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Mechanisms of Algal Toxin Production: From Genes to Environmental Triggers

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Abstract Algae toxins are toxic secondary metabolites produced by algae during water blooming, with a variety of chemical structure types and toxicological effects. With the eutrophication of water bodies and the intensification of climate change, harmful algae blooms in freshwater and marine ecosystems around the world occur frequently and releases a large number of toxins, posing a serious threat to ecosystems and human health. In order to reveal the internal mechanism of algatoxin production, researchers started from genetic and environmental factors and carried out multiomic studies such as genome, transcriptome, metabolomic and ecological experiments. This study reviews the classification, chemical structure and mechanism of action of common algae toxins, explores the ecological function of toxins in algae and the food chain migration process; summarizes the discovery and characteristics of genes and gene clusters related to algae toxin biosynthesis; analyzes the impact of environmental factors such as nutrients, light, temperature, hydrodynamics and biological interactions on the production of toxins, as well as the latest progress in toxin monitoring and prediction based on molecular markers, remote sensing and big data. Finally, a prospect is proposed for the insufficient progress of the current research, in order to provide a theoretical basis for algatoxin risk assessment, ecological management and prevention and control strategies.

Keywords Algae toxins; Gene clusters; Molecular regulation; Environmental factors; Monitoring and prediction

1 Introduction

Algae toxins are toxic secondary metabolites produced by toxin-producing algae (mainly cyanobacteria, dinoflagellate, diatoms, etc.) in water. They can be divided into several major categories such as hepatic toxins (such as microcystins), neurotoxins (such as paralytic shellfish toxin Saxitoxin, anatoxin, amnesia shellfish toxin Domoic acid), and diarrheal toxins (such as oxalic acid, Okadaic acid) and Okadaic toxins. These toxins have complex molecular structures and diverse toxicological mechanisms (such as microcystis toxins can inhibit protein phosphatases, while marine toxins often act on ion channels) (Zhou et al., 2021; Thomas et al., 2024).

Harmful Algal Blooms (HABs) are a rapid proliferation phenomenon of algae populations. They often break out under eutrophication conditions. They are accompanied by the release of a large number of algal toxins, resulting in hypoxia, reduced transparency in water, and poisoning events in aquatic organisms and humans through the food chain (Danil et al., 2021). For example, HABs can cause the water to reduce dissolved oxygen, hinder plant photosynthesis, and cause a large number of deaths such as fish and shellfish. At the same time, toxins are enriched through food webs, posing a serious threat to the safety of human drinking water and seafood. According to statistics, there are many food poisoning incidents caused by algatoxins every year around the world, which poses an ongoing challenge to public health. Therefore, in-depth research on the production mechanism of algae toxins, from gene regulation to environmental triggers, is of great significance to understanding the formation rules of harmful algae blooms and formulating pollution control strategies.

This study analyzes the ecological function of toxins in algae and the food chain migration process; introduces the impact of horizontal transfer such as transposons on the diffusion of toxin production capacity; elaborates on the molecular regulatory mechanisms at the level of gene regulation and epimodal modification, as well as major signaling pathways and regulatory factors; combines the latest progress in toxin monitoring and prediction of related technologies, aiming to improve the risk assessment and ecological management capabilities of algatoxins.

2 Types and Biological Functions of Algae Toxins

2.1 Chemical structure and mechanism of common algae toxins

There are many types of typical algae toxins, and there are obvious differences in their chemical structure and toxicological mechanism. For example, the microcystis toxins (MCs) produced by cyanobacteria are cyclic peptides, catalyzed by non-ribosomal peptide synthetase (NRPS) and polyketone synthetase (PKS). They are generally circulating peptides composed of 7 amino acids, which have a strong inhibitory effect on protein phosphatases 1 and 2A, resulting in increased risk of hepatocyte damage and liver cancer (Shishido et al., 2013). Neurotoxins include Anatoxin-a and paralytic shellfish toxin (PSP, mainly represented by Saxitoxin, STX), etc. They are mostly small-molecular alkaloids that cause neurotoxicity by blocking sodium channels or affecting the release of neurotransmitters. Amnesic shellfish toxins (polycarboxylic acids with glycol structure) produced by seaweed can overactivate glutamate receptors, leading to neuroexcitation toxicity (Maguire et al., 2018); Okada toxins and other diarrheal toxins (such as OA) are polyethers or fatty acid derivatives that cause diarrhea and cell damage by inhibiting protein phosphatase.

