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Numerical modelling of sediment–bacteria interaction processes in surface waters

Guanghai Gao^{a,*}, Roger A. Falconer^b, Binliang Lin^{b,c}

^a Key Laboratory of Pollution Processes and Environmental Criteria (Ministry of Education), College of Environmental Science and Engineering, Nankai University, Tianjin 300071, China

^b Cardiff School of Engineering, Cardiff University, The Parade, Cardiff CF24 3AA, UK

^c State Key Hydrosience and Engineering Laboratory, Tsinghua University, Beijing 100084, China

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ABSTRACT

Faecal bacteria exist in both free-living and attached forms in surface waters. The deposition of sediments can take faecal bacteria out of the water column and to the bed. The sediments can subsequently be re-suspended into the water column, which can then lead to the re-suspension of the faecal bacteria of the attached form back into the water column, where it may desorb from the sediments. Therefore, the fate and transport of faecal bacteria is highly related to the governing sediment transport processes, particularly where these processes are significant. However, little attempt has been made to model such processes in terms of predicting the impact of the sediment fluxes on faecal bacteria levels. Details are given of the refinement of a numerical model of faecal bacteria transport, where the sediment transport processes are significant. This model is based on the model DIVAST (Depth Integrated Velocities And Solute Transport). Analytical solutions for steady and uniform flow conditions were derived and used to test the sediment–bacteria interaction model. After testing the sediment–bacteria interaction model favourably against known results, the model was then set up for idealised case studies to investigate the effects of sediment on bacteria concentrations in the water column. Finally the model was applied to a simplified artificial flooding study to investigate the impact of suspended sediment fluxes on the corresponding bacteria transport processes. The model predictions have proved to be encouraging, with the results being compared to field measurements.

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1. Introduction

Faecal bacteria are widely used worldwide as indicators to monitor surface water quality. Faecal bacteria in surface waters can be considered to exist in two forms, either as free-living bacteria within the water column, or attached (or adsorbed) to suspended particles. The bacteria can be transported and diffused within the water column in their free-living form, or they can be adsorbed onto the sediments and then transported and diffused with the sediments. The

adsorbed bacteria can settle out when the suspended particles deposit on the bed and then be re-suspended with the particles into the overlying water column when the sediment particles are re-suspended.

Advances in numerical modelling of hydrodynamic and water quality processes have made such tools an invaluable means of predicting faecal contamination levels under different flow conditions. Numerical models used for predicting bacterial contamination have generally treated faecal bacteria as free-living in current studies, such as Lin and

* Corresponding author. Tel.: +86 15 022623290; fax: +86 22 23501117.

E-mail address: gaoguanghai@hotmail.com (G. Gao).

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Falconer (2001), Kashefipour et al (2002), and the deposition/re-suspension and adsorption/desorption processes are not generally included in the model and with little attempt being made to model such processes in terms of predicting the impact of the suspended sediment fluxes on bacteria levels in the water column. However, in recent years there have been many studies undertaken to study how bacteria exist in the sediments, with these studies frequently revealing higher numbers of indicator and pathogenic bacteria in the sediments than in the overlaying water column, both in marine and fresh water systems (Fries et al., 2006; Jamieson et al., 2004; Characklis et al., 2005). Fries et al. (2006) investigated the attachment of faecal indicator bacteria to particles in the Neuse river estuary, in eastern North Carolina, USA, and found that an overall average of 38% bacteria associated with particles. Characklis et al. (2005) found attachment ratios of typically 30–55% for enterococci in storm water. Gannon et al. (1983) showed that sedimentation was an important element in the overall faecal coliform disappearance rates in a river impoundment.

