Diverse and abundant multi-drug resistant *E. coli* in Matang mangrove estuaries, Malaysia

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E. coli, an important vector distributing antimicrobial resistance in the environment, was found to be multi-drug resistant, abundant, and genetically diverse in the Matang mangrove estuaries, Malaysia. One-third (34%) of the estuarine *E. coli* was multi-drug resistant. The highest antibiotic resistance prevalence was observed for aminoglycosides (83%) and beta-lactams (37%). Phylogenetic groups A and B1, being the most predominant *E. coli*, demonstrated the highest antibiotic resistant level and prevalence of integrons (integron I, 21%; integron II, 3%). Detection of phylogenetic group B23 downstream of fishing villages indicates human fecal contamination as a source of *E. coli* pollution. Enteroaggregative *E. coli* (1%) were also detected immediately downstream of the fishing village. The results indicated multi-drug resistance among *E. coli* circulating in Matang estuaries, which could be reflective of anthropogenic activities and aggravated by bacterial and antibiotic discharges from village lack of a sewerage system, aquaculture farms and upstream animal husbandry.

Introduction

*Escherichia coli* (*E. coli*), a component of the common intestinal microbiota in humans and warm-blooded animals, is an important indicator of fecal contamination in aquatic environments and food. Certain strains of *E. coli* are able to cause gastrointestinal and extraintestinal infections in humans. The pathogenic *E. coli* that cause gastrointestinal infections include enterohemorrhagic *E. coli* (EHEC), also referred to as Shiga toxin-producing *E. coli* (STEC) or verocytotoxic *E. coli* (VTEC), enteropathogenic *E. coli* (EPEC), enteroaggregative *E. coli* (EAEC), enterotoxigenic *E. coli* (ETEC), enteroinvasive *E. coli* (EIEC), and diffusely adherent *E. coli* (DAEC) (Galvin et al., 2010; Koczura et al., 2013). These pathogenic *E. coli*, together with other virulent strains of *E. coli* could cause extraintestinal infections in humans such as pyelonephritis, urinary tract infection, cystitis, neonatal meningitis, and bacteremia (Johnson and Stell, 2000; Galvin et al., 2010; Koczura et al., 2013).

*E. coli* is divided into four main phylogenetic groups A, B1, B2, and D, based on the presence and absence of, *chuA*, a gene that is responsible for heme transport in enterohemorrhagic O157:H7 *E. coli*; *yjaA*, an unknown functional gene which is identified in the recent complete genome sequence of *E. coli* K-12; and TSPE4.C2, an anonymously designated DNA fragment which is the non-coding region in *E. coli* strains (Clermont et al., 2000). These four phylogenetic groups of *E. coli* appear to have distinctive genetic and phenotypic characteristics that are associated with different ecological