An Innovative Microbial Consortium's Biodegradation of Tricresyl 聲 ♀ 镶 爛籠驖皛薵鄛 **狼**秋
北 秗狿駞槈 **퇃爛駠爛鳫**隃嫾 木 魱 鴲 鬱療徴疘鷽 腙韋 **鯫聣**鯫虩秲倞綪闍坧 夑妎 **鯂軔爛鯫駾鯫**虃秲倞緆闍坧爼 <u>鰍駾鰍滱秲倞阨闍坧憄導艷轳徟夌爛</u>礐鰍槷<sub>女</sub>買鱂 甝 鳫隃鑼稽 羵穮 該 꽯絡藣朖 **獹**稛睚驜**帔**箮馻 **溆**尾 **騾**黪韊媽韊**藌**瀌稛爛 邁穓 韃虊貛膄澞 井鬱坧鳫閁 鴲 퇃婥

Microbial consortium; Biodegradation; Toxicity

According to sequencing analysis, the cooperation of sphingobacterium, variovorax, and avobacterium was necessary for the degradation of TCPs. e 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 o ered fresh perspectives on TCP bioremediation in real environments [1-3].

To date, OPFRs have been eliminated by photocatalytic reduction and Fenton oxidation treatment. Microbial remediation, in contrast to these technologies, may o er a cost-e ective and environmentally bene cial solution for the degradation of organic pollutants. In order to accomplish this, pure strains possessing the ability to degrade TCP were e ectively 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 ve 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 e ciency was also limited by the weak adaptability of pure strains to unfavorable conditions. It was determined that microbial consortium degradation o ered the

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

## References

- Plummer KE, Siriwardena GM, Conway GJ, Risely K, Toms MP (2015) Is supplementary feeding in gardens a driver of evolutionary change in a migratory bird species? Glob Change Biol 21: 4353-4363.
- Robb GN, McDonald RA, Chamberlain DE and Bearhop S (2008) Food for thought: supplementary feeding as a driver of ecological change in avian populations