Isolation of Klebsiella pneumoniae from Sungai Skudai and in silico analysis of putative dehalogenase protein

ABSTRACT

Aims: The surplus use of herbicide Dalapon® contains 2,2-dichloropropionic acid (2,2-DCP) poses great danger to human and ecosystem due to its toxicity. Hence, this study focused on the isolation and characterization of a dehalogenase producing bacteria from Sungai Skudai, Johor, capable of utilizing 2,2-DCP as a carbon source and in silico analysis of its putative dehalogenase. Methodology and results: Isolation of the target bacteria was done by using 2,2-DCP-enriched culture as the sole carbon source that allows a bacterium to grow in 20 mM of 2,2-DCP at 30 °C with the corresponding doubling time of 8.89 ± 0.03 h. The isolated bacterium was then designated as Klebsiella pneumoniae strain YZ based on biochemical tests and basic morphological examination. The full genome of K. pneumoniae strain KLPN_25 (accession number: RRE04903) which obtained from NCBI database was screened for the presence of dehalogenase gene, assuming both strains YZ and KLPN_25 were the same organisms. A putative dehalogenase gene was then identified as type II dehalogenase from the genome sequence of strain KLPN_25. The protein structure of the type II dehalogenase of KLPN_25 strain was then pairwise aligned with the crystal structure of L-2-haloacid dehalogenase (L-DEX) Pseudomonas sp. strain YL as the template, revealing the existence of conserved amino acids residues, uniquely known to participate in the dehalogenation mechanism. The finding thus implies that the amino acid residues of type II dehalogenase possibly shares similar catalytic functions with the L-DEX. Conclusion, significance and impact of the study: In conclusion, this study confirmed the presence of new dehalogenase from the genus Klebsiella with potential to degrade 2,2-DCP from the river water. The structural information of type II dehalogenase provides insights for future work in designing haloacid dehalogenases.