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Modelling the fate and transport of faecal bacteria in estuarine and coastal waters

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1. Introduction

Pathogens are often responsible for the spread of waterborne diseases (Kashefipour et al., 2002). However, due to the difficulties of direct measurement of pathogens, indicator microorganisms have generally been used in water quality management (Chapra, 1997). Faecal indicator bacteria (FIB) groups, such as total coliform, faecal coliform, E. coli and enterococci, are used commonly around the world to measure the health hazards in bathing and shellfish harvesting waters (Thomann and Muller, 1987; Sanders et al., 2005). This is due principally to the fact that the faecal indicator bacteria can be easily quantified using laboratory tests and are generally not present in unpolluted waters, and the concentrations of these indicator bacteria tend to be correlated with the contamination level (Thomann and Muller, 1987). Various sources of faecal indicator bacteria exist in estuarine and coastal waters, which include: effluent outfalls, combined sewer overflows (CSO), diffuse source inputs etc. (Kashefipour et al., 2006). The importance of quantifying the effects of different bacteria sources has been emphasized in a recent work by Atwill et al. (2003), who suggest that nonpoint sources are important sources of faecal contamination. Sanders et al. (2005) assessed the effect of different faecal bacteria sources on surface water quality at an inter-tidal wetland, where sediment re-suspension was the dominant source of bacteria concentrations near the mouth and urban

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ABSTRACT

This paper details a numerical model developed to predict the fate and transport of faecal bacteria in receiving surface waters. The model was first validated by comparing model predicted faecal bacteria concentrations with available field measurements. The model simulations agreed well with the observation data. After calibration, the model was applied to investigate the effects of different parameters, including: tidal processes, river discharges from the upstream boundaries and bacteria inputs from the upstream boundaries, wastewater treatment works (WwTWs), rivers and combined sewer overflows (CSO), on the concentrations of faecal bacteria in the Ribble Estuary. The results revealed that the tide and upstream boundary bacteria inputs were the primary factors controlling the distribution of faecal bacteria. The bacteria inputs from the WwTWs in the model domain were generally found not to have a significant impact on distribution of faecal bacteria in the estuary.

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runoff controlled bacteria concentrations at inland sites. Hydrodynamic and hydrological processes play very important roles on the distribution of faecal bacteria and pathogen concentrations in river, estuarine and coastal waters. de Brauwere et al. (2011) found that tidal processes play a very important role on the distribution of bacteria concentrations in the Scheldt river and estuary. Ge et al. (2012) investigated the effects of waves on *E. coli* concentration distribution at an embayment beach.

The Ribble Estuary is located to the south of the Fylde coast, Lancashire, in the north west of England, (Fig. 1). Upstream of the estuary, there are three main rivers; namely the River Darwen, the River Douglas and the River Ribble (Fig. 1). At the mouth of the estuary there are two well-known seaside resorts, namely Lytham St Annes and Southport, with both being designated EU (European Union) bathing water sites. The Fylde Coast, which is located between Fleetwood in the north and the Ribble Estuary in the south, includes Blackpool, one of the most famous beaches, in England for tourism, receiving on average more than 17 million visitors a year. This stretch of coast includes some of the UK's premier resorts and bathing beaches and has been subject to significant infrastructure investments to reduce point-source impacts in achieving the standards of the 1976 Bathing Water Directive (BWD) (Stapleton et al., 2008). A major civil engineering investment program has been undertaken to reduce bacterial input to the estuary and enhance bathing water quality along the Fylde Coast. About £600 million was invested over the past 20 years on building new sewerage treatment plants along the Flyde Coast and the Ribble Estuary. Although the reduction in input bacterial loads has resulted in a significant decrease in the concentrations of bacterial indicators in the receiving



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Symbol list	
f	Coriolis parameter
Η	total depth of water
U, V	depth-averaged velocities in <i>x</i> , <i>y</i> directions respectively
3	depth-averaged eddy viscosity
ξ	water surface elevation above datum
ρ	fluid density
$ au_{xw}, au_{yw}$	surface wind shear stress components in <i>x</i> , <i>y</i> directions
$ au_{xb}$, $ au_{yb}$	bed shear stress components in x, y directions
Т	top width of the channel
ζ_R	water elevation
Q_R	discharge
β	momentum correction factor due to the non uniform
	velocity over the cross section
A	wetted cross section area
$R = \frac{A}{P}$	hydraulic radius
Р	wetted perimeter of the cross section
$U_R = Q_R/A$ cross-sectional averaged velocity	
С	bacterial concentration (cfu/100 ml)
C_0	source or sink of bacteria
D_{x}, D_{y}	depth averaged dispersion coefficients in x and y direc-
	tions, respectively
K _x	longitudinal dispersion coefficient
1	light irradiance (<i>cal/cm²/ady</i>)
K	decay rate for bacteria in the water column
K ₂₀	decay rate at $I = 20$ C
θ	a dimensionless temperature correction constant, typi-
т	cal values for θ are about 1.07
1	darkmass condition docuv rate at 20 °C
κ _n	calinity (not)
3	Samily (ppt) a light irradiance correction factor (0.00224 cm^2/cgl)
α_i	

waters, occasional higher bacterial counts have still been measured in recent years. As a result, the bathing waters still occasionally failed to comply with the EU mandatory water quality standards of the Bathing Framework Directive (Kashefipour, 2002). In addition, the Ribble catchment has been selected as a test area for the acquisition of environmental information, needed to underpin implementation of the revised Directive 2000/60/EC in the UK (Wither et al., 2005). The coastal system contains both bathing and shellfish harvesting waters and the Ribble river basin is the only UK research basin for studies linked to implementation of the Water Framework Directive (WFD) (Kay et al., 2005). The main objective of the current study is to better understand the effects of different factors, including tidal processes, upstream discharges and inputs of faecal bacteria from upstream rivers, combined sewer overflows (CSOs), diffuse sources and wastewater treatment works (WwTWs), on the distribution of faecal bacteria concentrations in the Ribble Estuary.

