmful and toxic microalgae, which enhance our ability to monitor and manage HABs effectively. It also highlighted the emerging environmental challenge posed by plastic debris in marine ecosystems. However, there are limitations that must be acknowledged to refine future research and interventions. These limitations, coupled with suggested future perspectives, can help guide subsequent studies aiming to further unravel the complexities of HAB dynamics and the plastisphere.

The current research is primarily focused on surface seawater, neglecting the investigation of harmful and toxic algae in the benthic layers. This oversight can lead to an incomplete understanding of the spatial distribution and full ecological impacts of HABs, as different environmental conditions and algal communities may exist in deeper waters. Sampling was conducted only during the dry and wet seasons, which does not allow for continuous, long-term monitoring of phytoplankton dynamics. This limitation restricts the ability to capture seasonal variations fully and understand long-term trends and fluctuations in phytoplankton communities, which are crucial for predicting and managing algal blooms effectively. In the case of VPA, only interactions among algal species were considered. This approach overlooks the potential influence of other biological factors such as bacteria and viruses, which can significantly impact algal growth and community dynamics through various interactions, including symbiosis, competition, and predation. The current work mainly relies on culture-independent approaches, such as high-throughput qPCR and 18SrRNA gene amplicon sequencing. Correlation analysis was conducted between the microbial community and environmental factors. It will be more important to set up lab experiments to validate if there is causality, rather than correlation. The study did not include measurements of algal toxins and quantification of microalgae-associated risk within the plastisphere. This is a significant oversight, as plastics can absorb and concentrate toxins produced by harmful algae. Without assessing the presence and concentration of toxins on plastic debris, it is difficult to fully understand the role that the plastisphere plays in the distribution and potential enhancement of algal toxin risks in marine environments. This limitation hinders the ability to evaluate the health risks posed by toxin-laden plastics to marine life and, by extension, to human health through bioaccumulation and the food chain.

To overcome these limitations, future studies should aim to include deeper water layers in their sampling regimen to provide a more holistic view of the algal communities across different marine strata. Additionally, extending the monitoring periods to encompass multiple seasons or even continuous year-round sampling could offer a more detailed picture of phytoplankton dynamics and their responses to environmental changes. Including a broader range of biological interactions in the analysis, particularly with non-algal microorganisms like bacteria and viruses, would also enrich the understanding of community dynamics and ecological balances. It might be relevant to isolate representative harmful and toxic taxa from seawater samples by employing culture-dependent methods to further consolidate the conclusions. Finally, quantifying the impacts of plastic pollution on marine microalgal communities and bloom events through simulation experiments and big-data modelling could yield more precise data on how different plastics affect marine life, thereby facilitating more targeted mitigation strategies against plastic pollution.

Appendix 1

This section provides detailed database information in this study.

1 Source of eukaryotic toxic and harmful microalgae species.

<table>
<tr><th colspan="4">Public website</th></tr>
<tr><td colspan="4">IOC-UNESCO Taxonomic Reference List of Harmful Micro Algae, Lundholm, N.; Churro, C.; Escalera, L.; Fraga, S.; Hoppenrath, M.; Iwataki, M.; Larsen, J.; Mertens, K.; Moestrup, Ø.; Murray, S.; Tillmann, U.; Zingone, A. (Eds) (2009 onwards). IOC-UNESCO Taxonomic Reference List of Harmful Micro Algae. Accessed at https://www.marinespecies.org/hab on 2024-10-26. doi:10.14284/362</td></tr>
<tr><th colspan="4">Paper search</th></tr>
<tr><th>Number</th><th>Author Full Names</th><th>Article Title</th><th>Source Title</th></tr>
<tr><td>1</td><td>Roselli, Leonilde; Caroppo, Carmela; Bevilacqua, Stanislao; Ciciriello, Pierangelo Cosimo; Ungaro, Nicola; Vadrucci, Maria Rosaria</td><td>Harmful algae and pressure-impact relationship: Noxious blooms and toxic microalgae occurrence from coastal waters of the Apulia region (Adriatic and Ionian Seas, Mediterranean)</td><td>MARINE ENVIRONMENTAL RESEARCH</td></tr>
<tr><td>2</td><td>Hargraves, PE; Maranda, L</td><td>Potentially toxic or harmful microalgae from the northeast coast</td><td>NORTHEASTERN NATURALIST</td></tr>
<tr><td>3</td><td>Hernandez-Becerril, David U.; Alonso-Rodriguez, Rosalba; Alvarez-Gongora, Cynthia; Baron-Campis, Sofia A.; Ceballos-Corona, Gerardo; Herrera-Silveira, Jorge; Del Castillo, Maria E. Meave; Juarez-Ruiz, Norma; Merino-Virgilio, Fanny; Morales-Blake, Alejandro; Ochoa, Jose L.; Orellana-Cepeda, Elizabeth; Ramirez-Camarena, Casimiro; Rodriguez-Salvadoro, Raciel</td><td>Toxic and harmful marine phytoplankton and microalgae (habs) in Mexican Coasts</td><td>JOURNAL OF ENVIRONMENTAL SCIENCE AND HEALTH PART A-TOXIC/HAZARDOUS SUBSTANCES & ENVIRONMENTAL ENGINEERING</td></tr>
<tr><td>4</td><td>Rodriguez-Palacio, M. C.; Crisostomo-Vazquez, L.; Alvarez-Hernandez, S.; Lozano-Ramirez, C.</td><td>Strains of toxic and harmful microalgae, from waste water, marine, brackish and fresh water</td><td>FOOD ADDITIVES AND CONTAMINANTS PART A-CHEMISTRY ANALYSIS CONTROL EXPOSURE & RISK ASSESSMENT</td></tr>
<tr><td>5</td><td>Zingone, A; Siano, R; D'Alelio, D; Sarno, D</td><td>Potentially toxic and harmful microalgae from coastal waters of the Campania region (Tyrrhenian Sea, Mediterranean Sea)</td><td>HARMFUL ALGAE</td></tr>
<tr><td>6</td><td>Zhang, Anqi; Liu, Honghan; Li, Chenhong; Chen, Changping; Liang, Junrong; Sun, Lin; Gao, Yahui</td><td>Relationship between toxic and harmful microalgae and environmental factors in typical mariculture areas of East China Sea</td><td>JOURNAL OF OCEANOLOGY AND LIMNOLOGY</td></tr>
<tr><td>7</td><td>Hofbauer, Wolfgang Karl</td><td>Toxic or Otherwise Harmful Algae and the Built Environment</td><td>TOXINS</td></tr>
<tr><td>8</td><td>Vershinin, A. O.; Orlova, T. Yu.</td><td>Toxic and harmful algae in the coastal waters of Russia</td><td>OCEANOLOGY</td></tr>
<tr><td>9</td><td>Yoshida, Takashi</td><td>Molecular-physiological and -ecological studies on toxic and</td><td>NIPPON SUISAN GAKKAISHI</td></tr>
</table>

		harmful algae	
10	Brown, Emily R.; Moore, Sam G.; Gaul, David A.; Kubanek, Julia	Differentiating toxic and nontoxic congeneric harmful algae using the non-polar metabolome	HARMFUL ALGAE
11	Casabianca, Silvia; Cornetti, Luca; Capellacci, Samuela; Vernesi, Cristiano; Penna, Antonella	Genome complexity of harmful microalgae	HARMFUL ALGAE
12	Daranas, AH; Norte, M; Fernández, JJ	Toxic marine microalgae	TOXICON
13	Bertin, Matthew J.; Zimba, Paul V.; Beauchesne, Kevin R.; Huncik, Kevin M.; Moeller, Peter D. R.	Identification of toxic fatty acid amides isolated from the harmful alga Prymnesium parvum carter	HARMFUL ALGAE
14	Zhang, Huajun; Wang, Hui; Zheng, Wei; Yao, Zhiyuan; Peng, Yun; Zhang, Su; Hu, Zhong; Tao, Zhen; Zheng, Tianling	Toxic Effects of Prodigiosin Secreted by Hahella sp KA22 on Harmful Alga Phaeocystis globosa	FRONTIERS IN MICROBIOLOGY
15	Ignatiades, Lydia; Gotsis-Skretas, Olympia	A Review on Toxic and Harmful Algae in Greek Coastal Waters (E. Mediterranean Sea)	TOXINS
16	Tester, Patricia A.; Litaker, R. Wayne; Berdalet, Elisa	Climate change and harmful benthic microalgae	HARMFUL ALGAE
17	Wikfors, Gary H.; Hegaret, Helene; Galimany, Eve; Sunila, Inke; Soudant, Philippe; Shumway, Sandra E.	Hemocyte responses in bivalve molluscs exposed to harmful or toxic algae:: Overview and preliminary synthesis	JOURNAL OF SHELLFISH RESEARCH
18	Fernandes-Salvador, Jose A.; Davidson, Keith; Sourisseau, Marc; Revilla, Marta; Schmidt, Wiebke; Clarke, Dave; Miller, Peter I.; Arce, Paola; Fernandez, Raul; Maman, Luz; Silva, Alexandra; Whyte, Callum; Mateo, Maria; Neira, Patricia; Mateus, Marcos; Ruiz-Villarreal, Manuel; Ferrer, Luis; Silke, Joe	Current Status of Forecasting Toxic Harmful Algae for the North-East Atlantic Shellfish Aquaculture Industry	FRONTIERS IN MARINE SCIENCE
19	Shi, Xinguo; Zou, Yazhen; Zhang, Yingjiao; Ding, Guangmao; Xiao, Yuchun; Lin, Senjie; Chen, Jianfeng	Salinity decline promotes growth and harmful blooms of a toxic alga by diverting carbon flow	GLOBAL CHANGE BIOLOGY
20	Bhat, S. R.	Reflections on the discovery of toxic species of marine micro-algae known to form harmful blooms	CURRENT SCIENCE
21	Chuong, Jeremy Jason Chin Chwan; Rahman, Mahbubur; Ibrahim, Nadiah; Heng, Lee Yook; Tan, Ling Ling; Ahmad, Asmat	Harmful Microalgae Detection: Biosensors versus Some Conventional Methods	SENSORS
22	Toebe, Kerstin	Whole cell hybridisation for monitoring harmful marine microalgae	ENVIRONMENTAL SCIENCE AND POLLUTION RESEARCH
23	Topal, M.; Topal, E. I. Arslan; Obek, E.	A green algae Cladophora fracta for accumulation of toxic/harmful pollutants causing environmental pollution in mine gallery waters	INTERNATIONAL JOURNAL OF ENVIRONMENTAL SCIENCE AND TECHNOLOGY
24	WAGNER, KH; SIDDIQI, I	Toxic components of microalgae scenedesmus obliquus	NATURWISSENSCHAFTEN
25	Mafra Jr., Luiz L. Mafra; Sunesen, Ines; Pires, Estela; Nascimento, Silvia Mattos; Alvarez, Gonzalo; Mancera-Pineda, Jose Ernesto; Torres, Gladys; Carnicer, Olga; Galindo, Jose Alexis Huamani; Ramirez, Sonia Sanchez;	Benthic harmful microalgae and their impacts in South America	HARMFUL ALGAE

	Martinez-Goicoecheaj, Ana; Morales-Benavides, Dilcia; Valerio-Gonzalez, Lorelys		
26	Zhao, Ting; Cao, Huidi; Jia, Yanfen; Han, Xiaotian; Yan, Tian; Yu, Rencheng	Information standardization for typical toxic and harmful algae in China's coastal waters-a case study of Karenia mikimotoi	JOURNAL OF OCEANOLOGY AND LIMNOLOGY
27	Lee, SJ; Kim, Y; Kim, HG; Seo, GM; Jeong, JH; Hong, YK	Algalytic activity of α-mannosidase on harmful marine microalgae	JOURNAL OF APPLIED PHYCOLOGY
28	CHEUNG, KC; CHU, LM; WONG, MH	Toxic effect of landfill leachate on microalgae	WATER AIR AND SOIL POLLUTION
29	Gol'din, Evgeny B.	Marine microalgae and their biocidal features in harmful organisms control	PHYCOLOGIA
30	Pearson, Leanne A.; D'Agostino, Paul M.; Neilan, Brett A.	Recent developments in quantitative PCR for monitoring harmful marine microalgae	HARMFUL ALGAE
31	Maso, Mercedes; Garces, Esther	Harmful microalgae blooms (HAB);: problematic and conditions that induce them	MARINE POLLUTION BULLETIN
32	Fukuyo, Yasywo	Toxic benthic microalgae in the western Pacific region	NIPPON SUISAN GAKKAISHI
33	Gustafsson, S.; Hultberg, M.; Figueroa, R. I.; Rengefors, K.	On the control of HAB species using low biosurfactant concentrations	HARMFUL ALGAE
34	Dolapsakis, Nicolas P.; Tzovenis, Ioannis; Kantourou, Paraskevi; Bitis, Ioannis; Economou-Amilli, Athena	Potentially harmful microalgae from lagoons of the NW Ionian sea, Greece	JOURNAL OF BIOLOGICAL RESEARCH-THESSALONIKI
35	Shurtleff, James; Rich, Phillip; Johnson, Tyler; Bettridge, Austin; Allred, Blake	Direct microalgae harvesting to prevent harmful algae blooms and produce renewable biofuel	ABSTRACTS OF PAPERS OF THE AMERICAN CHEMICAL SOCIETY
36	Guo, Ruoyu; Lu, Douding; Liu, Chenggang; Hu, Jiarong; Wang, Pengbin; Dai, Xinfeng	Toxic effect of nickel on microalgae Phaeodactylum tricornutum (Bacillariophyceae)	ECOTOXICOLOGY
37	Garr, Amber L.; Laramore, Susan; Krebs, William	Toxic Effects of Oil and Dispersant on Marine Microalgae	BULLETIN OF ENVIRONMENTAL CONTAMINATION AND TOXICOLOGY
38	Nagasaki, Keizo	Physiology, ecology, and molecular biology of viruses infecting harmful bloom-forming microalgae	NIPPON SUISAN GAKKAISHI
39	Penna, Antonella; Bertozzini, Elena; Battocchi, Cecilia; Galluzzi, Luca; Giacobbe, Maria Grazia; Vila, Magda; Garces, Esther; Luglie, Antonella; Magnani, Mauro	Monitoring of HAB species in the Mediterranean Sea through molecular methods	JOURNAL OF PLANKTON RESEARCH
40	Dhib, Amel; Fertouna-Bellakhal, Mouna; Turki, Souad; Aleya, Lotfi	Harmful planktonic and epiphytic microalgae in a Mediterranean Lagoon: The contribution of the macrophyte Ruppia cirrhosa to microalgae dissemination	HARMFUL ALGAE
41	Liu, Fuguo; Zhang, Chunyun; Wang, Yuanyuan; Chen, Guofu	A review of the current and emerging detection methods of marine harmful microalgae	SCIENCE OF THE TOTAL ENVIRONMENT
42	Magaletti, Erika; Borrello, Patrizia; Spada, Emanuela; Bataloni, Stefano; Di Girolamo, Irene; Giani, Michele	Surveillance of Potentially Toxic Benthic Microalgae Along the Italian Coast	JOURNAL OF COASTAL RESEARCH
43	Oloketuyi, S. F.; Mazzega, E.; Bernardinelli, G.; Hogberg,	Application of peroxidase-mimicking dnazyme-nanobody conjugate	FEBS OPEN BIO

	B.; de Marco, A.	for the detection of harmful microalgae	
44	Illoul, Hassina; Maso, Mercedes; Fortuno, Jose-Manuel; Cros, Lluisa; Morales-Blake, Alejandro; Seridji, Rabea	Potentially harmful microalgae in coastal waters of the Algiers area (Southern Mediterranean Sea)	CRYPTOGAMIE ALGOLOGIE
45	Burkholder, JM	Implications of harmful microalgae and heterotrophic dinoflagellates in management of sustainable marine fisheries	ECOLOGICAL APPLICATIONS
46	Mangoni, Olga; Imperatore, Concetta; Tomas, Carmelo R.; Costantino, Valeria; Saggiomo, Vincenzo; Mangoni, Alfonso	The New Carotenoid Pigment Moraxanthin Is Associated with Toxic Microalgae	MARINE DRUGS
47	Dizaji, Somayeh Zahedi; Fariman, Gilan Attaran; Zahedi, Mir Mahdi	Pigment content analysis in two HAB forming dinoflagellate species during the growth period	JOURNAL OF APPLIED PHYCOLOGY
48	Tan, Toh Hii; Leaw, Chui Pin; Leong, Sandric Chee Yew; Lim, Lay Peng; Chew, Siew Moon; Teng, Sing Tung; Lim, Po Teen	Marine micro-phytoplankton of Singapore, with a review of harmful microalgae in the region	RAFFLES BULLETIN OF ZOOLOGY
49	NIELSEN, MV; STROMGREN, T	Shell growth-response of mussels (mytilus-edulis) exposed to toxic microalgae	MARINE BIOLOGY
50	Mardones, Jorge I.; Shabala, Lana; Shabala, Sergey; Dorantes-Aranda, Juan Jose; Seger, Andreas; Hallegraeff, Gustaaf M.	Fish gill damage by harmful microalgae newly explored by microelectrode ion flux estimation techniques	HARMFUL ALGAE
51	Ben Gharbia, Hela; Yahia, Ons Kefi-Daly; Cecchi, Philippe; Masseret, Estelle; Amzil, Zouher; Herve, Fabienne; Rovillon, Georges; Nouri, Habiba; M'Rabet, Charaf; Couet, Douglas; Triki, Habiba Zmerli; Laabir, Mohamed	New insights on the species-specific allelopathic interactions between macrophytes and marine HAB dinoflagellates	PLOS ONE
52	Yu, Lili; Xia, Wei; Du, Hao	The toxic effects of petroleum pollutants to microalgae in marine environment	MARINE POLLUTION BULLETIN
53	Mantzorou, A.; Navakoudis, E.; Paschalidis, K.; Ververidis, F.	Microalgae: a potential tool for remediating aquatic environments from toxic metals	INTERNATIONAL JOURNAL OF ENVIRONMENTAL SCIENCE AND TECHNOLOGY
54	UPITIS, V; PAKALNE, D; SULCE, I	Optimal and toxic levels of elements for the cultivation of microalgae	6TH INTERNATIONAL TRACE ELEMENT SYMP 1989, VOLS 1-5
55	Ryu, Byung-Gon; Kim, Jungmin; Yoo, Gursong; Lim, Jun-Taek; Kim, Woong; Han, Jong-In; Yang, Ji-Won	Microalgae-mediated simultaneous treatment of toxic thiocyanate and production of biodiesel	BIORESOURCE TECHNOLOGY
56	Wang, Changyou; Li, Hongli; Wang, Xiulin; Zhang, Yong	Estimating Toxic Effect of Copper on Population of Microalgae Through a Three-dimensional Toxic Effect Growth Model	BULLETIN OF ENVIRONMENTAL CONTAMINATION AND TOXICOLOGY
57	He, N.; Duan, L. Y.; Sun, D.; Zhu, B.; An, M.; Duan, S. S.	Inhibitory effects of aqueous extracts of Eucalyptus tereticornis on HAB causing specie, Prorocentrum donghaiense	ALLELOPATHY JOURNAL
58	Mohamed, Zakaria A.	Potentially harmful microalgae and algal blooms in the Red Sea: Current knowledge and research needs	MARINE ENVIRONMENTAL RESEARCH
59	Masó, M; Garcés, E; Pagès, F; Camp, J	Drifting plastic debris as a potential vector for dispersing Harmful Algal Bloom (HAB) species	SCIENTIA MARINA

60	Ryu, J. A.; Park, S. J.; Kim, I. H.; Hwang, H. J.; Kim, C. H.; Nam, T. J.	Harmful Microalgae, Amphidinium cartarae, Regulates the IGF-IR Signaling Pathway in Human Colon Cancer Cells.	ENDOCRINE REVIEWS
61	Dyble, J.; Tester, P. A.; Litaker, R. W.	Effects of light intensity on cylindrospermopsin production in the cyanobacterial HAB species Cylindrospermopsis raciborskii	AFRICAN JOURNAL OF MARINE SCIENCE
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64	Yu, Zhiming; Wang, Zhongshi; Liu, Lidong	Electrophysiological techniques in marine microalgae study: A new perspective for harmful algal bloom (HAB) research	HARMFUL ALGAE
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71	Tas, S.; Yilmaz, I. N.	Potentially harmful microalgae and algal blooms in a eutrophic estuary in the Sea of Marmara (Turkey)	MEDITERRANEAN MARINE SCIENCE
72	Nan, Chunrong; Zhang, Haizhi; Lin, Shaozhen; Zhao, Guangqiang; Liu, Xueying	Allelopathic effects of Ulva lactuca on selected species of harmful bloom-forming microalgae in laboratory cultures	AQUATIC BOTANY
73	[Anonymous]	Metabolic pathways by which bay scallops modify phytosterols: Experimental approach and possible disruptions by hab species.	JOURNAL OF SHELLFISH RESEARCH
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79	Liu, Dongyang; Qv, Mingxiang; Dai, Dian; Wang, Xu; Zhu, Liandong	Toxic responses of freshwater microalgae Chlorella sorokiniana due to exposure of flame retardants	CHEMOSPHERE
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83	Vila, Magda; Camp, Jordi; Berdalet, Elisa	TOXIC MICROALGAE AND GLOBAL CHANGE Why have proliferations increased along the Mediterranean coast?	METODE SCIENCE STUDIES JOURNAL
84	Wang, Liping; Yan, Tian; Zhou, Mingjiang	Impacts of HAB species Heterosigma akashiwo on early development of the scallop Argopecten irradians Lamarck	AQUACULTURE
85	Meng, Xiangying; Chen, Cao; Bai, Mindong; Zhang, Zhitao; Cheng, Chao; Ma, Bin; Li, Jiaxin	Effect of hydroxyl radical on harmful microalgae: a potential technology for treatment of ship's ballast water	INDIAN JOURNAL OF GEO-MARINE SCIENCES
86	Antonella, Penna; Luca, Galluzzi	The quantitative real-time PCR applications in the monitoring of marine harmful algal bloom (HAB) species	ENVIRONMENTAL SCIENCE AND POLLUTION RESEARCH
87	Yang, Hyun Jun; Seo, Hye Jin; Kim, Yun Hee; Yun, Geon; Lee, Moo Joon; Yoo, Yeong Du; Shin, Kyong Ho; Choi, Keun-Hyung; Jang, Se Hyeon	Effects of harmful microalgae on the behavior and morphology of ephyrae of the moon jellyfish Aurelia aurita	MARINE POLLUTION BULLETIN
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90	Cerejo, M.; Dias, J. M.	Tidal transport and dispersal of marine toxic microalgae in a shallow, temperate coastal lagoon	MARINE ENVIRONMENTAL RESEARCH
91	Loera-Quezada, Maribel M.; Leyva-Gonzalez, Marco Antonio; Lopez-Arredondo, Damar; Herrera-Estrella, Luis	Phosphite cannot be used as a phosphorus source but is non-toxic for microalgae	PLANT SCIENCE
92	GARNHAM, GW; AVERY, SV; CODD, GA; GADD, GM	Interactions of microalgae and cyanobacteria with toxic metals and radionuclides: Physiology and environmental implications	CHANGES IN FLUXES IN ESTUARIES: IMPLICATIONS FROM SCIENCE TO