Suspended sediments can contribute to the disappearance of faecal bacteria from the water column in different ways. Attached faecal bacteria are adsorbed by the sediments from the water column during low energy flow conditions (Howell et al., 1996). Sediment concentrations also affect the light penetration rate in the water column, which further affects the decay rate of faecal bacteria (Stapleton et al., 2007). Allen et al. (1987) revealed that the water quality testing criteria generally do not take account of sediments as a potential reservoir of pathogens. The higher numbers of pathogenic levels occurring in sediments creates a potential health hazard from re-suspension and subsequent ingestion from increasing usage of recreational waters. Therefore, there is a need to obtain additional information on the survival of indicator and pathogenic bacteria in sediments and the factors which contribute to their survival (Allen et al., 1987). Jamieson et al. (2005) conducted field experiments in Swan Creek, Canada, by using the bacteria tracer *E. coli* NAR in their studies. They found that the bacteria tracer that re-appeared in the water column coincided with increases in the total suspended solids load, which indicated that the *E. coli* NAR were being re-suspended with the sediment load. *E. coli* NAR is a form of *E. coli* that is: resistant to nalidixic acid, non-pathogenic, rarely found in the natural environment and possesses survival characteristics similar to other *E. coli* (Jamieson et al., 2004).

Some faecal bacteria modelling efforts have been made to include sediment effects on bacteria. Steets and Holden (2003) included sediment effects on faecal bacteria fate and transport in a coastal lagoon by introducing a constant attachment ratio throughout the modelling period. Jamieson et al. (2005) developed a model for attached faecal bacteria for steady state flow conditions. Yang et al. (2008) and Stapleton et al. (2007) have recently developed bacteria transport models for the Severn Estuary. Both deposition and re-suspension processes were modelled for the attached bacteria. However, similar to Steets and Holden (2003), attachment ratios were assumed to be constant.

In this study, details are given of the refinement of a numerical model of faecal bacteria transport to include

sediment effects on bacteria fate and transport in surface waters, where the sediment transport processes are significant. This model is based on the model DIVAST (Depth Integrated Velocities And Solute Transport), which has been successfully applied to many sites, such as for predicting hydrodynamic and faecal bacteria transport processes in Swansea Bay (Lin and Falconer, 2001), faecal coliform transport in the Ribble Estuary (Kashefipour et al., 2002) and sediment transport processes in the Humber Estuary (Lin and Falconer, 1996).

2. Hydrodynamic modelling

For many estuarine and coastal water basins the vertical velocity component is relatively small in comparison with the horizontal velocity component. Hence the continuity and momentum equations can be integrated over the depth of flow and solved numerically to give the depth averaged velocity fields (Falconer, 1993). The depth integrated Reynolds Averaged Navier–Stokes equations are shown below:

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

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

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

where ξ = water elevation above (or below) datum; U, V = depth averaged velocity components in the 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 the x, y direction; τ_{xb}, τ_{yb} = bed shear stress component in the x, y directions; and $\bar{\varepsilon}$ = depth averaged eddy viscosity. The momentum correction factor, the wind and bed shear stresses, and the depth averaged viscosity are described in detail in Falconer (1993).

3. Suspended sediment transport modelling

Sediment transport formulations for predicting suspended sediment fluxes in depth integrated two-dimensional numerical models are generally based on solving the depth integrated form of the advective-diffusion equation, which can be shown to be of the form:

$$\frac{\partial SH}{\partial t} + \frac{\partial SUH}{\partial x} + \frac{\partial SVH}{\partial y} - \frac{\partial}{\partial x} \left(HD_x \frac{\partial S}{\partial x} \right) - \frac{\partial}{\partial y} \left(HD_y \frac{\partial S}{\partial y} \right) = E - D \quad (4)$$

where S = depth averaged suspended sediment concentration, E = sediment erosion rate, D = sediment deposition rate, and D_x, D_y = depth averaged dispersion coefficients in the x and y directions, respectively.

The depth averaged net sediment flux rate for non-cohesive sediment can be expressed in the form (Li et al., 2001; Yuan, 2007):

$$E - D = \gamma w_s (S_e - \alpha S) \quad (5)$$

where w_s = particle settling velocity, γ = a profile factor given by the ratio of the bed concentration S_a (i.e. the concentration at an elevation 'a' above bed) to the depth averaged equilibrium sediment concentration, S_e = depth-averaged equilibrium concentration, which can be determined from an appropriate sediment transport formula such as van Rijn (1984a, 1984b, 1993), with this being one of the most widely used formulations incorporated into computational models and included in the study reported herein, $\alpha = S_e/S$ is a sediment concentration profile factor. The equilibrium concentration is that value which occurs when the sediment flux vertically upwards from the bed due to turbulence is in equilibrium with the net sediment flux downwards due to the fall velocity associated with gravity.

