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SCREENING OF CATECHOL DIOXYGENASE GENE AMONG BACTERIAL COMMUNITIES ISOLATED FROM ANTHROPOGENIC CONTAMINATED AREA IN PAHANG, MALAYSIA

(2022) *Malaysian Journal of Biochemistry and Molecular Biology*, 2022, pp. 78-86.

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Abstract

The development of industrial, recreational, and urban areas in Pahang has introduced hydrocarbon pollution into the environment. The hydrocarbons impart a significant effect on the environment and human health, in both short- and long-term effects. Long-term exposure to these environmental pollutants may enhance the degradative abilities of the indigenous bacterial communities through the exhibition of catechol dioxygenase; an enzyme that can degrade hydrocarbons. In this study, bacteria communities that are tolerant towards hydrocarbons were successfully isolated and identified from two contaminated rivers and one pristine area. The presence of the catechol dioxygenase gene from the isolated bacterial samples was then screened using Polymerase Chain Reaction (PCR) amplification. A total of 33 hydrocarbon-tolerant bacteria were isolated from both contaminated and pristine areas. Five genera isolated from the contaminated areas; the *Bacillus*, *Lysinibacillus*, *Aeromonas*, *Shewanella*, and *Pseudomonas* strains were detected to harbour the catechol dioxygenase gene. Meanwhile, no catechol dioxygenase gene was detected in bacterial samples isolated from pristine area. Results obtained from the screening of the catechol dioxygenase gene can provide preliminary insight regarding the presence of catabolic enzymes particularly in different anthropogenic areas, which could provide a better understanding regarding the potential of catechol dioxygenase in eliminating toxic pollutants from the environment. © 2022 Malaysian Society for Biochemistry and Molecular Biology. All rights reserved.

Author Keywords

Anthropogenic area; Catechol dioxygenase; Hydrocarbon-tolerant; Polymerase chain reaction; Screening

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Publisher: Malaysian Society for Biochemistry and Molecular Biology

ISSN: 15112616

Language of Original Document: English

Abbreviated Source Title: Malays. J. Biochem. Mol. Biol.

2-s2.0-85175733880

Document Type: Article

Publication Stage: Final

Source: Scopus

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