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Formation and detection of marine algal toxins and their distribution in Chinese coastal waters

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ABSTRACT

Marine algal toxins, a diverse group of bioactive secondary metabolites produced by harmful algal species, pose significant threats to human health, marine ecosystems, and aquaculture economies. Driven by human activities and climate change, the increasing frequency and scale of harmful algal blooms have expanded the contamination scope of these toxins. This trend underscores an urgent need to better understand their formation and distribution, and to develop more effective methods for their detection and monitoring. This review summarizes recent advances in the formation, detection and monitoring of marine algal toxins, with special emphasis on cases of toxin distribution and pollution in Chinese coastal waters. Notably, advances in genomics and enzymology have begun to decipher the formation mechanism of these toxins, thus laying a fundamental basis for toxin research and risk management. Furthermore, the rapid development of detection technologies and the continuous strengthening of monitoring efforts enable us to track the formation and distribution of toxins in a more timely and accurate manner. Beyond their adverse effects, the unique bioactivities and mechanisms of action of marine algal toxins offer valuable molecular candidates for drug development or scientific research, underscoring the dual role of these natural products. Future research should prioritize the development of rapid, portable detection tools, elucidation of unresolved biosynthetic mechanisms, and exploration of safe therapeutic applications to better mitigate risks and explore the potential of these marine-derived compounds.

1. Introduction

Marine algal toxins are a large class of bioactive secondary metabolites produced by specific algal species, typically exhibiting distinctive chemical structures. These toxins generally demonstrate significant toxicity towards aquatic organisms, near-aquatic animals, and even humans, primarily by selectively targeting neuronal receptors, (Gerssen et al., 2010; Hidayat et al., 2025; Dawson and Holmes, 1999), inhibiting protein phosphatases (K Kiguchi et al., 1994; Costas et al., 2022), blocking/activating ion channels (Llewellyn, 2006; Rodríguez-Rodríguez et al., 2025). These aberrant activities can severely disrupt normal cellular metabolism, leading to host intoxication, including neurotoxicity (Hidayat et al., 2025), cardiotoxicity (Zabka et al., 2009), nephrotoxicity (Sitprija and Sitprija, 2019; Sanclemente-Paz, 2025) and hepatotoxicity (Li et al., 2023), and ultimately resulting in functional impairment or even death (Petroff et al., 2022; Cao et al., 2019; Xu et al., 2020).

In recent years, intensified coastal eutrophication coupled with accelerating climate change has driven a worldwide increase in both the frequency and spatial extent of harmful algal blooms (Hallegraeff et al.). These harmful algal produced toxins can accumulate in filter-feeding bivalves, herbivorous fish, and shellfish, subsequently posing a risk to humans through seafood consumption (Ly et al., 2024; Holmes and Lewis, 2022; Wang et al., 2024). This phenomenon not only creates critical public-health hazards but also imposes enormous economic losses on mariculture, while simultaneously undermining overall ecosystem health and stability (Dorantes-Aranda and José, 2023). Research on marine algal toxins is therefore essential for safeguarding

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food safety, supporting the sustainable development of marine economies, and preserving the integrity of marine ecosystems. However, current efforts on monitoring their distribution, understanding their formation, and developing detection/protection methods remain insufficient, highlighting the need for more comprehensive and integrated research to effectively address these challenges.

Here, in this review, we provide an account of the state of recent advances in the formation, application and detection of marine algal toxins, with special emphasis on cases of toxin distribution and pollution in Chinese coastal waters. The aim of this review is to systematically summarize current research findings, identify key knowledge gaps, and propose a reference framework for future investigations, thereby advancing scientific understanding and supporting practical management in this field.

2. Classification, formation, and potential applications

2.1. Classification of marine algal toxins

Marine algal toxins differ widely in chemical structure and mode of action. They can be classified according to their toxic effects and chemical structures. Based on the nature of their toxic effects in the host, marine algal toxins can be classified into five shellfish poisoning categories—Paralytic Shellfish Poisoning (PSP), Amnesic Shellfish Poisoning (ASP), Neurotoxic Shellfish Poisoning (NSP), Diarrhetic Shellfish Poisoning (DSP), and Azaspiracid Shellfish Poisoning (AZP)—alongside Ciguatera Poisoning (CP) (Fig. 1) (Daguer et al., 2018; Leal and Cristiano, 2022; Visciano et al., 2016).

Paralytic shellfish toxins (PSTs), which cause PSP, are one of the most widespread and highly potent class of marine algal toxins, with saxitoxin (STX) being a prominent representative (Fig. 1). These toxins are mainly produced by eukaryotic dinoflagellates in the genera *Alexandrium*, *Gymnodinium*, *Pyrodinium* and some cyanobacteria species. They can accumulate in edible bivalves, such as the butter clam, after they filter-feed on toxic dinoflagellates or cyanobacteria (Deng et al., 2025). By selectively blocking voltage-gated sodium channels, they induce neuromuscular paralysis that can lead to respiratory failure and death in humans or other mammals (Barchi and Weigele, 1979; Villegas and Barnola, 1972).

ASP is caused by amnesic shellfish toxins (ASTs), which are presented by domoic acid (DA) (Fig. 1). As a diatom-derived glutamate analogue, DA can over-activate brain kainate and AMPA receptors. This leads to calcium overload and excitotoxicity, resulting in potent neurotoxicity that selectively damages brain regions such as the hippocampus in both humans and marine animals (Bates et al., 2018; Pulido, 2008; Perl et al., 1990; Scholin et al., 2000).

Neurotoxic shellfish toxins (NSTs), which cause NSP, are produced primarily by dinoflagellates such as the genus *Karenia* and accumulate in shellfish of the species such as the clam *Mercenaria mercenaria* and the Pacific cupped oyster *Crassostrea gigas*. The principal component, brevetoxin (BTX) (Fig. 1), activates voltage-gated sodium channels, provoking Na^+ influx that underlies both respiratory irritation and neurotoxicity (Poli et al., 2000; Raposo-Garcia et al., 2023).

Diarrhetic shellfish toxins (DSTs), which cause DSP, are produced mainly by dinoflagellates of the genera *Dinophysis* and *Prorocentrum*. This group is represented by okadaic acid (OA) and its analogues (Fig. 1). OA shows gastrointestinal toxicity by inhibiting serine/threonine protein phosphatases PP1 and PP2A (Fu et al., 2019). Together with PSTs, these two toxin classes occur widely in coastal waters worldwide, posing a persistent threat to aquaculture and repeatedly causing human intoxications.

It is noteworthy that pectenotoxins (PTXs) and yessotoxins (YTXs) were historically classified under the category of DSP (Yasumoto et al., 1985). This was primarily due to their co-detection with the core diarrhetic toxins—OA and DTXs—in shellfish extracts during early screening methods reliant on mouse bioassays (Tubaro et al., 2010). However, advances in toxicological research have revealed fundamental differences between these two toxin groups and DSP in terms of both mechanism of action and clinical symptoms: PTXs primarily cause cytotoxicity by disrupting cytoskeletal and cell membrane integrity (Espiña and Rubiolo, 2008), and YTXs lead to cytotoxicity and systemic cardiovascular effects by interfering with intracellular calcium ion balance and the cytoskeleton—neither of which produces typical diarrhetic symptoms (Gao et al., 2024). Consequently, based on their distinct chemical structures and toxicological profiles, PTXs and YTXs have now been separated from the DSP classification and are recognized as two independent classes of marine algal toxins, parallel to DSP (Bouda et al., 2025). They are accordingly treated differently within the regulatory frameworks of many countries. This evolution in classification reflects a more scientific and refined understanding of the risks associated with these toxin groups.

Azaspiracids (AZAs) are polyether marine biotoxins that cause AZP (McMahon and Silke, 1996). Over 60 AZA analogues produced mainly by the protists *Azadinium* and *Amphidoma*, have been identified. Among these, AZA-1, AZA-2, and AZA-3 are the most prevalent and extensively studied (Furey et al., 2010). Their toxicity is characterized primarily by severe gastrointestinal symptoms, especially diarrhea, resulting from a multi-target mechanism by affecting potassium ion channels, sodium ion channels, chloride ion channels, and calcium ion channels (Boente-Juncal, et al., 2020, 2021; Yang et al., 2024).