The Ribble river basin has a range of land uses from low intensity grazing systems in the upper catchments, to some heavily urbanised and industrialised areas in the lower catchments. These diverse variations in the river basin characteristics, provide a range of excellent land use variability for model development and parameterization, thus the Ribble Estuary and the marine receiving waters provide a typical sink for a range of solutes advected into the estuarine and coastal basin following storm conditions. The range of characteristics of the system therefore provides the potential for transferability to other sites across the UK and internationally. The estuarine system contains both bathing and shellfish harvesting waters with considerable regulatory data records for relevant parameters. The Ribble Estuary is complex with a tidal reciprocating estuarine system and the shallow nearshore waters present a number of modelling challenges; these regulatory and modelling characteristics again, provide an environment ideal for transferring the modelling science advancements to other sites. The methods adopted in this study are generic and can readily be applied to other case study sites.

2. Material and methods

2.1. Hydrodynamic model

In modelling estuarine and riverine systems, the co-existence of one- and two-dimensional flow patterns is quite common. As suggested by Kashefipour et al. (2002) and Lin and Falconer (2005), in this study, an integrated one- and two-dimensional model, which was based on the DIVAST (Depth Integrated Velocities And Solute Transport) and FASTER (Flow And Solute Transport in Estuaries and Rivers) models were used. In the two-dimensional model, the depth-integrated equations are given below:

$$\frac{\partial\xi}{\partial t} + \frac{\partial UH}{\partial x} + \frac{\partial VH}{\partial y} = 0 \tag{1}$$

$$\frac{\partial UH}{\partial t} + \beta \left\{ \frac{\partial U^2 H}{\partial x} + \frac{\partial UVH}{\partial y} \right\} = fVH + gH \frac{\partial \xi}{\partial x} + \frac{\tau_{xw}}{\rho} - \frac{\tau_{xb}}{\rho} + 2\frac{\partial}{\partial x} \left(\overline{\varepsilon}H\frac{\partial U}{\partial x}\right) + \frac{\partial}{\partial y} \left[\overline{\varepsilon}H\left(\frac{\partial U}{\partial y} + \frac{\partial V}{\partial x}\right)\right] (2)$$

$$\begin{aligned} \frac{\partial VH}{\partial t} + \beta \left\{ \frac{\partial UVH}{\partial x} + \frac{\partial V^2 H}{\partial y} \right\} &= -fUH + gH \frac{\partial \xi}{\partial y} + \frac{\tau_{yw}}{\rho} - \frac{\tau_{yb}}{\rho} \\ &+ \frac{\partial}{\partial x} \left[\overline{\varepsilon} H \left(\frac{\partial U}{\partial y} + \frac{\partial V}{\partial x} \right) \right] + 2 \frac{\partial}{\partial y} \left(\overline{\varepsilon} H \frac{\partial V}{\partial y} \right) (3) \end{aligned}$$

where ξ = water elevation above (or below) datum; U,V = depth averaged velocity components in x, y directions; $H = \xi + h$ = total water depth; h = water depth below datum; β = momentum correction factor; f = Coriolis parameter; τ_{xw}, τ_{yw} = surface wind shear stress components in x, y direction; τ_{xb}, τ_{yb} = bed shear stress component in x, y directions; and $\overline{\varepsilon}$ = depth averaged eddy viscosity.

The one dimensional hydrodynamic equations can be expressed in the following form:

$$T\frac{\partial\zeta_R}{\partial t} + \frac{\partial Q_R}{\partial x} = 0 \tag{4}$$

$$\frac{\partial Q_R}{\partial t} + \frac{\partial}{\partial x} \left(\beta \frac{Q_R^2}{A} \right) + gA \frac{\partial \zeta_R}{\partial x} + g \frac{Q_R |Q_R|}{C^2 A R} = 0$$
(5)

where T = top with of the channel; $\zeta_R =$ water elevation; discharge; $\beta =$ momentum correction factor due to the non uniform velocity over the cross section; A = wetted cross section area; $R = \frac{A}{P} =$ hydraulic radius and P = wetted perimeter of the cross section.

2.2. Bacteria fate and transport model

In the faecal bacteria fate and transport model, the bacteria are normally modelled as a reactive tracer, wherein they will be transported by the flow processes once they enter the model domain and their concentrations are affected by faecal bacteria specific processes (de Brauwere et al., 2011). The bacteria transport model presented herein was developed by Gao et al. (2011a, b), which includes bacteria advection, mixing, dynamic growth/mortality, sedimentation and re-suspension processes. Download English Version:

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