			MANAGEMENT
93	Zhang, Cai; Chen, Xiaohua; Wang, Jiangtao; Tan, Liju	Toxic effects of microplastic on marine microalgae Skeletonema costatum: Interactions between microplastic and algae	ENVIRONMENTAL POLLUTION
94	Zhang Fengying; Shi Yanhong; Jiang Keji; Xu Zhaoli; Ma Lingbo	Sensitive and rapid detection of two toxic microalgae Alexandrium by loop-mediated isothermal amplification	ACTA OCEANOLOGICA SINICA
95	Sildever, Sirje; Kawakami, Yoko; Kannoa, Nanako; Kasai, Hiromi; Shiomoto, Akihiro; Katakura, Seiji; Nagai, Satoshi	Toxic HAB species from the Sea of Okhotsk detected by a metagenetic approach, seasonality and environmental drivers	HARMFUL ALGAE
96	Zhang, Chunyun; Chen, Guofu; Wang, Yuanyuan; Sun, Rui; Nie, Xiaoli; Zhou, Jin	MHBMDAA: Membrane-based DNA array with high resolution and sensitivity for toxic microalgae monitoring	HARMFUL ALGAE
97	Shin, HyeonSeok; Lee, Eunju; Shin, Jongoh; Ko, So-Ra; Oh, Hyung-Seok; Ahn, Chi-Yong; Oh, Hee-Mock; Cho, Byung-Kwan; Cho, Suhyung	Elucidation of the bacterial communities associated with the harmful microalgae Alexandrium tamarense and Cochlodinium polykrikoides using nanopore sequencing	SCIENTIFIC REPORTS
98	Tang, Ying Zhong; Kang, Yoonja; Berry, Dianna; Gobler, Christopher J.	The ability of the red macroalga, Porphyra purpurea (Rhodophyceae) to inhibit the proliferation of seven common harmful microalgae	JOURNAL OF APPLIED PHYCOLOGY
99	Wang, Zhaohui; Liu, Lei; Tang, Yali; Li, Aifeng; Liu, Chao; Xie, Changliang; Xiao, Lijuan; Lu, Songhui	Phytoplankton community and HAB species in the South China Sea detected by morphological and metabarcoding approaches	HARMFUL ALGAE
100	Mohd-Din, Monaliza; Hii, Kieng Soon; Abdul-Wahab, Mohd Firdaus; Mohamad, Shaza Eva; Gu, Haifeng; Leaw, Chui Pin; Lim, Po Teen	Spatial-temporal variability of microphytoplankton assemblages including harmful microalgae in a tropical semi-enclosed strait (Johor Strait, Malaysia)	MARINE ENVIRONMENTAL RESEARCH
101	Yuan, A.; Wang, B.; Li, J.; Lee, Joseph H. W.	A low-cost edge AI-chip-based system for real-time algae species classification and HAB prediction	WATER RESEARCH
102	Manzo, S.; Buono, S.; Rametta, G.; Miglietta, M.; Schiavo, S.; Di Francia, G.	The diverse toxic effect of sio2 and tio2 nanoparticles toward the marine microalgae Dunaliella tertiolecta	ENVIRONMENTAL SCIENCE AND POLLUTION RESEARCH
103	Natarajan, Lokeshwari; Omer, Sonal; Jetly, Nishta; Jenifer, M. Annie; Chandrasekaran, N.; Suraishkumar, G. K.; Mukherjee, Amitava	Eco-corona formation lessens the toxic effects of polystyrene nanoplastics towards marine microalgae Chlorella sp.	ENVIRONMENTAL RESEARCH
104	Rios, Francisco; Lechuga, Manuela; Lobato-Guarnido, Ismael; Fernandez-Serrano, Mercedes	Antagonistic Toxic Effects of Surfactants Mixtures to Bacteria Pseudomonas putida and Marine Microalgae Phaeodactylum tricornutum	TOXICS
105	Ni, Ziqi; Tan, Liju; Wang, Jiayin; Chen, Yanshan; Zhang, Na; Meng, Fanmeng; Wang, Jiangtao	Toxic effects of pristine and aged polystyrene and their leachate on marine microalgae Skeletonema costatum	SCIENCE OF THE TOTAL ENVIRONMENT
106	Gunasekaran, Dhivya; Chandrasekaran, Natarajan; Jenkins, David; Mukherjee, Amitava	Plain polystyrene microplastics reduce the toxic effects of zno particles on marine microalgae Dunaliella salina	JOURNAL OF ENVIRONMENTAL CHEMICAL ENGINEERING
107	Taylor, Joe D.; Berzano, Marco; Percy, Linda; Lewis, Jane	Evaluation of the MIDTAL microarray chip for monitoring toxic microalgae in the Orkney Islands, UK	ENVIRONMENTAL SCIENCE AND POLLUTION RESEARCH
108	Poot-Delgado, Carlos Antonio; Okolodkov, Yuri B.; Rendon-von Osten, Jaime	Spatio-temporal Variation of Harmful Planktonic Microalgae and Cyanobacteria Along the Central Coast of Campeche, Southeastern Gulf of Mexico	BULLETIN OF ENVIRONMENTAL CONTAMINATION AND TOXICOLOGY

109	Wu, Ganlin; Liu, Fuguo; Chen, Guofu; Wang, Yuanyuan; Wang, Yihan; Zhang, Chunyun	Establishment of a multiplex polymerase chain reaction detection assay for three common harmful microalgae in the East China Sea	ENVIRONMENTAL SCIENCE AND POLLUTION RESEARCH
110	Lin Jianing; Yan Tian; Zhang Qingchun; Zhou Mingjiang	Impact of several harmful algal bloom (HAB) causing species, on life history characteristics of rotifer Brachionus plicatilis Muller	CHINESE JOURNAL OF OCEANOLOGY AND LIMNOLOGY
111	Nishibori, Naoyoshi	Studies on the role of polyamines in the growth of harmful microalgae and the polyamine dynamics in coastal ecosystems	NIPPON SUISAN GAKKAISHI
112	Bruce, Karen L.; Ellis, Amanda V.; Leterme, Sophie C.; Khodakov, Dmitriy A.; Lenehan, Claire E.	Detection of harmful algal bloom causing microalgae using covalently immobilised capture oligonucleotide probes on glass and poly(dimethylsiloxane) surfaces	MICRO/NANO MATERIALS, DEVICES, AND SYSTEMS
113	Adam, Aimimuliani; Mohammad-Noor, Normawaty; Anton, Ann; Saleh, Ejria; Saad, Shahbudin; Shaleh, Sitti Raehanah Muhd	Temporal and spatial distribution of harmful algal bloom (HAB) species in coastal waters of Kota Kinabalu, Sabah, Malaysia	HARMFUL ALGAE
114	Manganelli, Maura	Blooms of toxic microorganisms in aquatic environments: marine microalgae and freshwater cyanobacteria. A brief review with a particular focus on the Italian situation Diffusion and health effects of toxic marine microalgae and freshwater cyanobacteria in Italy	RENDICONTI LINCEI-SCIENZE FISICHE E NATURALI
115	Schlesinger, Ami; Eisenstadt, Doron; Bar-Gil, Amicam; Carmely, Hilla; Einbinder, Shai; Gressel, Jonathan	Inexpensive non-toxic flocculation of microalgae contradicts theories; overcoming a major hurdle to bulk algal production	BIOTECHNOLOGY ADVANCES
116	Guo, Ziwei; He, Huan; Liu, Kunqian; Li, Zihui; Xi, Yanting; Liao, Zhicheng; Dao, Guohua; Huang, Bin; Pan, Xuejun	Toxic mechanisms of the antiviral drug arbidol on microalgae in algal bloom water at transcriptomic level	JOURNAL OF HAZARDOUS MATERIALS
117	Giri, Sayani; Mukherjee, Amitava	Ageing with algal EPS reduces the toxic effects of polystyrene nanoplastics in freshwater microalgae Scenedesmus obliquus	JOURNAL OF ENVIRONMENTAL CHEMICAL ENGINEERING
118	Khoshnamvand, Mehdi; Hanachi, Parichehr; Ashtiani, Saeed; Walker, Tony R.	Toxic effects of polystyrene nanoplastics on microalgae Chlorella vulgaris: Changes in biomass, photosynthetic pigments and morphology	CHEMOSPHERE
119	Choi, Chang Jae; Berges, John. A.; Young, Erica. B.	Rapid effects of diverse toxic water pollutants on chlorophyll a fluorescence: Variable responses among freshwater microalgae	WATER RESEARCH
120	Renaud, Florent; Oberhaensli, Francois; Teyssie, Jean-Louis; Miramand, Pierre; Temara, Ali; Warnau, Michel	Sorption-desorption kinetics and toxic cell concentration in marine phytoplankton microalgae exposed to Linear Alkylbenzene Sulfonate	MARINE POLLUTION BULLETIN
121	Nikonova, Alyona Alexandrovna; Mizandrontsev, Igor Borisovich; Bazhenov, Boris Nikolaevich; Khanaev, Igor Veniaminovich; Shabalina, Olesya Viktorovna; Afanasyeva, Alexandra Alexandrovna; Avezova, Tatiana Nikolaevna; Chindyavskaya, Anna Nikolaevna; Bityutsky, Alexander Nikolaevich; Kan, Andrey Yurievich; Karikh, Leonid Gennadievich; Dubrova, Kristina Sergeevna; Vorobyeva, Svetlana Semyonovna; Glyzina, Olga Yurievna	Toxic Effect of Anionic Surfactants on Freshwater Sponge Lubomirskia baikalensis and Its Endosymbiotic Microalgae Chlorella sp.	DIVERSITY-BASEL
122	Veldhuis, MJW; Wassmann, P	Bloom dynamics and biological control of a high biomass HAB	HARMFUL ALGAE

		species in European coastal waters:: A Phaeocystis case study	
123	Al-Aidaroos, Ali M.; Devassy, Reny P.; El-Sherbiny, Mohsen M.	Unusual dominance of harmful microalgae pseudo-nitzschia delicatissima cf. (cleve) heiden in the coastal waters of jeddah, central red sea	PAKISTAN JOURNAL OF BOTANY
124	Sun, Ying-ying; Meng, Kun; Su, Zhen-xia; Guo, Gan-lin; Pu, Yin-fang; Wang, Chang-hai	Isolation and purification of antialgal compounds from the red alga Gracilaria lemaneiformis for activity against common harmful red tide microalgae	ENVIRONMENTAL SCIENCE AND POLLUTION RESEARCH
125	Wang, Wanjun; Liao, Pan; Li, Guiying; Chen, Heng; Cen, Jingyi; Lu, Songhui; Wong, Po Keung; An, Taicheng	Photocatalytic inactivation and destruction of harmful microalgae Karenia mikimotoi under visible-light irradiation: Insights into physiological response and toxicity assessment	ENVIRONMENTAL RESEARCH
126	Malika, Moncer; Mounir, Ben Brahim; Mabrouka, Mahfoudhi; Lamia, Dammak Walha; Malika, Bel Hassen; Asma, Hamza	Multiannual trends of toxic and potentially toxic microalgae (Ostreopsis cf. Ovata, Prorocentrum lima, and Coolia monotis) in Sfax coasts (North of Gabes Gulf, Tunisia)	MARINE ECOLOGY-AN EVOLUTIONARY PERSPECTIVE
127	Rothenberger, Megan; Gleich, Samantha J.; Flint, Evan	The underappreciated role of biotic factors in controlling the bloom ecology of potentially harmful microalgae in the Hudson-Raritan Bay	HARMFUL ALGAE
128	Dalai, Swayamprava; Pakrashi, Sunandan; Bhuvaneshwari, M.; Iswarya, V.; Chandrasekaran, N.; Mukherjee, Amitava	Toxic effect of Cr(VI) in presence of n-tio2 and n-Al2O3 particles towards freshwater microalgae	AQUATIC TOXICOLOGY
129	Tsaloglou, Maria-Nefeli; Laouenan, Florian; Loukas, Christos-Moritz; Gabriel Monsalve, Lisandro; Thanner, Christine; Morgan, Hywel; Ruano-Lopez, Jesus M.; Mowlem, Matthew C.	Real-time isothermal RNA amplification of toxic marine microalgae using preserved reagents on an integrated microfluidic platform	ANALYST
130	Deepak, J. R.; Anbarasu, A.; Prabu, V.	Removal of Toxic Metal Presence in the Wastewater and Production of the Biomass from Microalgae Chlorella sp.	JOURNAL OF NANOMATERIALS
131	Hinder, Stephanie L.; Hays, Graeme C.; Brooks, Caroline J.; Davies, Angharad P.; Edwards, Martin; Walne, Anthony W.; Gravenor, Mike B.	Toxic marine microalgae and shellfish poisoning in the British isles: history, review of epidemiology, and future implications	ENVIRONMENTAL HEALTH
132	Zhao, Jiamin; Yang, Yingying; Li, Renjie; Song, Meijing; Yin, Danning; Ye, Xiaoyun; Chen, Xiurong	Heavy toxic sludge tolerance in microalgae: Effect of energy generation metabolisms from C. Humicola under IAA applications	JOURNAL OF CLEANER PRODUCTION
133	Zhang, Cai; Wang, Jiangtao; Tan, Liju; Chen, Xiaohua	Toxic effects of nano-zno on marine microalgae Skeletonema costatum: Attention to the accumulation of intracellular Zn	AQUATIC TOXICOLOGY
134	Barroso Garcia, Pilar; Rueda de la Puerta, Pilar; Parron Carreno, Tesifon; Marin Martinez, Porfirio; Guillen Enriquez, Javier	An epidemic outbreak with respiratory symptoms in the province of Almeria [Spain] due to toxic microalgae exposure	GACETA SANITARIA
135	Hernandez-Zamora, Miriam; Martinez-Jeronimo, Fernando	Exposure to the azo dye Direct blue 15 produces toxic effects on microalgae, cladocerans, and zebrafish embryos	ECOTOXICOLOGY
136	Kang, Yoonja; Gobler, Christopher J.	The brown tide algae, Aureococcus anophagefferens and Aureoumbra lagunensis (Pelagophyceae), allelopathically inhibit the growth of competing microalgae during harmful algal blooms	LIMNOLOGY AND OCEANOGRAPHY

137	Tayaban, Kuselah Mae M.; Pintor, Katherine L.; Vital, Pierangeli G.	Detection of potential harmful algal bloom-causing microalgae from freshwater prawn farms in Central Luzon, Philippines, for bloom monitoring and prediction	ENVIRONMENT DEVELOPMENT AND SUSTAINABILITY
138	Delegrange, A.; Vincent, D.; Courcot, L.; Amara, R.	Testing the vulnerability of juvenile sea bass (Dicentrarchus labrax) exposed to the harmful algal bloom (HAB) species Pseudo-nitzschia delicatissima	AQUACULTURE
139	Krasaesueb, Nattawut; Boonnorat, Jarungwit; Maneeruttanarungroj, Cherdsak; Khetkorn, Wanthanee	Highly effective reduction of phosphate and harmful bacterial community in shrimp wastewater using short-term biological treatment with immobilized engineering microalgae	JOURNAL OF ENVIRONMENTAL MANAGEMENT
140	Hallegraeff, Gustaaf M.	Transport of harmful marine microalgae via ship's ballast water: Management and mitigation with special reference to the Arabian Gulf region	AQUATIC ECOSYSTEM HEALTH & MANAGEMENT
141	Dias, P. Joana; Munoz, Julieta; Huisman, John M.; McDonald, Justin I.	Biosecurity monitoring of Harmful Algal Bloom (HAB) species in Western Australian waters: first confirmed record of Alexandrium catenella (Dinophyceae)	BIOINVASIONS RECORDS
142	Persson, Agneta; Smith, Barry C.; Alix, Jennifer H.; Wikfors, Gary H.	Properties and Behavior of Sexual Life Stages Underlying Dinoflagellate HAB Events of Cyst-Producing Species That Disrupt Fisheries and Aquaculture	REVIEWS IN FISHERIES SCIENCE & AQUACULTURE
143	Gueguen, Marielle; Lassus, Patrick; Laabir, Mohamed; Bardouil, MicheLe; Baron, Regis; Sechet, Veronique; Truquet, Philippe; Amzil, Zouher; Barille, Laurent	Gut passage times in two bivalve molluscs fed toxic microalgae:: Alexandrium minutum, A-catenella and Pseudo-nitzschia calliantha	AQUATIC LIVING RESOURCES
144	He, Dandan; Zeng, Youmei; Zhou, Guangming	The influence of microplastics on the toxic effects and biodegradation of bisphenol A in the microalgae Chlorella pyrenoidosa	AQUATIC ECOLOGY
145	Mansour, Abdallah Tageldein; Alprol, Ahmed E.; Abualnaja, Khamael M.; El-Beltagi, Hossam S.; Ramadan, Khaled M. A.; Ashour, Mohamed	The Using of Nanoparticles of Microalgae in Remediation of Toxic Dye from Industrial Wastewater: Kinetic and Isotherm Studies	MATERIALS
146	Pikula, Konstantin; Johari, Seyed Ali; Santos-Oliveira, Ralph; Golokhvast, Kirill	The Comparative Toxic Impact Assessment of Carbon Nanotubes, Fullerene, Graphene, and Graphene Oxide on Marine Microalgae Porphyridium purpureum	TOXICS
147	Liu, Dongyang; Yang, Wenfeng; Lv, Yuanfei; Li, Shuangxi; Qv, Mingxiang; Dai, Dian; Zhu, Liandong	Pollutant removal and toxic response mechanisms of freshwater microalgae Chlorella sorokiniana under exposure of tetrabromobisphenol A and cadmium	CHEMICAL ENGINEERING JOURNAL
148	Antonopoulou, Maria; Vlastos, Dimitris; Dormousoglou, Margarita; Bouras, Spyridon; Varela-Athanasatou, Maria; Bekakou, Irene-Eleni	Genotoxic and Toxic Effects of The Flame Retardant Tris(Chloropropyl) Phosphate (TCPP) in Human Lymphocytes, Microalgae and Bacteria	TOXICS
149	Davarpanah, Elham; Guilhermino, Lucia	Are gold nanoparticles and microplastics mixtures more toxic to the marine microalgae Tetraselmis chuii than the substances individually?	ECOTOXICOLOGY AND ENVIRONMENTAL SAFETY

150	Zingone, Adriana; Escalera, Laura; Aligizaki, Katerina; Fernandez-Tejedor, Margarita; Ismael, Amany; Montresor, Marina; Mozetic, Patricija; Tas, Seyfettin; Totti, Cecilia	Toxic marine microalgae and noxious blooms in the Mediterranean Sea: A contribution to the Global HAB Status Report	HARMFUL ALGAE
151	Muthuraman, R. M.; Murugappan, A.; Soundharajan, B.	Highly effective removal of presence of toxic metal concentrations in the wastewater using microalgae and pre-treatment processing	APPLIED NANOSCIENCE
152	Loukas, Christos-Moritz; McQuillan, Jonathan S.; Laouenan, Florian; Tsaloglou, Maria-Nefeli; Ruano-Lopez, Jesus M.; Mowlem, Matthew C.	Detection and quantification of the toxic microalgae Karenia brevis using lab on a chip mrna sequence-based amplification	JOURNAL OF MICROBIOLOGICAL METHODS
153	Hakamada, Mayu; Tokairin, Chihiro; Ishizuka, Hayate; Adachi, Kanna; Osawa, Toma; Aonuma, Shiori; Hirozumi, Ryosuke; Tsuchiya, Shigeki; Cho, Yuko; Kudo, Yuta; Konoki, Keiichi; Oshima, Yasukatsu; Nagasawa, Kazuo; Yotsu-Yamashita, Mari	Synthesis and Identification of decarbamoyloxysaxitoxins in Toxic Microalgae and their Reactions with the Oxygenase, sxtt, Reveal Saxitoxin Biosynthesis	CHEMISTRY-A EUROPEAN JOURNAL
154	Zhang, Weixia; Sun, Shuge; Du, Xueying; Han, Yu; Tang, Yu; Zhou, Weishang; Shi, Wei; Liu, Guangxu	Toxic impacts of microplastics and tetrabromobisphenol A on the motility of marine microalgae and potential mechanisms of action	GONDWANA RESEARCH
155	Sun, Ying-ying; Wang, Hui; Guo, Gan-lin; Pu, Yin-fang; Yan, Bin-lun; Wang, Chang-hai	Isolation, purification, and identification of antialgal substances in green alga Ulva prolifera for antialgal activity against the common harmful red tide microalgae	ENVIRONMENTAL SCIENCE AND POLLUTION RESEARCH
156	Penna, Antonella; Galluzzi, Luca	The quantitative real-time PCR applications in the monitoring of marine harmful algal bloom (HAB) species (vol 20, pg 6851, 2013)	ENVIRONMENTAL SCIENCE AND POLLUTION RESEARCH
157	Cho, Kichul; Ueno, Mikinori; Liang, Yan; Kim, Daekyung; Oda, Tatsuya	Generation of Reactive Oxygen Species (ROS) by Harmful Algal Bloom (HAB)-Forming Phytoplankton and Their Potential Impact on Surrounding Living Organisms	ANTIOXIDANTS
158	Chen, Junhui; Wang, Yanlong; Pan, Lei; Shen, Huihui; Fu, Dan; Fu, Boqiang; Sun, Chengjun; Zheng, Li	Separation and purification of two minor typical diarrhetic shellfish poisoning toxins from harmful marine microalgae via combined liquid chromatography with mass spectrometric detection	JOURNAL OF SEPARATION SCIENCE
159	Herrera-Sepulveda, Angelica; Hernandez-Saavedra, Norma Y.; Medlin, Linda K.; West, Nyree	Capillary electrophoresis finger print technique (CE-SSCP): an alternative tool for the monitoring activities of HAB species in Baja California Sur Costal	ENVIRONMENTAL SCIENCE AND POLLUTION RESEARCH
160	Bazzoni, Anna Maria; Caddeo, Tiziana; Pulina, Silvia; Padedda, Bachisio M.; Satta, Cecilia T.; Sechi, Nicola; Luglie, Antonella	Spatial distribution and multiannual trends of potentially toxic microalgae in shellfish farms along the Sardinian coast (NW Mediterranean Sea)	ENVIRONMENTAL MONITORING AND ASSESSMENT
161	Wang, Lei; Huang, Xulei; Lim, Dorothy Jingwen; Laserna, Anna Karen Carrasco; Li, Sam Fong Yau	Uptake and toxic effects of triphenyl phosphate on freshwater microalgae Chlorella vulgaris and Scenedesmus obliquus: Insights from untargeted metabolomics	SCIENCE OF THE TOTAL ENVIRONMENT
162	Petsas, A. S.; Vagi, M. C.; Pavlaki, M. D.; Smaragdaki, N. M.; Kostopoulou, M. N.; Lekkas, T. D.	Toxic effects of azinphos methyl and azinphos ethyl on growth and chlorophyll pigments production of marine unicellular microalgae tetraselmis suecica	PROCEEDINGS OF THE 13TH INTERNATIONAL CONFERENCE ON ENVIRONMENTAL SCIENCE AND TECHNOLOGY