Ciguatoxins (CTXs) are highly potent neurotoxins that cause CP. They are synthesized by benthic microalgae of the genera *Gambierdiscus* and *Fukuyoa*, and can be transmitted through the food web via fish that graze on these microalgae and subsequent predation, leading to CP

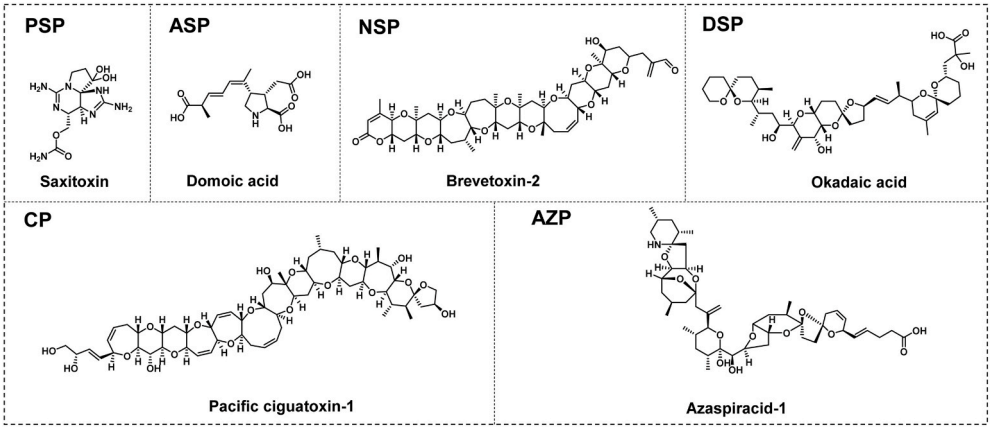


Fig. 1. The chemical structures of representative marine algal toxins based on the classification of toxic effects.

(Perkins et al., 2024; Holmes and Lewis, 2025; Pearn, 2001). Their primary mechanism of action is the binding to and persistent activation of voltage-gated sodium channels (VGSCs) on cell membranes. This leads to uncontrolled sodium influx, sustained membrane depolarization, and a cascade of effects in nerve and muscle cells, resulting in the diverse neurological, gastrointestinal, and cardiovascular symptoms characteristic of the illness (Cameron et al., 1991; Molgo et al., 1992; Bidard et al., 1984).

Chemical structure provides an alternative framework for classifying marine algal toxins. Based on the core chemical structures of these marine algal toxins, they can be broadly categorized into several major classes, including alkaloids, polyethers, cyclic imines (Visciano et al., 2016), and polypeptides (Fig. 2). Typical alkaloid-type toxins include saxitoxin and domoic acid; polyether-type toxins encompass okadaic acid, brevetoxins, yessotoxin, azaspiracid, pectenotoxin, and palytoxin; cyclic imine toxins comprise portimine, gymnodimine, and spiroimines (Fig. 2).

2.2. Formation of marine algal toxins

The classification above outlines the diversity of marine algal toxins from the perspectives of both toxin effects and chemical structures. Understanding the biosynthetic mechanism of toxins is a crucial link that connects their chemical nature, ecological functions, and risk evolution. While the unique chemical structures and biological properties of marine algal toxins have long captivated scientific interest, their formation mechanisms have remained elusive due to the complexity of their biosynthesis, which involves intricate metabolic pathways, genetic regulation, and food chain biomagnification (Chekan et al., 2020). Recent breakthroughs in genomics, transcriptomics, and metabolomics have driven progress in this field. Nevertheless, the biosynthetic mechanisms for most marine algal toxins have yet to be fully deciphered.

Among algal toxins, the biosynthetic pathways of alkaloid-type compounds are currently the best understood. The representative compound of PSTs, STX, can be produced by both cyanobacteria (e.g., *Dolichospermum circinale*) and dinoflagellates (e.g., *Alexandrium* sp.). Although several researches have been conducted on its biosynthetic process, the complete biosynthetic mechanism remains unclear due to the complex biosynthetic pathway, the difficulty in genetic manipulation of the producing strains, and the large genome size of dinoflagellates. Based on the previous studies, the biosynthetic pathway can be roughly inferred as follows (Fig. 3a): the multi-modular polyketide synthase SxtA catalyzes the methylation, decarboxylation, and condensation reactions of malonyl-CoA and arginine to generate the first key intermediate, intermediate 1 (Chun et al., 2018). Then, the amidinotransferase SxtG transfers the amidino group of arginine to intermediate 1 and yield intermediate 3 after spontaneous cyclization and dehydration. The oxidase SxtH was deduced to convert intermediate 3 to β-saxitoxinol via complex intramolecular rearrangement, thereby completing the skeleton construction process. Finally, the oxidase SxtT mediates a hydroxylation towards β-saxitoxinol and yield STX (Fig. 3a) (Lukowski, et al., 2018, 2020). In addition, further modifications catalyzed by enzymes such as GxtA, SxtN, and SxtSUL generate various derivatives of STX (Lukowski et al., 2019; Cullen et al., 2018).

A study led by Bradley S. Moore at the Scripps Institution of Oceanography revealed that the biosynthesis of the amnesic shellfish

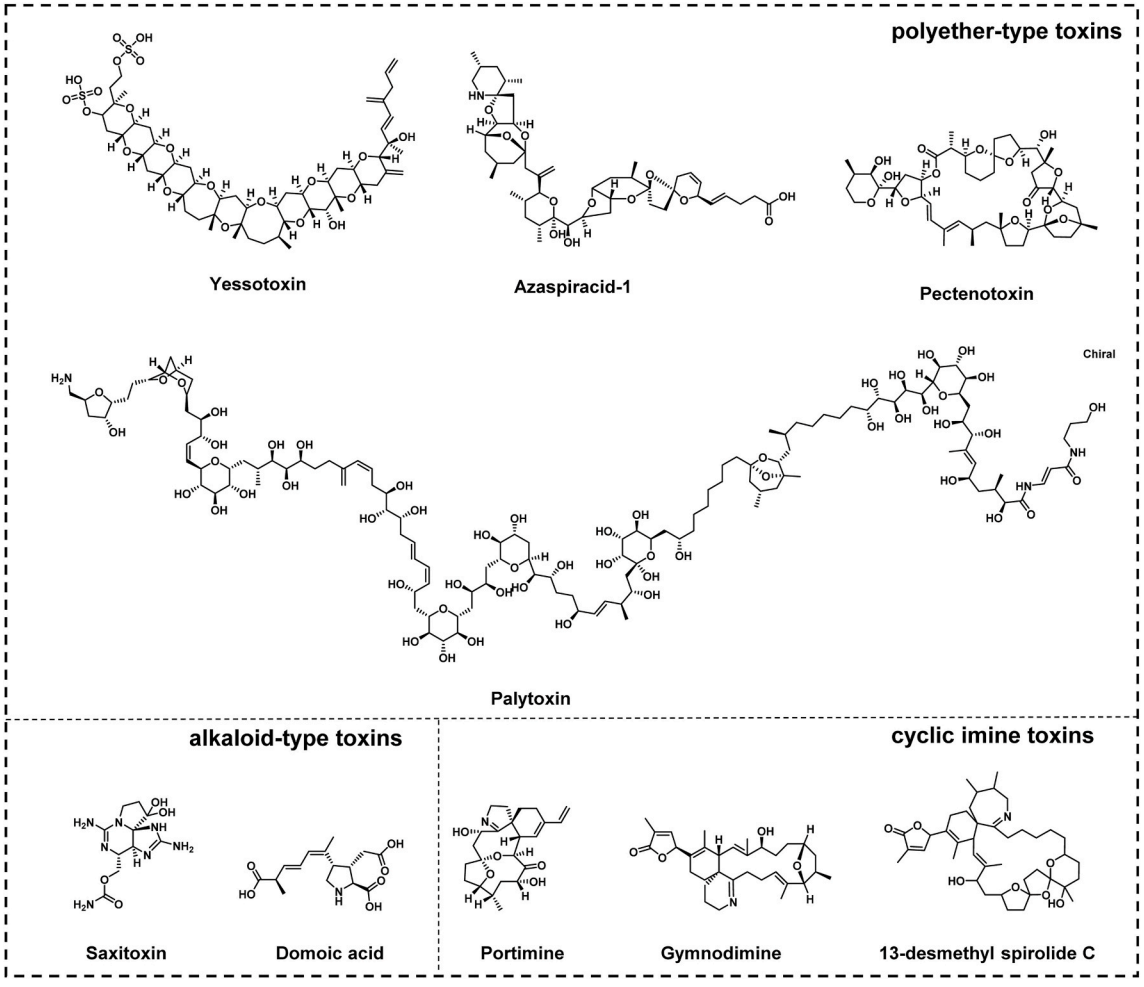


Fig. 2. Representative marine algal toxins based on the classification of chemical structures.