For modelling cohesive sediment transport the governing depth integrated advective-diffusion Eq. (4) is used, but with the net sediment flux being rewritten in the following form (Falconer and Chen, 1996):

$$D = \begin{cases} w_s S \left[1 - \frac{\tau_b}{\tau_{c,d}} \right] & \tau_b \leq \tau_{c,d} \\ 0 & \tau_b > \tau_{c,d} \end{cases} \quad (6)$$

$$E = \begin{cases} M \left[\frac{\tau_b - \tau_{c,e}}{\tau_{c,e}} \right] & \tau_b > \tau_{c,e} \\ 0 & \tau_b \leq \tau_{c,e} \end{cases} \quad (7)$$

where τ_b = bed shear stress, $\tau_{c,d}$ = critical shear stress for deposition, $\tau_{c,e}$ = critical shear stress for erosion and M = empirical erosion constant.

Most of the parameters included in the above formulations are sensitive to the sediment characteristics locally. During numerical modelling studies of estuarine flows the value used must be chosen with extreme care. Typically values of the critical stress for erosion and deposition are given in Van Rijn (1993) for a range of different mud types. For the empirical erosion coefficient M , reported values used in the current study for the Severn Estuary study are typically in the range of 0.00001–0.0005 for soft natural mud (Falconer and Chen, 1996).

4. Sediment–bacteria interaction model

4.1. Partition of bacteria between sediments and water

The total bacteria concentration in the water column C_T is given by:

$$C_T = C_d + C_p \quad (8)$$

where C_d = free-living bacteria concentration and C_p = attached bacteria concentration in the water column.

For a given concentration of suspended solids, the quantity of faecal bacteria on the particles is often expressed as a mass-specific concentration P (cfu/unit weight of suspended solids), so the volume-specific concentration on the particles C_p can be expressed as:

$$C_p = S \cdot P \quad (9)$$

where S = the suspended solid concentration, and P = the mass-specific bacteria concentration, which can be defined as follows:

$$S = \frac{M_s}{V_{w+s}} \quad (10)$$

$$P = \frac{CFU_p}{M_s} \quad (11)$$

where M_s = solid mass of sediment, V_{w+s} = total volume of the water and solids, and CFU_p = colony forming unit of attached bacteria.

Chapra (1997) expressed the tendency of bacteria to attach to the particles by using a partition coefficient of the form:

$$K_D = \frac{P}{C_d} \quad (12)$$

Assuming that the rate at which bacteria are adsorbed and/or desorbed from a particulate is fast, then a local equilibrium can be assumed to give:

$$C_T = C_d + K_D \cdot S \cdot C_d \quad (13)$$

which can be solved to give:

$$C_d = f_d C_T \quad (14)$$

and

$$f_d = \frac{1}{1 + K_D S} \quad (15)$$

where f_d is the fraction of free-living bacteria in the water column.

For the attached bacteria, we have:

$$C_p = f_p C_T \quad (16)$$

where

$$f_p = \frac{K_D S}{1 + K_D S} \quad (17)$$

and:

$$f_p + f_d = 1 \quad (18)$$

4.2. Exchange of bacteria at the sediment–water interface

4.2.1. Bacteria settlement

One of the effects of sediment transport on adsorbed bacteria is that when the sediment settles out then the adsorbed bacteria is also taken out of the water column to the bed sediments. The flux of adsorbed bacteria from the water column to the bed sediments, F_{dep} , can be expressed as:

$$F_{dep} = q_{dep} P \quad (19)$$

where F_{dep} = flux of adsorbed bacteria from the water column to the bed sediments (cfu/cm²/s), q_{dep} = sediment deposition flux (kg/m²/s), and $P = C_p/S$ attached faecal bacteria concentration on the suspended sediments (cfu/0.1 g).

