

## Prevalence and characterization of *Escherichia coli* in the Kelantan River and its adjacent coastal waters

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### ABSTRACT

The presence of *Escherichia coli* in river and sea water may cause different levels of infections and constitutes a risk to public health. In this study, water samples were collected from 15 sites along the Kelantan River, estuaries and its adjacent coastal waters to investigate the prevalence and diversity of *E. coli*. A membrane filtration technique was used to enumerate *E. coli* and phylogenetic grouping was performed using triplex polymerase chain reaction. *E. coli* abundance ranged from  $3.1 \times 10$  to  $1.6 \times 10^5$  colony forming units  $100 \text{ mL}^{-1}$ , and total suspended solids correlated significantly with *E. coli* abundance ( $r^2 = 0.165$ ,  $p < 0.001$ ) and rainfall ( $r^2 = 0.342$ ,  $p < 0.001$ ). Phylogenetic group B1 and A (59.4%) were the most prevalent, whereas groups B2 and D were least abundant. The higher abundance of phylogenetic group D at upstream sites of the Kelantan River suggested fecal contamination mainly of animal origin. Canonical-correlation analysis showed phylogenetic group B2, and phylogenetic groups A and D were greater in waters with higher inorganic nutrients (e.g.  $\text{NH}_4$ ,  $\text{NO}_2$  and  $\text{NO}_3$ ), whereas phylogenetic group B1 appeared to have better salinity tolerance between phylogenetic groups.

**Key words** | *E. coli*, fecal pollution, Kelantan River, phylogenetic groups

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### INTRODUCTION

*Escherichia coli* is a coliform subgroup commonly found in the intestine of both humans and animals. It is used as a marker for fecal pollution in aquatic system (Byamukama *et al.* 2005) and as an indicator to assess food hygiene and food safety. *E. coli* are mostly non-harmful but there are some pathogenic strains. These are responsible for infections of the human digestive system (e.g. enteroinvasive *E. coli* (EIEC), enteropathogenic *E. coli* (EPEC), enterotoxigenic *E. coli* (ETEC), enteroaggregative *E. coli* (EAEC), enterohaemorrhagic *E. coli* (EHEC), and diffusely adherent *E. coli* (DAEC)) (Hamelin *et al.* 2006), and human extraintestinal infections, such as nosocomial bacteremia, urinary tract infection, and myositis (Galvin *et al.* 2010). Most of

these pathotypes are of public health concern because their infectious dose is low and they are easily transmitted via food and water (Matic *et al.* 1997).

*E. coli* can be categorized into phylogroups A, B1, B2, and D based on the existence or absence of the following genes: (i) *chuA* (required for EHEC heme transport); (ii) *jyaA* (unknown function); and (iii) TSPE4.C2 (unknown DNA segment) (Clermont *et al.* 2000). Most commensal and obligatory pathogens (EHEC, ETEC, and EIEC) are found in phylogroup A and B1. Group A is predominantly found in humans, whereas group B1 is predominantly in animals. Phylogenetic group B2 and D are mostly virulent extraintestinal strains (Luna *et al.* 2010), whereas the virulent