



Isolation and molecular characterization of bacterial species from Sikog waterfall, Padawan, Sarawak

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ABSTRACT

Aims: Bacteria are microorganisms that are commonly distributed in any environment. They are also found abundantly in marine environments such as waterfalls and rivers. Some bacteria participate in various biological activities and possess no health risk; however, other species could be pathogenic and have been directly associated with various diseases in animals and humans. Therefore, it is crucial to analyze the antibiotic resistance profiles of bacteria in the research area based on regularly used antibiotics in clinical and agricultural contexts to establish a data baseline for health providers and public usage.

Methodology and results: Water samplings were done twice and collected from upstream, midstream, and downstream of the Sikog waterfall. A total of ninety isolates were isolated and analyzed using (GTG)₅ genetic fingerprinting to determine the genetic similarities. Based on the dendrogram generated using Gelj Version 2.0 software, 41 bacterial isolates were subjected to 16S rRNA gene sequencing for species identification. The Kirby-Bauer disk diffusion method was implemented to determine the level of susceptibility toward certain antibiotics. Sequence analysis was performed using BLAST, revealing that the isolates constitute 17 genera, including *Pseudomonas*, *Alcaligenes*, *Stenotrophomonas*, *Staphylococcus*, *Bacillus*, *Lysinibacillus*, *Rosellomorea*, *Citrobacter*, *Enterobacter*, *Kosakonia*, *Klebsiella*, *Escherichia*, *Serratia*, *Cronobacter*, *Aeromonas*, *Chromobacterium* and *Kocuria*. According to the overall antibiotic susceptibility analysis, streptomycin (10 µg) exhibited the highest rate of resistance among bacterial isolates, with 36.84%, followed by penicillin (10 units) (36.36%), rifampicin (5 µg) (27.27%) and ampicillin (10 µg) (26.32%).

Conclusion, significance and impact of study: The research findings revealed the predominant bacteria found in the recreational water of Sikog waterfall and their antibiotic susceptibility, which could be helpful in the treatment of bacterial infections for future clinical reference. Simultaneously, the public, particularly communities in the study area, should be informed about the potential health risk associated with diverse resistant enteric bacteria in the recreational water.

Keywords: 16S rRNA gene sequencing, antibiotic resistance, bacteria, (GTG)₅ PCR, Sikog waterfall

INTRODUCTION

The abundance of waterfalls in Sarawak is due to the topographical structure, climatic circumstances, and river conditions. Sikog waterfall, which is located in Padawan, Kuching, Sarawak, was chosen as a research site because it is a popular spot for outdoor activities such as camping and trekking. It is a place of indescribable beauty. Nevertheless, the nearby village still depends on the natural mountain river stream for their everyday needs and water supply. River water is also a vital resource for agriculture since various farms cultivate commodities such as pepper and other vegetation along the river.

Furthermore, this natural water body is also a reservoir for various microbes. Most bacteria found on the soil and surface water are non-pathogenic and play

critical functions in marine food webs and they undertake essential ecosystem processes such as nitrogen, carbon, and sulphur transformation. For instance, some *Acinetobacter* species found on surface water and soil have been associated with useful functions in the natural environment, such as oil spill detoxification, soil fertility improvement and microflora in human and plant bodies (Adewoyin and Okoh, 2018). Despite their natural presence in aquatic habitats, some bacteria have been linked to human infections through ingestion or exposure to contaminated water from recreational activities (Nollet and De Gelder, 2000). Despite the persistent efforts to ensure water safety, waterborne outbreaks continue to be reported globally (Ramírez-Castillo *et al.*, 2015).

Pathogenic bacteria and their antibiotic resistance associated with recreational water have been a significant