4.2.2. Bacteria re-suspension

The re-suspension of bacteria from the bed sediments to the water column F_{ero} , can be expressed as:

$$F_{\text{ero}} = q_{\text{ero}} P_b \quad (20)$$

where: F_{ero} = re-suspension of bacteria from the bed sediments to the water column (cfu/cm²/s), P_b = bacteria concentration on the bed sediments (cfu/0.1 g), and q_{ero} = sediment re-suspension flux rate (kg/m²/s).

To summarise, the net bacteria flux, F_{net} , due to settling and re-suspension of the sediments can be expressed as:

$$F_{\text{net}} = \max(q_{\text{ero}}, 0) P_b + \min(-q_{\text{dep}}, 0) P \quad (21)$$

4.2.3. Bacteria concentrations in the bed sediments

The concentration of bacteria on the bed sediments, P_b , varies depending on the exchange of bacteria between the water column and the bed sediments. However, another reduction also arises in the bed sediment concentration as a result of the decay of the bacteria within the bed sediments. Assuming that the deposited sediments from the water column to the bed and the bed sediments are well mixed immediately after deposition, then the exchange rate of bed bacteria concentration P_b can be expressed in the following form:

$$\frac{dP_b}{dt} = \frac{q_{\text{dep}}}{M_b} (P - P_b) - k_b P_b \quad (22)$$

where M_b = mass of bed sediments per unit area, and k_b = faecal bacteria decay/growth rate in the bed sediments.

Likewise, in Eq. (22), the mass of bed sediments per unit area, M_b , also varies temporarily as given by:

$$\frac{dM_b}{dt} = q_{\text{dep}} - q_{\text{ero}} \quad (23)$$

4.3. Governing equations for bacteria transport processes

4.3.1. Free-living bacteria transport

The fate and transport of free-living bacteria can be described by the following two-dimensional depth integrated advection-diffusion equation:

$$\begin{aligned} \frac{\partial C_d H}{\partial t} + \frac{\partial C_d U H}{\partial x} + \frac{\partial C_d V H}{\partial y} - \frac{\partial}{\partial x} \left(H D_x \frac{\partial C_d}{\partial x} \right) - \frac{\partial}{\partial y} \left(H D_y \frac{\partial C_d}{\partial y} \right) \\ = C_o^d + C_t^d - k C_d H \end{aligned} \quad (24)$$

where C_d = depth averaged free-living bacteria concentration, C_o^d = source or sink of free-living bacteria; C_t^d = transformation term defining the desorption of bacteria from the sediments to the free-living form and vice versa; and k = the decay rate of bacteria in the water column.

Eq. (24) has been solved to predict bacteria concentration levels for most studies of bacteria transport modelling, such as Kashefipour et al. (2002) and Lin and Falconer (2001), with this representation having been proven to represent the process accurately for the case where sediment transport is not significant. However, for studies where sediment transport processes are significant, then solving these equations alone will not give accurate results since the transport of bacteria through the process of sediment transport, via

erosion and deposition, have not been included in the transport model.

4.3.2. Attached bacteria transport

In studying the transport of attached bacteria, this part of the bacteria may be transported and diffused with the sediments. The fate and transport of attached bacteria can therefore be described by the following two-dimensional depth integrated advection-diffusion equation:

$$\begin{aligned} \frac{\partial H C_p}{\partial t} + \frac{\partial U H C_p}{\partial x} + \frac{\partial V H C_p}{\partial y} - \frac{\partial}{\partial x} \left(H D_x \frac{\partial C_p}{\partial x} \right) - \frac{\partial}{\partial y} \left(H D_y \frac{\partial C_p}{\partial y} \right) \\ = C_o^p + C_t^p + C_b^p - k C_p H \end{aligned} \quad (25)$$

where C_p = depth averaged attached bacteria concentration in the water column, C_o^p = source or sink of bacteria in its attached form; C_t^p = transformation term defining the adsorption of free-living bacteria to the attached bacteria form or vice versa; C_b^p = source term defining the attached bacteria from or to the bed sediments, for sediment erosion or deposition, respectively; and k = the decay rate for bacteria in the water column.

