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An Innovative Microbial Consortium's Biodegradation of Tricresyl Phosphate Isomers and the Toxicity Assessment of Its Main Products

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Abstract

Tri-o-cresyl phosphate (ToCP), tri-p-cresyl phosphate (TpCP), and tri-m-cresyl phosphate (TmCP) could all be completely broken down in 36, 24 h, and 12 h, respectively, by the novel microbial consortium ZY1. Intracellular enzymes were primarily responsible for the biodegradation of TCPs. ZY1 could also break down tris (2-chloroethyl) phosphate (TCEP), tris (1-chloro-2-propyl) phosphate (TCPP), bisphenol-A bis (diphenyl phosphate) (BDP), triphenyl phosphate (TPHP), 2-ethylhexyl diphenyl phosphate (EHDPP), and bisphenol-A bis (diphenyl phosphate) (BDP). The TCPs decrease in both freshwater and seawater suggested that high salinity may inhibit ZY1's ability to degrade. The breakdown products found indicated that TCPs were primarily metabolized by hydroxylation and hydrolysis. According to sequencing analysis, TCP degradation.

Keywords: Microbial consortium; Biodegradation; Toxicity

Introduction

According to sequencing analysis, the cooperation of sphingobacterium, variovorax, and flavobacterium was necessary for the degradation of TCPs. The degradation of TCPs may be facilitated by the cytochrome P450/NADPH-cytochrome P450 reductase and phosphatase, according to theories. Ultimately, based on the production of intracellular reactive oxygen species (ROS) and the apoptotic rate of A549 cells, the toxicity evaluation study discovered that the diester products' toxicity was lower than that of their parent compound. When considered collectively, these studies offered fresh perspectives on TCP bioremediation in real environments [1-3].

Methodology

To date, OPFRs have been eliminated by photocatalytic reduction and Fenton oxidation treatment. Microbial remediation, in contrast to these technologies, may offer a cost-effective and environmentally beneficial solution for the degradation of organic pollutants. In order to accomplish this, pure strains possessing the ability to degrade TCP were effectively isolated within the laboratory. According to Liu et al. (2019c), for instance, brevibacillus brevis was able to degrade 34.73%, 78.28%, and 89.17% of 1 mg/L ToCP, TmCP, and TpCP, respectively, in just five days. According to Wang, sphingopyxis eliminated 85.5% of the 0.27 mmol TCPs following a 7-day incubation period. However, the use of pure strain in the actual environment for TCP elimination may not be successful because the successful remediation [4-6].

Because the cooperative metabolic activities of complex microbial populations are always necessary for successful remediation in real environments, the degradation efficiency was also limited by the weak adaptability of pure strains to unfavorable conditions. It was determined that microbial consortium degradation offered the clearest benefit in restoring the environment. As a result of the diverse depolymerization processes of organic compounds that the various microorganisms in the microbial consortium formed, the toxic pollutants would mineralize into harmless products. Simultaneously, complex microbial communities' inherent compositional stability and performance allowed them to adapt to environmental perturbations more effectively than monoculture did [7-9].

Little research has been done on TCP reduction with the microbial consortium to date, and the transformation mechanism is unknown. Furthermore, while earlier research primarily concentrated on the toxicity of TCPs, there has been evidence to suggest that the ecological risk posed by degradation intermediates may be greater than that of the parent compound. The debromination products of 2, 2′, 4, 4′-tetrabromodiphenyl ether (BDE-47) were found by Tang to be more toxic than BDE-47 itself. Additionally, Chen proposed that TCP metabolites, particularly the hydroxylated metabolites, were more potent estrogen receptor antagonists than TCPs themselves, which may cause dysfunction of the testis structure. Thus, additional study of the degradation products' toxicity was required in order to improve understanding.

This work isolated the microbial consortium ZY1, which is able to degrade ToCP, TpCP, and TmCP. The crucial location of the degrading enzyme was established, and the three isomers' metabolic pathways were also suggested. Additionally, we investigated how the TCP treatment affected the microbial community and function genes. Evaluations of the primary degradation products' toxicity and the viability of bioaugmentation in freshwater and seawater using the microbial consortium ZY1 were conducted. Furthermore, ZY1's possible involvement in the degradation of other OPFRs was investigated [10].

Conclusion

Further clarification was provided regarding the role of extracellular and intracellular enzymes in the reduction of TCPs by the isolation of a novel microbial consortium ZY1, which possessed the ability to fully degrade three isomers. Two major pathways for TCP degradation have been proposed: hydrolysis and oxidative hydroxylation of TCPs.

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According to sequencing analysis, key degradation enzymes were also predicted, and sphingobacterium, variovorax, and flavobacterium may be involved in the removal of TCPs. The experiment on toxicity assessment.

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