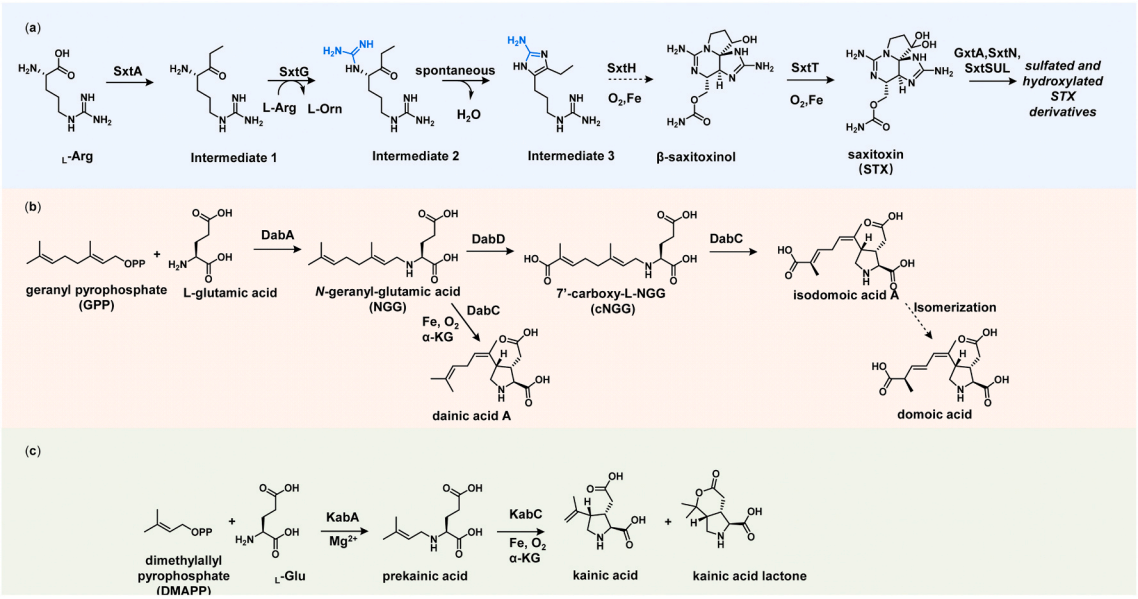


Fig. 3. Biosynthesis of alkaloid-type toxins. (**a**) The proposed biosynthetic pathway of STX; (**b**-**c**) The established biosynthetic pathway of DA and kainic acid, respectively.

toxin DA proceeds through four key enzymatic steps (Fig. 3b) (Steele et al., 2022). First, the terpene cyclase-like *N*-prenyltransferase DabA condenses geranyl diphosphate with L-glutamate to form *N*-geranyl-L-glutamate (NGG). Next, the cytochrome P450 monooxygenase DabD oxidizes NGG to yield cNGG. The α-ketoglutarate-dependent dioxygenase DabC then converts cNGG to isodomoic acid A via a cyclization reaction. Finally, an as-yet-uncharacterized isomerase converts isodomoic acid A into DA (Brunson et al., 2018). This pathway was delineated by integrating transcriptomic profiling with in vitro enzyme assays, and its validity was further corroborated by isolation of the intermediates and stable-isotope labeling experiments (Maeno et al., 2018). Another study by the same group demonstrated that the

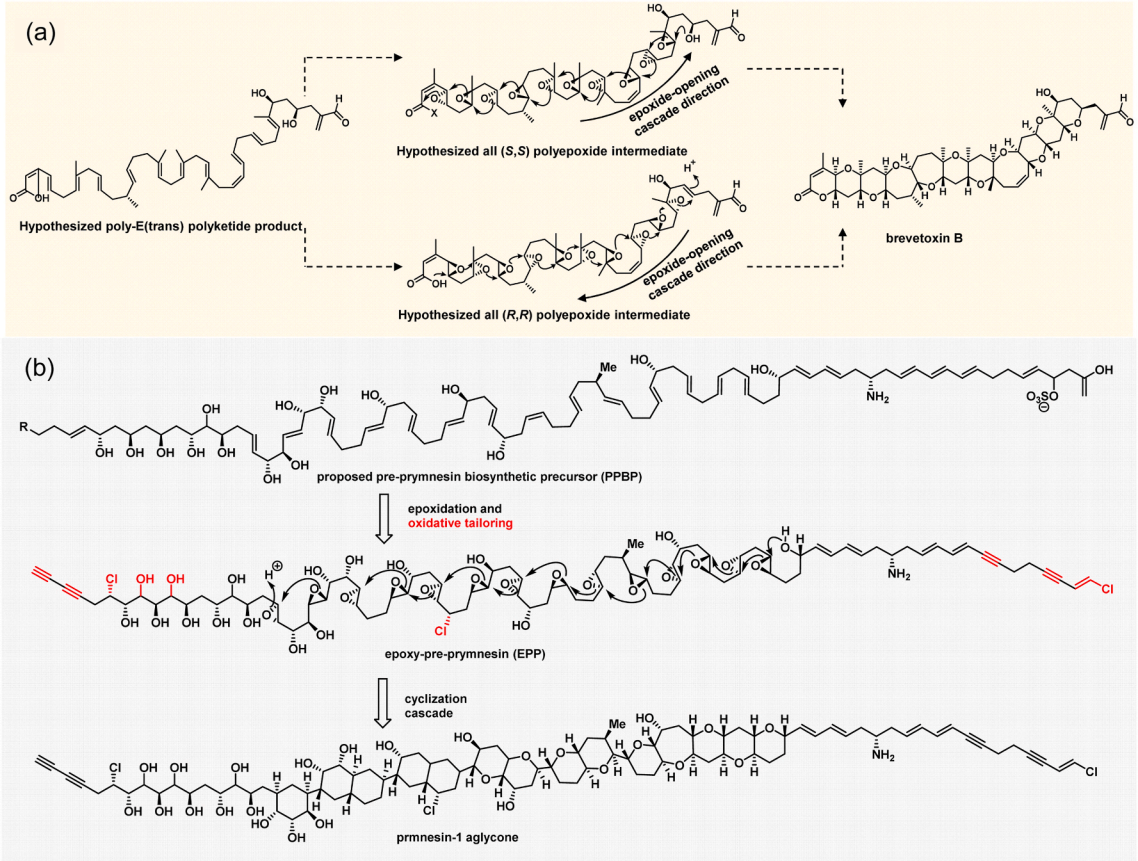


Fig. 4. Biosynthesis of polyether toxins. (**a**-**b**) The proposed biosynthetic pathways of brevetoxin B and prymnesin-1 aglycone, respectively.

analogue of DA, kainic acid, employs a similar biosynthetic pathway with DA (Fig. 3c) (John K. Brunson et al., 2018).

Polyether toxins possess complex chemical structures, and their biosynthesis is particularly intriguing. However, current understanding of their formation mechanisms remains very limited. The signature neurotoxic shellfish poison BTX, produced by the dinoflagellate *Karenia brevis* and related microalgae, possesses a molecular mass exceeding 850 Da and is characterized by a trans-fused polycyclic ether "ladder" architecture. Although isotope-labelling experiments have established that its carbon skeleton originates from polyketide precursors within the algal cell (Chekan et al., 2020), direct evidence for assembly via a canonical polyketide synthase (PKS) pathway is still lacking. The prevailing biosynthetic model, advanced by Nakanishi and co-workers (Nakanishi, 1985), proposes a "polyepoxide-cascade" scenario in which a polyunsaturated fatty-acid chain undergoes iterative epoxidation to generate an array of epoxides; subsequent enzyme-catalyzed, intramolecular epoxide-opening/ring-closure cascades would then forge the intricate polyether framework (Fig. 4a). This mechanism, however, is constrained by Baldwin's rule that favours exo-cyclization (smaller-ring formation) during nucleophilic attack of a hydroxyl group upon an epoxide (Baldwin, 1976; Vilotijevic and Jamison, 2010). In 2024, Xiao et al. provided the first demonstration that masking or attenuating the terminal hydroxyl nucleophile with a slowly removable THP group switches the entire cascade to an "epoxide → epoxonium" head-to-tail manifold, enabling consecutive endo-selective openings that deliver the fully endo polycyclic ether ladder in a single operation and offering a new mechanistic paradigm for BTX biosynthesis (Fig. 4a) (Xiao et al., 2024). Owing to the large and highly repetitive genome of dinoflagellates (up to more than 200 Gb) (Nicolaou et al., 2008), functional assignment of the underlying biosynthetic genes remains challenging. Future efforts need to integrate intermediate trapping, heterologous expression, enzymatic assays and in-vitro reconstitutions to elucidate the complete enzymatic choreography of BTX formation (Xiao et al., 2024).