163	Thiagarajan, Vignesh; Ramasubbu, Seenivasan	Extraction and characterization of sub-micron sized tio2 from toothpaste: evaluation of their toxic effects in marine microalgae Chlorella sp.	TOXICOLOGY AND ENVIRONMENTAL HEALTH SCIENCES
164	Chen, Daijie; Wang, Guobao; Chen, Chiyu; Feng, Zekai; Jiang, Yuanyuan; Yu, Hang; Li, Mengyao; Chao, Yuanqing; Tang, Yetao; Wang, Shizhong; Qiu, Rongliang	The interplay between microalgae and toxic metal(loid)s: mechanisms and implications in AMD phycoremediation coupled with Fe/Mn mineralization	JOURNAL OF HAZARDOUS MATERIALS
165	Wang, Jiayin; Tan, Liju; Ni, Ziqi; Zhang, Na; Li, Qi; Wang, Jiangtao	Is hydrodynamic diameter the decisive factor?-Comparison of the toxic mechanism of nsio2 and mps on marine microalgae Heterosigma akashiwo	AQUATIC TOXICOLOGY
166	Doblin, Martina A.; Coyne, Kathryn J.; Rinta-Kanto, Johanna M.; Wilhelm, Steven W.; Dobbs, Fred C.	Dynamics and short-term survival of toxic cyanobacteria species in ballast water from NOBOB vessels transiting the Great Lakes - implications for HAB invasions	HARMFUL ALGAE
167	Norén, F; Moestrup, O; Rehnstam-Holm, AS	Parvilucifera infectans Noren et Moestrup gen. Et sp nov (Perkinsozoa phylum nov.):: a parasitic flagellate capable of killing toxic microalgae	EUROPEAN JOURNAL OF PROTISTOLOGY
168	Wodeyar K, K. Abhilash; Akter, Sahina; Nama, Suman; Nayak, Binaya Bhusan; Gogoi, Pranab; Deshmukhe, Geetanjali; Jaiswar, Ashok Kumar; Landge, Asha Taterao; Layana, Porayil	Unveiling the spatio-temporal variation of harmful algal bloom (HAB) species assemblages and their relationship with environmental factors in a tidal creek environment	AQUATIC SCIENCES
169	Wang, Hao; Bouwman, Alexander F.; Wang, Junjie; Yu, Zhigang; Ran, Xiangbin	Competitive advantages of HAB species under changing environmental conditions in the coastal waters of the Bohai Sea, Yellow Sea and East China Sea	CONTINENTAL SHELF RESEARCH
170	Loukil-Baklouti, Amira; Feki-Sahnoun, Wafa; Hamza, Asma; Abdennadher, Moufida; Mahfoudhi, Mabrouka; Bouain, Abderrahmen; Jarboui, Othman	Controlling factors of harmful microalgae distribution in water column, biofilm and sediment in shellfish production area (South of Sfax, Gulf of Gabes) from southern Tunisia	CONTINENTAL SHELF RESEARCH
171	Ohkubo, Nobuyuki; Tomaru, Yuji; Yamaguchi, Haruo; Kitatsuji, Saho; Mochida, Kazuhiko	Development of a method to assess the ichthyotoxicity of the harmful marine microalgae Karenia spp. Using gill cell cultures from red sea bream (Pagrus major)	FISH PHYSIOLOGY AND BIOCHEMISTRY
172	Das, Soupam; Chandrasekaran, N.; Mukherjee, Amitava	Unmasking effects of masks: Microplastics released from disposable surgical face masks induce toxic effects in microalgae Scenedesmus obliquus and Chlorella sp.	COMPARATIVE BIOCHEMISTRY AND PHYSIOLOGY C-TOXICOLOGY & PHARMACOLOGY
173	Ebenezer, Vinitha; Ki, Jang-Seu	Quantification of toxic effects of the herbicide metolachlor on marine microalgae Ditylum brightwellii (Bacillariophyceae), Prorocentrum minimum (Dinophyceae), and Tetraselmis suecica (Chlorophyceae)	JOURNAL OF MICROBIOLOGY
174	Li, Ming; Wan, Chengyan; Pan, Xiaojie; Zou, Yi; Chang, Jianbo; Xie, Ping	Acute toxic effects of zinc, cadmium, and mercury on the growths of three unicellular green microalgae with relatively high initial densities	FRESENIUS ENVIRONMENTAL BULLETIN

175	Wang, Zikang; Yu, Simin; Nie, Yufan; Zhang, Ning; Zhu, Wentao; Zhou, Zhiqiang; Diao, Jinling	Interspecific insights into direct and indirect effects of acetochlor on interactions between daphnids and microalgae: Toxic, trophic, and grazer-infochemical responses	SCIENCE OF THE TOTAL ENVIRONMENT
176	Sanchez-Parra, Elisabet; Boutarfa, Soumia; Aboal, Marina	Are Cyanotoxins the Only Toxic Compound Potentially Present in Microalgae Supplements? Results from a Study of Ecological and Non-Ecological Products	TOXINS
177	Zhang, Chun Yun; Chen, Guo Fu; Cai, Pan Pan; Wang, Yuan Yuan; Guo, Chang Lu	Development and evaluation of a reverse dot blot assay for the simultaneous detection of common toxic microalgae along the Chinese coast	HARMFUL ALGAE
178	Moreira-Gonzalez, Angel Ramon; Brustolin, Marco Colossi; Mafra Junior, Luiz Laureno	Composition and abundance of benthic microalgae from the Estuarine Complex of Paranagua Bay (southern Brazil) with special emphasis on toxic species	OCEAN AND COASTAL RESEARCH
179	Orlova, Tatiana Yu.	Resting stages of planktonic microalgae in recent marine sediments from the east coast of Russia with special emphasis on toxic species	PROCEEDINGS OF THE RUSSIA-CHINA BILATERAL SYMPOSIUM ON MARINE ECOSYSTEMS UNDER THE GLOBAL CHANGE IN THE NORTHWESTERN PACIFIC
180	Oloketuyi, Sandra; Mazzega, Elisa; Zavasnik, Janez; Pungjunun, Kingkan; Kalcher, Kurt; de Marco, Ario; Mehmeti, Eda	Electrochemical immunosensor functionalized with nanobodies for the detection of the toxic microalgae Alexandrium minutum using glassy carbon electrode modified with gold nanoparticles	BIOSENSORS & BIOELECTRONICS
181	Moreira-Gonzalez, Angel R.; Domit, Camila; Rosa, Kaianan M. S.; Mafra Jr, Luiz L.	Occurrence of potentially toxic microalgae and diarrhetic shellfish toxins in the digestive tracts of green sea turtles (Chelonia mydas) from southern Brazil	HARMFUL ALGAE
182	Battocchi, Cecilia; Totti, Cecilia; Vila, Magda; Maso, Mercedes; Capellacci, Samuela; Accoroni, Stefano; Rene, Albert; Scardi, Michele; Penna, Antonella	Monitoring toxic microalgae Ostreopsis (dinoflagellate) species in coastal waters of the Mediterranean Sea using molecular PCR-based assay combined with light microscopy	MARINE POLLUTION BULLETIN
183	Toldra, Anna; Jauset-Rubio, Miriam; Andree, Karl B.; Fernandez-Tejedor, Margarita; Diogene, Jorge; Katakis, Ioanis; O'Sullivan, Ciara K.; Campas, Monica	Detection and quantification of the toxic marine microalgae Karlodinium veneficum and Karlodinium armiger using recombinase polymerase amplification and enzyme-linked oligonucleotide assay	ANALYTICA CHIMICA ACTA
184	Hu, Zhangxi; Xu, Ning; Gu, Haifeng; Chai, Zhaoyang; Takahashi, Kazuya; Li, Zhun; Deng, Yunyan; Iwataki, Mitsunori; Matsuoka, Kazumi; Tang, Ying Zhong	Morpho-molecular description of a new HAB species, Pseudocochlodinium profundisulcus gen. Et sp. Nov., and its LSU rrna gene based genetic diversity and geographical distribution	HARMFUL ALGAE
185	Shimada, Hiroshi; Sakamoto, Setsuko; Yamaguchi, Mineo; Imai, Ichiro	First record of two warm-water HAB species Chattonella marina (Raphidophyceae) and Cochlodinium polykrikoides (Dinophyceae) on the west coast of Hokkaido, northern Japan in summer 2014	REGIONAL STUDIES IN MARINE SCIENCE
186	Beyer, Valentin P.; Blockx, Jonas; Maciel, Ayessa Pires; Tyagi, Sakshi; Demir-Yilmaz, Irem; Formosa-Dague, Cecile; Muylaert, Koenraad; Thielemans, Wim	Use of PDMAEMA as a non-toxic synthetic flocculant for harvesting microalgae and evaluation of the influence of polymer size on flocculation behaviour	JOURNAL OF ENVIRONMENTAL CHEMICAL ENGINEERING

187	Bouquet, Aurelien; Perdrau, Marie Anais; Laabir, Mohamed; Foucault, Elodie; Chomerat, Nicolas; Rolland, Jean Luc; Abadie, Eric	Liza ramada Juveniles after Exposure to the Toxic Dinoflagellate Vulcanodinium rugosum: Effects on Fish Viability, Tissue Contamination and Microalgae Survival after Gut Passage	TOXINS
188	Zhang, YH; Fu, FX; Whereat, E; Coyne, KJ; Hutchins, DA	Bottom-up controls on a mixed-species HAB assemblage:: A comparison of sympatric Chattonella subsalsa and Heterosigma akashiwo (Raphidophyceae) isolates from the Delaware Inland Bays, USA	HARMFUL ALGAE
189	Machado, Rodrigo R.; Lourenco, Sergio O.	Nutritional properties of microalgae used as food for bivalve molluscs: a review	APLICACOES DA FICOLOGIA: ANAIS DO XI CONGRESSO BRASILEIRO DE FICOLOGIA E SIMPOSIO LATINO-AMERICANO SOBRE ALGAS NOCIVAS
190	Draredja, Mohamed Anis; Frihi, Hocine; Boualleg, Chahinaise; Gofart, Anne; Abadie, Eric; Laabir, Mohamed	Seasonal variations of phytoplankton community in relation to environmental factors in a protected meso-oligotrophic southern Mediterranean marine ecosystem (Mellah lagoon, Algeria) with an emphasis of HAB species	ENVIRONMENTAL MONITORING AND ASSESSMENT
191	Garcia-Balboa, C.; Baselga-Cervera, B.; Garcia-Sanchez, A.; Igual, J. M.; Lopez-Rodas, V.; Costas, E.	Rapid adaptation of microalgae to bodies of water with extreme pollution from uranium mining: An explanation of how mesophilic organisms can rapidly colonise extremely toxic environments	AQUATIC TOXICOLOGY
192	Naik, Ravidas Krishna; Naik, Milind Mohan; D'Costa, Priya Mallika; Shaikh, Fauzia	Microplastics in ballast water as an emerging source and vector for harmful chemicals, antibiotics, metals, bacterial pathogens and HAB species: A potential risk to the marine environment and human health	MARINE POLLUTION BULLETIN
193	Hazeem, Layla J.; Yesilay, Gamze; Bououdina, Mohamed; Perna, Simone; Cetin, Demet; Suludere, Zekiye; Barras, Alexandre; Boukherroub, Rabah	Investigation of the toxic effects of different polystyrene micro-and nanoplastics on microalgae Chlorella vulgaris by analysis of cell viability, pigment content, oxidative stress and ultrastructural changes	MARINE POLLUTION BULLETIN
194	Gerardo, Solis-Gonzalez; Alondra Alelie, Cortes-Tellez; Luis, Chacon-Garcia; Martha-Estrella, Garcia-Perez; Hector, Martinez-Flores E.; Maria Carmen, Bartolome Camacho	Prediction of the toxic impact on the freshwater microalgae Scenedesmus intermedius produced by the interaction of copper sulfate and copper oxychloride in a binary mixture with glyphosate	LIMNETICA
195	Touzet, Nicolas; Keady, Evelyn; Raine, Robin; Maher, Majella	Evaluation of taxa-specific real-time PCR, whole-cell FISH and morphotaxonomy analyses for the detection and quantification of the toxic microalgae Alexandrium minutum (Dinophyceae), Global Clade ribotype	FEMS MICROBIOLOGY ECOLOGY
196	BEHRINGER, DM; MEYER, KH; VEH, RW	Antibodies against neuroactive amino acids and neuropeptides. II. Simultaneous immunoenzymatic double staining with labeled primary antibodies of the same species and a combination of the ABC method and the hapten-anti-hapten bridge (HAB) technique.	JOURNAL OF HISTOCHEMISTRY & CYTOCHEMISTRY
197	Lourenco, Sergio O.; Barbarino, Elisabete; Bispo, Maria das	Effects of light intensity on growth, inorganic nitrogen storage, and	APLICACOES DA FICOLOGIA:

	Gracas S.; Borges, Davilma A.; Coelho-Gomes, Carina; Lavin, Paris L.; Santos, Fernanda	gross chemical composition of four marine microalgae in batch cultures	ANAIS DO XI CONGRESSO BRASILEIRO DE FICOLOGIA E SIMPOSIO LATINO-AMERICANO SOBRE ALGAS NOCIVAS

2 The taxonomic composition and sequence number of toxic algal species in HTMaDB.

Species_database	**Kingdom**	**Phylum**	**Class**	**Order**	**Family**	**Genus**	**SeqNumber**
Akashiwo_sanguinea	Alveolata	Dinoflagellata	Dinophyceae	Gymnodiniphycidae	Gymnodiniaceae	Akashiwo	15
Alexandrium_affine	Alveolata	Dinoflagellata	Dinophyceae	Gonyaulacales	Pyrocystaceae	Alexandrium	9
Alexandrium_andersonii	Alveolata	Dinoflagellata	Dinophyceae	Gonyaulacales	Pyrocystaceae	Alexandrium	5
Alexandrium_australiense	Alveolata	Dinoflagellata	Dinophyceae	Gonyaulacales	Pyrocystaceae	Alexandrium	1
Alexandrium_catenella	Alveolata	Dinoflagellata	Dinophyceae	Gonyaulacales	Pyrocystaceae	Alexandrium	23
Alexandrium_fragae	Alveolata	Dinoflagellata	Dinophyceae	Gonyaulacales	Pyrocystaceae	Alexandrium	1
Alexandrium_hiranoi	Alveolata	Dinoflagellata	Dinophyceae	Gonyaulacales	Pyrocystaceae	Alexandrium	2
Alexandrium_leei	Alveolata	Dinoflagellata	Dinophyceae	Gonyaulacales	Pyrocystaceae	Alexandrium	1
Alexandrium_limii	Alveolata	Dinoflagellata	Dinophyceae	Gonyaulacales	Pyrocystaceae	Alexandrium	2
Alexandrium_minutum	Alveolata	Dinoflagellata	Dinophyceae	Gonyaulacales	Pyrocystaceae	Alexandrium	11
Alexandrium_monilatum	Alveolata	Dinoflagellata	Dinophyceae	Gonyaulacales	Pyrocystaceae	Alexandrium	1
Alexandrium_ogatae	Alveolata	Dinoflagellata	Dinophyceae	Gonyaulacales	Pyrocystaceae	Alexandrium	2
Alexandrium_ostenfeldii	Alveolata	Dinoflagellata	Dinophyceae	Gonyaulacales	Pyrocystaceae	Alexandrium	50
Alexandrium_pacificum	Alveolata	Dinoflagellata	Dinophyceae	Gonyaulacales	Pyrocystaceae	Alexandrium	2
Alexandrium_pseudogonyaulax	Alveolata	Dinoflagellata	Dinophyceae	Gonyaulacales	Pyrocystaceae	Alexandrium	6
Alexandrium_tamarense	Alveolata	Dinoflagellata	Dinophyceae	Gonyaulacales	Pyrocystaceae	Alexandrium	59
Alexandrium_tamiyavanichii	Alveolata	Dinoflagellata	Dinophyceae	Gonyaulacales	Pyrocystaceae	Alexandrium	1
Alexandrium_taylorii	Alveolata	Dinoflagellata	Dinophyceae	Gonyaulacales	Pyrocystaceae	Alexandrium	1
Amphidinium_carterae	Alveolata	Dinoflagellata	Dinophyceae	Gymnodiniphycidae	Amphidiniaceae	Amphidinium	8
Amphidinium_gibbosum	Alveolata	Dinoflagellata	Dinophyceae	Gymnodiniphycidae	Amphidiniaceae	Amphidinium	1
Amphidinium_klebsii	Alveolata	Dinoflagellata	Dinophyceae	Gymnodiniphycidae	Amphidiniaceae	Amphidinium	1
Amphidinium_operculatum	Alveolata	Dinoflagellata	Dinophyceae	Gymnodiniphycidae	Amphidiniaceae	Amphidinium	2
Amphidoma_languida	Alveolata	Dinoflagellata	Dinophyceae	Gonyaulacales	Amphidomataceae	Amphidoma	3

Azadinium_dexteroporum	Alveolata	Dinoflagellata	Dinophyceae	Peridiniales	Amphidomataceae	Azadinium	2
Azadinium_poporum	Alveolata	Dinoflagellata	Dinophyceae	Peridiniales	Amphidomataceae	Azadinium	3
Azadinium_spinosum	Alveolata	Dinoflagellata	Dinophyceae	Peridiniales	Amphidomataceae	Azadinium	5
Centrodinium_punctatum	Alveolata	Dinoflagellata	Dinophyceae	Gonyaulacales	Ostreopsidaceae	Centrodinium	2
Coolia_canariensis	Alveolata	Dinoflagellata	Dinophyceae	Peridiniphycidae	Gonyaulacales	Coolia	2
Coolia_malayensis	Alveolata	Dinoflagellata	Dinophyceae	Peridiniphycidae	Gonyaulacales	Coolia	1
Dinophysis_acuminata	Alveolata	Dinoflagellata	Dinophyceae	Dinophysiales	Dinophysiaceae	Dinophysis	5
Dinophysis_acuta	Alveolata	Dinoflagellata	Dinophyceae	Dinophysiales	Dinophysiaceae	Dinophysis	1
Dinophysis_caudata	Alveolata	Dinoflagellata	Dinophyceae	Dinophysiales	Dinophysiaceae	Dinophysis	2
Dinophysis_fortii	Alveolata	Dinoflagellata	Dinophyceae	Dinophysiales	Dinophysiaceae	Dinophysis	1
Dinophysis_infundibulum	Alveolata	Dinoflagellata	Dinophyceae	Dinophysiales	Dinophysiaceae	Dinophysis	1
Dinophysis_miles	Alveolata	Dinoflagellata	Dinophyceae	Dinophysiales	Dinophysiaceae	Dinophysis	1
Dinophysis_norvegica	Alveolata	Dinoflagellata	Dinophyceae	Dinophysiales	Dinophysiaceae	Dinophysis	3
Dinophysis_tripos	Alveolata	Dinoflagellata	Dinophyceae	Dinophysiales	Dinophysiaceae	Dinophysis	1
Fukuyoa_paulensis	Alveolata	Dinoflagellata	Dinophyceae	Gonyaulacales	Pyrocystaceae	Fukuyoa	1
Fukuyoa_ruetzleri	Alveolata	Dinoflagellata	Dinophyceae	Gonyaulacales	Pyrocystaceae	Fukuyoa	2
Fukuyoa_yasumotoi	Alveolata	Dinoflagellata	Dinophyceae	Gonyaulacales	Pyrocystaceae	Fukuyoa	10
Gambierdiscus_australes	Alveolata	Dinoflagellata	Dinophyceae	Gonyaulacales	Pyrocystaceae	Gambierdiscus	18
Gambierdiscus_balechii	Alveolata	Dinoflagellata	Dinophyceae	Gonyaulacales	Pyrocystaceae	Gambierdiscus	4
Gambierdiscus_belizeanus	Alveolata	Dinoflagellata	Dinophyceae	Gonyaulacales	Pyrocystaceae	Gambierdiscus	7
Gambierdiscus_caribaeus	Alveolata	Dinoflagellata	Dinophyceae	Gonyaulacales	Pyrocystaceae	Gambierdiscus	1
Gambierdiscus_carolinianus	Alveolata	Dinoflagellata	Dinophyceae	Gonyaulacales	Pyrocystaceae	Gambierdiscus	5
Gambierdiscus_carpenteri	Alveolata	Dinoflagellata	Dinophyceae	Gonyaulacales	Pyrocystaceae	Gambierdiscus	8
Gambierdiscus_cheloniae	Alveolata	Dinoflagellata	Dinophyceae	Gonyaulacales	Pyrocystaceae	Gambierdiscus	1
Gambierdiscus_excentricus	Alveolata	Dinoflagellata	Dinophyceae	Gonyaulacales	Pyrocystaceae	Gambierdiscus	1
Gambierdiscus_holmesii	Alveolata	Dinoflagellata	Dinophyceae	Gonyaulacales	Pyrocystaceae	Gambierdiscus	2