2.2 The ecological function of toxins in algae: defense and competition

In addition to the occasional metabolites produced by algae, toxins often have important ecological significance. Existing research suggests that algatoxins may be used as a chemical defense substance for algae to inhibit competitive algae or to repel herbivorous organisms, thereby improving the competitiveness of toxin-producing populations. For example, some cyanobacteria secrete microcystis toxins or verbena toxins under nutritional deficiency or other stress conditions to affect the growth of coexisting populations; the production of anaphylactic toxins and paralytic shell toxins is also believed to reduce biological predation or competitors (Figure 1) (Teneva et al., 2023). In addition, toxins may also be related to stress tolerance in algae: studies have found that microcystis toxin plays a role in antioxidant stress and can help algae resist highlights or heavy metal stress; similarly, some dinoflagellate toxins are reported to be associated with population survival strategies under low temperature or low nutritional conditions. Algatoxins may play the role of signaling molecules, allelopathic substances or stress defense agents in the algae population ecology, so that toxin-producing algae have an advantage in resource competition and environmental stress. In addition, the accumulation of toxins through the food chain can weaken the growth and reproduction of algae predators or higher consumers, and also have an indirect effect on maintaining the stability of toxin-producing algae populations (Li, 2014).

2.3 Accumulation and transmission of toxins in the food chain

The transmission characteristics of algatoxins in the food chain are an important manifestation of their ecological harm. Toxins produced by algae can be enriched biologically through feeding of benthic organisms such as zooplankton and shellfish, and are further transmitted to fish, birds and even humans along the food chain. Studies have shown that microcystis and other algatoxins are often detected in fish and shellfish. After being ingested, they can "amplify" the toxicity in the food chain. For example, after eating toxic shellfish, top predators or humans can experience symptoms of food poisoning (Kershaw et al., 2021). At the same time, atmospheric aerosols are also a way to spread toxins. Tide explosions and waves can spray toxins into the air, and it will also cause poisoning after being inhaled by the respiratory tract. Therefore, algatoxins not only threaten native plankton and benthic invertebrates, but also affect higher trophic levels through the feeding chain, becoming the focus of attention of the entire ecosystem and even public health.

3 Genes and Gene Clusters Related to Algae Toxin Synthesis

3.1 Discovery and identification methods of genes related to toxin synthesis

With the development of molecular biology technology, toxin biosynthesis genes of toxin-producing algae are constantly being discovered. Traditional methods include designing primers using conserved sequences of known toxin synthase genes and detecting gene presence in unknown strains or environmental samples by PCR. For example, amplification of the microcystis toxin synthetase *mcyE* gene, the *anaC* gene of *anaC* gene and the paralytic castis toxin synthetase *sxtA* gene by conventional PCR can effectively detect and distinguish different types of toxin cyanobacteria (Ribeiro et al., 2020; Moraes et al., 2023). In recent years, high-throughput

sequencing and transcriptome analysis have played an important role in the discovery of toxin genes. American scientists analyzed marine diatom toxicity-producing gene clusters (such as the dodolalic acid synthesis gene cluster dabA-dabD of pseudo-rhombus algae) through comparative transcriptome analysis; similarly, genome sequencing revealed the composition of multiple toxin synthesis gene clusters in dinoflagellate and cyanobacteria (Lorenzi et al., 2019). In addition, metabolomics and isotope labeling techniques are also used to correlate specific metabolites with candidate genes, providing auxiliary evidence for the analysis of toxin synthesis pathways.

