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Bacterial community and their functional characteristics in leachate from Jeram and Jabor landfills

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Abstract

Aims: A landfill is one of the environments that nurtures a diverse microorganism community, which has the potential to carry various dioxygenase enzymes that can degrade possible contaminants in the landfill leachate. However, the information on the microbial community that is responsible for the degradation process is limited due to the culturedependent approach. The aim of this study was to assess the distribution of the bacteria that inhabited the landfills using 16S rRNA

gene amplicon sequencing approach.Methodology and results: The leachate sample collected from Jeram Sanitary Landfill, Selangor and Jabor-Jerangau Integrated Landfill, Pahang, was extracted and purified before being sent for 16S rRNA gene sequencing to proceed with the bioinformatics analyses. The findings show that 265 and 273 bacterial amplicon sequence variant (ASV) were sequenced for Jeram and Jabor landfills, respectively, with the dominant phyla Firmicutes for both leachate samples. On average, diverse genera associated with significant functions, such as cellulolytic bacteria (e.g., Taibaiella) with a percentage abundance of 0.3% and hydrogen-reducing bacteria (e.g., Anaerobic digester metagenome) with a percentage abundance of 0.375% were analyzed in the Jabor and Jeram landfill leachate, respectively. In addition, the Shannon index, which accounts for the species diversity of Jabor leachate, was lower than that of the Jeram leachate, and the Simpson index, which refers to random selection of the sample, was similar for both samples with no significant difference.Conclusion, significance and impact of study: Research findings indicate that both leachate samples contained diverse bacterial species. Using PICRUSt2, 10 metabolic pathways were predicted in both landfill leachates. Therefore, this approach can serve as a platform to analyze the distribution of bacterial communities and their functional characteristics in landfill leachate. © (2025), (Universiti Sains Malaysia). All rights reserved.

Author keywords

16S rRNA; landfill leachate; metabolism pathway; microbial community; PICRUSt2 prediction

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