Maitotoxin (MTX) is recognized as one of the most structurally complex natural products known to date. Its large molecular size and intricate ladder-frame polyether architecture imply biosynthesis through a sophisticated hybrid assembly line involving polyketide synthase and non-ribosomal peptide synthetase (PKS/NRPS) systems (Yang et al., 2024; Teufel and Müller, 2025). However, the large and complex genome of its producer, *Gambierdiscus*, has so far hindered any in-depth genetic or biochemical elucidation of maitotoxin biosynthesis. In contrast, significant progress has been made with the related prymnesin toxins. Their biosynthesis was proposed to follow a two-step pathway (Fig. 4b): first, the colossal linear polyene precursor is assembled by the recently discovered giant polyketide synthases PKZILLA-1 and PKZILLA-2; then, this precursor is converted into the characteristic "ladder" structure through sequential epoxidation and cyclization cascades. Similarly, polyether toxins such as okadaic acid (OA) and the dinophysistoxins (DTXs) are also considered to derive from polyketide pathways. Some progress has been achieved in identifying related the PKS encoding genes in their producer dinoflagellates like *Prorocentrum* spp. (Perez et al., 2008; Wan et al., 2023). Nevertheless, a comprehensive biosynthetic pathway—including the specific enzymes responsible for the formation of their characteristic cyclic ether rings—remains far from complete.

For other toxin classes, biosynthetic understanding remains in its infancy or is entirely lacking or poorly defined. For example, although azaspiracids (AZAs) type toxins are also hypothesized to derive from a polyketide pathway, no specific biosynthetic gene cluster or detailed enzymatic route has been identified to date, representing a significant knowledge gap in marine toxin research (Yang et al., 2024).

In recent years, the rapid development of high-throughput sequencing and molecular biology techniques has greatly deepened our understanding of the biosynthesis mechanism of marine algal toxins, advancing the research to the genomic and systems biology levels. First, with recent breakthroughs in sequencing technology, research on dinoflagellate genomics has expanded from an initial focus on symbiotic Symbiodiniaceae which has smaller genomes to a more diverse range of taxa such as *Amoebophrya ceratii (*Farhat et al., 2021), Polarella glacialis (Stephens et al., 2020), Prorocentrum cordatum (Dougan et al., 2023). This has revealed multiple independent genome expansion events (Hou et al., 2019; Chen et al., 2018), the critical role of horizontal gene transfer (Stephens et al., 2020; Wisecaver et al., 2013), and the extreme remodeling of nuclear protein composition—from histones to viral-derived proteins (DVNP) (Gornik, et al., 2012, 2019) and bacterial-derived proteins such as Major basic nuclear protein (MBNP) (Wong, 2019). These findings not only deepen our understanding of the biological processes in dinoflagellates but also provide a rare window into exploring eukaryotic genome plasticity, environmental adaptation, and symbiotic evolution. Second, the traditional view held that complex polyketide/polypeptide toxins in marine algal toxins might be synthesized through the coordinated action of multiple dispersed enzyme systems (Lin, 2024).

In 2024, the giant modular type I polyketide synthases PKZILLA-1 and PKZILLA-2, which comprise 140 and 99 domains encoded by genes exceeding 130 and 90 kbp respectively, have been identified from the golden alga Prymnesium parvum by Bradley Moore and coworkers (Timothy R. Fallon et al., 2024). Mechanistically, these mega synthases function via an assembly-line logic in which each module is responsible for one round of polyketide chain elongation and optional modification, ultimately assembling the large linear polyene precursor of prymnesin-1. In contrast to the well-studied PKS/NRPS systems found in microorganisms, plants, and animals—which typically comprise up to dozens of domains (Nivina et al., 2019)—the identification of this largest PKS system known to date has fundamentally transformed our understanding of polyketide assembly, particularly with regard to the evolutionary origin, transcriptional and translational efficiency, and catalytic mode of such a mega-protein. This finding lays the foundation for the development and implementation of alternative linked omics approaches to fully uncover the complete suite of prymnesin biosynthetic enzymes, while also offering the opportunity to dissect the enzymology of ladder-frame polyether biosynthesis and serving as a model to capture and dissect giant genes, transcripts, and proteins in specialized toxin biosynthesis (Teufel and Müller, 2025).

Toxin biosynthesis is not constitutively expressed but is instead tightly regulated by developmental stages and environmental factors. From an evolutionary ecological perspective, this coupling likely reflects a fundamental trade-off between growth, defense, and survival. For example, in Pseudo-nitzschia, which produces domoic acid, toxin production is closely associated with its sexual reproduction cycle, with toxin levels significantly increasing during later stages of sexual reproduction in certain species (Sauvey et al., 2019). Similarly, toxin content in Alexandrium species varies dynamically during the formation and germination of dormant cysts (Shin et al., 2021; Jiang et al., 2025). The formation of resistant cysts, coupled with enhanced toxin synthesis, underscores a dual ecological function. First, cysts and the vegetative cells released upon germination both carry high concentrations of toxins, which deter grazers and reduce predation risk, enhancing population survival during bloom decline (Xu and Kiørboe, 2018). Moreover, as resting structures, cysts tolerate adverse conditions such as low temperature and nutrient depletion, while the toxins accumulated within them not only protect the cysts but also reinforce their role as a highly toxic seed bank for the following season's bloom. This energy-intensive investment in toxin production is thus not a constant burden but a strategic allocation of resources to maximize survival during specific, high-risk life-cycle transitions, such as overwintering or seed-bed establishment. This ecological context is crucial for understanding why toxin biosynthesis is not constitutive but tightly regulated by endogenous developmental cues and exogenous environmental signals.

At the molecular level, this coupling manifests as the differential

transcriptional activation of toxin biosynthesis gene clusters under specific life cycle stages or environmental stresses, such as nutrient limitation (Wan et al., 2023). The regulation of toxin production by environmental factors is central to the ecological strategy of toxic phytoplankton. Extensive research shows that toxin synthesis is not static but is precisely controlled by abiotic factors such as temperature, light, and nutrients, directly linking toxin production to the environmental adaptation and survival strategies of algae. For example, in the azaspiracid-producing Azadinium spinosum, lower temperatures at 10 °C significantly increase cellular toxin quotas, while specific photoperiods and medium composition also jointly influence final toxin yields (Kilcoyne et al., 2019). In addition, seawater salinity also affects the accumulation of algal toxins. Samples collected by the researchers showed a significant negative correlation between algal toxin concentrations and salinity, suggesting that toxigenic microalgae may prefer to synthesize and accumulate phycotoxins in lower-salinity environments (Ji et al., 2026).

From an evolutionary ecology perspective, this environment-dependent regulation holds profound adaptive significance. As a chemical defense mechanism, toxin production necessarily involves a trade-off between cost and benefit. Theoretical models indicate that when resources such as nitrogen are sufficient, the cost of toxin production is minimal, consistent with the no-cost phenomenon observed in experiments. However, under nitrogen-limited conditions with high grazing pressure, maintaining high levels of toxin defense reduces the cell division rate by over 20%, making the cost substantial. This explains why toxin synthesis is strictly regulated: during summer blooms, when nutrients are often limiting and zooplankton grazing is active, investing in toxin production, though costly, provides survival benefits by reducing predation rates, giving algae with this regulatory capability an advantage in net growth rate (Chakraborty et al., 2019). Therefore, linking environmental signals, the transcriptional regulation of toxin biosynthetic gene clusters, and their ecological functions—such as defense against grazing—is key to a systemic understanding of the origin, evolution, and role of toxins in algal life history.