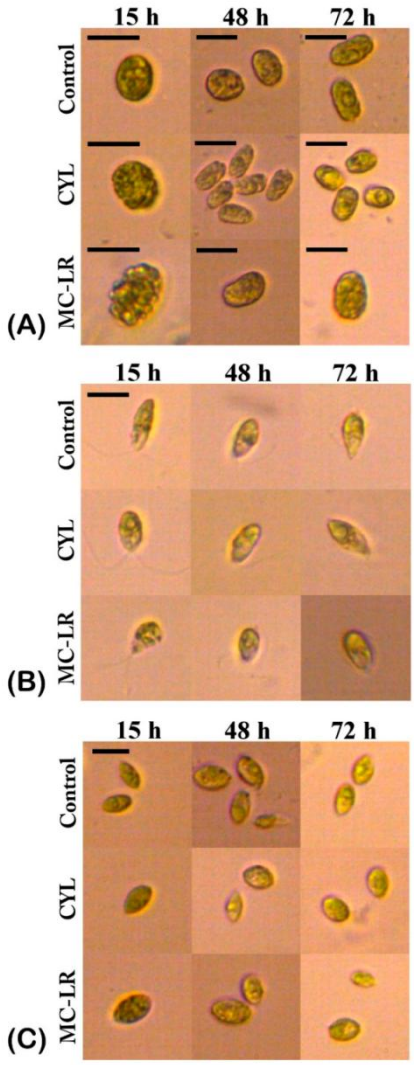

Figure 1 Morphology of *Chlamydomonas asymmetrica* (A), *Dunaliella salina* (B), and *Scenedesmus obtusiusculus* (C), after exposure to 1 μg/mL MC-LR and CYL for 15, 24, 48, and 72 h. Control: non-treated cell cultures. Bar = 10 μm (Adopted from Teneva et al., 2023)

3.2 Structural characteristics of key toxin synthesis gene clusters

Toxin synthesis genes in toxin-producing algae usually exist in clusters, encoding enzymes required for the complete biosynthetic pathway. Taking the cyanobacteria microcystis toxin as an example, the mcy gene cluster of *M. aeruginosa* PCC7806 spans about 55 kb, including a total of 10 open reading frames of mcyA-mcyJ, encoding biosynthetic enzymes such as multimodal polyketone synthetase (PKS) and non-ribosomal peptide synthetase (NRPS) (Rhee et al., 2012). The cluster is closely arranged in two directions of operon structures transcribed, providing a complete enzyme system for the synthesis of a complex peptide loop. Similarly, the gene cluster (ndaA–ndaF) of the cyclogenic toxin Nodularin is highly homologous to the mcy cluster and shares some of the core enzymes. The synthesized gene cluster of dinoflagellate paralytic cadoxin (PSTs) contains more than 20 genes, encoding enzymes such as PKS and aminotransferases required to synthesize STX; the oxalic acid

(*DabA-dabD*) gene cluster was found in some marine diatom genomes, indicating that non-cyanobacteria can also perform complex toxin biosynthesis. The common characteristics of these gene clusters are: the gene arrangement is compact, mostly in tandem structures, usually spanning tens of kb or even hundreds of kb intervals, the core encodes a complex biosynthetic enzyme, and there are often modified enzymes or regulatory elements on the side. This structural characteristic ensures efficient coordination of the toxin biosynthesis process and provides a basis for engineering replication and functional research.

3.3 Gene horizontal transfer and diffusion of toxin synthesis ability

Studies have shown that toxin synthesis gene clusters have strong mobility and mostly transfer horizontally between different species or strains. Genomic analysis found that transposase or integrase genes associated with multiple toxin-producing gene clusters existed next to each other. For example, mcy, NDA (cyclic cytoxin) and SXT (numbing) gene clusters can all detect relevant sequences on certain plasmids or transposal elements, suggesting that these large gene clusters may mediate transmission in populations through transposons (Popin et al., 2021). This horizontal transfer phenomenon allows relative populations that do not have the ability to produce toxins to change into toxic types by obtaining gene clusters, causing the rapid spread of toxin production capacity. In recent years, there has also been evidence that genomic rearrangements and gene deletions/repetitions of gene clusters are one of the sources of strain diversity. These studies show that toxin gene clusters are not rigid and unchanged, but are constantly spread and optimized through horizontal gene transfer and structural remodeling during evolution, so that the toxin synthesis capacity can be dynamically distributed in algae populations (Chen et al., 2024).

