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Response and Adaptation Mechanisms of Algal-Bacterial Symbiotic Systems Under Emerging Pollutant Stress

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Abstract. With the continuous advancement of industrialization and urbanization, emerging pollutants—including antibiotics and their resistance genes, personal care products, and microplastics—have been increasingly released into environmental matrices. Their persistence, bioaccumulation potential, and ecological risks have emerged as core research foci in global environmental science. As a pivotal component of aquatic ecosystems, the algal-bacterial symbiotic system fulfills an irreplaceable ecological role in material cycling, energy flow, and environmental purification. This study systematically reviews the categories, physicochemical properties, and environmental fates of typical emerging pollutants, elaborates on the community structure and core ecological functions of algal-bacterial symbiotic systems, and comprehensively analyzes the impacts of emerging pollutants on these systems at both physiological and molecular levels. Furthermore, it reveals the underlying response and adaptation mechanisms of the systems under pollutant stress. Finally, the limitations of current research are summarized, and future research directions are proposed, aiming to provide theoretical support and scientific references for the protection of aquatic ecological environments and the engineering application of algal-bacterial symbiotic systems.

Keywords: Emerging pollutants, Algal-bacterial symbiotic system, Stress response, Adaptation mechanism

1. Introduction

Rapid industrialization and urbanization have kept releasing emerging pollutants into water environments. These include antibiotics, personal care products, and microplastics, and such substances have already posed serious threats to the stability of aquatic ecosystems [1]. Taking river basins as an example, the distribution of antibiotic pollution shows clear spatial and seasonal differences. For instance, the detected concentration of macrolide antibiotics in the Liaohe River Basin reached 201.88 ng/L, while in the Haihe River Basin the concentration of quinolone antibiotics climbed as high as 248.66 ng/L. What is more, across six major river basins in China, antibiotic concentrations during the dry season are generally 1.48 to 7.36 times higher than those in the rainy season, and this situation brings moderatetohigh ecological risks to algae [2].

Microplastics have drawn widespread attention from researchers because they are highly persistent in the environment and have a strong ability to adsorb other pollutants. Their main sources

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include polymer particles in cosmetics, plastic raw materials, and various types of municipal solid waste [3]. Via electrostatic interactions, microplastics can form stable complexes with microorganisms [4]; at the same time, they can also go through interfacial adsorption and degradation processes, and microorganisms secrete extracellular polymeric substances (EPS) and extracellular enzymes, which then mediate these processes [5-7]. Research has shown that high concentrations of microplastics—anywhere from 10 to 100 mg/L—can greatly inhibit the biomass of algalbacterial symbiotic systems, reducing the ratio of chlorophyll a (Chl a) to mixed liquor suspended solids (MLSS) by 0.19 mg/g and also lowering the removal efficiency of organic matter, nitrogen, and phosphorus by 4.11% to 5.06% [8]. So overall, the combined stress coming from these emerging pollutants does pose a substantial threat to both the structural integrity and the functional stability of aquatic ecosystems.

Algalbacterial symbiotic systems are central drivers of material cycling and energy flow in aquatic ecosystems; they play a key role in regulating the biogeochemical cycles of carbon, nitrogen, and phosphorus, and they achieve this regulation through nutrient exchange and metabolic coupling between algal photosynthetic products and bacterial metabolism [9]. These systems have considerable potential for engineering applications in pollutant removal, but their functional performance depends heavily on the optimal regulation of environmental factors such as light intensity and pH [10]. That is why carrying out systematic research on how emerging pollutants affect algalbacterial symbiotic systems and on how these systems respond to such impacts has great theoretical and practical importance for the protection and management of aquatic ecological environments.