The biosynthetic capacity is an inherent molecular property of specific harmful algal species, defining their essential role as “risk sources”. When environmental conditions become favorable, these algae—equipped with dedicated biosynthetic pathways—gain a competitive advantage and form blooms, thereby inevitably driving the production and accumulation of their corresponding toxins. Consequently, elucidating the biosynthetic mechanisms of these toxins not only reveals the molecular basis of their formation but also provides a fundamental rationale for understanding their subsequent spatiotemporal distribution patterns.

2.3. Potential applications of marine algal toxins

Marine algal toxins have demonstrated broad application potential in the field of drug development and (or) scientific research due to their unique biological activities and mode of action. Several algal toxins have been found to possess potential medicinal value, such as for treating neurological disorders, anti-tumor effects, and anti-inflammatory applications (Gao et al., 2024).

Several marine algal toxins have attracted significant interest in the field of anticancer drug development due to their unique mechanisms of action. Notably, PSTs, a class of neurotoxins, have demonstrated anticancer properties. Studies have shown that appropriate doses of PSTs can delay tumor metastasis without obvious side effects in canine hemangiosarcoma models (Gao et al., 2024). OA, as a specific inhibitor of protein phosphatases PP1 and PP2A, can interfere with tumor cell signaling pathways, therefore inducing cell cycle arrest and apoptosis (Qiu et al., 2023). Yessotoxin has demonstrated high sensitivity toward specific tumor cells such as melanoma and lung cancer, and has shown tumor growth inhibitory effects in mouse experiments, making it a potential drug candidate for cancer treatment (Botana et al., 2014; Tobio et al., 2016).

STX, by regulating the release of glutamate and neuropeptides, has demonstrated analgesic effects in mouse models (Zhang, 2020; Li, 2022). Some algal toxins also exhibit immunomodulatory effects. For example, yessotoxin can regulate T-cell activity through the PKC and PP2A signaling pathways and inhibit histamine release from mast cells, providing a theoretical basis for its application in allergic disease treatment (Lopez et al., 2011). BTX, at low concentrations, can affect the metabolism and cytokine secretion of immune cells, showing potential immunomodulatory functions (Brammer-Robbins et al., 2022).Despite their broad pharmacological potential, the inherent toxicity of marine algal toxins poses a primary challenge to their clinical application (Bennett and AuthorAnonymous, 1988). Future research needs to further elucidate their mechanisms of action, optimize dosing regimens, and explore the possibility of structural modifications to balance efficacy and safety (Assuncao et al., 2017). With in-depth research, these natural products derived from the ocean are expected to provide new options for the treatment of various diseases.

3. Harmful algal blooms (HABs) and toxins distribution in Chinese coastal waters

As one of the marine regions most significantly affected by harmful algal blooms (HABs) worldwide, the coastal waters of China face persistent potential threats from algal toxins to ecological security, aquaculture, and public health. Therefore, discussing the distribution of HABs and algal toxins in this region carries stronger regional relevance and practical significance.

An analysis of reports from the Bulletin of Marine Ecological Early-Warning and Monitoring of China (2024) and the Bulletin of Marine Disasters of China 2020-2023 (Ministry of Natural ResourcesPRC, 2024; 2023, 2022, 2021, 2020) reveals that harmful algal blooms (HABs) in China's coastal waters have presented distinct spatio-temporal distribution patterns over the past decade, featured by prominent regional aggregation, notable interannual variability and localized episodic outbreaks. HABs prevalently occur in eutrophic coastal zones with complex hydrodynamic regimes, including the Pearl River Estuary, Bohai Sea, Hangzhou Bay, Yangtze River Estuary and Haikou Bay, with a concentrated outbreak period spanning from May to October annually. Such regularity is tightly linked to rising sea surface temperature, stable water column stratification and abundant nutrient availability. Spatially, the East China Sea dominates HAB occurrence, with its event frequency consistently accounting for over 40% of the national total. The Bohai Sea contributes more than 20% to the nationwide HAB occurrences. High-magnitude HAB events in the South China Sea are mostly short-lived and localized, while the Yellow Sea maintains a relatively moderate HAB frequency and limited coverage, contributing around 10% of national incidents (Table 1). Toxic HABs are predominantly dominated by Prorocentrum donghaiense, Margalefidinium polykrikoide and Phaeocystis globosa, while non-toxic bloom events are mainly driven by Noctiluca scintillans.

While we report a notable increase in the proportion of toxic red tides, a critical caveat must be explicitly acknowledged: due to changes in monitoring coverage/intensity, analytical methods, and detection limits over time, long term trend comparisons should be interpreted

Table 1
Recent HAB events in Chinese coastal waters (2020-2024).

Year	Number of HAB events	Cumulative area of HAB events (km^2)	Proportion of toxic algal blooms
2024	66	11731	Approximately 59%
2023	46	1466	Approximately 63%
2022	67	3328	Approximately 30%
2021	58	23277	Approximately 2%
2020	31	1748	Approximately 6%

with caution. For instance, the widespread adoption of liquid chromatography-tandem mass spectrometry (LC-MS/MS) as a standard method for lipophilic toxins was not uniform across all coastal monitoring stations before 2020. Consequently, variations in limits of detection (LOD) and quantification (LOQ) across different laboratories and time periods could lead to an "apparent increase" in detected toxicity, as more sensitive methods are more likely to detect trace levels. This does not invalidate the overall trend of increasing HAB frequency and distribution, but it does mean that the precise magnitude of the increase in "toxicity risk" must be regarded as an indicative directional signal rather than a precise quantitative measure. Moreover, the rising detection rate of marine algal toxins from 2020 to 2025 can also be attributed to China's increasing emphasis on marine environmental monitoring and protection. This trend has promoted improvements in monitoring coverage and intensity, representing non-objective factors contributing to the increase in detection data, rather than fully reflecting a natural increase in the actual occurrence levels of marine algal toxins (Ministry of Ecology and Environment, 2022).

The eutrophication of marine waters appears to be a key and direct factor driving the worsening of HABs. Excess nutrient inputs—primarily nitrogen and phosphorus from land-based runoff, agricultural fertilizers, and untreated wastewater—stimulate rapid proliferation of phytoplankton, including toxin-producing species, leading to increased frequency, intensity, and spatial extent of HABs. Climate change contributes through rising sea surface temperatures, ocean acidification, and altered stratification patterns, which can favor the growth of harmful algal species over benign ones and extend the seasonal window of bloom formation (Meng et al., 2024). Concurrently, intensifying human activities play a critical role. Large-scale excessive aquaculture, for instance, releases vast amounts of organic waste and uneaten feed into surrounding waters, creating localized eutrophic conditions that directly fuel HAB events (Hallegraeff et al., 2021; Yu, 2016). Additionally, global shipping transportation facilitates the introduction of non-native harmful algal species via ballast water discharge and hull fouling. This trend is also clearly documented in the 2019–2021 distribution dataset of toxic/harmful microalgae and algal toxins in Chinese coastal waters, which reveals distinct spatiotemporal dynamics in toxin spread (Zhang et al., 2024). A survey of relevant literature further indicates that the distribution of these marine algal toxins follows identifiable geographical and seasonal patterns (Fig. 5).