4 Molecular Regulation Mechanisms of Toxin Production

4.1 Transcriptional regulatory factors and signal transduction pathways

The expression of toxin biosynthetic gene clusters is regulated by a variety of transcription factors and signaling pathways. Taking the cyanobacterium microcystis toxin as an example, it is known that the nitrogen fixation regulator NtcA can directly bind to the promoter region of the mcy gene cluster to couple toxin synthesis with nitrogen metabolism. In addition, global regulators Fur (hepcidin) and Sigma factors may also regulate mcy cluster transcription by sensing metal or light changes. In dinoflagellate, although the specific transcription factor recognition mechanism is not clear, studies suggest that signals such as cell cycle, light intensity and nitrogen and phosphorus nutrient status can affect the expression of toxin genes. In terms of signaling, phosphorylation cascades, second messengers (such as circular AMPs), etc. may be involved in the interaction of nuclear factors and toxin genes (Zhu et al., 2016). Overall, the transcriptional regulatory network is complex and multi-level, involving environmental signal perception and fine regulation of transduction into target gene promoters, but the detailed mechanism is still being explored.

4.2 Effects of epigenetic modification on toxin synthesis

In addition to direct regulation of transcription factors, epigenetic mechanisms (such as DNA methylation, histone modification) may also participate in the regulation of toxin synthesis. In recent years, some scholars have explored the methylation pattern of the Microcystis genome through single-molecule real-time (SMRT) sequencing and other methods, and found that some regulatory genes have different methylation levels in the poison-producing strains, suggesting that they may affect gene expression activity (Stern et al., 2024). However, there are currently few reports on epigenetic regulation of algae toxin synthesis gene clusters. In the future, chromatin immunoprecipitation sequencing (ChIP-seq) and genome-wide methylomics can be used to evaluate the regulatory effect of methylation, acetylation and other modifications on mcy, sxt, and Ana cluster promoters to reveal the role of epigenetics in the regulation of toxin production (Popin et al., 2021).

4.3 Integration analysis of metabolic networks related to toxin synthesis

Toxin synthesis requires a large amount of precursors and energy, so its yield is often associated with the overall metabolic state of algae. Multiomics data integration analysis has been used to study the interconnection of toxin synthesis and other metabolic pathways. Through joint metabolomic-tratome analysis, it was found that conditions

rich in carbon sources are often conducive to the synthesis of carbon-rich toxins such as microcysticus toxins (Zhang et al., 2024); the nitrogen metabolism pathway is directly related to the supply of precursors for toxin production. When nutrients are unbalanced, excess energy and carbon sources may turn to toxin synthesis to maintain cellular homeostasis. Overall metabolic network analysis also reveals the cross-regulation of amino acid, lipid metabolism and toxin biosynthesis. Combining the metabolic pathway model helps to understand how algae balance growth and toxin production in resource allocation, providing a basis for dynamic regulatory models (Rawls et al., 2019).

4.4 Case analysis: case study on the regulation of dinoflagellate toxins by nitrite signal

Some studies have focused on the effects of specific signaling molecules on toxin production, such as the role of nitrite signals in the inorganic nitrogen form in dinoflagellate toxin synthesis. A study reported that supplementing different concentrations of nitrite in certain dinoflagellates with paralytic shellfish production changes the expression of the SXT gene cluster and toxin yield. This implies that different nitrogen sources or intermediate products act as signaling molecules to regulate toxin synthesis through nitrogen metabolism-related regulatory factors (Abassi et al., 2023). However, there are still few cases in this area, and more experiments are needed to verify them in combination with gene expression analysis. For example, using transcriptome technology to compare gene expression profiles before and after nitrite treatment can clarify changes in relevant signaling pathways and transcription factors such as NtcA or GlnB proteins, thereby revealing how nitrite affects the transcription of toxin synthesis gene clusters.