2. Research methods

AA bibliometric analysis using the Web of Science database has revealed that the research landscape, development trends, and hot topics in the field of emerging pollutants and algalbacterial symbiosis all have their own distinct features. When it comes to national distribution, research in this area has formed a development pattern where China sits right at the center, while European and American countries serve as important supporting players (Figure 1). China comes in first worldwide with a publication share of 53.64%, and this number really shows its strengths in research accumulation and investment. The United States follows behind with a share of 10.92%; meanwhile, eight other countries—including India and Italy—each account for somewhere between 2% and 6% of total publications, so these countries have gradually turned into key research forces in this field. This kind of distribution not only points to China's regional research advantages but also suggests that international collaboration on related work has been growing over time.

If we look at how things have changed over the years, driven by the world's growing concern about environmental issues, the annual number of publications in this field rose steadily—from 783 in 2014 up to 3301 in 2023 (Figure 2). After 2023, though, publication numbers showed a slight downward trend, dropping to 3154 in 2024 and then to 3029 in 2025; even so, the overall number has stayed pretty high. This suggests that research in this field has now entered a phase where things are steadily deepening and getting refined.

As for research hotspots, the field does show some obvious technologyoriented characteristics (Figure 3). TiO_2 photocatalysis (12.66%), advanced oxidation processes (10.12%), and adsorption technology (5.26%) are the core physicochemical remediation technologies, and they also represent the mainstream directions for controlling current emerging pollutants. Research related to atmospheric aerosols and air pollution makes up the second largest category, and this reflects how the field has been focusing on multimedia pollution issues that involve both water and air

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environments. Targeted research on typical emerging pollutants like microplastics and persistent organic pollutants accounts for about 2% to 3% of total research, and these areas have gradually emerged as important research branches. Technologies such as metalorganic framework materials and bioremediation account for a relatively small proportion, so they're still in the exploratory development stage. All in all, the research directions in this field match up well with the practical technical needs of emerging pollutant control: physicochemical remediation technologies are relatively mature and see wide use, while specialized research on emerging pollutants and the exploration of cuttingedge technologies (like new materials and bioremediation) have become key directions for future development.

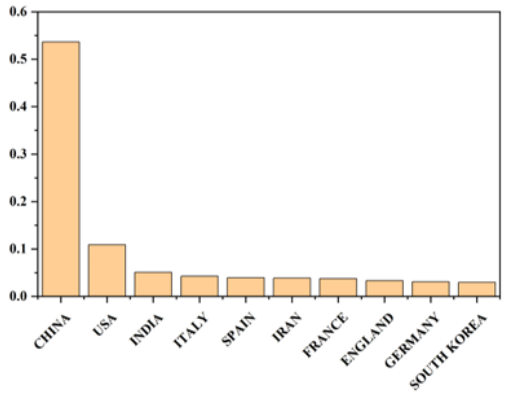

Figure 1. Distribution of the top 10 countries' publications in the field of emerging pollutants and algal-bacterial symbiosis

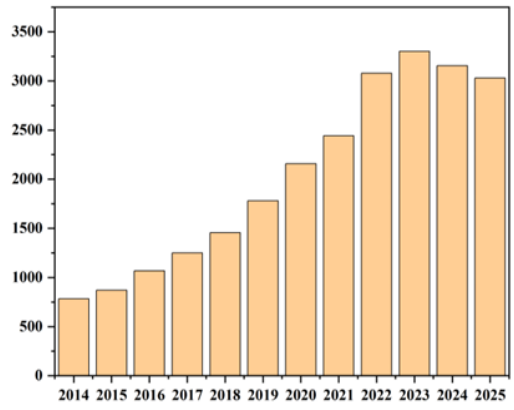

Figure 2. Annual publication trend in the field of emerging pollutants and algal-bacterial symbiosis from 2014 to 2025