4.3.3. Total bacteria transport

In order to predict bacteria concentrations correctly, both for free-living and attached bacteria, then the transport equation must be solved simultaneously in the numerical model for both bacterial components. However, there are difficulties in solving these equations accurately since the transformation terms are difficult to quantify. The transformation processes between the free-living and adsorbed state for the bacteria are very complex, so it is almost impossible to quantify these terms. Wu et al. (2005) pointed out that in modelling heavy metals there was a problem in using separate equations to model dissolved and particulate metals due to the complex nature of the transformation between the particulate and dissolved phase. Adding Eqs. (24) and (25) and using $C_t^d = -C_t^p$ gives

$$\begin{aligned} \frac{\partial H C_T}{\partial t} + \frac{\partial U H C_T}{\partial x} + \frac{\partial V H C_T}{\partial y} - \frac{\partial}{\partial x} \left(H D_x \frac{\partial C_T}{\partial x} \right) - \frac{\partial}{\partial y} \left(H D_y \frac{\partial C_T}{\partial y} \right) \\ = C_o^d + C_o^p + C_b^p - k C_T H \end{aligned} \quad (26)$$

where C_T = depth averaged total faecal bacteria concentration, $C_o^p = F_{\text{net}}$, which is a source term defining the attached bacteria from, or to, the bed sediments and F_{net} can be calculated from using Eq. (21) as follows:

$$F_{\text{net}} = \max(q_{\text{ero}}, 0) P_b + \min(-q_{\text{dep}}, 0) P$$

By solving the total bacteria transport equation, then the total bacterial concentration level C_T is determined, wherein Eqs. (14) and (16) can then be used to determine the free-living and attached bacteria levels respectively.

5. Sediment–bacteria interaction model verification

In this section analytical solutions of the sediment–bacteria interaction are detailed. Idealised cases are also set up to

investigate the effects of different environmental factors and parameters. The sediment–bacteria interaction model developed is based on the original DIVAST model framework which was originally developed by Falconer (1984). The DIVAST model has been used by many researchers (Wu et al., 2005; Lin and Falconer, 1997) in the past, so only the new sediment–bacteria interaction model has been tested against the analytical solutions for re-suspension and deposition of sediment and bacteria. In this section two analytical solutions for sediment–bacteria interaction case studies have been investigated, namely for a deposition and re-suspension test. These solutions were first derived and then the numerical model was set up for test cases. The numerically predicted results were compared with the analytical results in order to test the sediment–bacteria interaction properties of the numerical model.

5.1. Derivation of analytical solutions

5.1.1. Case 1: deposition test

This test was set up to represent the deposition processes of attached bacteria due to sediment–bacteria interactions, as illustrated in Fig. 1 and where P is the bacteria concentration on the suspended sediments in $\text{cfu}/(10^{-1} \text{ g})$, P_b is the bacteria concentration on the bed sediments in $\text{cfu}/(10^{-1} \text{ g})$, H is the water depth, h_b is the bed sediment thickness, S_0 is the initial sediment concentration in the water column in kg/m^3 , and which is set to a constant, and C_T is the total bacteria concentration in the water column in $\text{cfu}/100 \text{ ml}$.

To simplify this problem some basic assumptions have been made including:

1. The sediment particle size was assumed to be uniform across the domain, so that the settling velocity w_s was set to be a constant;
2. The initial sediment concentration S_0 was assumed to be greater than the equilibrium concentration S_e , which meant that the sediment and attached bacteria settled down onto the bed and the concentration of the sediment and bacteria in water column kept on decreasing until equilibrium had been reached;
3. The bacteria decay rate was assumed to be a constant.

Following on from these assumptions, the bacteria and sediment concentration in the water column and the bed sediments can be obtained analytically, with details of the solutions being given below.