Spatially, OA, dinophysistoxin-1 (DTX1) and pectenotoxin-2 (PTX2)—three lipophilic marine algal toxins—are ubiquitous throughout the Bohai Sea, Yellow sea, East China sea and South China Sea (Yu, 2016). This reflects the widespread distribution of marine algal

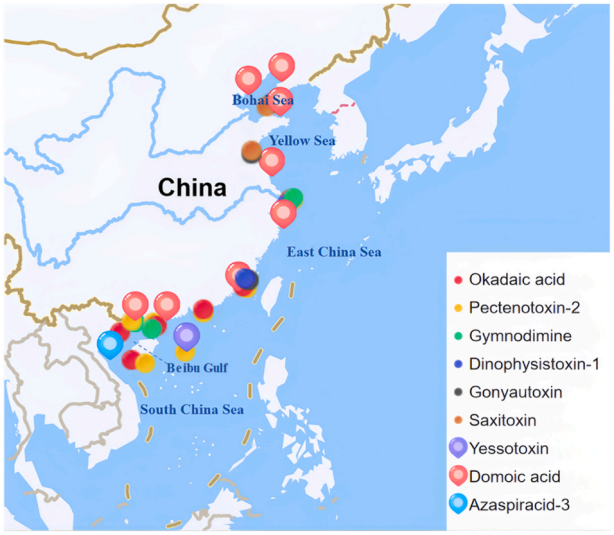


Fig. 5. Distribution of marine algal toxins in the coastal waters of China.

toxins in Chinese coastal waters and suggests potential threats to marine ecosystems and seafood safety. This is closely related to the extensive distribution of toxin-producing algae in these areas. For example, Dinophysis, which produces OA and DTX1, and dinoflagellates that produce PTX2, are widely distributed in Chinese coastal waters. Moreover, the detection rates of cyclic imine toxins are relatively high in the Yellow Sea, East China Sea, and South China Sea, while YTX is mainly concentrated in the East China Sea and Yellow Sea (Zhang et al., 2024). This may be associated with the unique environmental conditions and algal community structures of specific areas. It is worth noting that, as of now, the BTX type toxins have not been detected in Chinese coastal waters. In 2023, dissolved AZA3 was detected for the first time in the Beibu Gulf, marking the first occurrence of AZA3 in Chinese coastal seawater. Prior to this, AZAs had already been detected in shellfish and strain samples (Liu et al., 2019; Gu et al., 2013). In the Asia-Pacific region, AZAs are mainly derived from the dinoflagellate Azadinium poporum, which was known to inhabit temperate waters (Krock et al., 2014). Puget Sound strains can grow across 6.7–25.0 °C and salinity 15–35, with optimal growth at 20–23 °C, where temperature, rather than salinity, is the primary driver of growth rates. Field investigations confirmed that when temperature and salinity become favorable in June and July, the alga exhibits increased growth and becomes readily detectable (Dai et al., 2019). Its specific occurrence in the Beibu Gulf can be linked to its preference for moderate salinity and specific nutrient regimes found in this semi-enclosed basin, even though its overall cell abundance is low (Gu et al., 2013). Moreover, the fact that AZAs were detected earlier in shellfish but not in the dissolved phase may also be explained by the low monitoring intensity in the early years and the low sensitivity of the detection methodology. This case underscores that our spatiotemporal knowledge of toxin distribution is not a static picture but is dynamically shaped by both ecological processes and the evolving sensitivity and selectivity of our analytical tools.

Regarding toxin types, PSTs and DSTs dominate the marine algal

Table 2
Occurrence of marine algal toxins in Chinese coastal waters.

Marine region	Dominant marine algal toxin classes	Source algae
Bohai Sea	Pectenotoxin-2 (PTX2)	Dinoflagellates
	Okadaic acid (OA)	*Dinophysis* spp.
	Dinophysistoxin-1 (DTX1)	*Dinophysis* spp.
Yellow Sea	Pectenotoxin-2 (PTX2)	Dinoflagellates
	Okadaic acid (OA)	*Dinophysis* spp.; *Prorocentrum* spp.
	Dinophysistoxin-1 (DTX1)	*Dinophysis* spp.
	Gymnodimine (GYM)	Putative producer: *Karenia selliformis*
	Azaspiracid toxins (AZA1, AZA2)	Putative producer: *Azadinium poporum*
East China Sea	Domoic acid (DA)	*Pseudo-nitzschia* spp. (pennate diatoms)
	Okadaic acid (OA)	*Dinophysis* spp., *Prorocentrum* spp.
	Dinophysistoxin-1,2 (DTX1、DTX2)	*Dinophysis acuta/D. fortii*
	Gymnodimine (GYM)	Putative producer: *Karenia selliformis*
South China Sea	Neurotoxin β-N-methylamino-$_L$-alanine (BMAA)	*Trichodesmium* spp.
	Azaspiracid toxin-3 (AZA3)	Putative producer: *Azadinium poporum*
	Gymnodimine (GYM)	*Gymnodinium* spp.
	Okadaic acid (OA)	*Dinophysis* spp. , *Prorocentrum* spp.
	Pectenotoxin-2 (PTX2)	Dinoflagellates
	Yessotoxin (YTX) and homo-yessotoxin (h-YTX)	*Gonyaulax* spp., *Protoceratium reticulatum*
	13-Desmethylspirolide C (SPX1)	Putative producer: *Alexandrium ostenfeldii* complex

toxin spectrum in Chinese coastal waters (Table 2). PSTs are produced by Alexandrium species (e.g., A. catenella and A. pacificum), whereas DSTs originate from Dinophysis spp. High-incidence areas for both toxin types encompass the coasts of Guangdong and Fujian, the adjacent region of the Yangtze River estuary, and the northern Yellow Sea (Wang et al., 2023). During spring and summer, toxin concentrations in shellfish from certain off shore zones of Fujian and Dalian approach or even exceed the regulatory safety limits, indicating elevated regional risk (Table 2).

In recent years, with continuous advancements in environmental monitoring technologies, newly recorded toxic algal species and toxins have emerged. For example, the abundance of Alexandrium catenella cysts in sediments of the Yellow Sea and Bohai Sea has shown an increasing trend (Shao et al., 2012). In the Yangtze River Estuary of the East China Sea, Alexandrium pacificum dominates, and its distribution is closely linked to sediment types and the circulation regulated by the Kuroshio branch (Fu et al., 2009). Moreover, the synergistic effects of eutrophication and ocean acidification further enhance the toxicity of harmful blooms: elevated CO_2 and nitrate concentrations significantly increase PST production by A. minutum (Li, F. et al., 2023). In South China Sea, recurrent Phaeocystis globosa blooms have been found to release haemolytic toxins, posing a threat to both ecological safety and public health (Zhang et al., 2022).

The distribution of toxins shows obvious spatial heterogeneity and seasonal patterns, which is closely related to the ecological niche of the toxin-producing algae species, hydrological conditions, and eutrophication caused by human activities (Wang, 2025). These distribution characteristics not only reveal the risk hotspots of algal bloom toxins, but also provide key guidance for the construction of targeted monitoring networks and hierarchical early warning systems.

However, when interpreting toxin distribution data in Chinese coastal waters, it is also essential to consider the limitations arising from the underlying monitoring and methodological context. First, there are regional disparities in monitoring intensity, with more developed and aquaculture-intensive areas having denser monitoring networks. Second, advances in detection technology over time have significantly improved the sensitivity of toxin detection, meaning that the increase in reported toxin occurrences in recent years may partly reflect an "apparent increase" due to enhanced observational capacity. Additionally, sampling efforts are often concentrated in nearshore and surface waters, potentially underestimating conditions in open seas and deeper layers, while species identification based solely on morphology may introduce misidentification risks. Therefore, the spatiotemporal patterns and trends presented in this study result from the combined effects of environmental changes, the expansion of monitoring networks, and technological innovations in detection. When assessing long-term ecological changes, it is crucial to carefully distinguish between "artifacts of improved monitoring" and "true ecological signals".

4. Detection technologies for marine algal toxins and monitoring in Chinese coastal waters

After clearly understanding the distribution pattern and risk situation of algal toxins in China's coastal areas, how to accurately and promptly identify and quantify these toxins has become a key technical link for implementing effective early warnings, ensuring seafood safety, and conducting source control.

4.1. Biological techniques

Biological detection methods for marine algal toxins assess their toxic activity based on the specific responses of biological systems to the toxins. A variety of biological detection methods for marine algal toxins have been developed. (Meng and Feng, 2016). Among them, the mouse bioassay, as a classical method, played a significant role in the discovery and early research of unknown toxins and is still used as a toxicity equivalence reference for certain lipophilic toxins. However, this method only reflects the magnitude of toxicity and cannot determine the specific composition and concentration of toxins. It also suffers from poor reproducibility, ethical concerns, and specificity limitations, and is gradually being replaced by more sensitive and quantifiable chemical instrumental methods (Clarkson, 1981).