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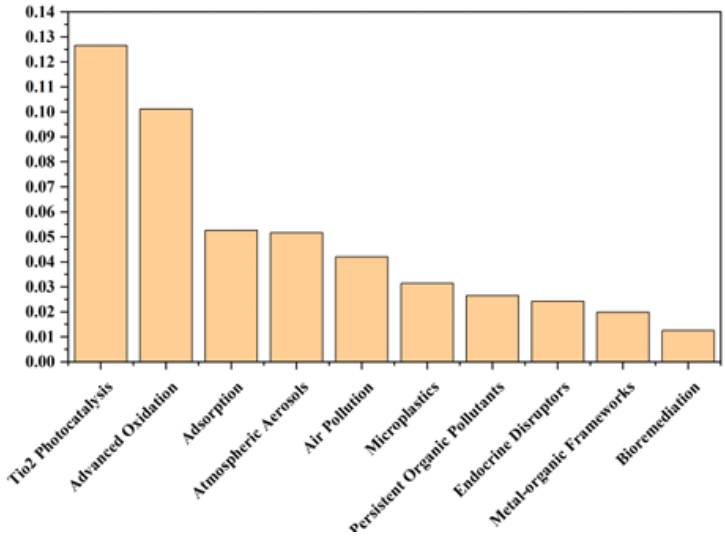

Figure 3. Distribution of the proportion of high-frequency keywords in the field of emerging pollutants and algal-bacterial symbiosis

3. Types and core characteristics of emerging pollutants

Emerging pollutants refer to contaminants derived from human activities that are clearly present in the environment and pose risks to human health and ecological systems. Due to their short production/use history or the late discovery of their hazards, relevant laws, regulations, and standards are either absent or incomplete. Such pollutants typically exhibit wide sources, low environmental concentrations, strong persistence, and significant biotoxicity, with uncertain removal efficiency by traditional water treatment processes [1]. Currently, internationally concerned emerging aquatic pollutants mainly include four categories: persistent organic pollutants, endocrine-disrupting chemicals, antibiotics, and microplastics. Among these, antibiotics, personal care products, and microplastics have the highest detection frequencies and widest distribution ranges in aquatic environments, with the most significant impacts on algal-bacterial symbiotic systems. Their specific characteristics are as follows:

3.1. Antibiotics

Antibiotics are secondary metabolites synthesized by microorganisms or artificially, primarily used to inhibit or kill pathogenic microorganisms [11]. Since their discovery, antibiotics have been widely applied in medical treatment, livestock and poultry breeding, and aquaculture. Common types of antibiotics include tetracyclines, quinolones, sulfonamides, and macrolides [12-14]; that said, antibiotics just can't be fully absorbed or put to use by humans and animals, so most of them end up entering the environment as parent compounds or metabolites through excretion [2]. Even at low concentrations—anywhere from 3.2 to 1128.4 ng/L—these antibiotics still retain a pretty high level of biological activity, they exert toxic effects on a variety of aquatic organisms, and they might even get transformed into compounds that are more active than the originals [1].

When you look at antibiotic pollution in China's river basins, it shows some clear spatial and temporal differences. Studies done on six major river basins (including the Liaohe River, the lower Yellow River, the Haihe River, the upper Yangtze River, the lower Pearl River, and Taihu Lake) have found that the detected concentrations of antibiotics vary quite a lot from one basin to another. The Liaohe River Basin is dominated by macrolides, Taihu Lake by sulfonamides, while the lower

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Yellow River, the Haihe River, the upper Yangtze River, and the lower Pearl River are all dominated by quinolones—their detected concentrations have reached 123.89, 248.66, 108.20, and 113.00 ng/L, respectively [2]. From a seasonal point of view, antibiotic concentrations tend to be higher during the dry season than they are during the rainy season.One reason is that runoff and dilution capacity decrease in the dry season; another reason is that antibiotic use increases during the high incidence of influenza in winter and spring. Ecological risk assessments have shown that antibiotics in the water bodies of each river basin pose moderate-to-high risks to algae. Among them, the lower Pearl River Basin has the highest risk, followed by the upper Yangtze River and Haihe River Basins [2]. More importantly, the widespread use of antibiotics can induce the formation of antibiotic resistance genes (ARGs), and the transfer and spread of these ARGs may lead to bacterial drug resistance, which in turn will pose long-term threats to human health [1,2].