5 Effects of Environmental Inducers on Algae Toxin Production

5.1 Changes in nutrient concentration and proportion

Nutrients (nitrogen, phosphorus) are key environmental factors that affect algae growth and toxin production. Studies have shown that under conditions of adequate and balanced nutrients, toxin-producing algae generally prefers rapid growth rather than large accumulation of toxins; while when nutrients are unbalanced (especially N or P-limited), algae tend to increase toxin synthesis as a coping strategy. Zeng Ling et al. (2018) pointed out that under low nitrogen or low phosphorus conditions, the individual toxin content of dinoflagellate *Prorocentrum lima* is significantly increased, and the effect of phosphorus restriction on toxin accumulation is often greater than that of nitrogen restriction (Figure 2) (Wan et al., 2023). This phenomenon may be because growth is inhibited when nutrients are restricted and excess carbon resources are redistributed for toxin synthesis. Furthermore, for nitrogen-rich toxins (such as microcystistoxins), their synthesis is inhibited when the nitrogen supply is insufficient, while it is relatively promoted when phosphorus is limited (Brandenburg et al., 2020). Overall, changes in nutrient concentration and N: P ratio significantly regulate algatoxin yield and type by affecting algae metabolism and energy distribution.

5.2 Light, temperature and hydrodynamic conditions

Light intensity and light cycle are important factors that affect the growth of photosynthetic toxin-producing algae. Generally speaking, moderate increase in light can enhance the photosynthesis and metabolic activity of the algae, thereby increasing the rate of toxin synthesis; but excessive or violent fluctuations may also lead to light inhibition and reduce toxin production. Temperature also significantly affects the production of algatoxins: each toxin-producing algae has its optimal toxin-producing temperature range, and toxin synthesis decreases when it is out of range. Warm and warm conditions often promote the reproduction and accumulation of toxins of cyanobacteria and dinoflagellate, which is also the main reason for the frequent occurrence of algae blooms and the increase in toxin levels in summer. In terms of hydrodynamic conditions, steady water bodies often promote the accumulation of phytoplankton algae, while strong mixing or disturbance can disintegrate the algae population and release intracellular toxins. But mixing can also disperse algae to different depths of the water column to change the light environment, thereby indirectly affecting toxin synthesis (Pavlidou et al., 2020). For example, circulating water sometimes produces high concentrations of dissolved toxins at night. Therefore, physical factors such as light, temperature and water fluidity comprehensively regulate the physiological state and nutritional acquisition of algae, thereby affecting the intensity and timing of toxin production.

