

The distribution and characteristics of bacteria in recreational river water of a community resort in Baram, Sarawak, Malaysian Borneo

¹Lihan, S., ¹Tian, P. K., ¹Chiew, T. S., ²Ching, C. L., ¹Shahbudin, A., ¹Hussain, H. and ³Mohd-Azlan, J.

¹Department of Molecular Biology, Faculty of Resource Science and Technology, Universiti Malaysia Sarawak, 94300 Kota Samarahan, Sarawak, Malaysia

²Institute of Biological Sciences, Faculty of Science, University of Malaya, 50603 Kuala Lumpur, Malaysia

³Department of Zoology, Faculty of Resource Science and Technology, Universiti Malaysia Sarawak, 94300 Kota Samarahan, Sarawak, Malaysia

Article history

Received: 16 May 2016

Received in revised form:
25 August 2016

Accepted: 29 August 2016

Keywords

Enterobacteriaceae
antibiogram
GTG-PCR
Recreational water

Abstract

Enterobacteriaceae is a large family within the Gram-negative bacteria that primarily inhabits in the gastrointestinal tract of human and animals. The bacteria within this group are readily survived in the environment with some species found living free in the water where energy sources are scarce, making them ideal indicators for faecal contamination of the river water. Some species within the family have been used as indicator for the presence of pathogenic bacteria whilst on the other hand some species have been directly associated with various diseases in human and animals. The main aim of this research study was to determine the distribution and characteristics of the *Enterobacteriaceae* in water samples collected from river and waterfalls within a community resort. The health risk associated with the bacteria was analysed with regard to their susceptibility to antibiotics. Samples were collected from surface water and water falling down directly from waterfalls of river within the community resort. The samples collected were plated onto Eosine Methylene Blue agar (EMBA) for the isolation of the *Enterobacteriaceae*. Bacterial colonies growing on the agar were randomly picked, purified, stocked and then identified using API 20E identification kit. DNA fingerprinting using (GTG)5-PCR was utilised to determine their genetic profiles before the isolates were grouped into a dendrogram using RAPDistance software package. The level of antibiotic susceptibility of the bacteria isolates was analysed using disc diffusion technique. This study confirmed the presence of *Enterobacter*, *Klebsiella*, *Citrobacter*, *Pantoea* and *Serratia* in the water samples with their single and multiple antibiotic resistance and susceptible characteristics. The dendrogram presented in this study shows genetic similarities and differences among the strains, suggesting while there is a potential for single distribution of a clone, there is also possibility of the distribution of different strains within species in the water environment. Therefore, awareness on the potential risk associated with genetically diverse intermediate and resistant enteric bacteria in the recreational water should be communicated to the public especially communities within the study area.

© All Rights Reserved

Introduction

The *Enterobacteriaceae* group of bacteria consists of the harmless symbionts and pathogens of human and environmental species such as commonly found bacteria *Escherichia coli*, *Klebsiella* spp., *Enterobacter* spp. and many others (Cabral, 2010). The coliforms are among the group of indicator bacteria that have been used to measure of water quality. Besides, they are among the major contributions to the contaminants of surface and recreational waters in developing countries (Cabral, 2010).

Diseases-causing *Enterobacteriaceae* have

the capability to invade their host in many ways because they possess some important characteristics like motility, colonization factors, endotoxin and enterotoxin (Guentzel, 1996; Peterson, 1996). Some species are motile because they possess several flagella distributed around their perimeter. Apart from that, the enterobacterial colonization factors consist of hairy appendages which can make them bind tightly to their host. The endotoxins are the cell membrane constituent of Gram-negative bacteria including *Enterobacteriaceae*, which trigger infected individuals to have high fever (Peterson, 1996).

Pollution of water especially with faeces

*Corresponding author.

Email: lsamuel@frst.unimas.my