Gambierdiscus_honu	Alveolata	Dinoflagellata	Dinophyceae	Gonyaulacales	Pyrocystaceae	Gambierdiscus	1
Gambierdiscus_lapillus	Alveolata	Dinoflagellata	Dinophyceae	Gonyaulacales	Pyrocystaceae	Gambierdiscus	1
Gambierdiscus_lewisii	Alveolata	Dinoflagellata	Dinophyceae	Gonyaulacales	Pyrocystaceae	Gambierdiscus	1
Gambierdiscus_pacificus	Alveolata	Dinoflagellata	Dinophyceae	Gonyaulacales	Pyrocystaceae	Gambierdiscus	10
Gambierdiscus_polynesiensis	Alveolata	Dinoflagellata	Dinophyceae	Gonyaulacales	Pyrocystaceae	Gambierdiscus	6
Gambierdiscus_scabrosus	Alveolata	Dinoflagellata	Dinophyceae	Gonyaulacales	Pyrocystaceae	Gambierdiscus	55
Gambierdiscus_silvae	Alveolata	Dinoflagellata	Dinophyceae	Gonyaulacales	Pyrocystaceae	Gambierdiscus	2
Gambierdiscus_toxicus	Alveolata	Dinoflagellata	Dinophyceae	Gonyaulacales	Pyrocystaceae	Gambierdiscus	14
Gonyaulax_bohaiensis	Alveolata	Dinoflagellata	Dinophyceae	Gonyaulacales	Gonyaulacaceae	Gonyaulax	1
Gonyaulax_spinifera	Alveolata	Dinoflagellata	Dinophyceae	Gonyaulacales	Gonyaulacaceae	Gonyaulax	6
Gymnodinium_catenatum	Alveolata	Dinoflagellata	Dinophyceae	Gymnodiniales	Gymnodiniaceae	Gymnodinium	11
Heterocapsa_bohaiensis	Alveolata	Dinoflagellata	Dinophyceae	Peridiniales	Heterocapsaceae	Heterocapsa	2
Heterocapsa_borneoensis	Alveolata	Dinoflagellata	Dinophyceae	Peridiniales	Heterocapsaceae	Heterocapsa	1
Heterocapsa_circularisquama	Alveolata	Dinoflagellata	Dinophyceae	Peridiniales	Heterocapsaceae	Heterocapsa	1
Heterocapsa_horiguchii	Alveolata	Dinoflagellata	Dinophyceae	Peridiniales	Heterocapsaceae	Heterocapsa	1
Heterocapsa_niei	Alveolata	Dinoflagellata	Dinophyceae	Peridiniales	Heterocapsaceae	Heterocapsa	3
Heterocapsa_pygmaea	Alveolata	Dinoflagellata	Dinophyceae	Peridiniales	Heterocapsaceae	Heterocapsa	10
Karenia_bicuneiformis	Alveolata	Dinoflagellata	Dinophyceae	Gymnodiniales	Kareniaceae	Karenia	1
Karenia_brevis	Alveolata	Dinoflagellata	Dinophyceae	Gymnodiniales	Kareniaceae	Karenia	14
Karenia_mikimotoi	Alveolata	Dinoflagellata	Dinophyceae	Gymnodiniales	Kareniaceae	Karenia	7
Karenia_papilionacea	Alveolata	Dinoflagellata	Dinophyceae	Gymnodiniales	Kareniaceae	Karenia	1
Karenia_selliformis	Alveolata	Dinoflagellata	Dinophyceae	Gymnodiniales	Kareniaceae	Karenia	1
Karlodinium_veneficum	Alveolata	Dinoflagellata	Dinophyceae	Gymnodiniales	Kareniaceae	Karlodinium	25
Lingulodinium_polyedra	Alveolata	Dinoflagellata	Dinophyceae	Gonyaulacales	Lingulodiniaceae	Lingulodinium	10
Margalefidinium_fulvescens	Alveolata	Dinoflagellata	Dinophyceae	Gymnodiniales	Gymnodiniaceae	Margalefidinium	3
Margalefidinium_polykrikoides	Alveolata	Dinoflagellata	Dinophyceae	Gymnodiniales	Gymnodiniaceae	Margalefidinium	27

Ostreopsis_ovata	Alveolata	Dinoflagellata	Dinophyceae	Gonyaulacales	Pyrocystaceae	Ostreopsis	3
Ostreopsis_rhodesiae	Alveolata	Dinoflagellata	Dinophyceae	Gonyaulacales	Pyrocystaceae	Ostreopsis	3
Ostreopsis_siamensis	Alveolata	Dinoflagellata	Dinophyceae	Gonyaulacales	Pyrocystaceae	Ostreopsis	2
Pfiesteria_piscicida	Alveolata	Dinoflagellata	Dinophyceae	Thoracosphaerales	Pfiesteriaceae	Pfiesteria	35
Pfiesteria_shumwayae	Alveolata	Dinoflagellata	Dinophyceae	Thoracosphaerales	Pfiesteriaceae	Pfiesteria	1
Phalacroma_mitra	Alveolata	Dinoflagellata	Dinophyceae	Dinophysiales	Oxyphysiaceae	Phalacroma	4
Phalacroma_rotundatum	Alveolata	Dinoflagellata	Dinophyceae	Dinophysiales	Oxyphysaceae	Phalacroma	2
Polykrikos_hartmannii	Alveolata	Dinoflagellata	Dinophyceae	Gymnodiniales	Gymnodiniaceae	Polykrikos	1
Prorocentrum_cassubicum	Alveolata	Dinoflagellata	Dinophyceae	Prorocentrales	Prorocentraceae	Prorocentrum	1
Prorocentrum_concavum	Alveolata	Dinoflagellata	Dinophyceae	Prorocentrales	Prorocentraceae	Prorocentrum	1
Prorocentrum_cordatum	Alveolata	Dinoflagellata	Dinophyceae	Prorocentrales	Prorocentraceae	Prorocentrum	12
Prorocentrum_emarginatum	Alveolata	Dinoflagellata	Dinophyceae	Prorocentrales	Prorocentraceae	Prorocentrum	2
Prorocentrum_hoffmannianum	Alveolata	Dinoflagellata	Dinophyceae	Prorocentrales	Prorocentraceae	Prorocentrum	2
Prorocentrum_leve	Alveolata	Dinoflagellata	Dinophyceae	Prorocentrales	Prorocentraceae	Prorocentrum	3
Prorocentrum_lima	Alveolata	Dinoflagellata	Dinophyceae	Prorocentrales	Prorocentraceae	Prorocentrum	12
Prorocentrum_mexicanum	Alveolata	Dinoflagellata	Dinophyceae	Prorocentrales	Prorocentraceae	Prorocentrum	3
Prorocentrum_panamense	Alveolata	Dinoflagellata	Dinophyceae	Prorocentrales	Prorocentraceae	Prorocentrum	1
Prorocentrum_rhathymum	Alveolata	Dinoflagellata	Dinophyceae	Prorocentrales	Prorocentraceae	Prorocentrum	6
Prorocentrum_texanum	Alveolata	Dinoflagellata	Dinophyceae	Prorocentrales	Prorocentraceae	Prorocentrum	1
Protoceratium_reticulatum	Alveolata	Dinoflagellata	Dinophyceae	Gonyaulacales	Pyrocystaceae	Protoceratium	6
Protoperidinium_crassipes	Alveolata	Dinoflagellata	Dinophyceae	Peridiniphycidae	Peridiniales	Protoperidinium	3
Pyrodinium_bahamense	Alveolata	Dinoflagellata	Dinophyceae	Gonyaulacales	Pyrocystaceae	Pyrodinium	6
Pyrodinium_bahamense_var._compressum	Alveolata	Dinoflagellata	Dinophyceae	Gonyaulacales	Pyrocystaceae	Pyrodinium	6
Takayama_acrotrocha	Alveolata	Dinoflagellata	Dinophyceae	Gymnodiniphycidae	Kareniaceae	Takayama	1
Vicicitus_globosus	Stramenopiles	Ochrophyta	Dictyochophyceae	Dictyochales	Dictyochaceae	Vicicitus	1
Chattonella_marina	Stramenopiles	Ochrophyta	Raphidophyceae	Chattonellales	Chattonellaceae	Chattonella	6

Chattonella_marina_var._antiqua	Stramenopiles	Ochrophyta	Raphidophyceae	Chattonellales	Chattonellaceae	Chattonella	4
Chattonella_marina_var._ovata	Stramenopiles	Ochrophyta	Raphidophyceae	Chattonellales	Chattonellaceae	Chattonella	3
Chattonella_subsalsa	Stramenopiles	Ochrophyta	Raphidophyceae	Chattonellales	Chattonellaceae	Chattonella	12
Fibrocapsa_japonica	Stramenopiles	Ochrophyta	Raphidophyceae	Chattonellales	Chattonellaceae	Fibrocapsa	4
Heterosigma_akashiwo	Stramenopiles	Ochrophyta	Raphidophyceae	Chattonellales	Chattonellaceae	Heterosigma	53
Nitzschia_bizertensis	Stramenopiles	Ochrophyta	Diatomea	Bacillariophytina	Bacillariophyceae	Nitzschia	1
Pseudochattonella_farcimen	Stramenopiles	Ochrophyta	Dictyochophyceae	Florenciellales	Florenciellales incertae sedis	Pseudochattonella	3
Pseudochattonella_verruculosa	Stramenopiles	Ochrophyta	Dictyochophyceae	Florenciellales	Florenciellales incertae sedis	Pseudochattonella	6
Pseudo-nitzschia_australis	Stramenopiles	Ochrophyta	Diatomea	Bacillariophytina	Bacillariophyceae	Pseudo-nitzschia	3
Pseudo-nitzschia_batesiana	Stramenopiles	Ochrophyta	Diatomea	Bacillariophytina	Bacillariophyceae	Pseudo-nitzschia	1
Pseudo-nitzschia_brasiliana	Stramenopiles	Ochrophyta	Diatomea	Bacillariophytina	Bacillariophyceae	Pseudo-nitzschia	3
Pseudo-nitzschia_caciantha	Stramenopiles	Ochrophyta	Diatomea	Bacillariophytina	Bacillariophyceae	Pseudo-nitzschia	1
Pseudo-nitzschia_calliantha	Stramenopiles	Ochrophyta	Diatomea	Bacillariophytina	Bacillariophyceae	Pseudo-nitzschia	1
Pseudo-nitzschia_cuspidata	Stramenopiles	Ochrophyta	Diatomea	Bacillariophytina	Bacillariophyceae	Pseudo-nitzschia	2
Pseudo-nitzschia_delicatissima	Stramenopiles	Ochrophyta	Diatomea	Bacillariophytina	Bacillariophyceae	Pseudo-nitzschia	1
Pseudo-nitzschia_fraudulenta	Stramenopiles	Ochrophyta	Diatomea	Bacillariophytina	Bacillariophyceae	Pseudo-nitzschia	1
Pseudo-nitzschia_fukuyoi	Stramenopiles	Ochrophyta	Diatomea	Bacillariophytina	Bacillariophyceae	Pseudo-nitzschia	3
Pseudo-nitzschia_galaxiae	Stramenopiles	Ochrophyta	Diatomea	Bacillariophytina	Bacillariophyceae	Pseudo-nitzschia	1
Pseudo-nitzschia_granii	Stramenopiles	Ochrophyta	Diatomea	Bacillariophytina	Bacillariophyceae	Pseudo-nitzschia	1
Pseudo-nitzschia_kodamae	Stramenopiles	Ochrophyta	Diatomea	Bacillariophytina	Bacillariophyceae	Pseudo-nitzschia	1
Pseudo-nitzschia_lundholmiae	Stramenopiles	Ochrophyta	Diatomea	Bacillariophytina	Bacillariophyceae	Pseudo-nitzschia	2
Pseudo-nitzschia_multiseries	Stramenopiles	Ochrophyta	Diatomea	Bacillariophytina	Bacillariophyceae	Pseudo-nitzschia	6
Pseudo-nitzschia_pseudodelicatissima	Stramenopiles	Ochrophyta	Diatomea	Bacillariophytina	Bacillariophyceae	Pseudo-nitzschia	1
Pseudo-nitzschia_pungens	Stramenopiles	Ochrophyta	Diatomea	Bacillariophytina	Bacillariophyceae	Pseudo-nitzschia	4
Pseudo-nitzschia_seriata	Stramenopiles	Ochrophyta	Diatomea	Bacillariophytina	Bacillariophyceae	Pseudo-nitzschia	1
Pseudo-nitzschia_simulans	Stramenopiles	Ochrophyta	Diatomea	Bacillariophytina	Bacillariophyceae	Pseudo-nitzschia	1

Pseudo-nitzschia_subcurvata	Stramenopiles	Ochrophyta	Diatomea	Bacillariophytina	Bacillariophyceae	Pseudo-nitzschia	1
Pseudo-nitzschia_turgidula	Stramenopiles	Ochrophyta	Diatomea	Bacillariophytina	Bacillariophyceae	Pseudo-nitzschia	2
Chrysochromulina_leadbeateri	Chromista	Haptophyta	Prymnesiophyceae	Prymnesiales	Chrysochromulinaceae	Chrysochromulina	1
Phaeocystis_globosa	Chromista	Haptophyta	Prymnesiophyceae	Phaeocystales	Phaeocystaceae	Phaeocystis	22
Phaeocystis_pouchetii	Chromista	Haptophyta	Prymnesiophyceae	Phaeocystales	Phaeocystaceae	Phaeocystis	4
Prymnesium_calathiferum	Chromista	Haptophyta	Coccolithophyceae	Prymnesiales	Prymnesiaceae	Prymnesium	2
Prymnesium_faveolatum	Chromista	Haptophyta	Coccolithophyceae	Prymnesiales	Prymnesiaceae	Prymnesium	1
Prymnesium_parvum	Chromista	Haptophyta	Coccolithophyceae	Prymnesiales	Prymnesiaceae	Prymnesium	4
Prymnesium_polylepis	Chromista	Haptophyta	Coccolithophyceae	Prymnesiales	Prymnesiaceae	Prymnesium	17
Prymnesium_zebrinum	Chromista	Haptophyta	Coccolithophyceae	Prymnesiales	Prymnesiaceae	Prymnesium	1

3 The taxonomic composition and sequence number of harmful algal species in HTMaDB.

Species_database	**Kingdom**	**Phylum**	**Class**	**Order**	**Family**	**Genus**	**SeqNumber**
Alexandrium_cohorticula	Alveolata	Dinoflagellata	Dinophyceae	Gonyaulacales	Pyrocystaceae	Alexandrium	1
Alexandrium_margalefii	Alveolata	Dinoflagellata	Dinophyceae	Gonyaulacales	Pyrocystaceae	Alexandrium	1
Alexandrium_insuetum	Alveolata	Dinoflagellata	Dinophyceae	Gonyaulacales	Pyrocystaceae	Alexandrium	2
Asterionellopsis_glacialis	Stramenopiles	Ochrophyta	Diatomea	Bacillariophytina	Bacillariophyceae	Asterionellopsis	4
Aureococcus_anophagefferens	Stramenopiles	Ochrophyta	Pelagophyceae	Pelagomonadales	Pelagomonadaceae	Aureococcus	20
Aureoumbra_lagunensis	Stramenopiles	Ochrophyta	Pelagophyceae	Sarcinochrysidales	Sarcinochrysidaceae	Aureoumbra	3
Blixaea_quinquecornis	Alveolata	Dinoflagellata	Dinophyceae	Peridiniphycidae	Peridiniales	Blixaea	2
Chaetoceros_affinis	Stramenopiles	Ochrophyta	Diatomea	Chaetocerotales	Chaetocerotaceae	Chaetoceros	1
Chaetoceros_atlanticus	Stramenopiles	Ochrophyta	Diatomea	Chaetocerotales	Chaetocerotaceae	Chaetoceros	1
Chaetoceros_constrictus	Stramenopiles	Ochrophyta	Diatomea	Chaetocerotales	Chaetocerotaceae	Chaetoceros	2
Chaetoceros_convolutus	Stramenopiles	Ochrophyta	Diatomea	Chaetocerotales	Chaetocerotaceae	Chaetoceros	1
Chaetoceros_curvisetus	Stramenopiles	Ochrophyta	Diatomea	Chaetocerotales	Chaetocerotaceae	Chaetoceros	1
Chaetoceros_danicus	Stramenopiles	Ochrophyta	Diatomea	Chaetocerotales	Chaetocerotaceae	Chaetoceros	4
Chaetoceros_debilis	Stramenopiles	Ochrophyta	Diatomea	Chaetocerotales	Chaetocerotaceae	Chaetoceros	3
Chaetoceros_decipiens	Stramenopiles	Ochrophyta	Diatomea	Chaetocerotales	Chaetocerotaceae	Chaetoceros	1
Chaetoceros_diadema	Stramenopiles	Ochrophyta	Diatomea	Chaetocerotales	Chaetocerotaceae	Chaetoceros	1
Chaetoceros_laevisporus	Stramenopiles	Ochrophyta	Diatomea	Chaetocerotales	Chaetocerotaceae	Chaetoceros	3
Chaetoceros_pseudocurvisetus	Stramenopiles	Ochrophyta	Diatomea	Chaetocerotales	Chaetocerotaceae	Chaetoceros	2
Chaetoceros_rostratus	Stramenopiles	Ochrophyta	Diatomea	Chaetocerotales	Chaetocerotaceae	Chaetoceros	5
Chaetoceros_socialis	Stramenopiles	Ochrophyta	Diatomea	Chaetocerotales	Chaetocerotaceae	Chaetoceros	2
Chaetoceros_simplex	Stramenopiles	Ochrophyta	Diatomea	Chaetocerotales	Chaetocerotaceae	Chaetoceros	1
Chaetoceros_tenuissimus	Stramenopiles	Ochrophyta	Diatomea	Chaetocerotales	Chaetocerotaceae	Chaetoceros	1
Chaetoceros_throndsenii	Stramenopiles	Ochrophyta	Diatomea	Chaetocerotales	Chaetocerotaceae	Chaetoceros	4

Chaetoceros_tortissimus	Stramenopiles	Ochrophyta	Diatomea	Chaetocerotales	Chaetocerotaceae	Chaetoceros	2
Chaetoceros_lorenzianus	Stramenopiles	Ochrophyta	Diatomea	Chaetocerotales	Chaetocerotaceae	Chaetoceros	1
Chaetoceros_wighamii	Stramenopiles	Ochrophyta	Diatomea	Chaetocerotales	Chaetocerotaceae	Chaetoceros	1
Coscinodiscus_radiatus	Stramenopiles	Ochrophyta	Diatomea	Coscinodiscales	Coscinodiscaceae	Coscinodiscus	4
Coolia_monotis	Alveolata	Dinoflagellata	Dinophyceae	Peridiniphycidae	Gonyaulacales	Coolia	4
Cylindrotheca_closterium	Stramenopiles	Ochrophyta	Diatomea	Bacillariophytina	Bacillariophyceae	Cylindrotheca	46
Cyclotella_meneghiniana	Stramenopiles	Ochrophyta	Diatomea	Bacillariophytina	Mediophyceae	Cyclotella	29
Dictyocha_fibula	Stramenopiles	Ochrophyta	Dictyochophyceae	Dictyochales	Dictyochaceae	Dictyocha	1
Dictyocha_speculum	Stramenopiles	Ochrophyta	Dictyochophyceae	Dictyochales	Dictyochaceae	Dictyocha	1
Dinophysis_hastata	Alveolata	Dinoflagellata	Dinophyceae	Dinophysiales	Dinophysaceae	Dinophysis	1
Diplopsalis_lenticula	Alveolata	Dinoflagellata	Dinophyceae	Peridiniphycidae	Peridiniales	Diplopsalopsis	1
Dunaliella_salina	Chloroplastida	Chlorophyta	Chlorophyceae	Chlamydomonadales	Dunaliellaceae	Dunaliella	39
Eucampia_zodiacus	Stramenopiles	Ochrophyta	Diatomea	Bacillariophytina	Mediophyceae	Eucampia	1
Eutreptiella_gymnastica	Discoba	Euglenozoa	Euglenophyceae	Eutreptiales	Eutreptiaceae	Eutreptiella	5
Euglena_viridis	Discoba	Euglenozoa	Euglenophyceae	Euglenales	Euglenaceae	Euglena	1
Gonyaulax_digitale	Alveolata	Dinoflagellata	Dinophyceae	Peridiniphycidae	Gonyaulacales	Gonyaulax	1
Gonyaulax_polygramma	Alveolata	Dinoflagellata	Dinophyceae	Peridiniphycidae	Gonyaulacales	Gonyaulax	2
Gonyaulax_verior	Alveolata	Dinoflagellata	Dinophyceae	Peridiniphycidae	Gonyaulacales	Gonyaulax	1
Gymnodinium_aureolum	Alveolata	Dinoflagellata	Dinophyceae	Gymnodiniphycidae	Gymnodiniaceae	Gymnodinium	7
Gymnodinium_impudicum	Alveolata	Dinoflagellata	Dinophyceae	Gymnodiniphycidae	Gymnodiniaceae	Gymnodinium	5
Guinardia_delicatula	Stramenopiles	Ochrophyta	Diatomea	Coscinodiscophytina	Rhizosolenids	Guinardia	5
Guinardia_flaccida	Stramenopiles	Ochrophyta	Diatomea	Coscinodiscophytina	Rhizosolenids	Guinardia	5
Halamphora_coffeiformis	Stramenopiles	Ochrophyta	Diatomea	Bacillariophytina	Bacillariophyceae	Halamphora	8
Heterocapsa_rotundata	Alveolata	Dinoflagellata	Dinophyceae	Peridiniphycidae	Peridiniales	Heterocapsa	2
Heterocapsa_triquetra	Alveolata	Dinoflagellata	Dinophyceae	Peridiniphycidae	Peridiniales	Heterocapsa	5
Heterocapsa_pygmaea	Alveolata	Dinoflagellata	Dinophyceae	Peridiniphycidae	Peridiniales	Heterocapsa	2

Lauderia_annulata	Stramenopiles	Ochrophyta	Diatomea	Bacillariophytina	Mediophyceae	Lauderia	3
Lepidodinium_chlorophorum	Alveolata	Dinoflagellata	Dinophyceae	Gymnodiniphycidae	Gymnodiniaceae	Lepidodinium	4
Leptocylindrus_danicus	Stramenopiles	Ochrophyta	Diatomea	Coscinodiscophytina	Rhizosolenids	Leptocylindrus	4
Leptocylindrus_minimus	Stramenopiles	Ochrophyta	Diatomea	Coscinodiscophytina	Rhizosolenids	Leptocylindrus	2
Levanderina_fissa	Alveolata	Dinoflagellata	Dinophyceae	Gymnodiniphycidae	Gymnodiniales familia incertae sedis	Levanderina	1
Lithodesmioides_polymorpha	Stramenopiles	Ochrophyta	Diatomea	Bacillariophytina	Mediophyceae	Lithodesmioides	1
Noctiluca_scintillans	Alveolata	Dinoflagellata	Dinophyceae	Noctilucales	Noctilucaceae	Noctiluca	5
Nitzschia_longissima	Stramenopiles	Ochrophyta	Diatomea	Bacillariophytina	Bacillariophyceae	Nitzschia	3
Ostreopsis_lenticularis	Alveolata	Dinoflagellata	Dinophyceae	Gonyaulacales	Pyrocystaceae	Ostreopsis	1
Paralia_sulcata	Stramenopiles	Ochrophyta	Diatomea	Coscinodiscophytina	Melosirids	Paralia	2
Phalacroma_rapa	Alveolata	Dinoflagellata	Dinophyceae	Dinophysiales	Oxyphysiaceae	Phalacroma	3
Plagioselmis_prolonga	Chromista	Cryptophyta	Cryptophyceae	Pyrenomonadales	Geminigeraceae	Plagioselmis	2
Plagioselmis_nannoplanctica	Chromista	Cryptophyta	Cryptophyceae	Pyrenomonadales	Geminigeraceae	Plagioselmis	3
Proboscia_alata	Stramenopiles	Ochrophyta	Diatomea	Coscinodiscophytina	Rhizosolenids	Proboscia	2
Prorocentrum_dentatum	Alveolata	Dinoflagellata	Dinophyceae	Prorocentrales	Prorocentraceae	Prorocentrum	3
Prorocentrum_donghaiense	Alveolata	Dinoflagellata	Dinophyceae	Prorocentrales	Prorocentraceae	Prorocentrum	5
Prorocentrum_gracile	Alveolata	Dinoflagellata	Dinophyceae	Prorocentrales	Prorocentraceae	Prorocentrum	1
Prorocentrum_micans	Alveolata	Dinoflagellata	Dinophyceae	Prorocentrales	Prorocentraceae	Prorocentrum	10
Prorocentrum_redfieldii	Alveolata	Dinoflagellata	Dinophyceae	Prorocentrales	Prorocentraceae	Prorocentrum	3
Prorocentrum_triestinum	Alveolata	Dinoflagellata	Dinophyceae	Prorocentrales	Prorocentraceae	Prorocentrum	3
Protodinium_simplex	Alveolata	Dinoflagellata	Dinophyceae	Gymnodiniphycidae	Suessiaceae	Protodinium	3
Pseudocochlodinium_profundisulcus	Alveolata	Dinoflagellata	Dinophyceae	Dinophyceae ordo incertae sedis	Dinophyceae familia incertae sedis	Pseudocochlodinium	1
Pyrophacus_steinii	Alveolata	Dinoflagellata	Dinophyceae	Gonyaulacales	Pyrocystaceae	Pyrophacus	1
Scrippsiella_acuminata	Alveolata	Dinoflagellata	Dinophyceae	Peridiniphycidae	Thoracosphaeraceae	Scrippsiella	8
Scrippsiella_trochoidea	Alveolata	Dinoflagellata	Dinophyceae	Peridiniphycidae	Thoracosphaeraceae	Scrippsiella	6
Skeletonema_tropicum	Stramenopiles	Ochrophyta	Diatomea	Bacillariophytina	Mediophyceae	Skeletonema	7

