

Long-term and short-term variations of *Escherichia coli* population structure in tropical coastal waters

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Abstract In this study, monthly and daily samplings were carried out at Klang, an eutrophic estuary, and at Port Dickson, an oligotrophic coastal water system. *Escherichia coli* concentration was measured via culture method, and the phylogenetic structure of *E. coli* population was via Clermont typing. Average *E. coli* concentration at Klang was higher than Port Dickson ($t = 2.97$, $df = 10$, $p < 0.05$), and daily sampling did not show any apparent temporal variation at both sites. At Klang, salinity was inversely correlated with coliform ($R^2 = 0.216$, $df = 25$, $p < 0.05$), suggesting that river flow was a mode of transport for coliform. Although *E. coli* concentration was higher at the eutrophic site, *E. coli* population structure at both Klang and Port Dickson were similar and showed neither long-term nor short-term variations. This study showed the predominance of commensal groups A and B1 in tropical coastal waters of Peninsular Malaysia.

Keywords Faecal pollution · Clermont typing · *E. coli* loading rate · Straits of Malacca

Introduction

Escherichia coli (*E. coli*) is a commensal bacterium in the large intestine of human and other warm blooded

animals. The presence of *E. coli* is widely used as faecal pollution indicator in water quality assessment (Cho et al. 2010). Faecal pollution has been reported for different water bodies, e.g. fresh water (river or lake) (Ferguson et al. 2003) and salt water (seawater, coastal water and estuarine water) (Gabutti et al. 2004; Orsi et al. 2008) and is a serious problem since it represents a health risk to both animals and humans (Wilkinson et al. 2006; Orsi et al. 2008). Faecal pollution can be introduced from multiple sources, e.g. agricultural runoff, industrial waste, inadequately treated sewage from urban areas and other anthropogenic input (Geldreich 1996; Ferguson et al. 2003).

At present, the population structure of *E. coli* is characterised into four main phylogenetic groups (A, B1, B2 and D) (Herzer et al. 1990; Gordon et al. 2008). Both groups A and B1 are commensals where group A is predominant in humans, and group B1 is predominant in animals (Tenailon et al. 2010), whereas groups B2 and D are usually pathogenic and can cause extraintestinal infections (Picard et al. 1999; Clermont et al. 2000). The distribution of *E. coli* phylogenetic groups has been attributed to environmental factors such as dietary, climatic conditions and geographic (Duriez et al. 2001; Unno et al. 2009). As the population structure of *E. coli* in humans in tropical countries are mainly groups A and B1 (Escobar-Páramo et al. 2004), it is essential to investigate whether the *E. coli* population structure in tropical coastal waters reflected that found in humans. Moreover, *E. coli* groups A and B1 are now emerging as intestinal pathogenic strains (Escobar-Páramo et al. 2004; Li et al. 2010). At present much remains unknown of the *E. coli* population structure in tropical coastal waters, and only Orsi et al. (2008) have reported *E. coli* population structure albeit in a tropical river.

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