Cytotoxicity assays based on sensitive cell lines offer high throughput but are susceptible to interference from sample matrices. Immunoassays such as enzyme-linked immunosorbent assay (ELISA), chemiluminescence immunoassay (CLIA), and lateral flow immunochromatographic assay (LFIA), utilize the specific binding between antigens and antibodies, demonstrating substantial potential for rapid on-site screening and high-throughput detection. Immunoassays are highly sensitive, rapid to perform, and suitable for large-scale on-site screening, making them common preliminary screening tools for regulatory agencies, but may cross-react with structurally analogous compounds (W.R.G. Baeyens et al., 1998; Liu et al., 2022; Al-Tabban et al., 2024). Enzyme activity inhibition assays, by simulating the physiological mechanisms of toxin action, offer new pathways for cost-effective and rapid detection of specific algal toxins (Tang et al., 2025).

Furthermore, biosensor technology, which integrates biological recognition elements with physical transducers, enables rapid, real-time, and online monitoring of toxins (Zhang et al., 2018). It shows significant potential for portability and automation and has become one of the research hotspots in the development of marine algal toxin detection technologies.

4.2. Chemical analytical techniques

Continuous refinement of chemical analytical techniques has secured them a central role in marine algal toxin detection (Zhang and Li, 2024). These methods typically rely on solvent extracts or chromatographically resolved fractions, after which toxins are identified and quantified by spectroscopic or mass-spectrometric detection. The main chemical detection methods are high-performance liquid chromatography (HPLC), liquid chromatography–mass spectrometry (LC-MS) and its tandem mass spectrometry variant (LC-MS/MS), high resolution mass spectrometry (HRMS), liquid chromatography-high resolution mass spectrometry (LC-HR-MS), capillary electrophoresis (CE) and Raman spectroscopy (Chen et al., 2019).

Compared with other methods, the LC-MS detection technology has the advantages of strong specificity, short analysis time, high sensitivity, and the ability to simultaneously determine different types of marine algal toxins. Currently, it has become the most effective instrumental analysis method in the field of marine algal toxin detection, and mainly for quantitative purpose. Corresponding LC-MS analysis methods have been established for almost every type of marine algal toxin. However, conventional LC-MS/MS methods based on low-resolution mass spectrometry (LRMS) are susceptible to matrix effects (ME), which can compromise both the identification and quantification of analytes. With advances in instrumental platforms, high-resolution mass spectrometry (HRMS) has attracted increasing attention in toxin detection (Zendong et al., 2015). HRMS offers the advantage of non-targeted analysis, enabling retrospective screening of acquired data. The combination of liquid chromatography with high-resolution mass spectrometry (LC-HRMS) integrates the strengths of both techniques, allowing for the screening of a large number of compoundsin a single run, performing non-targeted analysis, and facilitating retrospective toxin detection. However, manual processing and verification—commonplace in quantitative LC-MS/MS—are not feasible for LC-HRMS due to the vast number of detectable analytes. (Costa et al., 2022; Klijnstra et al., 2021; Panda et al., 2022).

Recent studies on phycotoxin detection in Chinese marine waters have consistently shown that LC-MS remains the predominant method for identifying and quantifying common algal toxins. Advanced chemical analysis techniques are pivotal for accurately characterizing marine

algal toxins in environmental samples. For instance, in a basin-wide survey of the Beibu Gulf, LC-MS was employed to quantify 12 target phycotoxins, revealing the widespread presence of domoic acid, pectenotoxin-2, homo-yessotoxin, and gymnodimine A, with clear spatial gradients linked to environmental drivers (Ji et al., 2026). In another methodological advance, a novel solid-phase extraction (SPE) coupled with LC-MS/MS approach was developed to simultaneously enrich and detect 35 dissolved algal toxins from seawater, achieving remarkable sensitivity (detection limits as low as 2.0×10^{-4} ng/L) and successfully identifying nine toxins—including first-reported isomers in China—in coastal waters (Wang et al., 2026). These examples underscore how modern instrumental methods enable precise, multi-toxin profiling and support large-scale monitoring of toxin distribution and dynamics.

4.3. Application scenario of different methods

Currently, the detection of marine algal toxins faces multiple challenges. First, sample matrices such as shellfish tissues, algal suspensions, or sediments are highly complex, containing abundant lipids, proteins, pigments, and other interferents. These can lead to significant matrix effects during extraction, purification, and instrumental analysis, compromising the accuracy of both qualitative and quantitative determinations (Cortese et al., 2020). Second, a given toxin class often comprises numerous structurally similar analogues—for example, saxitoxin and its dozens of congeners (Deng et al., 2025), as well as the okadaic acid and its analogues (Novelli et al., 2021). These analogues and isomers exhibit highly similar chromatographic behavior and even mass spectrometric patterns, imposing stringent demands on separation resolution and identification capability. Third, toxin concentrations in environmental or biological samples span an extremely wide range, from trace levels up to concentrations exceeding regulatory toxicity thresholds, requiring detection methods to combine a broad dynamic range with high sensitivity. Moreover, the physicochemical properties of different toxins vary markedly, including polarity, thermal stability, acid–base behavior, and solubility.

Overall, these challenges have limited the universality and standardization of detection methods, while also driving the development of new strategies such as multi-technology integration, non-targeted screening, and online monitoring. The mouse bioassay method, as the earliest classic method, was widely used globally and played an important role in the discovery and research of unknown toxins. However, it can only determine the overall toxicity level, but cannot identify the exact toxins, and its repeatability is poor. Moreover, with the increasing opposition from animal protection advocates, its application scope has become increasingly limited. With the rapid development of chemical analysis instruments, LC-MS/MS spectrometry has now become the reference method for quantitative detection of various lipophilic toxins and plays an important role in regulatory control (Ji et al., 2026). Enzyme-linked immunosorbent assay is widely used for high-throughput screening of specific toxins (such as saxitoxin). Emerging technologies, including cell-based assays and biosensors, are currently mainly in the research and validation stages and have not yet been routinely applied in regulatory monitoring. This methodological framework ensures reliable compliance testing and also provides space for integrating validated new methods.

Therefore, the selection of an appropriate detection method is fundamentally dictated by the target toxin's chemistry, sample type, and required data quality (Table 3). Based on their chemical characteristic, for toxin groups with high structural diversity and significant differences in toxicity among analogues, such as PSTs and AZAs, LC-MS/MS is the suitable method for quantitative regulation. Although ELISA offers a rapid screening method, its high cross-reactivity in these groups can yield a “false positive” by detecting non-toxic structural analogues, making it unsuitable for confirmation. Among other immunoassay formats, CLIA provides enhanced sensitivity through its enzyme-catalyzed chemiluminescent signal, while LFIA enables simple, equipment-free operation for rapid on-site preliminary screening. Conversely, for poorly characterized or newly emerging toxins, where reference standards are scarce, the high resolving power and non-targeted acquisition capabilities of HRMS are indispensable for discovery and identification, even though it is less practical for routine high-throughput quantification. Biosensors provide a solution to bridge the gap between on-site screening and laboratory confirmation by offering rapid, portable, and quantifiable detection. However, the reliability of this method when handling complex samples needs further improvement. While they enable on-site monitoring of toxins such as saxitoxin, their sensitivity to matrix interference and limited multiplexing capability restricts them to preliminary screening rather than regulatory confirmation.

4.4. Toxin monitoring program in China

Chinese coastal waters are among the areas most prone to HABs and are also one of the marine regions most significantly impacted by algal

Table 3
Strengths and limitations of different analytical methods and related application scenarios.