Skeletonema_costatum	Stramenopiles	Ochrophyta	Diatomea	Bacillariophytina	Mediophyceae	Skeletonema	29
Skeletonema_marinoi	Stramenopiles	Ochrophyta	Diatomea	Bacillariophytina	Mediophyceae	Skeletonema	48
Skeletonema_menzelii	Stramenopiles	Ochrophyta	Diatomea	Bacillariophytina	Mediophyceae	Skeletonema	1
Skeletonema_pseudocostatum	Stramenopiles	Ochrophyta	Diatomea	Bacillariophytina	Mediophyceae	Skeletonema	17
Takayama_pulchella	Alveolata	Dinoflagellata	Dinophyceae	Gymnodiniphycidae	Kareniaceae	Takayama	1
Takayama_xiamenensis	Alveolata	Dinoflagellata	Dinophyceae	Gymnodiniphycidae	Kareniaceae	Takayama	1
Teleaulax_acuta	Chromista	Cryptophyta	Cryptophyceae	Pyrenomonadales	Geminigeraceae	Teleaulax	3
Tenuicylindrus_belgicus	Stramenopiles	Ochrophyta	Diatomea	Coscinodiscophytina	Rhizosolenids	Tenuicylindrus	3
Thalassiosira_allenii	Stramenopiles	Ochrophyta	Diatomea	Bacillariophytina	Mediophyceae	Thalassiosira	1
Thalassiosira_curviseriata	Stramenopiles	Ochrophyta	Diatomea	Bacillariophytina	Mediophyceae	Thalassiosira	2
Thalassiosira_gravida	Stramenopiles	Ochrophyta	Diatomea	Bacillariophytina	Mediophyceae	Thalassiosira	8
Thalassiosira_lundiana	Stramenopiles	Ochrophyta	Diatomea	Bacillariophytina	Mediophyceae	Thalassiosira	1
Thalassiosira_mala	Stramenopiles	Ochrophyta	Diatomea	Bacillariophytina	Mediophyceae	Thalassiosira	1
Thalassiosira_minima	Stramenopiles	Ochrophyta	Diatomea	Bacillariophytina	Mediophyceae	Thalassiosira	5
Thalassiosira_minuscula	Stramenopiles	Ochrophyta	Diatomea	Bacillariophytina	Mediophyceae	Thalassiosira	3
Thalassionema_nitzschioides	Stramenopiles	Ochrophyta	Diatomea	Bacillariophytina	Mediophyceae	Thalassionema	1
Thalassiosira_pseudonana	Stramenopiles	Ochrophyta	Diatomea	Bacillariophytina	Mediophyceae	Thalassiosira	18
Thalassiosira_punctigera	Stramenopiles	Ochrophyta	Diatomea	Bacillariophytina	Mediophyceae	Thalassiosira	7
Thalassiosira_rotula	Stramenopiles	Ochrophyta	Diatomea	Bacillariophytina	Mediophyceae	Thalassiosira	19
Thalassiosira_weissflogii	Stramenopiles	Ochrophyta	Diatomea	Bacillariophytina	Mediophyceae	Thalassiosira	10
Tripos_dens	Alveolata	Dinoflagellata	Dinophyceae	Gonyaulacales	Ceratiaceae	Tripos	1
Tripos_furca	Alveolata	Dinoflagellata	Dinophyceae	Gonyaulacales	Ceratiaceae	Tripos	6
Tripos_fusus	Alveolata	Dinoflagellata	Dinophyceae	Gonyaulacales	Ceratiaceae	Tripos	2
Tripos_lineatus	Alveolata	Dinoflagellata	Dinophyceae	Gonyaulacales	Ceratiaceae	Tripos	1
Tripos_muelleri	Alveolata	Dinoflagellata	Dinophyceae	Gonyaulacales	Ceratiaceae	Tripos	1
Tryblionella_compressa	Stramenopiles	Ochrophyta	Diatomea	Bacillariophytina	Bacillariophyceae	Tryblionella	2

Appendix 2

This section provides detailed sampling information in this study.

1 The detailed information of sampling locations in Hong Kong coastal seawater.

Sample ID	Description	Longitude	Latitude
S1	Eastern Waters	114.218333	22.408611
S2	Eastern Waters	114.205	22.450556
S3	Eastern Waters	114.274167	22.46
S4	Eastern Waters	114.275278	22.434444
S5	Eastern Waters	114.335	22.476944
S6	Eastern Waters	114.3071	22.523683
S7	Eastern Waters	114.3618	22.57305
S8	Eastern Waters	114.40945	22.48765
S9	Eastern Waters	114.289444	22.343056
S10	Eastern Waters	114.296389	22.286111
S11	Eastern Waters	114.3325	22.276111
S12	Eastern Waters	114.343333	22.249722
S13	Eastern Waters	114.304167	22.289444
S14	Eastern Waters	114.379722	22.265
S15	Eastern Waters	114.394167	22.355
S16	Southern Waters	114.322222	22.366667
S17	Southern Waters	114.257222	22.234167
S18	Southern Waters	114.256389	22.205
S19	Southern Waters	114.286389	22.155278
S20	Southern Waters	114.175556	22.1875
S21	Southern Waters	114.189444	22.227222
S22	Southern Waters	114.130833	22.228056
S23	Southern Waters	114.073333	22.278333
S24	Southern Waters	114.055	22.353333
S25	Southern Waters	114.119722	22.331667
S26	Southern Waters	114.117222	22.311667
S27	Southern Waters	114.1525	22.299167
S28	Southern Waters	114.009722	22.238889
S29	Southern Waters	114.002778	22.188056
S30	Southern Waters	113.939444	22.185556
S31	Southern Waters	113.881389	22.166944

S32	Western Waters	113.827983	22.224317
S33	Western Waters	113.975	22.323056
S34	Western Waters	113.875	22.289722
S35	Western Waters	113.919722	22.431944
S36	Western Waters	113.905278	22.361111

2. The detailed information of sampling locations of coastal plastisphere.

Sample ID	Group	Description	Region	Longitude	Latitude
EnvHKSumMc1	Ambient	Marine Culture	Hong Kong	114.32278	22.36583
EnvHKSumMR1	Ambient	Marine Reserve	Hong Kong	114.27630	22.25900
EnvHKSumMR2	Ambient	Marine Reserve	Hong Kong	114.27630	22.25900
EnvHKSumMR3	Ambient	Marine Reserve	Hong Kong	114.27630	22.25900
EnvHKSumMR4	Ambient	Marine Reserve	Hong Kong	114.27630	22.25900
EnvHKSumPort1	Ambient	Port	Hong Kong	114.27446	22.38152
EnvHKSumWWTP2	Ambient	WWTP	Hong Kong	114.11727	22.31137
EnvHKWinBeach1	Ambient	Beach	Hong Kong	114.18930	22.23140
EnvHKWinBeach2	Ambient	Beach	Hong Kong	114.18930	22.23140
EnvHKWinBeach3	Ambient	Beach	Hong Kong	114.18930	22.23140
EnvHKWinEs1	Ambient	Estuary	Hong Kong	114.21694	22.40194
EnvHKWinEs2	Ambient	Estuary	Hong Kong	114.21694	22.40194
EnvHKWinEs4	Ambient	Estuary	Hong Kong	114.21694	22.40194
EnvHKWinEs5	Ambient	Estuary	Hong Kong	114.21694	22.40194
EnvHKWinMc1	Ambient	Marine Culture	Hong Kong	113.98209	22.46892
EnvHKWinMc10	Ambient	Marine Culture	Hong Kong	114.32278	22.36583
EnvHKWinMc11	Ambient	Marine Culture	Hong Kong	114.13045	22.22385
EnvHKWinMc12	Ambient	Marine Culture	Hong Kong	114.13045	22.22385
EnvHKWinMc13	Ambient	Marine Culture	Hong Kong	114.13045	22.22385
EnvHKWinMc15	Ambient	Marine Culture	Hong Kong	114.13045	22.22385
EnvHKWinMc2	Ambient	Marine Culture	Hong Kong	113.98209	22.46892
EnvHKWinMc3	Ambient	Marine Culture	Hong Kong	113.98209	22.46892
EnvHKWinMc4	Ambient	Marine Culture	Hong Kong	113.98209	22.46892
EnvHKWinMc5	Ambient	Marine Culture	Hong Kong	113.98209	22.46892
EnvHKWinMc6	Ambient	Marine Culture	Hong Kong	114.32278	22.36583
EnvHKWinMc7	Ambient	Marine Culture	Hong Kong	114.32278	22.36583
EnvHKWinMc8	Ambient	Marine Culture	Hong Kong	114.32278	22.36583
EnvHKWinMc9	Ambient	Marine Culture	Hong Kong	114.32278	22.36583
EnvHKWinMR1	Ambient	Marine Reserve	Hong Kong	114.27632	22.25902
EnvHKWinPort1	Ambient	Port	Hong Kong	114.27446	22.38152
EnvHKWinPort2	Ambient	Port	Hong Kong	114.27446	22.38152
EnvHKWinPort3	Ambient	Port	Hong Kong	114.27446	22.38152
EnvHKWinPort4	Ambient	Port	Hong Kong	114.27446	22.38152
EnvHKWinPort5	Ambient	Port	Hong Kong	114.27446	22.38152

EnvHKWinWWTP1	Ambient	WWTP	Hong Kong	114.11727	22.31137
EnvHKWinWWTP2	Ambient	WWTP	Hong Kong	114.11727	22.31137
EnvHKWinWWTP3	Ambient	WWTP	Hong Kong	114.11727	22.31137
EnvHKWinWWTP4	Ambient	WWTP	Hong Kong	114.11727	22.31137
EnvQDSumBeach1	Ambient	Beach	Hong Kong	120.49433	36.09085
EnvQDSumBeach2	Ambient	Beach	Hong Kong	120.49433	36.09085
EnvQDSumBeach4	Ambient	Beach	Hong Kong	120.49433	36.09085
EnvQDSumBeach5	Ambient	Beach	Hong Kong	120.49433	36.09085
EnvQDSumEs1	Ambient	Estuary	Hong Kong	120.31518	36.25501
EnvQDSumEs2	Ambient	Estuary	Hong Kong	120.31518	36.25501
EnvQDSumEs3	Ambient	Estuary	Hong Kong	120.31518	36.25501
EnvQDSumMc1	Ambient	Marine Culture	Hong Kong	120.23318	36.19174
EnvQDSumMc2	Ambient	Marine Culture	Hong Kong	120.23318	36.19174
EnvQDSumMc4	Ambient	Marine Culture	Hong Kong	120.23318	36.19174
EnvQDSumMc5	Ambient	Marine Culture	Hong Kong	120.23318	36.19174
EnvQDSumMR1	Ambient	Marine Reserve	Hong Kong	120.17625	35.88025
EnvQDSumMR2	Ambient	Marine Reserve	Hong Kong	120.17625	35.88025
EnvQDSumMR3	Ambient	Marine Reserve	Hong Kong	120.17625	35.88025
EnvQDSumPort1	Ambient	Port	Hong Kong	120.30023	36.07129
EnvQDSumPort2	Ambient	Port	Hong Kong	120.30023	36.07129
EnvQDSumPort3	Ambient	Port	Hong Kong	120.30023	36.07129
EnvQDSumPort4	Ambient	Port	Hong Kong	120.30023	36.07129
EnvQDSumPort5	Ambient	Port	Hong Kong	120.30023	36.07129
EnvQDSumWWTP1	Ambient	WWTP	Hong Kong	120.34792	36.15289
EnvQDSumWWTP2	Ambient	WWTP	Hong Kong	120.34792	36.15289
EnvQDSumWWTP3	Ambient	WWTP	Hong Kong	120.34792	36.15289
EnvQDSumWWTP4	Ambient	WWTP	Hong Kong	120.34792	36.15289
EnvQDSumWWTP5	Ambient	WWTP	Hong Kong	120.34792	36.15289
EnvQDWinBeach1	Ambient	Beach	Hong Kong	120.49433	36.09085
EnvQDWinBeach2	Ambient	Beach	Hong Kong	120.49433	36.09085
EnvQDWinBeach3	Ambient	Beach	Hong Kong	120.49433	36.09085
EnvQDWinBeach4	Ambient	Beach	Hong Kong	120.49433	36.09085
EnvQDWinBeach5	Ambient	Beach	Hong Kong	120.49433	36.09085
EnvQDWinEs1	Ambient	Estuary	Hong Kong	120.31518	36.25501
EnvQDWinEs2	Ambient	Estuary	Hong Kong	120.31518	36.25501
EnvQDWinEs3	Ambient	Estuary	Hong Kong	120.31518	36.25501
EnvQDWinEs4	Ambient	Estuary	Hong Kong	120.31518	36.25501

EnvQDWinEs5	Ambient	Estuary	Hong Kong	120.31518	36.25501
EnvQDWinMc1	Ambient	Marine Culture	Hong Kong	120.23318	36.19174
EnvQDWinMc2	Ambient	Marine Culture	Hong Kong	120.23318	36.19174
EnvQDWinMc3	Ambient	Marine Culture	Hong Kong	120.23318	36.19174
EnvQDWinMc4	Ambient	Marine Culture	Hong Kong	120.23318	36.19174
EnvQDWinMc5	Ambient	Marine Culture	Hong Kong	120.23318	36.19174
EnvQDWinMR1	Ambient	Marine Reserve	Hong Kong	120.17625	35.88025
EnvQDWinMR2	Ambient	Marine Reserve	Hong Kong	120.17625	35.88025
EnvQDWinMR3	Ambient	Marine Reserve	Hong Kong	120.17625	35.88025
EnvQDWinMR4	Ambient	Marine Reserve	Hong Kong	120.17625	35.88025
EnvQDWinMR5	Ambient	Marine Reserve	Hong Kong	120.17625	35.88025
EnvQDWinPort1	Ambient	Port	Hong Kong	120.30023	36.07129
EnvQDWinPort2	Ambient	Port	Hong Kong	120.30023	36.07129
EnvQDWinPort3	Ambient	Port	Hong Kong	120.30023	36.07129
EnvQDWinPort4	Ambient	Port	Hong Kong	120.30023	36.07129
EnvQDWinPort5	Ambient	Port	Hong Kong	120.30023	36.07129
EnvQDWinWWTP1	Ambient	WWTP	Hong Kong	120.34792	36.15289
EnvQDWinWWTP2	Ambient	WWTP	Hong Kong	120.34792	36.15289
EnvQDWinWWTP3	Ambient	WWTP	Hong Kong	120.34792	36.15289
EnvQDWinWWTP4	Ambient	WWTP	Hong Kong	120.34792	36.15289
EnvQDWinWWTP5	Ambient	WWTP	Hong Kong	120.34792	36.15289
PlaHKSumMc1	Plastisphere	Marine Culture	Hong Kong	114.32278	22.36583
PlaHKSumMR1	Plastisphere	Marine Reserve	Hong Kong	114.27630	22.25900
PlaHKSumMR2	Plastisphere	Marine Reserve	Hong Kong	114.27630	22.25900
PlaHKSumMR3	Plastisphere	Marine Reserve	Hong Kong	114.27630	22.25900
PlaHKSumMR4	Plastisphere	Marine Reserve	Hong Kong	114.27630	22.25900
PlaHKSumPort1	Plastisphere	Port	Hong Kong	114.27446	22.38152
PlaHKSumWWTP2	Plastisphere	WWTP	Hong Kong	114.11727	22.31137
PlaHKWinBeach1	Plastisphere	Beach	Hong Kong	114.18930	22.23140
PlaHKWinBeach2	Plastisphere	Beach	Hong Kong	114.18930	22.23140
PlaHKWinBeach3	Plastisphere	Beach	Hong Kong	114.18930	22.23140
PlaHKWinEs1	Plastisphere	Estuary	Hong Kong	114.21694	22.40194
PlaHKWinEs2	Plastisphere	Estuary	Hong Kong	114.21694	22.40194
PlaHKWinEs4	Plastisphere	Estuary	Hong Kong	114.21694	22.40194
PlaHKWinEs5	Plastisphere	Estuary	Hong Kong	114.21694	22.40194
PlaHKWinMc1	Plastisphere	Marine Culture	Hong Kong	113.98209	22.46892
PlaHKWinMc10	Plastisphere	Marine Culture	Hong Kong	114.32278	22.36583

PlaHKWinMc11	Plastisphere	Marine Culture	Hong Kong	114.13045	22.22385
PlaHKWinMc12	Plastisphere	Marine Culture	Hong Kong	114.13045	22.22385
PlaHKWinMc13	Plastisphere	Marine Culture	Hong Kong	114.13045	22.22385
PlaHKWinMc15	Plastisphere	Marine Culture	Hong Kong	114.13045	22.22385
PlaHKWinMc2	Plastisphere	Marine Culture	Hong Kong	113.98209	22.46892
PlaHKWinMc3	Plastisphere	Marine Culture	Hong Kong	113.98209	22.46892
PlaHKWinMc4	Plastisphere	Marine Culture	Hong Kong	113.98209	22.46892
PlaHKWinMc5	Plastisphere	Marine Culture	Hong Kong	113.98209	22.46892
PlaHKWinMc6	Plastisphere	Marine Culture	Hong Kong	114.32278	22.36583
PlaHKWinMc7	Plastisphere	Marine Culture	Hong Kong	114.32278	22.36583
PlaHKWinMc8	Plastisphere	Marine Culture	Hong Kong	114.32278	22.36583
PlaHKWinMc9	Plastisphere	Marine Culture	Hong Kong	114.32278	22.36583
PlaHKWinMR1	Plastisphere	Marine Reserve	Hong Kong	114.27632	22.25902
PlaHKWinPort1	Plastisphere	Port	Hong Kong	114.27446	22.38152
PlaHKWinPort2	Plastisphere	Port	Hong Kong	114.27446	22.38152
PlaHKWinPort3	Plastisphere	Port	Hong Kong	114.27446	22.38152
PlaHKWinPort4	Plastisphere	Port	Hong Kong	114.27446	22.38152
PlaHKWinPort5	Plastisphere	Port	Hong Kong	114.27446	22.38152
PlaHKWinWWTP1	Plastisphere	WWTP	Hong Kong	114.11727	22.31137
PlaHKWinWWTP2	Plastisphere	WWTP	Hong Kong	114.11727	22.31137
PlaHKWinWWTP3	Plastisphere	WWTP	Hong Kong	114.11727	22.31137
PlaHKWinWWTP4	Plastisphere	WWTP	Hong Kong	114.11727	22.31137
PlaQDSumBeach1	Plastisphere	Beach	Qingdao	120.49433	36.09085
PlaQDSumBeach2	Plastisphere	Beach	Qingdao	120.49433	36.09085
PlaQDSumBeach4	Plastisphere	Beach	Qingdao	120.49433	36.09085
PlaQDSumBeach5	Plastisphere	Beach	Qingdao	120.49433	36.09085
PlaQDSumEs1	Plastisphere	Estuary	Qingdao	120.31518	36.25501
PlaQDSumEs2	Plastisphere	Estuary	Qingdao	120.31518	36.25501
PlaQDSumEs3	Plastisphere	Estuary	Qingdao	120.31518	36.25501
PlaQDSumMc1	Plastisphere	Marine Culture	Qingdao	120.23318	36.19174
PlaQDSumMc2	Plastisphere	Marine Culture	Qingdao	120.23318	36.19174
PlaQDSumMc4	Plastisphere	Marine Culture	Qingdao	120.23318	36.19174
PlaQDSumMc5	Plastisphere	Marine Culture	Qingdao	120.23318	36.19174
PlaQDSumMR1	Plastisphere	Marine Reserve	Qingdao	120.17625	35.88025
PlaQDSumMR2	Plastisphere	Marine Reserve	Qingdao	120.17625	35.88025
PlaQDSumMR3	Plastisphere	Marine Reserve	Qingdao	120.17625	35.88025
PlaQDSumPort1	Plastisphere	Port	Qingdao	120.30023	36.07129

PlaQDSumPort2	Plastisphere	Port	Qingdao	120.30023	36.07129
PlaQDSumPort3	Plastisphere	Port	Qingdao	120.30023	36.07129
PlaQDSumPort4	Plastisphere	Port	Qingdao	120.30023	36.07129
PlaQDSumPort5	Plastisphere	Port	Qingdao	120.30023	36.07129
PlaQDSumWWTP1	Plastisphere	WWTP	Qingdao	120.34792	36.15289
PlaQDSumWWTP2	Plastisphere	WWTP	Qingdao	120.34792	36.15289
PlaQDSumWWTP3	Plastisphere	WWTP	Qingdao	120.34792	36.15289
PlaQDSumWWTP4	Plastisphere	WWTP	Qingdao	120.34792	36.15289
PlaQDSumWWTP5	Plastisphere	WWTP	Qingdao	120.34792	36.15289
PlaQDWinBeach1	Plastisphere	Beach	Qingdao	120.49433	36.09085
PlaQDWinBeach2	Plastisphere	Beach	Qingdao	120.49433	36.09085
PlaQDWinBeach3	Plastisphere	Beach	Qingdao	120.49433	36.09085
PlaQDWinBeach4	Plastisphere	Beach	Qingdao	120.49433	36.09085
PlaQDWinBeach5	Plastisphere	Beach	Qingdao	120.49433	36.09085
PlaQDWinEs1	Plastisphere	Estuary	Qingdao	120.31518	36.25501
PlaQDWinEs2	Plastisphere	Estuary	Qingdao	120.31518	36.25501
PlaQDWinEs3	Plastisphere	Estuary	Qingdao	120.31518	36.25501
PlaQDWinEs4	Plastisphere	Estuary	Qingdao	120.31518	36.25501
PlaQDWinEs5	Plastisphere	Estuary	Qingdao	120.31518	36.25501
PlaQDWinMc1	Plastisphere	Marine Culture	Qingdao	120.23318	36.19174
PlaQDWinMc2	Plastisphere	Marine Culture	Qingdao	120.23318	36.19174
PlaQDWinMc3	Plastisphere	Marine Culture	Qingdao	120.23318	36.19174
PlaQDWinMc4	Plastisphere	Marine Culture	Qingdao	120.23318	36.19174
PlaQDWinMc5	Plastisphere	Marine Culture	Qingdao	120.23318	36.19174
PlaQDWinMR1	Plastisphere	Marine Reserve	Qingdao	120.17625	35.88025
PlaQDWinMR2	Plastisphere	Marine Reserve	Qingdao	120.17625	35.88025
PlaQDWinMR3	Plastisphere	Marine Reserve	Qingdao	120.17625	35.88025
PlaQDWinMR4	Plastisphere	Marine Reserve	Qingdao	120.17625	35.88025
PlaQDWinMR5	Plastisphere	Marine Reserve	Qingdao	120.17625	35.88025
PlaQDWinPort1	Plastisphere	Port	Qingdao	120.30023	36.07129
PlaQDWinPort2	Plastisphere	Port	Qingdao	120.30023	36.07129
PlaQDWinPort3	Plastisphere	Port	Qingdao	120.30023	36.07129
PlaQDWinPort4	Plastisphere	Port	Qingdao	120.30023	36.07129
PlaQDWinPort5	Plastisphere	Port	Qingdao	120.30023	36.07129
PlaQDWinWWTP1	Plastisphere	WWTP	Qingdao	120.34792	36.15289
PlaQDWinWWTP2	Plastisphere	WWTP	Qingdao	120.34792	36.15289
PlaQDWinWWTP3	Plastisphere	WWTP	Qingdao	120.34792	36.15289

PlaQDWinWWTP4	Plastisphere	WWTP	Qingdao	120.34792	36.15289
PlaQDWinWWTP5	Plastisphere	WWTP	Qingdao	120.34792	36.15289

Appendix 3

This section provides a database of the experimental results of the thesis.

