Research Progress on the Degradation of *o*-cresol by Algal-bacterial Symbiotic System

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Abstract: This review delves into the application of the algal-bacterial symbiotic system for o-cresol degradation, which is a promising method that can cut costs and boost degradation efficiency. Nevertheless, the complexity of these symbiotic systems is a crucial factor that has a significant impact on both o-cresol degradation and the subsequent resource recovery process. The review centers on the latest progress in o-cresol degradation using the algal-bacterial symbiotic system. It carries out a systematic analysis of degradation pathways, taking into account environmental conditions, synergistic mechanisms, and research approaches. Key degradation mechanisms are elucidated through examining metabolic routes and interfacial interactions between microbial communities. Furthermore, the paper identifies current challenges in optimizing these symbiotic systems for practical applications and proposes potential solutions, including bioaugmentation strategies, advanced monitoring technologies, and system stability enhancement approaches. This comprehensive analysis provides insights for improving bioremediation efficiency and enabling value-added resource conversion in phenolic compound treatment processes.

Keywords: Algal-bacterial Symbiotic Systems; O-Cresol; Degradation Mechanisms; Key Algal-Bacterial Combinations with Functional Enhancements

1. Introduction

o-Cresol (2-methylphenol), a highly toxic and recalcitrant aromatic organic pollutant, is widely present in industrial wastewater from coking, coal chemical, and petrochemical industries. It exhibits strong corrosiveness and high toxicity, posing risks to human health through inhalation, dermal contact, and other pathways. Conventional physicochemical treatment methods face challenges such as high costs and secondary pollution generation, while biological treatment technologies have emerged as a research hotspot due to their environmental friendliness and cost-effectiveness. The algal-bacterial symbiotic system, which integrates the degradation capacity of microorganisms with the photosynthetic advantages of algae, has demonstrated significant potential in recent years for treating refractory pollutants like *o*-cresol. This review summarizes research progress in the system's degradation mechanisms and functional enhancement through key algal-bacterial combinations, while outlining future research directions.

2. The Mechanism of *o*-cresol Degradation in an Algal-bacterial Symbiotic System

The algal-bacterial symbiosis system (ABS) integrates the pollutant-degrading capabilities of bacteria with the ability of algae to remove contaminants such as nitrogen and phosphorus. It is recognized as a representative manifestation of water self-purification processes in natural aquatic environments. Through synergistic interactions between algae and microorganisms, the ABS achieves efficient degradation of *o*-cresol. The underlying mechanisms primarily involve the following aspects.

2.1 Synergistic Metabolism of Biodegradation and Photo-driven Processes

Bacteria can remove small amounts of persistent organic pollutants (POPs) from wastewater through biodegradation. The synergistic interaction between microalgae and bacteria can enhance bacterial activity and improve the system's tolerance to persistent organic pollutants. Studies have shown that Nitrosomonas combined with nitrifying sludge can effectively degrade antibiotics and other pollutants through co-metabolism, while certain antibiotics like sulfamethoxazole can only be efficiently degraded via co-metabolism with ammonia-oxidizing bacteria [1]. The diverse microbial communities present in wastewater can interact with microalgae to remove specific contaminants through biodegradation. By leveraging the photosynthetic properties of microalgae in conjunction with the metabolic and respiratory activities of bacteria in algal-bacterial systems, it becomes possible to achieve the removal and degradation of organic pollutants and heavy metals in wastewater.

Phenol does not volatilize or adsorb to sediments and suspended particles in aquatic environments, but biodegradation and indirect reactions mediated by photochemically generated hydroxyl radicals and peroxy radicals are important transport mechanisms [2]. Chronic bioaccumulation and biodegradation of organic pollutants by microorganisms constitute the second stage of phenolic compound removal. Bacteria are the most commonly used microorganisms in biological treatment due to their high biodegradation rates of pollutants [3]. Roell et al. [4] found that phenol utilization requires a highly active tricarboxylic acid cycle (TCA cycle). Experimental results on phenol removal by Spirulina maxima demonstrated that the high removal efficiency (97.5%) was primarily attributed to biodegradation rather than bioadsorption [5]. El-Sheekh et al. [6] conducted similar studies on algae for degrading polycyclic aromatic compounds and phenolic substances. After cellular uptake, phenol is broken down into intermediate metabolites, further confirming that its removal is a biodegradation process.

