



# Prevalence and Diversity of Antibiotic Resistant *Escherichia coli* From Anthropogenic-Impacted Larut River

Chui Wei Bong<sup>1,2\*</sup>, Kyle Young Low<sup>2,3</sup>, Lay Ching Chai<sup>1,2</sup> and Choon Weng Lee<sup>1,2</sup>

<sup>1</sup> Institute of Biological Sciences, Universiti Malaya, Kuala Lumpur, Malaysia, <sup>2</sup> Institute of Ocean and Earth Sciences (IOES), Universiti Malaya, Kuala Lumpur, Malaysia, <sup>3</sup> Institute for Advanced Studies, Universiti Malaya, Kuala Lumpur, Malaysia

## OPEN ACCESS

### Edited by:

Luther King Abia Akebe,  
University of KwaZulu-Natal,  
South Africa

### Reviewed by:

Daniel Gyamfi Amoako,  
National Institute for Communicable  
Diseases (NICD), South Africa  
Vicente de Paulo Martins,  
University of Brasilia, Brazil

### \*Correspondence:

Chui Wei Bong  
cwbong@um.edu.my;  
lee@um.edu.my

### Specialty section:

This article was submitted to  
Environmental Health and Exposome,  
a section of the journal  
Frontiers in Public Health

**Received:** 13 October 2021

**Accepted:** 20 January 2022

**Published:** 10 March 2022

### Citation:

Bong CW, Low KY, Chai LC and  
Lee CW (2022) Prevalence and  
Diversity of Antibiotic Resistant  
*Escherichia coli* From  
Anthropogenic-Impacted Larut River.  
Front. Public Health 10:794513.  
doi: 10.3389/fpubh.2022.794513

Aquatic environments, under frequent anthropogenic pressure, could serve as reservoirs that provide an ideal condition for the acquisition and dissemination of antibiotic resistance genetic determinants. We investigated the prevalence and diversity of antibiotic-resistant *Escherichia coli* by focusing on their genetic diversity, virulence, and resistance genes in anthropogenic-impacted Larut River. The abundance of *E. coli* ranged from (estimated count) Est 1 to  $4.7 \times 10^5$  (colony-forming units per 100 ml) CFU 100 ml<sup>-1</sup> to Est 1 to  $4.1 \times 10^5$  CFU 100 ml<sup>-1</sup> with phylogenetic group B1 (46.72%), and A (34.39%) being the most predominant. The prevalence of multiple antibiotic resistance phenotypes of *E. coli*, with the presence of *tet* and *sul* resistance genes, was higher in wastewater effluents than in the river waters. These findings suggested that *E. coli* could be an important carrier of the resistance genes in freshwater river environments. The phylogenetic composition of *E. coli* and resistance genes was associated with physicochemical properties and antibiotic residues. These findings indicated that the anthropogenic inputs exerted an effect on the *E. coli* phylogroup composition, diversification of multiple antibiotic resistance phenotypes, and the distribution of resistance genes in the Larut River.

**Keywords:** *Escherichia coli*, anthropogenic activities, antibiotic, resistant, resistance genes

## INTRODUCTION

*Escherichia coli* (*E. coli*) of the family *Enterobacteriaceae*, is a Gram-negative, facultative anaerobe, non-spore-forming, rod-shaped, commensal, and potentially pathogenic bacterium that resides largely in the gastrointestinal tracts of warm-blooded vertebrate animals (1–3). Most *E. coli* strains are harmless, and only some are pathogenic. The pathogenic *E. coli* can be classified as either intestinal pathogenic *E. coli* (IPEC) or extraintestinal pathogenic *E. coli* (ExPEC). The IPECs are major diarrhoeagenic pathogens that cause gastroenteritis with six intestinal pathotype subgroups: enterohemorrhagic *E. coli* (EHEC), enteropathogenic *E. coli* (EPEC), enteroaggregative *E. coli* (EAEC), enterotoxigenic *E. coli* (ETEC), enteroinvasive *E. coli* (EIEC), and diffusely adherent *E. coli* (DAEC). Meanwhile, ExPEC consists of three human pathotype subgroups: neonatal-meningitis *E. coli* (NMEC), uropathogenic *E. coli* (UPEC), sepsis-associated pathogenic *E. coli* (SePEC), and the avian pathogenic *E. coli* (APEC) (4).