1 In situ environmental parameters and nutrients in Hong Kong coastal seawater

Sample ID	**In-situ parameters**				**Nutrients ($\mu g \cdot L^{-1}$)**				
	Temp (ºC)	**Salinity**	**pH**	**DO ($mg\ L^{-1}$)**	**NO_3^-**	**NO_2^-**	**NH_4^+**	**PO_4^{3-}**	**SiO_3^{2-}**
Wet_S1	30.2	17.5	8.22	5.52	16.7	7.47	42.1	31.5	1487
Wet_S2	33.1	24.9	8.50	2.39	7.35	1.52	55.8	48.2	605
Wet_S3	32.9	27.2	8.35	8.75	6.96	1.33	31.6	45.4	263
Wet_S4	31.3	26.2	8.38	5.55	7.89	1.94	41.7	10.8	478
Wet_S5	30.7	31.9	8.26	5.57	7.33	1.60	33.2	8.26	189
Wet_S6	30.8	32.1	8.18	8.21	7.05	1.23	26.0	5.16	206
Wet_S7	30.9	30.2	8.23	5.83	7.15	1.46	48.5	18.3	157
Wet_S8	30.4	30.5	8.25	5.55	7.33	1.39	40.2	8.18	114
Wet_S9	31.6	31.9	8.19	9.50	6.59	1.06	35.9	39.1	228
Wet_S10	30.4	32.6	8.24	9.60	6.75	1.17	55.5	17.3	121
Wet_S11	30.4	32.5	8.29	9.70	6.76	1.38	42.6	11.2	126
Wet_S12	30.2	31.5	8.24	10.2	6.58	0	47.4	7.05	100
Wet_S13	30.3	32.6	8.25	10.0	6.66	1.18	57.1	10.4	89.2
Wet_S14	30.4	31.6	8.25	10.1	6.79	1.85	47.2	11.8	81.3
Wet_S15	30.7	32.0	8.27	9.80	6.80	1.52	31.1	9.03	95.5
Wet_S16	31.5	32.4	8.06	8.10	6.67	1.17	39.9	16.0	189
Wet_S17	28.1	31.3	8.08	5.56	14.3	10.6	62.0	11.8	129
Wet_S18	27.9	31.1	8.10	5.83	15.1	11.4	52.3	19.9	127
Wet_S19	28.9	30.5	8.17	6.48	11.0	6.33	41.2	17.8	100
Wet_S20	29.0	29.6	8.15	6.39	17.9	14.3	42.9	19.5	114
Wet_S21	28.8	29.7	8.15	6.65	17.3	12.5	38.6	19.0	110
Wet_S22	28.4	28.5	8.06	5.07	43.1	39.0	66.1	17.9	250
Wet_S23	29.0	27.3	8.14	6.00	47.4	43.1	75.8	34.9	311
Wet_S24	29.3	24.5	7.96	4.78	86.4	85.2	79.2	64.6	642
Wet_S25	28.1	28.2	7.95	3.74	46.7	42.9	130	49.6	447
Wet_S26	28.1	27.3	7.74	3.27	66.7	64.6	2101	103.0	635
Wet_S27	28.6	28.2	7.97	5.96	39.9	36.4	120	17.1	380
Wet_S28	29.3	28.0	8.15	5.95	113	115	12.7	77.5	864

Wet_S29	29.6	27.9	8.31	7.80	34.9	29.0	99.6	42.7	306
Wet_S30	30.1	28.2	8.31	7.17	23.9	20.1	66.9	47.8	207
Wet_S31	30.1	27.7	8.14	6.67	18.0	13.0	31.1	24.9	143
Wet_S32	30.8	21.3	7.94	5.48	27.1	22.0	77.7	0	170
Wet_S33	30.2	22.1	7.90	5.74	168	175	2.43	86.7	1181
Wet_S34	30.4	23.4	7.96	5.48	122	125	27.6	47.3	660
Wet_S35	30.6	20.3	7.81	5.29	113	114	0	34.9	681
Wet_S36	31.0	18.8	7.88	6.52	149	153	53.4	91.2	992
Dry_S1	19.7	31.8	7.76	6.74	8.12	7.33	85.7	4.80	258
Dry_S2	20.2	31.9	7.82	6.18	3.02	2.40	34.1	3.10	99
Dry_S3	19.6	32.0	7.83	5.91	2.93	1.69	13.1	2.99	105
Dry_S4	19.7	32.1	7.67	6.57	2.30	1.42	13.5	6.36	139
Dry_S5	19.1	32.6	7.90	6.54	2.24	1.56	11.7	8.86	123
Dry_S6	20.1	32.8	8.07	5.92	1.84	0.95	20.5	4.57	87.6
Dry_S7	19.6	32.9	7.98	5.86	1.72	0.42	28.9	5.62	63.4
Dry_S8	18.9	33.0	8.06	5.74	0	0.93	15.8	4.20	63.3
Dry_S9	18.8	33.3	7.92	5.47	2.33	0.93	45.2	2.89	74.6
Dry_S10	20.0	33.6	7.89	5.78	2.53	1.44	34.9	7.61	89.6
Dry_S11	19.5	33.6	7.88	5.72	5.65	4.28	51.9	8.63	113
Dry_S12	19.5	33.9	7.73	5.54	3.82	3.02	26.2	4.91	82.6
Dry_S13	19.5	33.7	7.88	5.87	4.97	3.79	64.5	7.70	108
Dry_S14	19.2	33.9	7.72	5.75	7.29	6.05	50.7	7.67	114
Dry_S15	19.1	33.6	7.83	5.84	6.42	5.42	52.5	7.53	125
Dry_S16	19.3	33.3	7.79	5.99	2.11	1.96	52.3	5.95	96.1
Dry_S17	18.3	33.1	7.86	5.90	6.28	5.69	74.2	6.51	62.4
Dry_S18	18.2	33.4	7.19	5.87	8.62	7.90	85.3	12.0	129
Dry_S19	20.4	34.0	7.78	6.05	3.05	2.32	52.8	5.43	92.6
Dry_S20	18.2	33.3	7.68	6.12	4.84	4.21	43.1	7.84	113
Dry_S21	18.5	33.0	7.85	6.74	2.66	2.01	46.7	5.90	75.0
Dry_S22	19.2	32.7	7.82	6.18	2.79	2.53	125	10.2	69.7
Dry_S23	18.4	33.1	7.72	5.91	4.99	4.26	144	7.87	79.2
Dry_S24	18.7	32.7	8.06	6.57	4.76	4.42	141	16.4	75.5
Dry_S25	18.8	32.5	7.91	6.54	5.61	4.98	226	13.1	74.1
Dry_S26	18.6	33.0	7.87	5.92	7.22	6.12	127	6.36	67.6
Dry_S27	18.9	31.4	7.80	5.86	9.53	8.85	1212	12.7	165
Dry_S28	18.8	32.6	7.87	5.74	6.55	5.59	135	3.81	111
Dry_S29	18.5	32.2	7.78	5.47	4.22	3.50	113	0.12	82.4

Dry_S30	19.1	33.0	7.88	5.78	3.78	3.38	72.0	2.45	75.0
Dry_S31	19.1	33.2	7.86	5.72	4.67	3.92	72.7	1.91	81.8
Dry_S32	18.9	32.9	7.83	5.54	5.17	4.72	72.7	3.18	81.1
Dry_S33	19.6	30.8	7.95	5.87	9.63	8.58	152	10.2	52.1
Dry_S34	19.1	32.9	7.91	5.75	4.27	3.50	45.2	1.28	78.2
Dry_S35	19.7	30.6	7.85	5.84	7.69	6.80	108	9.61	61.9
Dry_S36	19.4	30.4	8.04	5.99	10.8	9.63	135	8.43	76.0

2 Concentrations of LATs in dissolved seawater and SPM in sampling location.

Sample location	**Wet season (ng L^{-1})**								**Dry season (ng L^{-1})**							
	Dissolved phase				SPM				Dissolved phase				SPM			
	PTX-2	OA	GYM	DTX-1	PTX-2	OA	GYM	DTX-1	PTX-2	OA	GYM	DTX-1	PTX-2	OA	GYM	DTX-1
S1	0.85	0.68	0.18	<LOD	0.16	<LOD	0.01	<LOD	0.31	1.23	1.43	0.03	0.18	0.00	0.03	<LOD
S2	0.31	1.12	0.31	<LOD	0.06	<LOD	0.01	<LOD	0.69	1.94	1.76	0.04	0.22	0.00	0.05	<LOD
S3	1.38	0.78	0.18	<LOD	0.07	<LOD	0.01	<LOD	1.01	1.10	0.98	0.05	0.36	0.00	0.07	<LOD
S4	1.39	1.02	0.29	<LOD	0.04	<LOD	0.02	<LOD	1.08	1.89	1.68	0.06	0.29	0.00	0.02	<LOD
S5	1.97	1.03	0.16	<LOD	0.01	<LOD	0.00	<LOD	1.06	1.64	1.39	0.11	0.53	0.00	0.02	<LOD
S6	1.56	1.54	0.23	<LOD	0.05	<LOD	0.03	<LOD	5.38	1.60	0.45	0.64	1.89	0.00	0.01	<LOD
S7	0.10	0.31	0.01	<LOD	0.04	<LOD	0.02	<LOD	0.90	0.63	0.30	0.10	1.21	0.10	0.01	<LOD
S8	0.87	1.51	0.06	<LOD	0.04	<LOD	0.01	<LOD	0.93	0.37	0.26	0.09	1.78	0.11	0.01	<LOD
S9	1.13	0.48	0.34	<LOD	0.11	<LOD	0.00	<LOD	0.58	0.57	0.05	0.06	0.63	0.03	0.00	<LOD
S10	1.83	0.98	0.46	<LOD	0.00	<LOD	0.00	<LOD	0.15	0.18	0.00	0.03	1.69	0.05	0.02	0.11
S11	1.44	0.44	0.74	<LOD	0.28	<LOD	0.01	<LOD	0.41	0.52	0.00	0.04	0.97	0.02	0.00	0.05
S12	1.51	0.11	0.51	<LOD	0.20	<LOD	0.01	<LOD	0.24	0.34	0.06	0.02	0.08	0.01	0.00	<LOD
S13	0.97	0.46	0.78	<LOD	0.20	<LOD	0.01	<LOD	0.65	0.31	0.18	0.04	0.79	0.01	0.00	<LOD
S14	1.29	0.31	0.32	<LOD	0.24	<LOD	0.03	<LOD	0.09	0.18	0.09	0.01	1.25	0.02	0.00	<LOD
S15	1.00	0.39	0.55	<LOD	0.25	<LOD	0.01	<LOD	0.58	0.32	0.00	0.09	1.73	0.04	0.00	<LOD
S16	1.03	0.62	0.43	<LOD	0.18	<LOD	0.01	<LOD	0.93	0.94	0.11	0.12	0.69	0.03	0.00	<LOD
S17	0.50	0.17	0.34	<LOD	0.23	<LOD	0.01	<LOD	1.46	0.73	0.13	0.14	0.58	0.03	0.00	<LOD

S18	0.63	0.09	0.14	<LOD	0.02	<LOD	0.00	<LOD	0.51	0.45	0.10	0.09	0.32	0.00	0.00	<LOD
S19	0.68	0.19	0.16	<LOD	0.14	<LOD	0.00	<LOD	0.02	0.03	0.01	0.00	0.09	0.00	0.00	<LOD
S20	0.48	0.07	0.08	<LOD	0.03	<LOD	0.00	<LOD	0.64	0.38	0.00	0.06	1.69	0.04	0.00	<LOD
S21	0.64	0.08	0.13	<LOD	0.03	<LOD	0.00	<LOD	0.93	0.86	0.00	0.00	0.88	0.03	0.00	<LOD
S22	0.59	0.21	0.14	<LOD	0.05	<LOD	0.01	<LOD	0.88	1.07	0.00	0.00	2.37	0.04	0.00	<LOD
S23	0.78	0.18	0.09	<LOD	0.12	<LOD	0.00	<LOD	0.18	0.56	0.00	0.00	0.80	0.03	0.00	<LOD
S24	0.21	0.37	0.01	<LOD	0.07	<LOD	0.00	<LOD	0.70	0.67	0.01	0.00	1.56	0.03	0.00	<LOD
S25	0.19	0.15	0.05	<LOD	0.07	<LOD	0.02	<LOD	0.18	0.37	0.11	0.00	0.89	0.00	0.00	<LOD
S26	0.55	0.26	0.05	<LOD	0.05	<LOD	0.00	<LOD	0.21	0.34	0.17	0.00	0.84	0.00	0.00	<LOD
S27	0.38	0.38	0.05	<LOD	0.02	<LOD	0.01	<LOD	1.47	0.58	0.17	0.00	1.14	0.00	0.00	<LOD
S28	0.25	0.33	0.02	<LOD	0.10	<LOD	0.02	<LOD	0.19	0.40	0.22	0.02	0.37	0.00	0.00	<LOD
S29	0.2	0.33	0.01	<LOD	0.09	<LOD	0.00	<LOD	0.30	0.33	0.15	0.03	0.82	0.02	0.00	<LOD
S30	0.11	0.15	0.01	<LOD	0.09	<LOD	0.00	<LOD	0.23	0.31	0.10	0.02	0.57	0.00	0.00	<LOD
S31	0.55	0.26	0.05	<LOD	0.14	<LOD	0.02	<LOD	0.57	0.47	0.15	0.04	1.15	0.03	0.00	<LOD
S32	0.12	0.15	0.01	<LOD	0.05	<LOD	0.00	<LOD	0.35	0.42	0.12	0.02	4.90	0.00	0.00	<LOD
S33	0.18	0.08	0.04	<LOD	0.04	<LOD	0.00	<LOD	0.29	0.71	0.03	0.06	1.14	0.02	0.00	<LOD
S34	0.35	0.12	0.02	<LOD	0.05	<LOD	0.00	<LOD	0.35	0.32	0.11	0.01	1.08	0.00	0.00	<LOD
S35	0.2	0.16	0.02	<LOD	0.04	<LOD	0.00	<LOD	0.29	0.79	0.01	0.06	0.74	0.00	0.00	<LOD
S36	0.19	0.12	0.01	<LOD	0.03	<LOD	0.00	<LOD	0.58	0.75	0.00	0.10	1.36	0.00	0.00	<LOD

3 In situ environmental parameters and nutrients of plastisphere surrounding environment.

Sample ID	**Temp**	**pH**	**Salinity**	**DOC**	**NO_3^-**	**PO_4^{3-}**
EnvHKSumMc1	27.8	8.3	32	3.274	2	0.44
EnvHKSumMR1	30.1	8.2	32	7.297	2.4	0.21
EnvHKSumMR2	30.2	8.11	33	5.681	2.9	0.21
EnvHKSumMR3	30.2	8.16	29	19.6	2	0.24
EnvHKSumMR4	30.3	8.16	29	13.48	1.1	0.28
EnvHKSumPort1	31.4	8.01	23	12.97	1.7	0.15
EnvHKSumWWTP2	30.8	7.44	27	3.829	2.6	0.22
EnvHKWinBeach1	18.967	7.81	35.63	5.138	3.3	0.19
EnvHKWinBeach2	18.966	7.8	35.66	5.128	2.3	0.37
EnvHKWinBeach3	18.985	7.81	35.68	5.294	1.5	0.3
EnvHKWinEs1	20.071	7.95	34.95	7.056	1	0.36
EnvHKWinEs2	20.047	7.91	34.98	7.015	1.5	0.28
EnvHKWinEs4	20.02	7.89	34.89	3.996	0.5	0.05
EnvHKWinEs5	19.92	7.9	35.27	4.555	1.2	0.04
EnvHKWinMc1	22.134	7.59	29.54	7.467	1.6	1.71
EnvHKWinMc10	16.164	7.9	34.54	2.81	1.8	0.18
EnvHKWinMc11	17.81	7.99	35.44	2.647	1.7	0.53
EnvHKWinMc12	17.93	7.97	35.48	2.653	1.8	0.57
EnvHKWinMc13	17.998	8.01	35.47	2.656	1	0.35
EnvHKWinMc15	17.982	8	35.43	2.727	1	0.33
EnvHKWinMc2	22.278	7.6	29.43	9.211	1.3	1.59
EnvHKWinMc3	22.345	7.56	29.44	7.804	1.3	1.54
EnvHKWinMc4	21.869	7.41	29.41	8.466	1.8	1.21
EnvHKWinMc5	22.026	7.53	29.69	17.86	1.4	1.15
EnvHKWinMc6	16.185	7.95	34.33	4.122	1.3	0.27
EnvHKWinMc7	16.158	7.91	34.54	3.753	1.8	0.15
EnvHKWinMc8	16.189	7.86	34.54	3.813	1.6	0.27
EnvHKWinMc9	16.099	7.88	34.54	2.73	1.4	0.08
EnvHKWinMR1	15.652	8.01	34.21	2.809	1.7	0.65
EnvHKWinPort1	17.456	7.89	26.19	2.792	1.1	1.65
EnvHKWinPort2	18.402	7.99	34.07	2.751	1	0.46
EnvHKWinPort3	18.689	8.09	33.35	3.046	1.2	0.41
EnvHKWinPort4	18.569	8.02	34.42	2.396	1	0.69

EnvHKWinPort5	18.16	7.99	35.34	4.131	1.2	0.31
EnvHKWinWWTP1	17.881	7.84	35.03	3.843	0.9	0.47
EnvHKWinWWTP2	17.894	7.84	34.58	3.611	0.8	0.58
EnvHKWinWWTP3	18.35	7.83	34.08	4.325	1.6	0.36
EnvHKWinWWTP4	18.113	7.8	33.95	4.191	1.5	0.52
EnvQDSumBeach1	27.5	8.3	24.5	1.3821	0.171	0.189
EnvQDSumBeach2	27.7	8.2	24	1.066	0.035	0.318
EnvQDSumBeach4	27.8	8.2	24.4	2.1802	0.039	0.19
EnvQDSumBeach5	28	8.3	23.9	1.1783	0.085	0.239
EnvQDSumEs1	30.8	8.6	19.6	3.0857	0.498	0.134
EnvQDSumEs2	30.8	8.7	18.2	3.1053	0.619	0.142
EnvQDSumEs3	30.3	8.9	20.6	1.564	0.34	0.222
EnvQDSumMc1	30.7	8.2	23.2	1.8028	0.099	0.211
EnvQDSumMc2	31.3	8.2	23.1	1.7373	0.104	0.308
EnvQDSumMc4	31.1	8.2	23.6	1.5619	0.081	0.293
EnvQDSumMc5	31.6	8.2	23.4	1.685	0.086	0.2
EnvQDSumMR1	28.7	8.3	24.6	2.2215	0.009	0.245
EnvQDSumMR2	28.2	8.3	24.4	1.3169	0.009	0.267
EnvQDSumMR3	28	8.3	24.7	0.6398	0.009	0.332
EnvQDSumPort1	27.8	8.1	23.5	0.6984	0.02	0.209
EnvQDSumPort2	29.5	8.1	24.1	1.5084	0.075	0.218
EnvQDSumPort3	28.2	8.2	24.3	1.6302	0.201	0.151
EnvQDSumPort4	28.9	8.2	24.2	0.5761	0.069	0.272
EnvQDSumPort5	27.8	8.3	24.3	0.08	0.005	0.32
EnvQDSumWWTP1	30.8	7.9	24.3	2.1985	0.272	0.166
EnvQDSumWWTP2	28.5	8.2	24.3	0.9544	0.183	0.223
EnvQDSumWWTP3	28.4	8.2	24.6	1.0662	0.143	0.262
EnvQDSumWWTP4	28.1	8.1	24.8	1.0851	0.076	0.21
EnvQDSumWWTP5	28	8.2	24.8	1.0615	0.051	0.273
EnvQDWinBeach1	6.2	8.5	27.8	6.11	0.008	0.108
EnvQDWinBeach2	7	8.49	27.7	6.155	0.008	0.128
EnvQDWinBeach3	6.6	8.52	27.7	5.297	0.228	0.12
EnvQDWinBeach4	7	8.51	27.7	5.67	0.016	0.082
EnvQDWinBeach5	6.1	8.5	27.8	5.807	0.011	0.003
EnvQDWinEs1	7.2	8.08	11.2	19.015	2.701	0.098
EnvQDWinEs2	7.5	8.1	8.44	19.468	5.555	0.166
EnvQDWinEs3	7.2	8.37	13.7	20.168	5.08	0.116

EnvQDWinEs4	7.4	8.42	8.72	19.153	8.502	0.14
EnvQDWinEs5	7.6	8.38	8.66	18.007	3.181	0.099
EnvQDWinMc1	4.5	8.49	27.3	6.836	0.045	0.152
EnvQDWinMc2	4.6	8.5	28.1	6.532	0.025	0.12
EnvQDWinMc3	5.1	8.52	27.8	6.154	0.042	0.117
EnvQDWinMc4	5	8.5	27.5	4.525	0.027	0.098
EnvQDWinMc5	6.8	8.52	26.9	6.406	0.075	0.106
EnvQDWinMR1	6.2	8.5	27	4.551	0.017	0.001
EnvQDWinMR2	5.5	8.52	26.8	5.511	0.007	0.002
EnvQDWinMR3	6.3	8.49	27.6	5.877	0.001	0.001
EnvQDWinMR4	5.6	8.53	27.2	5.215	0.008	0.003
EnvQDWinMR5	6.1	8.49	26.9	5.876	0.01	0.001
EnvQDWinPort1	6.1	8.46	26.9	7.147	0.008	0.001
EnvQDWinPort2	5.9	8.45	27.3	7.658	0.018	0.001
EnvQDWinPort3	5.7	8.44	27.6	11.553	0.036	0.001
EnvQDWinPort4	6.3	8.49	27.7	3.473	0.066	0.001
EnvQDWinPort5	5.7	8.46	27.2	3.855	0.121	0.001
EnvQDWinWWTP1	5.7	8.42	27	8.437	0.251	0.079
EnvQDWinWWTP2	6.3	8.44	26.7	7.571	0.285	0.093
EnvQDWinWWTP3	6	8.44	26.7	8.144	0.357	0.074
EnvQDWinWWTP4	6.7	8.44	26.7	7.348	0.327	0.081
EnvQDWinWWTP5	6.2	8.42	26.7	7.878	0.245	0.117

4 Polymer identification of plastics.

Site	Polymer	HQI	Site	Polymer	HQI
Beach	Resin	81.22	WWTP	Polystyrene	72.73
	Ethylene propylene copolymer	81.24		Polypropylenes	72.89
	Polypropylenes	82.93		Polypropylenes	78.85
	Polypropylenes	86.63		Propylene-ethylene copolymer	85.7
	Polypropylenes	91.8		Polypropylene-co-ethylene	94.18
Reserve	Propylene-ethylene copolymer	74.43	Port-1	Polystyrene	79.85
	Polyethylene terephthalate	76.65		Ethylene-Propylene copolymer	82.67
	Polyethylenes	82.9		Polyethylenes	85.68
	Polyamide-6,6	91.6		Polypropylenes	86.96
	Low-moecular	91.82		Polyethylenes	88.67

	polyethylene				
Port-2	Polyethylenes	76.74	Estuary-1	Polyethylene, chlorinated	73.38
	Polyethylene-co-Propylene copolymer	81.87		Polyethylenes	86.42
	Polypropylenes	88.33		Ethylene copolymer	87.78
	Polyethylene Terephthalate	91.33		Polyethylenes	90.04
	Polyethylenes	92.28		Polypropylene isotactic	90.85
Estuary-2	Polyethylenes	81.21		Low-molecular polyethylene	91.42
	Polypropylenes	85.46	Marine culture-1	Polypropylene	79.74
	Polyethylene Terephthalate	90.05		Polyethylenes	81.71
	Polyethylenes	90.47		Polyethylene Terephthalate	82.12
	Polyethylenes	90.72		Propylene-ethylene copolymer	83.88
Marine culture-5	Polystyrene	72.75		Polypropylenes	84.54
	Polypropylenes	79.7		Polyethylene-co-Propylene copolymer	89.68
	Polyester	81.05		Ethylene-propylene copolymer	93.53
	Polypropylenes	82	Marine culture-6	Polyethylene Terephthalate	70.28
	Butadiene rubber	84.82		Polypropylenes	80
	Polyethylene-co-Propylene copolymer	92.72		Polystyrenes	81.09
	Ethylene-propylene copolymer	93.78		Polypropylenes	89.8
Marine culture-10	Polystyrene	74.07		Polypropylenes	93.12
	Polyester urethane	74.77			
	Polyethylenes	82.21			
	Polypropylenes	85.62			
	Polypropylenes	90.83			
	Polyethylenes	90.9			

Appendix 4

This section provides bioinformatic and statistical results of the thesis.