Methods	Technologies	Strengths	Limitations	Toxin types	Application scenario
Spectrometric methods	LC-MS/MS LC-HRMS GC-MS	Excellent accuracy and sensitivity; Multi-toxin and analogue profiling in a single run; Low sample consumption	High instrumental cost; Requirement for skilled operators; Time-intensive sample pretreatment and analysis; Lack of portability	Lipophilic and hydrophilic marine biotoxins (DA, STX, OA, etc.)	Confirmatory qualitative and (or) quantitative analysis; Identification of unknown toxins
Immunoanalytical method	ELISA LFIA CLIA	High specificity (ELISA/CLIA); Simple, rapid, low-cost, and portable (LFIA); Commercial kits available; Suitable for batch screening	Cross-reactivity and varying sensitivity among analogues (ELISA); Low sensitivity and semi-quantitative (LFIA); Poor stability and high background (CLIA)	STX, OA, DA, DTX, etc.	Batch screening (ELISA); On-site rapid screening (LFIA); Rapid-response moderate-sensitivity detection (CLIA)
Biosensor method	Organic sensors Cell sensors Enzyme sensors Receptor sensors Immune sensors DNA sensors	High sensitivity; Quantifiable; Real-time output; Molecular recognition (label-free and easily modifiable)	Poor quantitative accuracy; Limited capability for simultaneous multi-target detection; Inadequate stability in complex samples	STX, OA, AZAs, etc.	On-site semiquantitative detection; Ultra-trace sample research; Mobile enforcement

toxins. Recently, China has made many efforts in the monitoring of marine red tides and algal toxins. For example, the project "harmful algae and algal toxins in coastal waters of China: investigation and database" (Yan, 2022), funded by the Ministry of Science and Technology of China, has conducted large-scale systematic offshore cruise surveys in China's coastal waters. As report goes, 2637 survey stations were deployed and 4066 field samples were collected. The research team comprehensively analyzed marine algal toxins in phytoplankton and shellfish, and several algal toxin species have been newly recorded in China's coastal environments at the regional scale, including azaspiracid, cyclic imines, and β-N-methylamino-$_L$-alanine. The findings were published in the dataset "Distribution Dataset of Toxic and Harmful Microalgae and Algal Toxins in Coastal Waters of China from 2019 to 2021", which included 106 microalgae distribution maps and 29 algal toxin distribution maps for Chinese coastal seas (Zhang et al., 2024). Simultaneously, the project established the nation's first publicly accessible national algal toxin database. By the end of 2022, it had amassed 186,000 records of species, toxin, and environmental data. The established platform provides real-time data for red tide emergency response, aquaculture self-monitoring, and customs supervision.

In addition to research programs, the Ministry of Natural Resources of China annually releases the "China Marine Disaster Bulletin". This bulletin systematically archives and spatially represents the timing, location, areal extent, and other key parameters of all recorded HAB events occurring throughout the year (2023; 2022; 2021; 2020). Data are acquired through an integrated, multi-source observational network that includes coastal monitoring stations, satellite remote sensing, profiling floats, volunteer vessels, unmanned aerial vehicles, and in-situ sampling campaigns (2024). The observational suite captures the full data chain—sea-surface temperature, nutrient concentrations, phytoplankton community composition, biotoxin levels in shellfish, and associated fisheries losses. Concurrently, the bulletin disseminates exemplary case studies of HAB emergency response, technical guidelines for disaster prevention and mitigation, and science-outreach brochures. By offering a one-stop, authoritative reference on the status, trends, and countermeasures of HAB and toxin hazards, the bulletin enhances the capacity for marine disaster risk reduction and fosters broad public awareness of ocean stewardship and ecological security.

Under the current industry standards for marine algal toxin testing in imported and exported seafood products—issued and implemented under the authority of the General Administration of Quality Supervision, Inspection and Quarantine (AQSIQ)—the vast majority of common algal toxin types are systematically covered. The testing methodology system is relatively comprehensive, encompassing traditional biological assays such as the mouse bioassay (AQSIQ, 2013) and the fluorescent protein phosphatase inhibition assay (AQSIQ, 2008), as well as newer techniques like ELISA (AQSIQ, 2010). For chemical instrumental analysis, the highly efficient and sensitive liquid chromatography-tandem mass spectrometry (LC-MS/MS) serves as the mainstream technology and is currently the most widely applied in practice (AQSIQ, 2015).

These industry standards are consistently updated in response to technological advancements and regulatory needs. Through the timely repeal of outdated standards and the issuance and implementation of new ones, the testing system is ensured to maintain its scientific rigor, applicability, and timeliness, meeting the practical requirements of current food safety supervision and international trade.In the face of the increasing uncertainty in the occurrence time and space of algal blooms, developing more rapid, portable and low-cost on-site detection technologies, as well as achieving simultaneous screening of multiple toxins and early warning, remain important directions for future technological development and management practices. These technological advancements and the improvement of the monitoring system together constitute the cornerstone for addressing the challenge of algal toxins and ensuring the safety of marine ecology and seafood.

5. Conclusions and perspectives

Marine algal toxins represent a double-edged sword. On one hand, they pose significant threats to aquaculture industries and food safety. These toxins can accumulate through the food chain, ultimately causing human poisoning—or even death—through consumption of contaminated shellfish and fish. Therefore, a key focus in addressing this challenge lies in fundamentally understanding the formation mechanisms of marine algal toxins, enhancing the intensity and frequency of detection, and developing therapeutic drugs for marine algal toxin poisoning. On the other hand, due to their unique biological activities and mechanisms of action, low doses of marine algal toxins demonstrate therapeutic potential for neurological diseases, cancer, and other conditions, highlighting their potential medicinal value. However, how to balance the toxicity and therapeutic effects of marine algal toxins is the key issue that needs to be addressed, with the optimization of the chemical structure of candidate toxin being an important direction.From the recent trends in the occurrence of HABs and marine algal toxin outbreaks in Chinese coastal waters, it is evident that human activities are exerting an increasing influence on the oceans. The excessive proliferation of algae has led to more frequent HABs, which in turn intensifies the threat posed by algal toxins to both food safety and marine ecosystems. In response, monitoring and mitigation technologies targeting these toxins continue to advance, strengthening our capacity to confront such challenges. China has conducted research and disseminated information on both HAB outbreaks and algal toxins distribution in its coastal regions. These initiatives have provided a data foundation and decision-making support for risk warnings, scientific prevention, and integrated management of algal toxins. Notably, rapid progress in gene sequencing and editing is progressively revealing the biosynthetic mechanisms of these complex molecules. A clear understanding of these biosynthetic mechanisms is essential to trace toxin origins, thereby providing a molecular and genetic basis for early-stage monitoring and mitigation strategies.

At present, the following issues mainly exist: Firstly, the mechanism of toxin production is not yet fully understood, especially in the complex environment where climate change and eutrophication interact; Secondly, the monitoring system has limitations in terms of temporal and spatial coverage, and lacks convenient and sensitive on-site rapid detection methods; Thirdly, research on the synergistic effects of multiple toxins, the migration and transformation laws in the food chain, and the impact of long-term low-dose exposure on human health is still insufficient; Fourthly, the medicinal development of algal toxins is still limited by their toxicity, and breakthroughs need to be achieved through structural optimization and in-depth exploration of pharmacological mechanisms.

Looking ahead, future research should prioritize a mechanism-driven and integrated framework to better understand and manage marine algal toxins. In particular, advancing a systems-level understanding of toxin biosynthesis—through multi-omics approaches and ecological modeling—will definitely improve the prediction of HAB events and toxin outbreaks. In parallel, there is a continued need to develop portable, highly sensitive, and real-time detection technologies—such as biosensors and microfluidic platforms—to enhance spatial–temporal resolution and enable on-site applications, thereby strengthening risk assessment and rapid response capacity. Notably, China has established and continues to reinforce a nationwide monitoring and early-warning network for HABs and algal toxins, integrating routine surveillance, emergency response, and data-sharing. However, long-term, continuous, and stable monitoring, combined with multi-factor data analysis incorporating environmental changes, ecological shifts, and species migration, will help further elucidate the dynamic patterns of algal toxin distribution, variation, and threat status in the relevant sea areas, thereby enabling early risk prediction.

In parallel, although marine algal toxins present undeniable risks to food safety and ecosystem health, they also harbor untapped medicinal

potential. Future efforts should move beyond single-toxin studies toward a more comprehensive evaluation of toxin mixtures, focusing on their synergistic effects, food chain transfer, and long-term low-dose health impacts. From a translational perspective, unlocking the medicinal value of marine algal toxins will require precise control of their toxicity through structural optimization and in-depth pharmacological investigation. Strategies such as structure–activity relationship (SAR) analysis, synthetic biology, and enzyme engineering will facilitate the development of safer and more selective analogues. Ultimately, by bridging environmental science and biomedical research, it is possible to both mitigate the risks of algal toxins and harness their unique bioactivities for therapeutic innovation.

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Fangyuan Cheng: Writing – original draft. **Junfeng Zhang:** Writing – original draft. **Qianqian Li:** Writing – original draft. **Bo Hu:** Writing – review & editing. **Hao-Bing Yu:** Writing – review & editing. **Shengying Li:** Writing – review & editing. **Xingwang Zhang:** Conceptualization, Writing – review & editing.

Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

Data availability

Data will be made available on request.

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