3.2. Personal care products

Microplastics are plastic particles with a maximum size of ≤5 mm; they are ubiquitous and slowly degrading pollutants in aquatic environments and soil. Their primary sources include polymer particles added to cosmetics and cleaning products, raw material particles used in plastic industrial production, and secondary fragments generated by physical, chemical, and biological degradation of large plastic waste [1,3]. Microplastics are characterized by long environmental persistence, high stability, strong fragmentation potential, large specific surface area, and strong adsorption capacity for other pollutants [1,3]. Studies have shown that microplastics are prone to photooxidative degradation under light exposure, with more significant degradation in small, shallow lakes. Once microplastics are released into aquatic environments, they can undergo migration and transformation in both marine and freshwater ecosystems [1].

The potential toxicity of microplastics comes from two main aspects. One is the monomers, oligomers, and various additives that are released from the plastic matrix itself. The other is the persistent organic pollutants and heavy metals that microplastics can enrich from the surrounding water environment. As a kind of carrier, microplastics form combined pollution before they enter the bodies of organisms; their accumulation in organisms can lead to a variety of physiological abnormalities, such as digestive system damage, growth retardation, and immune dysfunction. They also pose potential threats to human health through biomagnification along food chains. In addition, the long-term accumulation of microplastics can change the physicochemical properties of the surrounding environment—for example, it can affect soil permeability and water mobility—and this change further interferes with the material cycling processes of the entire ecosystem [3].

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4. Algal-bacterial symbiotic system: structure, function and nutrient exchange mechanism

The algal-bacterial symbiotic system is a complex ecosystem formed when photosynthetic autotrophic algae and chemoheterotrophic bacteria interact with each other in a mutualistic manner. As a core component of aquatic ecosystems, this system's structural stability has a direct effect on how well it functions; algae and bacteria work together through synergistic interactions to get material cycling and environmental purification done. Their specific structures and functional characteristics are described in more detail below.

In this kind of symbiotic system, the algal component is made up mostly of phytoplankton, and that includes representative groups like Chlorophyta, Cyanophyta, and Bacillariophyta. The dominant species within these groups include Chlorella, Scenedesmus, and Chlamydomonas (from Chlorophyta); Nostoc and Anabaena (from Cyanophyta); and Navicula and Nitzschia (from Bacillariophyta) [9]. These algae have a pretty high photosynthetic efficiency, which allows them to synthesize a large amount of organic substrates; beyond that, they can also provide carbon sources, energy, and growth factors for the symbiotic bacteria that live alongside them.

The bacterial component of this system is mainly heterotrophic, and it belongs to groups like Proteobacteria, Bacteroidetes, and Firmicutes. Common genera under these groups include Bacillus, Pseudomonas, Acinetobacter, and Lactobacillus, and each of these genera has its own distinct metabolic functions. For instance, it can efficiently break down organic matter into inorganic nutrients, and Pseudomonas has a strong ability to degrade various pollutants as well; these two genera work alongside algae to get environmental purification done. The way species match up with each other, plus how balanced their proportions are between algae and bacteria—these two factors directly determine the system's structural stability and its functional specificity. Different species can build specific symbiotic relationships through synergistic effects, and by doing that, they optimize the ecological functions of the whole system. Scanning electron microscopy observations have shown that microalgal cells can adhere firmly to fungal hyphae using extracellular polymers, and this forms a threedimensional network structure that really helps with gas exchange and nutrient flow; having said that, if fungi grow too much, they'll end up disrupting the balance of the entire symbiotic system.