Algae release oxygen through photosynthesis, promoting the aerobic bacteria to oxidize and decompose o-cresol. Meanwhile, metabolic or respiratory byproducts of bacteria (such as CO_2) provide raw materials for algal photosynthesis [7]. Therefore, the synergistic interaction between bacteria and algae can degrade organic pollutants, achieving the goal of wastewater purification. Wang et al. [8] found that when applying algal-bacterial symbiotic technology to treat organic pollutants in coking wastewater, the symbiotic system produced higher concentrations of EPS, which helped the system resist toxic pollutants. This symbiotic system not only improves the settling performance of bacteria and algae but also enhances their resistance to external toxic substances and harsh environmental conditions, ensuring safe and efficient degradation of organic compounds in industrial wastewater.

2.2 Symbiotic Relationship Regulated by Signaling Molecules

During the interaction between bacteria and algae, bacteria secrete signaling molecules that induce morphological changes in algae, while algae release specific chemical substances that inhibit bacterial quorum sensing (QS). In recent years, exploring microbial behaviors in the phycosphere from the perspective of chemical ecology—particularly microbial chemical ecology—has gradually emerged as a new research highlight. Notable examples include algal allelopathy and bacterial quorum sensing signals. Allelopathy refers to the direct or indirect, promotive or inhibitory effects of chemicals released by organisms into the environment on neighboring organisms within a micro-environmental region. Significant progress has been made in developing novel herbicides from allelopathic substances or utilizing allelopathy to optimize agricultural practices [9]. Under environmental stress, the allelopathic effects of microalgae play a critical role in their survival and competition. QS, a unique regulatory mechanism in bacteria, modulates population density, promotes biofilm formation, coordinates population behavior, and activates specific gene expression [10,11]. For instance, QS alters cell membrane surface properties and bacterial motility, influencing sludge granulation. Valle et al. [12] found that *N*-acyl homoserine lactones (AHLs) are crucial for biofilm formation, bacterial aggregation, and sludge granulation. Tan et al. [13,14] demonstrated that QS enhances adenosine-triphosphate (ATP) synthesis, increases extracellular polymer content in sludge, and facilitates aerobic granular sludge formation. In algal-bacterial symbiotic systems, bacterial QS can influence certain physiological behaviors of algae. Krysciak et al. [15] identified pentapeptide compounds in sponge-associated bacteria, confirming that these signaling molecules mediate mutual sensing between bacteria and sponge cells, accelerating bacterial biofilm formation on sponge surfaces and fostering the establishment of algal-bacterial symbiosis.

3. Key Algal-Microbial Consortium and Functional Enhancement

3.1 Screening and Application of High-efficiency Degrading Bacteria

The treatment of wastewater containing cresols has attracted widespread attention. Compared with physicochemical methods, biological methods demonstrate advantages such as cost-effectiveness, safety, lower treatment thresholds, minimal residue, and absence of secondary pollution, making them more advantageous in practical applications. Representative studies in this field include: Masahiro et al. achieved complete degradation of *o*-cresol in a three-phase bioreactor, with initial concentrations ranging from 30 to 600 mg/L, and the degradation process conformed to the Haldane model [16]; Christian Kennes et al. [17] effectively produced methane using a UASB reactor fed with *p*-cresol and volatile fatty acids; Jiang Yan, Wen Jianping, and colleagues from Tianjin University [18,19] reported that Candida tropicalis completely degraded 280 mg/L of *m*-cresol within 52 hours with high efficiency. However, wastewater containing multiple phenolic compounds discharged from industries such as coking, petrochemicals, oil-gas manufacturing, chemical fibers, and pharmaceuticals often exhibits significantly higher concentrations than these reported levels. To enhance the efficiency of biological methods in treating high-concentration phenolic wastewater, in addition to improving traditional processes, it is crucial to intensify efforts in screening and cultivating high-efficiency degrading microbial strains.