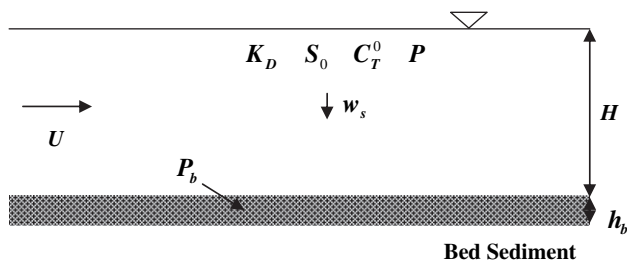


Fig. 1 – Illustration of test case set up.

Under steady flow conditions the governing equation for total bacteria can be simplified to the following form:

$$\frac{dC_T}{dt} = \frac{1}{H} C_b^p - kC_T \quad (27)$$

where C_b^p represents the reduction of bacteria due to the deposition of sediments, which is given as:

$$C_b^p = q_{\text{dep}} P = \gamma w_s P (S_e - \alpha S) \quad (28)$$

and

$$P = C_d K_D = \frac{K_D C_T}{1 + K_D S} \quad (29)$$

where k is the decay rate.

Hence, Eq. (27) can be expressed in the following form:

$$\frac{dC_T}{dt} = \frac{\gamma w_s}{H} \frac{K_D C_T}{1 + K_D S} (S_e - \alpha S) - kC_T \quad (30)$$

The sediment concentration in this equation can be obtained by solving the sediment transport equation. For steady and uniform flow conditions, the governing equation for suspended sediment transport can be simplified to give:

$$\frac{dS}{dt} = \frac{\gamma w_s}{H} (S_e - \alpha S) \quad (31)$$

Yuan (2007) derived an analytical solution for this sediment transport Eq. (31), given as:

$$S = \frac{1}{\alpha} S_e + \left(S_0 - \frac{1}{\alpha} S_e \right) e^{-\lambda t} \quad (32)$$

where

$$\lambda = \frac{\alpha \gamma w_s}{H} \quad (33)$$

For the derivation of the analytical solution for Eq. (30), an operator splitting scheme proposed in Lin and Falconer (1997) is used. This equation can be treated as the combination of the following two equations:

$$\frac{dC_T}{dt} = \frac{\gamma w_s}{H} \frac{K_D C_T}{1 + K_D S} (S_e - \alpha S) \quad (34)$$

$$\frac{dC_T}{dt} = -kC_T \quad (35)$$

Yuan (2007) derived the analytical solution of Eq. (34) to validate his heavy metal model, together with the analytical solution for $dC_T/dt = -kC_T$ given as $C_T = C_T^0 e^{-kt}$. Hence the analytical solution of Eq. (30) can be obtained by combining these two analytical solutions to give:

$$C_T = \frac{\alpha + K_D [S_e + (\alpha S^0 - S_e) e^{-\lambda t}]}{\alpha (1 + K_D S^0)} C_T^0 e^{-kt} \quad (36)$$

5.1.2. Case 2: re-suspension test

This case is based on the deposition test, except that the initial conditions are now changed so that the initial sediment concentration S_0 is set lower than the equilibrium value S_e and the initial bacteria concentration in the bed sediments P_b is set to be a constant other than zero.

In this case the fate and transport of the total bacteria can also be expressed using Eq. (30), but here C_b^p represents the source of bacteria due to sediment erosion, giving:

$$C_b^p = q_{\text{ero}} P_b = \gamma w_s P_b (S_e - \alpha S) \quad (37)$$

Assuming a first order decay for the bacteria concentration in the bed sediments, then we get:

$$P_b = P_b^0 e^{-k_b t} \quad (38)$$

$$\frac{dC_T}{dt} = \frac{\gamma w_s}{H} P_b^0 e^{-k_b t} (S_e - \alpha S) - k C_T \quad (39)$$

which gives the analytical solution as:

$$C_T = \left[C_T^0 + \frac{P_b^0}{\alpha} (S_e - \alpha S^0) (1 - e^{-\lambda t}) \right] e^{-k t} \quad (40)$$

5.2. Verification of model against analytical solutions

In this section details are given of the testing of the sediment–bacteria interaction model against the analytical solutions derived in the previous section.