1 The differential ASVs between the plastisphere (enriched) and the ambient (depleted) phytoplankton community.

ID	$\log_2$CPM	Level	ID	$\log_2$CPM	Level	ID	$\log_2$CPM	Level	ID	$\log_2$CPM	Level
ASV_51	14.27694	Enriched	ASV_873	9.04205	Enriched	ASV_1195	7.8738	Depleted	ASV_686	9.07972	Depleted
ASV_29	14.8988	Enriched	ASV_2505	7.04359	Enriched	ASV_277	10.64113	Depleted	ASV_1315	7.44628	Depleted
ASV_370	11.0917	Enriched	ASV_792	8.70156	Enriched	ASV_745	8.30355	Depleted	ASV_279	10.26384	Depleted
ASV_239	12.184	Enriched	ASV_1885	7.89681	Enriched	ASV_304	10.29413	Depleted	ASV_998	8.64273	Depleted
ASV_135	12.90295	Enriched	ASV_3181	6.74108	Enriched	ASV_160	11.56931	Depleted	ASV_932	7.85574	Depleted
ASV_44	14.19868	Enriched	ASV_2933	6.77713	Enriched	ASV_1080	7.7326	Depleted	ASV_493	9.3872	Depleted
ASV_190	12.09706	Enriched	ASV_195	11.08615	Enriched	ASV_663	8.69255	Depleted	ASV_682	8.0979	Depleted
ASV_38	14.87331	Enriched	ASV_2281	7.11727	Enriched	ASV_1068	7.48669	Depleted	ASV_1211	7.79563	Depleted
ASV_249	12.07192	Enriched	ASV_985	8.51717	Enriched	ASV_15	15.23821	Depleted	ASV_1555	7.23997	Depleted
ASV_1358	8.28062	Enriched	ASV_1326	8.17306	Enriched	ASV_653	8.94893	Depleted	ASV_4271	9.31407	Depleted
ASV_457	10.44725	Enriched	ASV_1152	7.91642	Enriched	ASV_1239	7.31894	Depleted	ASV_126	11.1056	Depleted
ASV_828	9.12886	Enriched	ASV_644	12.09975	Enriched	ASV_639	9.81806	Depleted	ASV_1047	7.83228	Depleted
ASV_827	9.39247	Enriched	ASV_561	9.64329	Enriched	ASV_1304	7.33697	Depleted	ASV_1117	7.7183	Depleted
ASV_162	12.36436	Enriched	ASV_902	8.86777	Enriched	ASV_247	10.6357	Depleted	ASV_318	10.18774	Depleted
ASV_423	11.49086	Enriched	ASV_1161	8.11915	Enriched	ASV_555	9.03394	Depleted	ASV_1222	7.40094	Depleted
ASV_707	9.44698	Enriched	ASV_2244	7.06992	Enriched	ASV_810	8.99102	Depleted	ASV_1034	7.69751	Depleted

ASV_208	12.20323	Enriched	ASV_188	12.1253	Enriched	ASV_168	11.43672	Depleted	ASV_1038	7.57413	Depleted
ASV_55	14.93803	Enriched	ASV_492	9.78311	Enriched	ASV_634	8.73382	Depleted	ASV_972	8.37969	Depleted
ASV_118	13.03003	Enriched	ASV_246	11.80886	Enriched	ASV_861	8.10797	Depleted	ASV_288	10.61649	Depleted
ASV_70	13.84342	Enriched	ASV_1249	8.07863	Enriched	ASV_788	8.07142	Depleted	ASV_1054	7.94009	Depleted
ASV_137	12.55404	Enriched	ASV_1032	9.29455	Enriched	ASV_552	8.75201	Depleted	ASV_167	12.09774	Depleted
ASV_240	11.36267	Enriched	ASV_705	9.02664	Enriched	ASV_60	12.75308	Depleted	ASV_1434	7.51513	Depleted
ASV_363	10.78133	Enriched	ASV_1614	7.26577	Enriched	ASV_352	10.32539	Depleted	ASV_940	7.9978	Depleted
ASV_36	15.05311	Enriched	ASV_933	8.63138	Enriched	ASV_765	8.8643	Depleted	ASV_627	8.80169	Depleted
ASV_1324	8.22985	Enriched	ASV_1656	7.59571	Enriched	ASV_502	9.39861	Depleted	ASV_521	9.55057	Depleted
ASV_1467	8.26929	Enriched	ASV_1512	7.49688	Enriched	ASV_336	10.81066	Depleted	ASV_916	7.97616	Depleted
ASV_171	12.5131	Enriched	ASV_325	10.38047	Enriched	ASV_64	12.96203	Depleted	ASV_384	9.94556	Depleted
ASV_18	15.20766	Enriched	ASV_2056	7.2178	Enriched	ASV_1140	7.6471	Depleted	ASV_1042	7.9035	Depleted
ASV_224	11.94717	Enriched	ASV_1591	9.32573	Enriched	ASV_367	10.37899	Depleted	ASV_1115	8.0868	Depleted
ASV_1287	7.99647	Enriched	ASV_1357	8.20289	Enriched	ASV_749	8.2248	Depleted	ASV_148	11.30772	Depleted
ASV_150	12.21365	Enriched	ASV_1010	8.64459	Enriched	ASV_287	10.48627	Depleted	ASV_856	8.18199	Depleted
ASV_499	10.18812	Enriched	ASV_4278	6.85903	Enriched	ASV_438	10.61921	Depleted	ASV_1063	7.67085	Depleted
ASV_405	10.17404	Enriched	ASV_1146	8.40051	Enriched	ASV_726	8.57128	Depleted	ASV_812	8.32538	Depleted
ASV_117	12.93695	Enriched	ASV_1708	7.53906	Enriched	ASV_440	9.12727	Depleted	ASV_800	8.53142	Depleted
ASV_1888	7.28229	Enriched	ASV_2144	7.07713	Enriched	ASV_942	7.89887	Depleted	ASV_63	13.04906	Depleted
ASV_1380	8.38098	Enriched	ASV_2020	7.37874	Enriched	ASV_223	10.52093	Depleted	ASV_329	10.30281	Depleted
ASV_229	11.11439	Enriched	ASV_1009	8.19085	Enriched	ASV_631	8.97038	Depleted	ASV_1345	7.2506	Depleted
ASV_1433	7.73095	Enriched	ASV_1806	7.39647	Enriched	ASV_214	11.40476	Depleted	ASV_599	9.24836	Depleted

ASV_121	13.10264	Enriched	ASV_28	13.84634	Enriched	ASV_197	11.10437	Depleted	ASV_814	8.12084	Depleted
ASV_761	9.28349	Enriched	ASV_2967	7.0915	Enriched	ASV_443	9.45095	Depleted	ASV_1029	7.9115	Depleted
ASV_922	8.37668	Enriched	ASV_1791	7.43835	Enriched	ASV_192	10.75176	Depleted	ASV_673	8.37615	Depleted
ASV_1506	8.05922	Enriched	ASV_259	10.94241	Enriched	ASV_69	12.29824	Depleted	ASV_1027	7.77894	Depleted
ASV_677	9.45154	Enriched	ASV_2774	6.71779	Enriched	ASV_925	7.50168	Depleted	ASV_935	7.92239	Depleted
ASV_337	10.97035	Enriched	ASV_179	13.61298	Enriched	ASV_672	9.17364	Depleted	ASV_1427	7.28252	Depleted
ASV_799	9.01338	Enriched	ASV_886	8.7673	Enriched	ASV_754	8.29847	Depleted	ASV_99	11.51951	Depleted
ASV_477	10.05915	Enriched	ASV_1124	8.5722	Enriched	ASV_306	10.52432	Depleted	ASV_772	8.80826	Depleted
ASV_1605	7.60851	Enriched	ASV_1170	8.22554	Enriched	ASV_210	10.36778	Depleted	ASV_1127	7.52184	Depleted
ASV_1341	8.15287	Enriched	ASV_703	9.3964	Enriched	ASV_750	8.45302	Depleted	ASV_1217	7.91768	Depleted
ASV_376	10.24316	Enriched	ASV_1739	10.1386	Enriched	ASV_756	8.37702	Depleted	ASV_1374	7.42831	Depleted
ASV_204	11.89785	Enriched	ASV_572	9.76255	Enriched	ASV_658	8.72319	Depleted	ASV_512	9.81602	Depleted
ASV_955	9.02952	Enriched	ASV_583	7.45696	Enriched	ASV_365	10.15589	Depleted	ASV_1060	7.76186	Depleted
ASV_1962	7.30342	Enriched	ASV_2969	6.76876	Enriched	ASV_1355	7.51093	Depleted	ASV_693	8.61299	Depleted
ASV_1302	8.91889	Enriched	ASV_2046	7.53915	Enriched	ASV_713	8.13642	Depleted	ASV_453	9.65067	Depleted
ASV_189	11.96604	Enriched	ASV_157	11.94915	Depleted	ASV_737	7.85495	Depleted	ASV_581	9.35887	Depleted
ASV_93	12.77542	Enriched	ASV_6	16.18883	Depleted	ASV_193	11.65696	Depleted	ASV_995	8.43104	Depleted
ASV_387	10.82676	Enriched	ASV_107	12.29854	Depleted	ASV_1391	7.07378	Depleted	ASV_1182	7.43642	Depleted
ASV_850	8.89894	Enriched	ASV_22	14.12823	Depleted	ASV_149	11.83658	Depleted	ASV_1252	7.7411	Depleted
ASV_1457	7.78917	Enriched	ASV_221	10.75624	Depleted	ASV_533	9.17069	Depleted	ASV_1228	7.72285	Depleted
ASV_1090	7.91257	Enriched	ASV_98	12.41815	Depleted	ASV_481	8.92712	Depleted	ASV_130	12.18017	Depleted
ASV_1446	7.80209	Enriched	ASV_116	12.17288	Depleted	ASV_297	10.81258	Depleted	ASV_4	16.76444	Depleted

ASV_1774	7.27277	Enriched	ASV_410	9.72433	Depleted	ASV_565	8.60153	Depleted	ASV_882	8.23296	Depleted
ASV_219	11.78763	Enriched	ASV_432	9.70195	Depleted	ASV_217	10.65817	Depleted	ASV_1162	8.04574	Depleted
ASV_592	9.83439	Enriched	ASV_341	9.8971	Depleted	ASV_742	8.02348	Depleted	ASV_636	8.57681	Depleted
ASV_734	9.30324	Enriched	ASV_434	10.00243	Depleted	ASV_1259	7.50861	Depleted	ASV_1462	7.1069	Depleted
ASV_1296	7.89483	Enriched	ASV_87	12.62018	Depleted	ASV_1580	7.38008	Depleted	ASV_905	7.983	Depleted
ASV_747	9.35401	Enriched	ASV_271	10.63706	Depleted	ASV_250	10.78597	Depleted	ASV_460	9.36927	Depleted
ASV_324	11.04965	Enriched	ASV_1022	9.38931	Depleted	ASV_1095	7.67141	Depleted	ASV_675	8.40292	Depleted
ASV_49	14.0219	Enriched	ASV_265	15.26419	Depleted	ASV_511	9.24796	Depleted	ASV_1103	7.86694	Depleted
ASV_1366	7.6314	Enriched	ASV_586	11.34399	Depleted	ASV_248	10.82689	Depleted	ASV_1153	7.99099	Depleted
ASV_202	12.00932	Enriched	ASV_522	9.45322	Depleted	ASV_253	11.20338	Depleted	ASV_1305	7.54442	Depleted
ASV_422	10.03416	Enriched	ASV_258	10.82056	Depleted	ASV_735	8.32936	Depleted	ASV_500	9.69932	Depleted
ASV_1996	7.39775	Enriched	ASV_147	13.94487	Depleted	ASV_100	12.40005	Depleted	ASV_21	15.04211	Depleted
ASV_392	10.116	Enriched	ASV_447	9.67732	Depleted	ASV_411	10.2753	Depleted	ASV_1093	8.1428	NotSig
ASV_963	8.85196	Enriched	ASV_20	14.17246	Depleted	ASV_233	11.36921	Depleted	ASV_305	8.62823	NotSig
ASV_428	10.63665	Enriched	ASV_23	14.51835	Depleted	ASV_452	9.52771	Depleted	ASV_591	9.43978	NotSig
ASV_1294	8.00758	Enriched	ASV_429	9.61736	Depleted	ASV_997	7.96913	Depleted	ASV_559	9.34428	NotSig
ASV_787	9.17344	Enriched	ASV_2	17.01591	Depleted	ASV_266	10.75849	Depleted	ASV_371	10.42992	NotSig
ASV_299	11.20664	Enriched	ASV_268	10.70847	Depleted	ASV_957	7.47824	Depleted	ASV_946	8.52128	NotSig
ASV_83	13.25921	Enriched	ASV_1181	7.37858	Depleted	ASV_1186	7.27626	Depleted	ASV_731	8.8513	NotSig
ASV_951	8.50808	Enriched	ASV_73	13.06342	Depleted	ASV_1238	7.12332	Depleted	ASV_1521	7.96726	NotSig
ASV_1441	7.8537	Enriched	ASV_1052	8.03395	Depleted	ASV_151	12.02405	Depleted	ASV_541	9.28014	NotSig
ASV_2189	7.2164	Enriched	ASV_338	9.64991	Depleted	ASV_1024	7.86271	Depleted	ASV_1201	7.56929	NotSig

ASV_496	9.81768	Enriched	ASV_85	12.67127	Depleted	ASV_1236	7.45118	Depleted	ASV_895	8.16899	NotSig
ASV_2018	7.04847	Enriched	ASV_456	9.70514	Depleted	ASV_1048	8.46731	Depleted	ASV_965	8.41456	NotSig
ASV_1317	7.59799	Enriched	ASV_725	8.15868	Depleted	ASV_1370	7.14949	Depleted	ASV_296	10.75604	NotSig
ASV_1267	8.12369	Enriched	ASV_775	8.74411	Depleted	ASV_59	12.40503	Depleted	ASV_1447	7.41949	NotSig
ASV_1050	8.25887	Enriched	ASV_865	7.70372	Depleted	ASV_468	9.29335	Depleted	ASV_538	9.87408	NotSig
ASV_1670	7.81662	Enriched	ASV_466	9.49389	Depleted	ASV_732	8.64161	Depleted	ASV_1311	8.06813	NotSig
ASV_1338	8.24955	Enriched	ASV_529	9.44002	Depleted	ASV_588	9.2224	Depleted	ASV_1531	7.30823	NotSig
ASV_1501	8.21046	Enriched	ASV_216	10.98475	Depleted	ASV_907	8.05547	Depleted	ASV_1527	7.55005	NotSig
ASV_444	10.10465	Enriched	ASV_628	8.75981	Depleted	ASV_662	9.19416	Depleted	ASV_630	9.71509	NotSig
ASV_2199	7.14436	Enriched	ASV_19	14.22622	Depleted	ASV_506	9.81204	Depleted	ASV_885	8.49645	NotSig
ASV_790	9.25156	Enriched	ASV_1213	7.50203	Depleted	ASV_274	10.91048	Depleted	ASV_571	8.82669	NotSig
ASV_1248	8.03812	Enriched	ASV_1137	7.89911	Depleted	ASV_825	8.65034	Depleted	ASV_323	10.7291	NotSig
ASV_710	9.47399	Enriched	ASV_475	10.12785	Depleted	ASV_417	10.13119	Depleted	ASV_574	9.55941	NotSig
ASV_758	9.12953	Enriched	ASV_446	9.92227	Depleted	ASV_519	9.23832	Depleted	ASV_733	8.3549	NotSig
ASV_2130	7.21328	Enriched	ASV_212	11.57344	Depleted	ASV_1025	7.75219	Depleted	ASV_1330	7.18894	NotSig
ASV_1882	7.37305	Enriched	ASV_364	10.12793	Depleted	ASV_205	11.11638	Depleted	ASV_1766	7.32748	NotSig
ASV_868	8.66584	Enriched	ASV_7	16.24191	Depleted	ASV_926	8.17798	Depleted	ASV_1126	7.89449	NotSig
ASV_720	9.42483	Enriched	ASV_312	10.15841	Depleted	ASV_822	8.77058	Depleted	ASV_1573	7.38997	NotSig
ASV_1482	7.48312	Enriched	ASV_515	15.25519	Depleted	ASV_154	11.92886	Depleted	ASV_1843	7.24919	NotSig
ASV_977	8.62317	Enriched	ASV_43	13.36514	Depleted	ASV_971	7.99359	Depleted	ASV_1189	8.25312	NotSig
ASV_818	8.3949	Enriched	ASV_391	10.07661	Depleted	ASV_401	10.25279	Depleted	ASV_349	8.76482	NotSig
ASV_1114	8.00708	Enriched	ASV_201	10.75577	Depleted	ASV_920	8.03871	Depleted	ASV_56	10.98571	NotSig

ASV_1454	7.9037	Enriched	ASV_585	8.92592	Depleted	ASV_441	9.60772	Depleted	ASV_158	11.60468	NotSig
ASV_2831	6.80028	Enriched	ASV_412	12.24663	Depleted	ASV_689	9.11577	Depleted	ASV_602	9.2051	NotSig
ASV_261	10.45364	Enriched	ASV_697	8.54856	Depleted	ASV_1588	7.34621	Depleted	ASV_1172	7.94028	NotSig
ASV_2420	8.03003	Enriched	ASV_448	9.53378	Depleted	ASV_1764	7.15589	Depleted	ASV_235	8.73525	NotSig
ASV_199	11.16654	Enriched	ASV_373	9.98695	Depleted	ASV_1119	7.36238	Depleted	ASV_276	8.55702	NotSig
ASV_1171	8.19338	Enriched	ASV_615	8.5363	Depleted	ASV_779	8.7877	Depleted	ASV_1312	7.96585	NotSig
ASV_1129	8.35357	Enriched	ASV_608	9.20426	Depleted	ASV_131	11.99109	Depleted	ASV_1877	7.27459	NotSig
ASV_927	8.66013	Enriched	ASV_664	8.4753	Depleted	ASV_80	12.96885	Depleted	ASV_836	8.00303	NotSig
ASV_290	10.93584	Enriched	ASV_437	9.54993	Depleted	ASV_485	9.87469	Depleted	ASV_721	8.21536	NotSig
ASV_504	8.12233	Enriched	ASV_763	8.50829	Depleted	ASV_326	10.24109	Depleted	ASV_1183	7.91912	NotSig
ASV_1207	8.00318	Enriched	ASV_284	10.4765	Depleted	ASV_540	9.59456	Depleted			
ASV_1478	7.84489	Enriched	ASV_234	11.16498	Depleted	ASV_381	10.4144	Depleted			
ASV_778	8.92695	Enriched	ASV_528	8.75337	Depleted	ASV_209	11.20881	Depleted			

