

Treatment of Dye Wastewater by Mixed Bacterial Flora Co-cultivation System

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Abstract

Printing and dyeing wastewater is recognized as one of the most difficult wastewaters at home and abroad because it contains dyes with stable chemical properties and difficult to be biodegraded. It has become one of the research hotspots to screen microorganisms that can efficiently decolorize and degrade dyes and apply them to the treatment of printing and dyeing wastewater. The decolorization and degradation of dyes by a single decolorizing bacteria has shortcomings such as low efficiency, incomplete degradation, and easy formation of secondary pollution. Mixed bacteria can not only overcome these shortcomings, but also have its own significant advantages, such as synergistic improvement of decolorization efficiency and environmental conditions. The development of mixed bacteria co-culture system is expected to solve the problem of refractory printing and dyeing wastewater.

Keywords

Co-culture System; Metabolic Level; Mixed Bacterial Flora; Wastewater.

1. Construction of Mixed Bacterial Flora Co-culture System

Due to the wide application of new synthetic dyes with more complex structures and more stable properties, the challenges faced by traditional bioprocessing technologies are becoming more and more severe. Fungi have many advantages in the treatment of textile printing and dyeing wastewater, such as complete decolorization and degradation of pollutants, kinetic advantages, and extracellular degradation. However, fungi inevitably have certain limiting factors in the treatment of dye wastewater, such as sensitivity to environmental changes, slow proliferation, nitrogen-limited cultivation, unstable enzyme production, and long degradation time [1]. The most critical problem of the single fungal treatment system is that the system is unstable, and bacteria begin to breed and become dominant strains after 20-30 days of operation.

There are complex ecological relationships among microorganisms, including cooperative metabolism, induction, intermediate quorum sensing, and gene transfer. Genomics studies have shown that closely related or other species of microorganisms in the system can induce the expression or high expression of these genes [2,3]. Therefore, mixing two or more microorganisms to treat complex wastewater will be an effective biological treatment method. Different types of mixed culture systems have also emerged, such as bacteria-bacteria mixed culture systems, bacteria-fungus mixed culture systems, and fungi-fungus mixed culture systems. Among them, the bacteria-fungus mixed culture system is the most common mixed culture system.

Combined with the advantages of high degradability, high adaptability and fast bacterial growth rate of fungi, the combined co-culture system of fungi and bacteria was used to treat various types of industrial wastewater. The results showed that the treatment effect of the mixed culture system was

better than that of single fungi or bacteria [4,5]. However, due to the synergistic effect between fungi, microbial co-culture is more efficient in degrading toxic substances and waste disposal. Samta et al. [6] reported that a mixed fungal treatment system composed of *Penicillium oxalicum* SAR-3, *Aspergillus niger* SAR-6 and *Aspergillus flavus* SAB-3 could efficiently degrade azo dyes and actual printing and dyeing wastewater. Kuhar et al. [7] reported that the fungal co-culture system composed of *Ganoderma lucidum* and *Trametes versicolor* achieved rapid and complete decolorization of malachite green under solid-state fermentation conditions, and the content of laccase was significantly increased. But so far, there are few reports on the treatment of printing and dyeing wastewater by the co-culture fungal system.

2. Optimization of Mixed Bacterial Flora Co-cultivation System

The construction, operation and operation of the mixed culture system will have a certain impact on the decolorization and degradation of dyes. Therefore, these process conditions must be optimized to achieve the best decolorization and degradation effect. Zhang Jinping[8] constructed a mixed culture system of fungi and bacteria, and optimized the conditions such as treatment time, inoculation ratio, inoculation sequence, ventilation, and dye concentration. After a certain period of time, the decolorization rate and degradation rate of the dye were measured. Simultaneously inoculated, and the inoculation ratio was 2:1, the shaking culture achieved a high decolorization rate and degradation rate for 12 h, and still had a strong tolerance to the high concentration of 320 mg/L dye. When Dong Xinjiao [4] constructed a fungus-bacteria mixed culture system to degrade cyanide in sewage, they mixed one cyanide-resistant fungus with eight cyanide-reducing bacteria in equal volumes, and used the cyanide degradation rate as an indicator to carry out the analysis of the mixed strains. In order to optimize the combination, the cyanide reduction rate of the mixed system composed of 8# bacteria and fungi was the highest, reaching 99.5% within 24 h. Although fungi have great potential in textile printing and dyeing wastewater treatment, the research and application of fungi in wastewater treatment are very limited. The researchers put forward the bioaugmentation technology (Bioaugmentation) of adding functional microorganisms to the treatment system off-line and online, and studied the effect of this technology to enhance the removal of pentachlorophenol (PCP), dyes, naphthalene and other pollutants from aerobic activated sludge. performance [9]. The mixed bacterial flora has active co-metabolism, which is easy to form a synergistic effect, stimulate the production of a variety of dye-degrading enzymes, and achieve a more complete and thorough degradation of dyes. Therefore, actively explore the construction of a mixed bacterial flora treatment system to achieve environmentally friendly treatment of dye wastewater. It is the main research direction in the field of efficient sewage treatment in the future.