The core of the algalbacterial symbiotic system lies in the efficient twoway nutrient exchange that happens between algae and bacteria. This mechanism does more than just support the system's structural stability and functional efficiency—it also lays a foundation for its central role in material cycling and energy flow throughout the ecosystem. To be more specific, algae fix CO_2 through photosynthesis to synthesize organic matter, and this process provides carbon sources, oxygen, and growth factors for the bacterial component. In return, bacteria mineralize organic matter to supply

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inorganic nutrients (like nitrogen and phosphorus) and CO_2 back to the algae, and they also secrete plant hormones that can help regulate algal growth. This mutualistic cycle allows the system to stay stable even when it's in a nutrientpoor environment [10].

Through the biogeochemical transformation of elements like carbon, nitrogen, and phosphorus, this symbiotic system acts as a key link that connects the inorganic environment with biological communities, and it helps promote energy flow and material balance across the ecosystem [11]. Precisely because of this efficient material exchange network, the algalbacterial symbiotic system can flexibly adjust its community structure and metabolic strategies when facing environmental stresses—things like nutrient deficiency, temperature fluctuations, or pollutant exposure—so that it can keep its ecological functions going. This ability really shows that the system has a strong capacity to adapt to its environment [12].

5. Impacts of emerging pollutants on algal-bacterial symbiotic systems

As important biological units for aquatic ecological restoration and wastewater treatment, the functional stability of algal-bacterial symbiotic systems is increasingly threatened by emerging pollutants in the environment. Emerging pollutants such as antibiotics are widely detected in aquatic environments, where they can interfere with the physiological metabolism and molecular regulatory networks of algae and bacteria in symbiotic systems, thereby impairing the ecological functions of the entire system.

5.1. Impacts at the physiological level

5.1.1. Impacts on the growth rates of symbiotic algae and bacteria

Emerging pollutants often show a typical hormetic effect on the growth of algae and bacteria in algal-bacterial symbiotic systems. That is, at low concentrations they can promote growth, but at high concentrations they inhibit it. For example, when Microcystis aeruginosa is exposed to low concentrations of the polychlorinated biphenyl congener 2-fluorobiphenyl (2-FBP) and the allelochemical gallic acid (GA), its growth gets stimulated. After 15 days of exposure to 0.5 μg/L and 1 μg/L of 2-FBP, algal density increased by 33.33% and 46.34% respectively [9]. In the same way, low concentrations of GA also had a certain promoting effect on the growth of this alga, indicating that these compounds can act as "pollutant activators" and support algal growth when their concentrations are in an appropriate range [9]. However, when the concentration of 2-FBP reaches 2 μg/L and GA reaches 10 mg/L, algal growth is significantly inhibited, with inhibition rates of 34.50% and 77.90% respectively, and the combined inhibition rate of the two pollutants can even reach 88.70% [9].In algal-bacterial co-culture systems, the inoculation ratio is a key factor affecting the growth of different microorganisms. Relevant research has found that the optimal inoculation ratio of Chlorella sorokiniana and Aspergillus oryzae is 1:1. If the proportion of fungal spores in the system is too high, it increases the overall biomass of the co-culture system but reduces the relative biomass and oil content of microalgae [15]. This happens because excessive fungi block the light needed for microalgal growth, inhibiting normal photosynthesis and growth, and finally leading to a serious imbalance in the growth states of the two organisms [15]. Scanning electron microscopy observations have also confirmed that microalgal cells can firmly adhere to the surface of fungal hyphae through extracellular polymers, forming a three-dimensional network structure that facilitates gas exchange and nutrient flow, though excessive fungal growth breaks the original balance of the co-culture system [15].In addition, bacterial communities in the symbiotic system can

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significantly promote microalgal growth. In a symbiotic system composed of activated sludge and Chlorella, the biomass of Chlorella in the co-culture groups was significantly higher than that in the pure culture groups at every time point of the experiment. After 7 days of culture, the biomass of the co-culture groups was about 1.66 times that of the pure culture groups, with the most obvious difference appearing on the 4th day, when co-culture biomass was 1.83 times higher than that of the pure culture groups [16]. This result shows that bacterial communities can effectively promote microalgal proliferation through material exchange and signal communication.

