

The Rampancy of Multiple- Drug Resistant Bacteria Isolated from Surface Water of Satow Waterfall, Bau Sarawak

Khairunnisa Mohammad Hamdi*, Samuel Lihan

Institute of Biodiversity and Environmental Conservation, Universiti Malaysia Sarawak, 94300 Kota Samarahan, Sarawak, Malaysia

Corresponding author: khairunnisahamdi87@gmail.com

Received: 25th July 2022

Accepted: 23rd August 2022

Published: 30th October 2022

Abstract

Antimicrobial resistance (AMR) is universally acknowledged as a serious threat to human health, well-being, and prosperity. Many therapeutically important antibiotic resistance genes are thought to have arisen in the environment. Antibiotics are no longer effective in treating infections caused by multi- and pan-resistant bacteria (dubbed "superbugs") that have spread rapidly around the world [1]. Furthermore, AMR bacteria and antimicrobial resistant genes can thrive and proliferate in natural waterbodies because they can act as both recipients and natural reservoirs for the bacteria and genes. Toxic exposure to AMR bacteria and ARGs puts recreationists in danger, reducing their ability to combat illnesses.

Considering Satow Waterfall, Bau is a renowned water-based recreational destination, an assessment of their physiochemical water quality characteristics and the prevalence of AMR bacteria was conducted to corroborate the safety of the water. A total of nine water samples were collected at the surface water (0–30 cm depth) of the upstream, midstream, and downstream. The water quality index (WQI) of the sampling stations ranged from 92.60 to 95, classifying the water under Class I. However, the water is microbiologically polluted. During Trip 2, the highest level of coliform was found in the middle stream at 2.59×10^5 cfu/mL, which is above the regulatory standard set by the Malaysian Department of Environment (DOE).

A total of 100 isolated bacteria were subjected to (GTG)₅-genomic fingerprinting analysis to evaluate the degree of genetic similarity among the samples and thus enable the selection of appropriate clonal representatives. Fifty-four bacterial isolates were chosen as representatives and identified by 16S rDNA sequencing, which confirmed the existence of 21 bacterial genera as shown in Figure 1. All identified isolates were tested against 15 antibiotics of various classes, namely, streptomycin (S), Kanamycin (K), cefotaxime (CTX), cephalothin (KF), tetracycline (TE), doxycycline (DO), carbenicillin (CAR), sulfamethoxazole (SXT), ofloxacin (OFX), levofloxacin (LEV), erythromycin (E), meropenem (MEM), ertapenem (ETP), vancomycin (VA) and chloramphenicol (C) employing the Clinical and Laboratory Standards Institute (CLSI) protocols.

The antibiotic susceptibility test (AST) demonstrated substantial resistance to SXT (41%), E (41%) and CAR (39%), as well as high susceptibility to C (85%), followed by LEV (78%) and OFX (72%). The Multiple

Official Journal of Faculty of Medicine, Universiti Sultan Zainal Abidin, Malaysia.

Antibiotic Resistance Index (MARI) evaluation demonstrated the MARI varied from 0–0.60, with 33% of the isolates having a MARI greater than 0.20 (Figure 1).

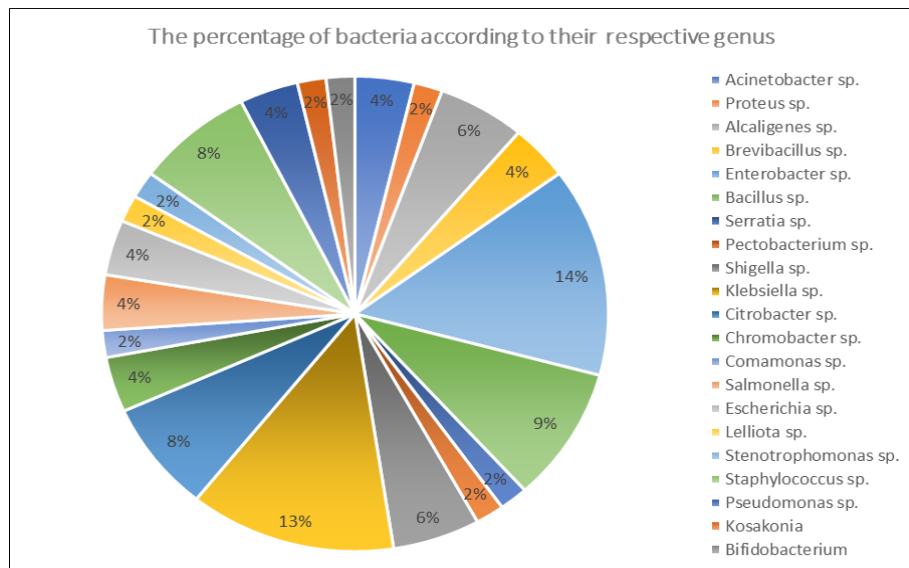


Figure 1: The percentage of bacteria according to respective genus

In this study, we found that the occurrence of MAR bacteria in water environment where there's an undisclosed source of antibiotic utilisation is still inevitable, highlighting the necessity to constantly monitor the water quality and the pervasiveness of MAR bacteria in recreational water.

Keywords

16S rDNA sequencing, Antibiotic resistance Water quality

Acknowledgement

The authors would like to thank the Institute of Biodiversity and Environment, UNIMAS, and the Faculty of Resource Science and Technology, UNIMAS, for their assistance in providing the facilities. This study was supported by the Tun Zaidi Chair under grant no. F07/TZC/1915/2019

Reference

1. Rath, L., 2021. *What Are CRE 'Superbug' Infections?* [online] WebMD. Available at: <<https://www.webmd.com/a-to-z-guides/cre-superbug-infections>> [Accessed 14 June 2022].