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# Spatial variability of *E. coli* in an urban salt-wedge estuary

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ABSTRACT

This study investigated the spatial variability of a common faecal indicator organism, *Escherichia coli*, in an urban salt-wedge estuary in Melbourne, Australia. Data were collected through comprehensive depth profiling in the water column at four sites and included measurements of temperature, salinity, pH, dissolved oxygen, turbidity, and *E. coli* concentrations. Vertical variability of *E. coli* was closely related to the salt-wedge dynamics; in the presence of a salt-wedge, there was a significant decrease in *E. coli* concentrations with depth. Transverse variability was low and was most likely dwarfed by the analytical uncertainties of *E. coli* measurements. Longitudinal variability was also low, potentially reflecting minimal die-off, settling, and additional inputs entering along the estuary. These results were supported by a simple mixing model that predicted *E. coli* concentrations based on salinity measurements. Additionally, an assessment of a sentinel monitoring station suggested routine monitoring locations may produce conservative estimates of *E. coli* concentrations in stratified estuaries.


## 1. Introduction

Increased faecal contamination of estuarine and coastal waters around the world represents major issue in water quality management today due to its implications on public health trough associated aquatic recreation and aquaculture. Additionally, elevated faecal pollution levels can have substantial economic implications through costs associated with medical treatment of waterborne illnesses caused by faecal pathogens directly, or indirectly by impacting tourist activities and associated local businesses (e.g. closure of beaches). For example, estimated cost for treatment of waterborne illnesses for only two beaches in California, USA was $3.3 million per annum (Dwight et al., 2005). As such, increased efforts are needed to understand faecal microorganism dynamics in estuarine environment, which in turn would lead to effective mitigation strategies and, ultimately, to improved recreational water quality.

Understanding faecal microorganism dynamics in an estuarine system starts with collecting information about the levels of faecal pollution. This is achieved through monitoring programs, which commonly involve collection of water samples from discrete points within the analysed estuary. Often, due to logistical and financial constraints, sampling sites are sparsely distributed along the system, and water samples collected from these sites are assumed being representative of faecal microbe levels within an entire estuarine reach. However, the choice of the precise sampling location can have significant impact on the measured faecal microorganism levels especially in the case of such complex environments. For example, Quilliam et al. (2011) highlighted the importance of spatial variability by showing that samples taken within the same *cross-section*, but on opposite sides of an estuary, led to contrasting classifications of microbial water quality. Nevertheless, in spite of the importance of the issue, literature lacks comprehensive studies on spatial variability of faecal microorganisms within estuarine environment, thus leaving a significant knowledge gap in understanding this aspect of faecal microorganism dynamics.

Furthermore, numerical models are increasingly being used to help understand faecal microorganism dynamics in estuaries and serve as a management tool for defining effective mitigation strategies (Salomon and Pommepuy, 1990; Kashefipour et al., 2002; Garcia-Armisen et al., 2006; de Brauwere et al., 2011; Gao et al., 2011; Liu and Huang, 2012; Bedri et al., 2013; de Brauwere et al., 2014; Gao et al., 2015; Liu et al., 2015). These models are typically complex 1D/2D or 3D hydrodynamic-microorganism models – consistent with the complexity of the environment and the processes modelled. It is well established that as the complexity of a model increases, so does the need for data quantity and quality for model testing (Grayson and Blöschl, 2001), in order to be able to fully exploit model capabilities. Despite this, data supporting the spatial dimensionality of models is often missing. For example, some studies have collected longitudinal profiles of estuarine faecal microorganism concentrations (Salomon and Pommepuy, 1990; de Brauwere et al., 2011), but none have measured vertical concentration profiles of faecal microorganisms, which is essential for testing 3D models. It is clear that lack of understanding the spatial variability of faecal microbes within a water body can hinder the robustness of such models and limit

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their application. Finally, application of improperly validated models and associated decision-making could have serious implications both in terms of management costs and water quality benefits.

The aim of this study was to characterize the spatial variability of a commonly used faecal indicator organism (*Escherichia coli*) in a highly stratified, salt-wedge estuary in Melbourne, Victoria, Australia. Data were collected and analysed to understand the factors influencing vertical variability (i.e. along the depth of water column), transverse variability (i.e. across the estuary), and longitudinal variability (i.e. along the estuary). An additional objective was to test the assumption of representativeness of a single *E. coli* sample collected from a fixed, routine monitoring station of the overall *E. coli* levels within that cross-section.

## 2. Methods

### 2.1. Study site

The Yarra River is located in south-eastern Australia and is the major river which flows through the urban metropolis of Melbourne. It has a total length of 242 km and drains a catchment of 4000 km$^2$ comprising forested headwater reaches, predominantly rural mid-reaches and urbanised lower reaches, before discharging into Port Philip Bay. The last 22 km represent its estuarine section, which has a well-defined upstream boundary (i.e. an artificial weir, Dights Falls, which prevents tidal propagation upstream). The estuary is used for secondary contact water recreation (especially rowing, kayaking, and fishing) while primary contact recreation is either restricted due to boat navigation or is not recommended due to frequently high levels of faecal indicator microbes (Department of Sustainability and Environment, 2012).