5.1.2. Impacts on the growth rates of symbiotic algae and bacteria

Photosynthesis is an important basis for algal growth and material accumulation. Many kinds of emerging pollutants interfere with the normal photosynthetic system of algae, thereby disrupting normal metabolic activities. When Microcystis aeruginosa is exposed to 2-FBP and GA, the content of Chl a and the maximum photosynthetic efficiency of the algae show a concentration-dependent change trend that is consistent with the growth state. The Chl a content in low-concentration treatment groups is significantly higher than that in the control group, while high-concentration exposure can reduce Chl a content by up to 88.00% [9]. The trend of first increasing and then decreasing in Chl a content and maximum photosynthetic efficiency indicates that the regulation of photosynthetic efficiency inhibits the conversion of light energy and the ability of algae to respond to external stress [9]. Related research suggests that photosystem II (PSII) may be a key target for pollutants to act on, because high concentrations of GA can cause serious damage to the structure of the algal photosynthetic system and lead to blockage of the photosynthetic electron transport chain [9].

Transcriptome analysis has further revealed the molecular regulation mechanism of photosynthesis under co-culture conditions. In the algal-bacterial co-culture system, the expression of photosynthetic pigment genes in Chlorella sorokiniana shows a downregulated trend [15]. When the alga-fungus ratio increases from 1:10 to 2:1, the contents of Chl a, chlorophyll b, and carotenoids all show a decreasing trend [15]. This phenomenon is mainly caused by the light-shielding effect of fungal hyphae and the aggregation of algal cells under co-culture conditions; these factors hinder light penetration, limit the light utilization efficiency of microalgae, and then negatively affect the synthesis of photosynthetic pigments in chloroplasts [15].

Similarly, in the symbiotic system composed of activated sludge and Chlorella, genes related to photosynthesis, photosynthetic antenna proteins, and chlorophyll synthesis are significantly enriched. Among them, 20 genes in the photosynthesis pathway and 7 genes in the photosynthetic antenna protein pathway are downregulated [16]. This result further confirms that the complex light conditions and material exchange relationships in the symbiotic system can form a precise regulatory network, and this network controls the expression of genes related to algal photosynthesis..

5.2. Impacts at the molecular level

5.2.1. Transcriptomic and proteomic changes of symbiotic systems under pollutant stress

Emerging pollutant stress produces clear regulatory effects on gene expression and protein synthesis in algalbacterial symbiotic systems. The system can activate internal stress response mechanisms to deal with pollutant exposure by inducing or inhibiting the transcription of functional genes and adjusting the expression levels of related proteins. At the transcriptome level, the gene expression

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profiles of the system change obviously under emerging pollutant stress. When Microcystis aeruginosa is exposed to 2FBP and GA, the expression of genes related to extracellular polymer synthesis in the algae changes noticeably, and the rfbB and rfbD genes show a significant upregulated expression trend under lowconcentration stimulation [9]. In addition, functional genes related to EPS synthesis and biofilm formation—including lptC, OA58_RS20610, and pgm—also show an obvious upregulated expression state after exposure to low concentrations of pollutants [9]. In algal-bacterial co-culture systems, transcriptome analysis revealed a more complex gene expression regulatory network. After co-culture of Chlorella sorokiniana and Aspergillus oryzae, 2383 differentially expressed genes (DEGs) were identified in Chlorella sorokiniana (1175 upregulated, 1207 downregulated), and 3608 DEGs in Aspergillus oryzae (1495 upregulated, 2113 downregulated) [15]. Gene Ontology (GO) enrichment analysis showed that DEGs were primarily concentrated in binding, catalytic activity, cellular components, and cell membrane components [15]. Kyoto Encyclopedia of Genes and Genomes (KEGG) pathway analysis indicated that DEGs in Chlorella sorokiniana were mainly enriched in ribosome biogenesis, protein export, and RNA polymerase activity, while those in Aspergillus oryzae were enriched in DNA replication, endoplasmic reticulum protein processing, and the tricarboxylic acid cycle [15].

