



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

Aziz Ghaderpour^{1,2}, Wing Sze Ho¹, Li-Lee Chew^{1,2}, Chui Wei Bong^{1,2},
Ving Ching Chong^{1,2}, Kwai-Lin Thong^{1,2} and Lay Ching Chai^{1,2*}

¹ Faculty of Science, Institute of Biological Science, University of Malaya, Kuala Lumpur, Malaysia, ² Institute of Ocean and Earth Sciences, University of Malaya, Kuala Lumpur, Malaysia

OPEN ACCESS

Edited by:

Rustam Aminov,
Technical University of Denmark,
Denmark

Reviewed by:

Veijo Kisand,
University of Tartu, Estonia
Daniela Ceccarelli,
University of Maryland, USA

*Correspondence:

Lay Ching Chai,
Faculty of Science, Institute of
Biological Sciences, University of
Malaya, 50603 Kuala Lumpur,
Malaysia
lcchai@um.edu.my

Specialty section:

This article was submitted to
Antimicrobials, Resistance and
Chemotherapy,
a section of the journal
Frontiers in Microbiology

Received: 10 April 2015

Accepted: 02 September 2015

Published: 29 September 2015

Citation:

Ghaderpour A, Ho WS, Chew L-L,
Bong CW, Chong VC, Thong K-L and
Chai LC (2015) Diverse and abundant
multi-drug resistant *E. coli* in Matang
mangrove estuaries, Malaysia.
Front. Microbiol. 6:977.
doi: 10.3389/fmicb.2015.00977

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.

Keywords: *E. coli*, Matang mangrove estuaries, antibiotic resistance, phylogenetic groups

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