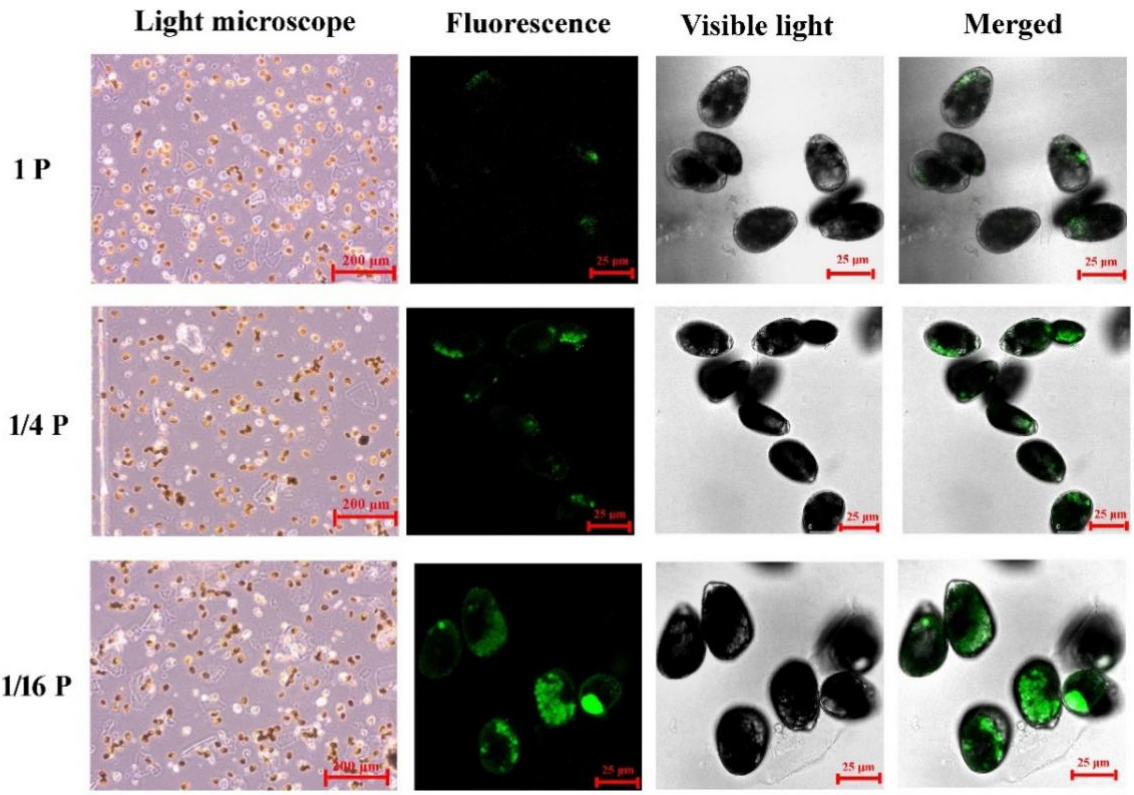

Figure 2 Light microscopy (LM) and confocal microscopy (CLSM) images of *P. lima* cells in P-limited conditions and a control. Representative confocal microscope images of *P. lima* cells showing oil bodies with green fluorescence are displayed (Adopted from Wan et al., 2023)

5.3 Microbial community and symbiosis/competitive relationship

The interaction between algae and symbiotic or competitive microorganisms is also an important factor in affecting toxin production. Certain concomitant bacteria promote algae growth and toxin synthesis, such as indirectly affecting toxin levels by providing vitamins or breaking down nutrients. Conversely, inhibitory or competitive microbial communities may reduce the growth rate of toxin production by producing antagonistic substances or competing nutrients. In natural water bodies, pathogenic microorganisms or special bacteria can also degrade toxins and alleviate toxin accumulation (Zeng et al., 2020). Clusters of bacterial genes that have the ability to degrade microcystis toxins (such as mlrA-D) have been found to break the toxin into a nontoxic component. Therefore, water body microbial community structure, bacterial and algae symbiosis and microbial competition may all significantly regulate the production and decomposition process of algatoxins.

5.4 Case analysis: research on the relationship between nutrient salt and toxin level in freshwater lakes

In many freshwater nutritious lakes (such as Taihu Lake in China, Dianchi Lake, etc.), research has found that nutrient load is highly correlated with microcystis toxin content. Specifically, the input of excess nitrogen and phosphorus nutrients promotes the outbreak of microcysticus, but long-term high nitrogen often makes phosphorus in water a limiting factor, and the concentration of cytotoxin tends to increase when phosphorus is relatively scarce. Monitoring data show that in these lakes, when the temperature rises in spring and summer accompanied by the peak of nitrogen and phosphorus input, the microcystis community proliferates rapidly and produces a large number of MCs; after the nutrients are consumed in autumn, the MCs released by the rupture of the algae maintain a high level of water toxicity (Schampera and Hellweger, 2024). Therefore, lake nutrition regulation strategies (such as reducing exogenous nitrogen and phosphorus load) are crucial to control algatoxin levels, and fine adjustments to nutrient structure will also affect the final toxin output (Lawson and Young, 2025). These research cases highlight the key role of nutrition management in ecological restoration and toxin prevention.