3. Advances in Microbial Interaction Studies at Metabolic Level

Microorganisms in the microbial aggregate system can regulate the macroscopic characteristics of microorganisms through the interaction mechanism. Therefore, it is of great significance to study the microscopic effects of various microorganisms in the microbial aggregate system to understand the macroscopic manifestation principle and further study on wastewater treatment. There are various symbiotic mechanisms of microorganisms in microbial aggregates, and one of the mainstream research methods is to study the signal transmission mechanism between microorganisms from the metabolic level, so as to analyze the interaction between microorganisms.

Signal transduction refers to the growth, metabolism and character expression of another microorganism by using metabolites secreted by microorganisms themselves, and the mechanism of interaction between microorganisms can be studied from the molecular level by using metabolites. Studies have shown that quorum sensing molecules secreted by bacteria, such as phthalide high serine lactone, can affect the growth and development of microalgae. After bacteria such as *Sheva* and *Bacillus* SPP., accumulate with microalgae, they produce algae-soluble metabolites. Studies have shown that the interaction between bacteria and algae in the process of colonization is the main reason for the good effect of the bacteria and algae accumulation system on wastewater treatment. Compared

with the free bacteria-algae system, the bacteria-algae aggregate system has stronger metabolic functions and generally has better treatment effect on wastewater than the free bacteria-algae system. Therefore, the study of complex interactions in the bacteria-algae aggregate system has become one of the current research hotspots. Bacteria or fungi have a great influence on the growth of microalgae in the process of microalgal aggregation, so the influence of bacteria on the metabolism level of microalgae has been widely concerned. Goecke et al. found that bacteria can influence the morphogenesis of algae and induce microalgae to produce metabolites with defense mechanisms for themselves during the interaction of microorganisms in the bacterial-algal aggregation system. In the aggregation experiment of the composite strain and microalgae, the removal effect of nitrogen and phosphorus and the synthesis of fatty acids in microalgae cells were mostly improved.

At present, there are few studies on the interaction of bacteria and algae on the level of metabolic molecules to affect wastewater treatment, so the specific mechanism is still not perfect. Studies show that the presence of bacteria can directly affect the metabolism of microalgae, and then affect the wastewater treatment effect to a certain extent. Chen Taojing compared and analyzed the difference of metabolome of chlorella-Pseudomonas H4 aggregate system in wastewater treatment, and the analysis results showed that the microscopic influence of H4 on the metabolites of Chlorella resulted in the great difference in pollutant removal between the aggregate system and the free system of Chlorella. The presence of bacteria can change the environmental factors, and the change of environmental factors can affect the metabolism of microalgae, and then affect the wastewater treatment effect to a certain extent, which may be the reason for the regulation of microalgae metabolism. For example, Maza-Marquez studied the increase of dissolved oxygen by 7 mg L⁻¹ in microalgal bacterial aggregates. Newman's study showed that when the dissolved oxygen content in water changed, the expression of alkaline phosphatase activity in microalgae also changed to some extent. Therefore, the presence of bacteria can directly affect microalgae or indirectly affect the environment, thus affecting the metabolism of microalgae.

At present, most studies focus on bacterial and microalgal aggregates, but there are few reports on fungus-microalgal aggregates. Therefore, it is necessary and promising to study the influence of microalgal interactions on wastewater treatment from the metabolic level of fungus-microalgal aggregates.

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