Currently, multiple strains of high-efficiency *o*-cresol degrading bacteria have been screened, such as *Pseudomonas sp.* TJKYLJF-01 (CGMCC No. 10177), which can completely degrade 1000 mg/L *o*-cresol within 48 hours and tolerate concentrations up to 1500 mg/L, making it suitable for bioaugmentation treatment of coking wastewater. Another strain (named MeP) was isolated from soil samples at a coking plant in Huangshi, Hubei Province, capable of efficiently degrading phenolic pollutants like *o*-cresol. Identified as *Pseudomonas* sp., this strain completely degraded 200 mg/L *o*-cresol within 7 days. This achievement lays a foundation for subsequent studies on gene expression, metabolic pathways, and intermediate products during phenolic pollutant degradation, while also facilitating future targeted modifications of the strain, which will significantly expand its application potential and value. Additionally, a team from the Chinese Academy of Sciences (CAS) elucidated the "chemomimetic" biocatalytic system (Cre gene cluster) in Corynebacterium glutamicum. Through a three-step reaction involving phosphorylation, oxidation, and hydrolysis, this system converts *o*-cresol into metabolizable intermediates such as *p*-hydroxybenzoic acid and achieves selective oxidation of aliphatic carbon-hydrogen bonds, offering a novel strategy for complex phenolic degradation. Zhang group also isolated a quinoline-degrading *Comamonas* sp. strain (designated Z1), investigating the effects of substrate concentration, pH, and metal ions on its ability to degrade *o*-cresol and *p*-cresol. This work not only enriches microbial resources for cresol degradation but also provides theoretical support for the biological treatment of phenolic-containing industrial wastewater.

3.2 Selection and Functional Expansion of Algae

Microalgae are single-celled organisms characterized by rapid growth and high biomass content, and they are widely applied in various bioengineering fields:

(1) Nutritional applications: Microalgae contain abundant nutrients, including polysaccharides, lipids, proteins, trace elements essential for the human body, and bioactive compounds. These components can be utilized in the production of food and beverages [20,21].

(2) Bioenergy production: As a biomass energy source, microalgae are rich in lipids and are recognized as a crucial feedstock for third-generation biofuels. The entire production and processing cycle of microalgae-based biofuels is environmentally friendly, as the energy output exceeds the energy input, and the CO_2 fixation capacity surpasses CO_2 emissions, offering significant economic and environmental benefits [22].

(3) Wastewater treatment: Beyond nitrogen

fixation and phosphorus removal, certain microalgae species, such as Chlorella, possess a negatively charged cell surface that enables the adsorption of suspended particles, organic matter, and heavy metal pollutants in wastewater [23].

For different wastewater qualities, it is necessary to construct distinct bacterial-algal symbiotic systems to enhance the removal of specific pollutants. Microalgae species are diverse and vary in functionality. Chlorella and Scenedesmus, among others, are widely utilized due to their high specific surface area and strong adsorption capacity. Studies have found that a symbiotic system combining Scenedesmus with fungi significantly improves the removal efficiency of *o*-cresol, particularly demonstrating superior performance during the advanced treatment stage. Zhang Caisong investigated the growth and *o*-cresol degradation capabilities of three microalgal species (*Scenedesmus obliquus*, *Microcystis aeruginosa*, and *Selenastrum capricornutum*) under varying initial concentrations of *o*-cresol. The study ultimately identified Selenastrum capricornutum as the optimal algal species for subsequent *o*-cresol degradation experiments.

4. Challenges and Future Prospects

The algal-bacterial symbiotic system demonstrates broad prospects in *o*-cresol degradation due to its high efficiency, low energy consumption, and environmental friendliness. However, two key challenges remain unresolved: the toxic inhibition of algae by high-concentration *o*-cresol and the stability of microbial-algal communities under complex water quality conditions. Future research should focus on breaking through fundamental mechanisms of algal-bacterial synergy, developing engineered consortia with enhanced toxicity resistance, and integrating artificial intelligence for system parameter optimization to promote large-scale applications. Concurrently, combining synthetic biology with materials science could enable the creation of multifunctional integrated systems, while exploring resource recovery pathways (such as biomass energy extraction) to provide sustainable solutions for industrial wastewater treatment.

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