2 Identified harmful and toxic ASVs in plastisphere and ambient seawater.

ID	**Species**	**Type**	**ID**	**Species**	**Type**	**ID**	**Species**	**Type**
ASV_19	*Akashiwo sanguinea*	Toxic	ASV_3021	*Dunaliella salina*	Harmful	ASV_214	*Leptocylindrus danicus*	Harmful
ASV_3137	*Akashiwo sanguinea*	Toxic	ASV_3079	*Dunaliella salina*	Harmful	ASV_2803	*Leptocylindrus danicus*	Harmful
ASV_1222	*Alexandrium andersonii*	Toxic	ASV_3131	*Dunaliella salina*	Harmful	ASV_126	*Levanderina fissa*	Harmful
ASV_3341	*Alexandrium andersonii*	Toxic	ASV_3115	*Dunaliella salina*	Harmful	ASV_1349	*Lingulodinium polyedra*	Toxic
ASV_2215	*Alexandrium cohorticula*	Harmful	ASV_3164	*Dunaliella salina*	Harmful	ASV_2274	*Lingulodinium polyedra*	Toxic
ASV_754	*Alexandrium hiranoi*	Toxic	ASV_3187	*Dunaliella salina*	Harmful	ASV_3681	*Margalefidinium fulvescens*	Toxic
ASV_233	*Alexandrium ostenfeldii*	Toxic	ASV_3301	*Dunaliella salina*	Harmful	ASV_800	*Margalefidinium polykrikoides*	Toxic
ASV_686	*Alexandrium ostenfeldii*	Toxic	ASV_3348	*Dunaliella salina*	Harmful	ASV_1189	*Nitzschia longissima*	Harmful
ASV_167	*Alexandrium tamarense*	Toxic	ASV_3358	*Dunaliella salina*	Harmful	ASV_1739	*Nitzschia longissima*	Harmful
ASV_485	*Alexandrium tamarense*	Toxic	ASV_3363	*Dunaliella salina*	Harmful	ASV_69	*Noctiluca scintillans*	Harmful
ASV_2400	*Amphidinium klebsii*	Toxic	ASV_3405	*Dunaliella salina*	Harmful	ASV_100	*Noctiluca scintillans*	Harmful
ASV_814	*Asterionellopsis glacialis*	Harmful	ASV_3584	*Dunaliella salina*	Harmful	ASV_223	*Noctiluca scintillans*	Harmful
ASV_1589	*Aureococcus anophagefferens*	Harmful	ASV_3631	*Dunaliella salina*	Harmful	ASV_3551	*Noctiluca scintillans*	Harmful
ASV_1809	*Aureococcus anophagefferens*	Harmful	ASV_3840	*Dunaliella salina*	Harmful	ASV_107	*Plagioselmis prolonga*	Harmful
ASV_3590	*Aureococcus anophagefferens*	Harmful	ASV_3884	*Dunaliella salina*	Harmful	ASV_441	*Plagioselmis prolonga*	Harmful
ASV_935	*Azadinium poporum*	Toxic	ASV_3891	*Dunaliella salina*	Harmful	ASV_1115	*Plagioselmis prolonga*	Harmful
ASV_336	*Chaetoceros curvisetus*	Harmful	ASV_3925	*Dunaliella salina*	Harmful	ASV_1335	*Plagioselmis prolonga*	Harmful
ASV_1788	*Chaetoceros debilis*	Harmful	ASV_3943	*Dunaliella salina*	Harmful	ASV_304	*Polykrikos hartmannii*	Toxic
ASV_212	*Chaetoceros diadema*	Harmful	ASV_3956	*Dunaliella salina*	Harmful	ASV_411	*Prorocentrum cordatum*	Toxic
ASV_3005	*Chaetoceros diadema*	Harmful	ASV_4094	*Dunaliella salina*	Harmful	ASV_452	*Prorocentrum cordatum*	Toxic

ASV_2221	*Chaetoceros lorenzianus*	Harmful	ASV_4181	*Dunaliella salina*	Harmful	ASV_512	*Prorocentrum cordatum*	Toxic
ASV_4750	*Chaetoceros pseudocurvisetus*	Harmful	ASV_4193	*Dunaliella salina*	Harmful	ASV_572	*Prorocentrum cordatum*	Toxic
ASV_3399	*Chaetoceros rostratus*	Harmful	ASV_4194	*Dunaliella salina*	Harmful	ASV_733	*Prorocentrum cordatum*	Toxic
ASV_2824	*Chaetoceros simplex*	Harmful	ASV_4205	*Dunaliella salina*	Harmful	ASV_731	*Prorocentrum cordatum*	Toxic
ASV_2330	*Chaetoceros socialis*	Harmful	ASV_4211	*Dunaliella salina*	Harmful	ASV_749	*Prorocentrum cordatum*	Toxic
ASV_2883	*Chaetoceros socialis*	Harmful	ASV_4277	*Dunaliella salina*	Harmful	ASV_1038	*Prorocentrum cordatum*	Toxic
ASV_2	*Chaetoceros tenuissimus*	Harmful	ASV_4311	*Dunaliella salina*	Harmful	ASV_1315	*Prorocentrum cordatum*	Toxic
ASV_2533	*Chaetoceros throndsenii*	Harmful	ASV_4338	*Dunaliella salina*	Harmful	ASV_1464	*Prorocentrum cordatum*	Toxic
ASV_3299	*Chrysochromulina leadbeateri*	Toxic	ASV_4383	*Dunaliella salina*	Harmful	ASV_1812	*Prorocentrum cordatum*	Toxic
ASV_4113	*Chrysochromulina leadbeateri*	Toxic	ASV_4406	*Dunaliella salina*	Harmful	ASV_1877	*Prorocentrum cordatum*	Toxic
ASV_4878	*Chrysochromulina leadbeateri*	Toxic	ASV_4437	*Dunaliella salina*	Harmful	ASV_2213	*Prorocentrum cordatum*	Toxic
ASV_296	*Coscinodiscus radiatus*	Harmful	ASV_4459	*Dunaliella salina*	Harmful	ASV_2506	*Prorocentrum cordatum*	Toxic
ASV_1236	*Coscinodiscus radiatus*	Harmful	ASV_4704	*Dunaliella salina*	Harmful	ASV_2784	*Prorocentrum cordatum*	Toxic
ASV_2862	*Coscinodiscus radiatus*	Harmful	ASV_4743	*Dunaliella salina*	Harmful	ASV_2869	*Prorocentrum cordatum*	Toxic
ASV_6	*Cyclotella meneghiniana*	Harmful	ASV_4772	*Dunaliella salina*	Harmful	ASV_3347	*Prorocentrum cordatum*	Toxic
ASV_99	*Cyclotella meneghiniana*	Harmful	ASV_4947	*Dunaliella salina*	Harmful	ASV_3481	*Prorocentrum cordatum*	Toxic
ASV_148	*Cyclotella meneghiniana*	Harmful	ASV_4993	*Dunaliella salina*	Harmful	ASV_3488	*Prorocentrum cordatum*	Toxic
ASV_216	*Cyclotella meneghiniana*	Harmful	ASV_5114	*Dunaliella salina*	Harmful	ASV_3605	*Prorocentrum cordatum*	Toxic
ASV_438	*Cyclotella meneghiniana*	Harmful	ASV_160	*Eucampia zodiacus*	Harmful	ASV_3689	*Prorocentrum cordatum*	Toxic
ASV_810	*Cyclotella meneghiniana*	Harmful	ASV_453	*Eucampia zodiacus*	Harmful	ASV_3816	*Prorocentrum cordatum*	Toxic
ASV_4422	*Cyclotella meneghiniana*	Harmful	ASV_1162	*Eucampia zodiacus*	Harmful	ASV_4252	*Prorocentrum cordatum*	Toxic
ASV_118	*Cylindrotheca closterium*	Harmful	ASV_365	*Fibrocapsa japonica*	Toxic	ASV_4310	*Prorocentrum cordatum*	Toxic
ASV_179	*Cylindrotheca closterium*	Harmful	ASV_1576	*Fibrocapsa japonica*	Toxic	ASV_4350	*Prorocentrum cordatum*	Toxic
ASV_189	*Cylindrotheca closterium*	Harmful	ASV_2055	*Fibrocapsa japonica*	Toxic	ASV_4451	*Prorocentrum cordatum*	Toxic

ASV_246	*Cylindrotheca closterium*	Harmful	ASV_2536	*Fibrocapsa japonica*	Toxic	ASV_4910	*Prorocentrum cordatum*	Toxic
ASV_423	*Cylindrotheca closterium*	Harmful	ASV_3897	*Fibrocapsa japonica*	Toxic	ASV_636	*Prorocentrum rhathymum*	Toxic
ASV_559	*Cylindrotheca closterium*	Harmful	ASV_4922	*Gonyaulax polygramma*	Harmful	ASV_1859	*Prorocentrum rhathymum*	Toxic
ASV_631	*Cylindrotheca closterium*	Harmful	ASV_2319	*Gonyaulax spinifera*	Toxic	ASV_2415	*Prorocentrum rhathymum*	Toxic
ASV_799	*Cylindrotheca closterium*	Harmful	ASV_3954	*Gonyaulax spinifera*	Toxic	ASV_265	*Prorocentrum triestinum*	Harmful
ASV_778	*Cylindrotheca closterium*	Harmful	ASV_3287	*Gonyaulax verior*	Harmful	ASV_1837	*Prorocentrum triestinum*	Harmful
ASV_873	*Cylindrotheca closterium*	Harmful	ASV_586	*Guinardia flaccida*	Harmful	ASV_4514	*Protoceratium reticulatum*	Toxic
ASV_1341	*Cylindrotheca closterium*	Harmful	ASV_1182	*Gymnodinium catenatum*	Toxic	ASV_20	*Protodinium simplex*	Harmful
ASV_1467	*Cylindrotheca closterium*	Harmful	ASV_1511	*Gymnodinium catenatum*	Toxic	ASV_284	*Protodinium simplex*	Harmful
ASV_1882	*Cylindrotheca closterium*	Harmful	ASV_3218	*Gymnodinium catenatum*	Toxic	ASV_448	*Protodinium simplex*	Harmful
ASV_1946	*Cylindrotheca closterium*	Harmful	ASV_171	*Halamphora coffeiformis*	Harmful	ASV_2431	*Protodinium simplex*	Harmful
ASV_2966	*Cylindrotheca closterium*	Harmful	ASV_208	*Halamphora coffeiformis*	Harmful	ASV_3445	*Protoperidinium crassipes*	Toxic
ASV_2985	*Cylindrotheca closterium*	Harmful	ASV_239	*Halamphora coffeiformis*	Harmful	ASV_693	*Prymnesium parvum*	Toxic
ASV_4397	*Cylindrotheca closterium*	Harmful	ASV_370	*Halamphora coffeiformis*	Harmful	ASV_1399	*Prymnesium parvum*	Toxic
ASV_4496	*Cylindrotheca closterium*	Harmful	ASV_538	*Halamphora coffeiformis*	Harmful	ASV_1425	*Prymnesium parvum*	Toxic
ASV_4847	*Cylindrotheca closterium*	Harmful	ASV_707	*Halamphora coffeiformis*	Harmful	ASV_1944	*Prymnesium parvum*	Toxic
ASV_234	*Dictyocha fibula*	Harmful	ASV_720	*Halamphora coffeiformis*	Harmful	ASV_2234	*Prymnesium parvum*	Toxic
ASV_3130	*Dinophysis acuminata*	Toxic	ASV_747	*Halamphora coffeiformis*	Harmful	ASV_3232	*Prymnesium parvum*	Toxic
ASV_4797	*Dinophysis acuminata*	Toxic	ASV_955	*Halamphora coffeiformis*	Harmful	ASV_3670	*Prymnesium parvum*	Toxic
ASV_1580	*Dinophysis miles*	Toxic	ASV_965	*Halamphora coffeiformis*	Harmful	ASV_4166	*Prymnesium parvum*	Toxic
ASV_4135	*Dinophysis miles*	Toxic	ASV_1114	*Halamphora coffeiformis*	Harmful	ASV_4424	*Prymnesium parvum*	Toxic
ASV_85	*Dunaliella salina*	Harmful	ASV_1124	*Halamphora coffeiformis*	Harmful	ASV_4967	*Prymnesium parvum*	Toxic
ASV_193	*Dunaliella salina*	Harmful	ASV_1172	*Halamphora coffeiformis*	Harmful	ASV_4972	*Prymnesium parvum*	Toxic
ASV_204	*Dunaliella salina*	Harmful	ASV_1207	*Halamphora coffeiformis*	Harmful	ASV_5053	*Prymnesium parvum*	Toxic

ASV_229	*Dunaliella salina*	Harmful	ASV_1248	*Halamphora coffeiformis*	Harmful	ASV_653	*Prymnesium polylepis*	Toxic
ASV_253	*Dunaliella salina*	Harmful	ASV_1287	*Halamphora coffeiformis*	Harmful	ASV_1137	*Prymnesium polylepis*	Toxic
ASV_274	*Dunaliella salina*	Harmful	ASV_1312	*Halamphora coffeiformis*	Harmful	ASV_2682	*Prymnesium polylepis*	Toxic
ASV_364	*Dunaliella salina*	Harmful	ASV_1324	*Halamphora coffeiformis*	Harmful	ASV_4585	*Prymnesium polylepis*	Toxic
ASV_417	*Dunaliella salina*	Harmful	ASV_1358	*Halamphora coffeiformis*	Harmful	ASV_1119	*Pseudo-nitzschia australis*	Toxic
ASV_437	*Dunaliella salina*	Harmful	ASV_1501	*Halamphora coffeiformis*	Harmful	ASV_2571	*Pseudo-nitzschia australis*	Toxic
ASV_506	*Dunaliella salina*	Harmful	ASV_1854	*Halamphora coffeiformis*	Harmful	ASV_571	*Pseudo-nitzschia cuspidata*	Toxic
ASV_585	*Dunaliella salina*	Harmful	ASV_1962	*Halamphora coffeiformis*	Harmful	ASV_23	*Pseudo-nitzschia delicatissima*	Toxic
ASV_599	*Dunaliella salina*	Harmful	ASV_2056	*Halamphora coffeiformis*	Harmful	ASV_4271	*Pseudo-nitzschia delicatissima*	Toxic
ASV_634	*Dunaliella salina*	Harmful	ASV_2141	*Halamphora coffeiformis*	Harmful	ASV_4448	*Pseudo-nitzschia delicatissima*	Toxic
ASV_663	*Dunaliella salina*	Harmful	ASV_2268	*Halamphora coffeiformis*	Harmful	ASV_4662	*Pseudo-nitzschia delicatissima*	Toxic
ASV_662	*Dunaliella salina*	Harmful	ASV_2295	*Halamphora coffeiformis*	Harmful	ASV_4901	*Pseudo-nitzschia delicatissima*	Toxic
ASV_689	*Dunaliella salina*	Harmful	ASV_2526	*Halamphora coffeiformis*	Harmful	ASV_266	*Pseudochattonella verruculosa*	Toxic
ASV_822	*Dunaliella salina*	Harmful	ASV_2542	*Halamphora coffeiformis*	Harmful	ASV_2484	*Pseudocochlodinium profundisulcus*	Harmful
ASV_827	*Dunaliella salina*	Harmful	ASV_2580	*Halamphora coffeiformis*	Harmful	ASV_3202	*Pseudocochlodinium profundisulcus*	Harmful
ASV_825	*Dunaliella salina*	Harmful	ASV_2799	*Halamphora coffeiformis*	Harmful	ASV_5111	*Pseudocochlodinium profundisulcus*	Harmful
ASV_972	*Dunaliella salina*	Harmful	ASV_3046	*Halamphora coffeiformis*	Harmful	ASV_1195	*Pyrophacus steinii*	Harmful
ASV_998	*Dunaliella salina*	Harmful	ASV_3074	*Halamphora coffeiformis*	Harmful	ASV_64	*Skeletonema marinoi*	Harmful
ASV_1024	*Dunaliella salina*	Harmful	ASV_3281	*Halamphora coffeiformis*	Harmful	ASV_259	*Skeletonema marinoi*	Harmful
ASV_1051	*Dunaliella salina*	Harmful	ASV_3513	*Halamphora coffeiformis*	Harmful	ASV_73	*Teleaulax acuta*	Harmful
ASV_1291	*Dunaliella salina*	Harmful	ASV_3613	*Halamphora coffeiformis*	Harmful	ASV_197	*Teleaulax acuta*	Harmful

ASV_1323	*Dunaliella salina*	Harmful	ASV_3712	*Halamphora coffeiformis*	Harmful	ASV_287	*Teleaulax acuta*	Harmful
ASV_1347	*Dunaliella salina*	Harmful	ASV_3779	*Halamphora coffeiformis*	Harmful	ASV_697	*Teleaulax acuta*	Harmful
ASV_1352	*Dunaliella salina*	Harmful	ASV_3869	*Halamphora coffeiformis*	Harmful	ASV_985	*Teleaulax acuta*	Harmful
ASV_1474	*Dunaliella salina*	Harmful	ASV_3872	*Halamphora coffeiformis*	Harmful	ASV_1656	*Teleaulax acuta*	Harmful
ASV_1449	*Dunaliella salina*	Harmful	ASV_3940	*Halamphora coffeiformis*	Harmful	ASV_1754	*Teleaulax acuta*	Harmful
ASV_1539	*Dunaliella salina*	Harmful	ASV_3969	*Halamphora coffeiformis*	Harmful	ASV_1751	*Teleaulax acuta*	Harmful
ASV_1614	*Dunaliella salina*	Harmful	ASV_4210	*Halamphora coffeiformis*	Harmful	ASV_1876	*Teleaulax acuta*	Harmful
ASV_1632	*Dunaliella salina*	Harmful	ASV_4964	*Halamphora coffeiformis*	Harmful	ASV_1926	*Teleaulax acuta*	Harmful
ASV_1645	*Dunaliella salina*	Harmful	ASV_147	*Heterocapsa triquetra*	Harmful	ASV_2074	*Teleaulax acuta*	Harmful
ASV_1724	*Dunaliella salina*	Harmful	ASV_456	*Heterosigma akashiwo*	Toxic	ASV_2086	*Teleaulax acuta*	Harmful
ASV_1735	*Dunaliella salina*	Harmful	ASV_1153	*Heterosigma akashiwo*	Toxic	ASV_2257	*Teleaulax acuta*	Harmful
ASV_1906	*Dunaliella salina*	Harmful	ASV_1441	*Heterosigma akashiwo*	Toxic	ASV_2299	*Teleaulax acuta*	Harmful
ASV_1890	*Dunaliella salina*	Harmful	ASV_1531	*Heterosigma akashiwo*	Toxic	ASV_2324	*Teleaulax acuta*	Harmful
ASV_1952	*Dunaliella salina*	Harmful	ASV_1643	*Heterosigma akashiwo*	Toxic	ASV_2472	*Teleaulax acuta*	Harmful
ASV_1983	*Dunaliella salina*	Harmful	ASV_1774	*Heterosigma akashiwo*	Toxic	ASV_3337	*Teleaulax acuta*	Harmful
ASV_2018	*Dunaliella salina*	Harmful	ASV_1956	*Heterosigma akashiwo*	Toxic	ASV_3534	*Teleaulax acuta*	Harmful
ASV_2081	*Dunaliella salina*	Harmful	ASV_2126	*Heterosigma akashiwo*	Toxic	ASV_4279	*Teleaulax acuta*	Harmful
ASV_2197	*Dunaliella salina*	Harmful	ASV_2632	*Heterosigma akashiwo*	Toxic	ASV_4441	*Teleaulax acuta*	Harmful
ASV_2235	*Dunaliella salina*	Harmful	ASV_3861	*Heterosigma akashiwo*	Toxic	ASV_4515	*Teleaulax acuta*	Harmful
ASV_2244	*Dunaliella salina*	Harmful	ASV_4028	*Heterosigma akashiwo*	Toxic	ASV_4793	*Teleaulax acuta*	Harmful
ASV_2284	*Dunaliella salina*	Harmful	ASV_4072	*Heterosigma akashiwo*	Toxic	ASV_5052	*Teleaulax acuta*	Harmful
ASV_2283	*Dunaliella salina*	Harmful	ASV_4558	*Heterosigma akashiwo*	Toxic	ASV_1101	*Tenuicylindrus belgicus*	Harmful
ASV_2361	*Dunaliella salina*	Harmful	ASV_4647	*Heterosigma akashiwo*	Toxic	ASV_349	*Thalassiosira allenii*	Harmful
ASV_2406	*Dunaliella salina*	Harmful	ASV_4783	*Heterosigma akashiwo*	Toxic	ASV_1183	*Thalassiosira curviseriata*	Harmful

ASV_2481	*Dunaliella salina*	Harmful	ASV_5082	*Heterosigma akashiwo*	Toxic	ASV_3440	*Thalassiosira curviseriata*	Harmful
ASV_2587	*Dunaliella salina*	Harmful	ASV_932	*Karenia mikimotoi*	Toxic	ASV_3827	*Thalassiosira curviseriata*	Harmful
ASV_2651	*Dunaliella salina*	Harmful	ASV_1117	*Karenia mikimotoi*	Toxic	ASV_21	*Thalassiosira mala*	Harmful
ASV_2620	*Dunaliella salina*	Harmful	ASV_861	*Karlodinium veneficum*	Toxic	ASV_158	*Thalassiosira mala*	Harmful
ASV_2689	*Dunaliella salina*	Harmful	ASV_1025	*Karlodinium veneficum*	Toxic	ASV_765	*Thalassiosira pseudonana*	Harmful
ASV_2690	*Dunaliella salina*	Harmful	ASV_2572	*Karlodinium veneficum*	Toxic	ASV_279	*Thalassiosira weissflogii*	Harmful
ASV_2714	*Dunaliella salina*	Harmful	ASV_4856	*Karlodinium veneficum*	Toxic	ASV_1550	*Thalassiosira weissflogii*	Harmful
ASV_2765	*Dunaliella salina*	Harmful	ASV_1510	*Lauderia annulata*	Harmful	ASV_2823	*Thalassiosira weissflogii*	Harmful
ASV_2774	*Dunaliella salina*	Harmful	ASV_205	*Lepidodinium chlorophorum*	Harmful	ASV_4168	*Thalassiosira weissflogii*	Harmful
ASV_2860	*Dunaliella salina*	Harmful	ASV_312	*Lepidodinium chlorophorum*	Harmful	ASV_466	*Tripos fusus*	Harmful
ASV_2933	*Dunaliella salina*	Harmful	ASV_502	*Lepidodinium chlorophorum*	Harmful			
ASV_3016	*Dunaliella salina*	Harmful	ASV_4183	*Lepidodinium chlorophorum*	Harmful			

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Publications from the Current PhD Study

1. **Li Zhang**#, Anqi Xiong#, Changchao Li, Xintong Liu, Xiaohua Zhang, Shihao Gong, Meng Yan, Xian Qin, Yang Liu, Zhangxi Hu, James Kar-Hei Fang, Huanfeng Duan, Hongbin Liu, Leo L. Chan, Ling N. Jin (2024). Ecological pattern of microalgal communities and associated risks in coastal ecosystems. *ISME Communications*. (Major revision)
2. **Li Zhang**#, Ziqian Xu#, Changchao Li, Xi Pan, Yijing Wang, Xiaohua Zhang, Xintong Liu, Anqi Xiong, Yan Wang, Xinru Zhang, Yongkang Zhao, Shuping Ji, Jian Liu, Meng Yan, James K.H. Fang, Ling N. Jin (2025). Microalgae and associated ecological risks in coastal plastispheres. *Water Research X* (under review)
3. Xintong Liu; Bo Liang; Siyu Yao; Anqi Xiong; Xiaohua Zhang; Yajing Sun; **Li Zhang**; Changchao Li; Yuefei Ruan; Meng Yan; Yuen Wa Ho; James Kar-Hei; Wang Fang, Bei; Frederic Leusch; Daniel Schlenk; Wenhua Liu; Kenneth Mei Yee Leung; Ling Jin, (2024). Interplay of Natural Toxins and Anthropogenic Contaminants in Species-Specific Seawater Cytotoxicity: Insights from Cetacean Skin Fibroblasts. *Environmental Science & Technology* (under review)