6 Multi-Level Regulatory Model For Toxin Production

6.1 Gene-environmental interaction model

Toxin production is the result of the interaction between genes' intrinsic abilities and external environmental conditions. Existing research proposes a gene-environment interaction regulation model, which believes that the expression of gene clusters is driven by environmental signal input, and gene products (toxins) may also feedback to regulate growth and metabolism. The microcystis toxin mcy gene cluster is affected by the nitrogen regulator NtcA, which reflects the genome's response to exogenous nutritional status; at the same time, MCs are believed to be able to affect the iron metabolism and signaling pathways of microcystis itself (indirectly regulate gene expression), forming a positive and negative feedback circle (Wei et al., 2024). When external conditions change (nutrition, temperature, light intensity, etc.), the gene expression model is quickly adjusted to adapt to the new environment. This type of interaction model emphasizes that simple gene cluster annotation is not enough to predict toxin yield, and environmental variables need to be integrated into the model to more accurately describe the space-time dynamics of toxins.

6.2 Dynamic regulation of toxin synthesis and metabolic energy distribution

In algae cells, toxin biosynthesis requires a large amount of energy and precursor substances, so the dynamic regulation of toxin synthesis is closely related to the distribution of cell metabolic energy. Research shows that when cell growth rate slows down (such as entering a stable period), the immediate yield of toxins can remain unchanged or relatively increased, resulting in an increase in cell toxicity (Salvador et al., 2016). This is because during the growth restricted phase, excess energy is redistributed to toxin biosynthesis. On the contrary, during the rapid growth period, energy is mainly used for cell reproduction, and the amount of newly synthesized toxins is low. This energy distribution model illustrates the relationship between growth kinetics and toxin concentration, and also provides a theoretical basis for understanding the laws of toxin accumulation at different growth stages. A dynamic metabolic model constructed incorporating multiomics data can be used to simulate how algae regulate energy flow to balance growth and toxin production under different environmental conditions.

6.3 Comprehensive regulatory network revealed by multiomics data

In recent years, the joint analysis of multipleomics (genome, transcriptome, proteome, metabolomic, epigenetic group, etc.) has made breakthroughs in algatoxin research. By integrating these data, a complete toxin synthesis regulatory network map can be drawn. Single-cell sequencing technology can identify gene modules with the greatest differences in expression between toxic and avirulent strains; proteome-metabolomic analysis reveals changes in toxin precursor supply and transporters; epilogue data supplement the modification information at the transcriptional regulation level. Combining these high-dimensional data can establish a hierarchical network model from gene-transcription-protein-metabolism, identify key regulatory nodes and pathways, and provide multi-scale explanations for predicting toxin production. This type of comprehensive regulatory network research is becoming a hot topic in the future, and it is expected to describe the full dynamics of toxin production at the single cell level (Erwin et al., 2023; Li et al., 2024).

7 Technological Progress in Monitoring and Predicting Algae Toxin Production

7.1 Real-time monitoring method based on molecular markers

With the analysis of toxin synthesis gene clusters, real-time monitoring based on gene markers has become an effective means to quickly detect the poison-producing populations in algae flowers. Traditional ecological monitoring methods are difficult to quickly distinguish between toxin-producing and non-toxin-producing algae strains, while molecular technologies such as PCR and qPCR can detect the abundance of toxin synthetic genes (such as mcyE, anaC, sxtA, etc.) to evaluate the potential toxicity risks in real time. In addition, high-throughput sequencing technologies (such as 18S/16S sequencing or functional gene-based metagenomics) can quickly obtain microbial community structure and toxin gene diversity in water bodies, providing a basis for early warning. In recent years, environmental DNA (eDNA) detection methods have also been developed, which can directly amplify and quantify the scattered DNA in water samples without distinguishing between cells or DNA regions,

so as to achieve sensitive monitoring of pollutants (Liu and Han, 2025). These molecular marker methods have high sensitivity, high specificity and automation characteristics, and are suitable for rapid early warning of algatoxin events.