5.2.1. Case 1: deposition

The computational parameters were set as follows:

1. Water depth = 1 m;
2. Parameters for sediment transport: $\alpha = 1$, $\gamma = 1$ and the fall velocity $w_s = 0.001$ m/s and the equilibrium sediment concentration S_e was set to 1 kg/m³;
3. The partition coefficient K_D was set to 10 l/g, as suggested in Bai and Lung (2005) and the initial sediment and water column bacterial concentrations were set to be 2 kg/m³ and 100 cfu/100 ml respectively. These parameter values gave an initial ratio of attached to total bacteria of about 0.952. The decay rate in the water column was set to 1 day⁻¹.
4. The initial bacteria bed concentration was assumed to be zero.

The comparisons between the model calculated and analytical solutions are shown in Fig. 2. From these plots it can be seen that the model predicted results are nearly identical to the analytical solution for the bacteria and suspended sediment concentrations. Fig. 2 shows that the sediment deposition processes reach the equilibrium condition after about 3600 s, or 1 h. After reaching equilibrium conditions the sediment concentrations were kept at a constant level. The decay process meant that the total bacteria concentration kept reducing after equilibrium conditions had been achieved for the sediment transport. It can be seen that the bacteria loss due to sediment deposition occurred in a fairly short time compared to the loss due to decay.

5.2.2. Case 2: re-suspension

The set up of the numerical model for this case was the same as that for Case 1, except for changes in some initial conditions. For this case $S_0 = 0$, $C_T = 0$ and $P_b^0 = 100$ cfu/0.1 g.

The comparison between the model predicted and analytical solutions are shown in Fig. 3. From these results it can be seen that the model results are again nearly identical to the analytical results, for both the bacteria and suspended sediment concentrations. Fig. 3 shows that the sediment re-suspension processes reached equilibrium conditions

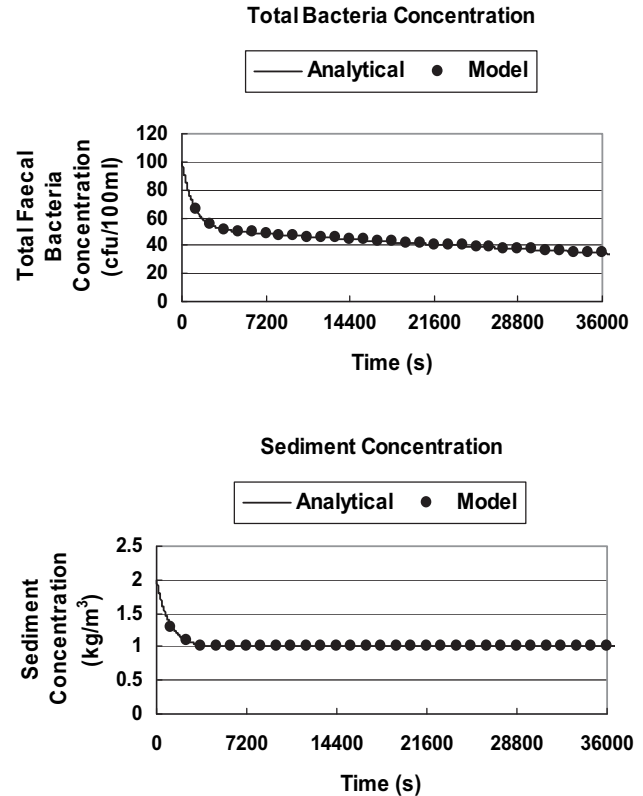


Fig. 2 – Comparison of bacteria and sediment concentrations for deposition test.

again after about 3600 s or 1 h. After equilibrium conditions had been reached the sediment concentration remained at a constant level. The bacteria concentration level decreased gradually, which was due to bacterial decay. During the re-suspension process the decay processes were suppressed by the rapid increase in the bacteria level due to re-suspension.

6. Idealised case application

The sediment–bacteria interaction model has been shown to solve the governing equations accurately and can therefore be used with some confidence in investigating the effects of sediments on the fate and transport of bacteria. In this section idealised test cases were set up to study the effects of removing bacteria from the water column and the subsequent re-suspension of bacteria from the bed.

