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Bacterial degradation of 2, 4-dichlorophenol: Catabolic genes detection and enzyme characterization

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The widespread use of chemicals and their frequent release into the environment is the major cause of pollution, worldwide. Chlorophenolic compounds, such as 2, 4-dichlorophenol (2, 4-DCP), are classified as priority pollutants due to their recalcitrance, persistence, toxicity, carcinogenicity and mutagenicity. The aims of this study were: to isolate 2, 4-DCP degrading microorganisms indigenous to contaminated sites in Durban, South Africa, and establish their degradation potential, to detect the presence of 2, 4-DCP catabolic genes in selected isolates, and to characterize the enzymes involved in the degradation process. Following enrichment in mineral salt medium (MSM) supplemented with 2, 4-DCP (40 ppm) as the sole carbon and energy source, three 2, 4-DCP degrading bacteria were isolated and identified as Pseudomonas chlororaphis strain UFB2, Klebsiella pneumoniae strain KPNIH39 and Klebsiella pneumoniae strain DHQP1002001 based on the 16S rRNA gene sequence analysis. These isolates were able to degrade between 49.01% and 75.11% of 2, 4-DCP within 10 days, with the degradation rate constant ranging between 0.07 and 0.14 mg/L/d. The PCR amplification of the catabolic genes involved in 2, 4-DCP degradation revealed the presence of the phenol hydroxylase (600 and 715 bp), catechol 1, 2-dioxygenase (467 and 507 bp), muconate isomerase (651 and 494 bp), cis-dienelactone hydrolase (491 and 567 bp), and trans-dienelactone hydrolase (491 and 567 bp) in Pseudomonas chlororaphis and Klebsiella pneumonia, respectively. The absence of catechol 2,3-dioxygenase gene in these isolates suggests that the organisms most likely follow ortho-pathway for 2, 4-DCP degradation. This study will therefore assist in contaminated sites and alleviate pollution of chlorophenolic compounds in the environment.

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