7.2 Remote sensing and big data-driven toxin prediction model

Satellite remote sensing technology can indirectly monitor the occurrence of algae blooms and estimate the concentration of chlorophyll by detecting changes in the water color spectrum, but it is still difficult to judge the specific toxin type. In recent years, methods combining machine learning and big data analysis have been used to construct toxin prediction models. Some studies use multi-source data (meteorology, nutrients, historical algae bloom event records, water quality parameters, etc.) to predict potential algae bloom outbreaks and toxin concentration trends. Integrated models such as deep neural networks and random forests have made progress in experiments, which can screen out the key environmental factors driving toxin accumulation and make dynamic predictions (a study combined with hydrodynamic model and pollution source distribution to achieve real-time forecasts of exogenous nitrogen and phosphorus input in lakes and microcystic toxin concentrations). Looking ahead, combining remote sensing high-frequency monitoring with machine learning models can achieve more timely and accurate toxin risk warnings and provide support for ecological management of large-scale waters such as reservoirs and lakes.

7.3 New high sensitivity analysis technology for toxin detection

At the laboratory analysis level, with the advancement of instrument technology, algatoxin detection has entered the era of high sensitivity. Liquid chromatography-mass spectrometry (LC-MS/MS) technology can quantify multiple algatoxin isomers simultaneously, with sensitivity reaching the nanogram level, and has become the current detection standard; immunoassay methods (ELISA, colloidal gold) are widely used for rapid on-site screening due to their simple operation. In addition, new nanosensors and molecular probes are also under development, enabling direct dilution-free measurement and low-cost detection. More and more research focuses on real-time detection devices in the field, such as multi-functional instruments based on microfluidic chips, or portable devices that can be read through mobile phones, which will provide a more convenient means to respond to algatoxin events in a timely manner.

8 Conclusions and Prospects

At present, significant progress has been made in the research on the mechanism of algae toxin production both at the genetic level and in environmental response. Researchers have identified a variety of toxin-synthesis gene clusters and their core regulatory factors, such as NtcA-mediated nitrogen response pathways; combined with molecular and ecological evidence, a comprehensive regulatory network of gene-metabolism-environment has been gradually constructed. However, there are also shortcomings in the research: many key regulatory elements (such as feedback regulation of nonstructural proteins and metabolic intermediates) have not been clarified; the role of epigenetic regulation and genomic plasticity in toxin production needs to be further revealed; the mechanism of environmental factors affecting each factor is complex, and the interaction effects between factors still lack quantitative description. In addition, most current monitoring and prediction methods rely on empirical models, and prediction accuracy and timeliness need to be improved.

The study of algatoxin production mechanism has important implications for ecological management. Revealing the association between toxin synthesis and environmental stress and nutritional fluctuations can provide early warning indicators for algae burn prevention and control, such as reducing toxin risk by controlling nitrogen and phosphorus input structure. The improvement of the genetic marker monitoring system will make early warning more targeted.

The focus of future research includes: applying gene editing and synthetic biology tools to verify the functions of key regulatory factors; developing multi-scale and multi-parameter dynamic models to integrate gene information and environmental variables; deepening the application of multiomics in ecological niche and evolutionary perspectives, and understanding the origin and adaptability of toxin gene clusters. In addition, a comprehensive

toxin monitoring and early warning platform combining machine learning and Internet of Things technology will also become a research hotspot. Through the above efforts, it is expected to achieve a full-chain management strategy from basic research to application level, providing reliable support for responding to the increasingly frequent harmful algae blooms and toxin hazards under the background of global climate change.

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Conflict of Interest Disclosure

The authors confirm that the study was conducted without any commercial or financial relationships and could be interpreted as a potential conflict of interest.

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