Under co-culture conditions, the expression of methyltransferase and RNA synthesis-related genes in Chlorella sorokiniana was significantly up-regulated, indicating that the growth potential of microalgae had been enhanced. In contrast, the carbohydrate metabolism and tricarboxylic acid cycle of Aspergillus oryzae were inhibited, suggesting competition for organic matter between microalgae and fungi in the co-culture system [15]. The endoplasmic reticulum protein processing pathway of Aspergillus oryzae had the most significant number of DEGs, and co-culture can promote fungal protein synthesis—a process critical for fungal growth, development, and cellular homeostasis [15].

Experiments with dialysis membrane-isolated co-culture have confirmed that bacterial secretions can remotely regulate the expression of algal genes. Activated sludge induced differential expression of 5846 genes in Chlorella, among which 3786 were up-regulated and 2060 were down-regulated. The up-regulated genes were enriched in carbon/nitrogen metabolism, organic matter transport, and plant signal transduction, while the down-regulated genes were involved in chlorophyll synthesis and photosynthesis.

5.2.2. Response mechanisms of symbiotic systems to pollutant stress

Under the stress pressure from emerging pollutants, algal-bacterial symbiotic systems can quickly activate internal stress response mechanisms and signal transduction pathways to better cope with external pressure, thereby keeping the structure and various functions of the whole system at a stable level. Both algae and bacteria can remove reactive oxygen species (ROS) that accumulate in cells and reduce oxidative damage by synthesizing a variety of antioxidant substances (such as glutathione and vitamin C) as well as stress-resistant proteins (including heat shock proteins and cold shock proteins) [16].At the same time, such symbiotic systems can transmit the stress signals they receive through several important pathways—including the mitogen-activated protein kinase (MAPK) signaling pathway and the calcium signaling pathway—and further regulate downstream gene expression and physiological metabolism, finally achieving adaptive adjustment to external pollutant stress. For example, stress caused by antibiotics can effectively activate the two-component signal transduction system in bacteria, and then regulate the expression level of resistance genes and the activity of efflux pumps, so as to pump antibiotics out of cells and reduce the accumulation concentration of pollutants inside cells. Meanwhile, algae can sense pollutant

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stress through the calcium signaling pathway, and this lets them induce efficient expression of a series of stressresponserelated genes, which then helps boost their own stress resistance. On top of that, algae and bacteria can exchange information and communicate with each other using signal substances like quorum sensing molecules; together, they adjust and optimize the system's stress response strategies, and that further raises the overall stress resistance level of the whole symbiotic system.

6. Conclusions and prospects

This study has systematically introduced the types, physicochemical characteristics, and environmental fate of typical emerging pollutants—including antibiotics, personal care products, and microplastics. It has also analyzed in detail the structural composition and key ecological functions of algal-bacterial symbiotic systems, discussed the effects of these pollutants on the systems from both physiological and molecular levels, and further clarified the response and adaptation mechanisms of the systems under pollutant stress.

Emerging pollutants are widely distributed in aquatic environments and have obvious persistence and biotoxicity. Their effects on algal-bacterial symbiotic systems usually follow a typical hormetic rule: low concentrations stimulate the systems, while high concentrations inhibit their growth and functions. At the physiological level, emerging pollutants can affect the growth rates of algae and bacteria in symbiotic systems, interfere with normal algal photosynthesis, and change the content of photosynthetic pigments and photosynthetic efficiency. At the molecular level, they can regulate the expression of functional genes and the synthesis of related proteins in algae and bacteria, and induce the activation of stress response pathways. In response to such stress, algal-bacterial symbiotic systems can activate antioxidant mechanisms, regulate signal transduction pathways, and carry out interspecific information exchange to adapt to the external pollutant environment and maintain the stability of their own structure and functions.

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