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

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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 4.7×10^5 (colony-forming units per 100 ml) CFU 100 ml^{-1} to Est 1 to 4.1×10^5 CFU 100 ml^{-1} 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).