The Yarra River estuary is categorised as a highly-stratified, salt-wedge estuary (Beckett et al., 1982) and is micro-tidal (i.e. having a tidal range <2 m, (Dyer, 1997)). Water level fluctuations within Port Philip Bay average 0.5 m but vary between 0.3 and 0.9 m. The tidal pattern is semi-diurnal with a significant diurnal variation (Beckett et al., 1982).

The major input of fresh water to the estuary is the Yarra River, which contributes about 70% of the total flow at the estuary mouth (Sokolov and Black, 1996). Other freshwater inputs include Gardiners Creek in the upper estuary (~7.5 km downstream of the Dights Falls) and Maribyrnong River and Moonee Ponds Creek in the lower part of the estuary. Additionally, there are >200 stormwater drains discharging directly to the estuary, some of which have pipe diameters >3 m (Daly et al., 2013; Jovanovic et al., 2015).

### 2.2. Depth profiling

The depth profiling was done at four key cross-sections, spanning the entire estuary: at Abbotsford, Hawthorn, Morell Bridge and South Bank, located 0.5, 6.2, 10.1 and 12.4 km from the beginning of the estuary, respectively (Fig. 1). To understand the spatial variability of *E. coli* within the estuary, depth profiling was conducted by collecting water samples and taking in-situ water quality measurements at increments of 25 to 50 cm below the water surface (increments depended on the position of salt-wedge, with coarser resolution applied below the halocline, where variability in water quality was significantly lower). In-situ water quality measurements were made using a multi-parameter probe (Hydrolab DS5X): Temperature (Temp; °C), Salinity (Sal; psu), Turbidity (Turb; NTU), pH, and dissolved oxygen (DO; mg/L). Water samples were retrieved using a peristaltic pump which had the inlet suction pipe attached to the multi-parameter probe. Samples were collected into 200 ml sterile PET bottles and stored in coolers on ice until transported to the Environmental and Public Heath Microbiology Laboratory (EPHM Lab) at Monash University where they were analysed for *E. coli*, well within 12 h of collection (McCarthy et al., 2008), using the Colilert method (IDEXX Laboratories, 2013).

Single- and double-pass depth profiling methods were used to provide the necessary data for assessment of the spatial variability of *E. coli*. The specific aim of the single pass profiling was to provide data for assessing cross-sectional and transverse variability of *E. coli*. This procedure entailed moving in one direction along the estuary (i.e. from South Bank to Abbotsford) and sampling three verticals across the width of each *cross-section* at each monitoring site. One vertical was positioned at the thalweg, while the other two were distributed evenly across the width of the estuarine *cross-section* depending on the thalweg position. All three depth profiles within the *cross-section* were obtained within 10–30 min of each other. This enabled a *cross-sectional* analysis of

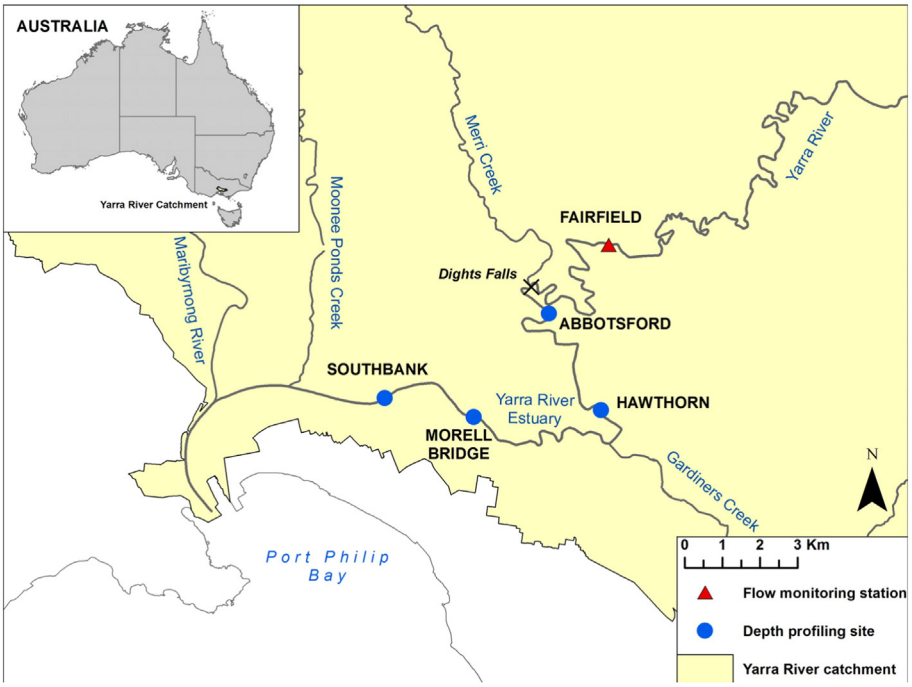


**Fig. 1.** Yarra River Estuary and four depth profiling sites: Abbotsford, Hawthorn, Morell Bridge and South Bank.

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