6.1. Removal of bacteria from the water column due to sediment

6.1.1. Effect of the partition coefficient

In order to investigate the effect of the partition coefficient on the removal of bacteria from the water column, partition coefficient K_D values of 10 l/g, 1 l/g, 0.1 l/g and 0.01 l/g were used. The initial bacteria bed concentration was assumed to be zero, the initial sediment concentration was set to be 2 kg/m³ and the initial bacteria concentration in the water column was set to 100 cfu/100 ml. The decay rate in the water column was

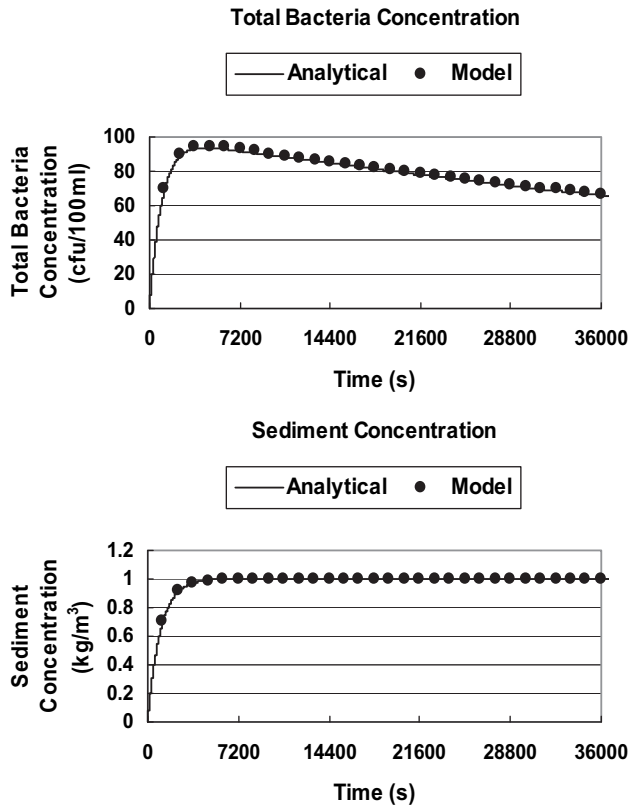


Fig. 3 – Comparison of bacteria and sediment concentrations for re-suspension test.

set to 1 day^{-1} . The parameters for sediment transport were set to: $\alpha = 1$, $\gamma = 1$ and the fall velocity $w_s = 0.001 \text{ m/s}$ and the equilibrium sediment concentration S_e was set to be 1 kg/m^3 .

The numerical model results are shown in Fig. 4. It was observed that with a higher partition coefficient then lower total bacteria concentrations were predicted in the water column. The reason for this finding is that the higher partition coefficient gave higher ratios of attached to total bacteria for the same sediment concentrations, which meant that more bacteria were deposited on the bed and thereby giving a lower concentration in the water column.

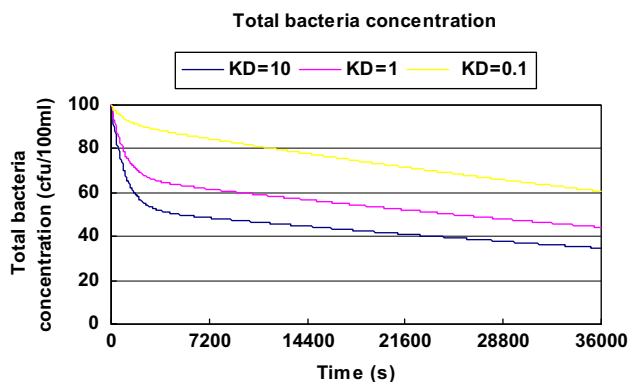


Fig. 4 – Removal of bacteria with different partition coefficients.

6.1.2. Effect of different sediment sizes giving different settling velocities

Settling velocities of $w_s = 0.001 \text{ m/s}$, 0.0001 m/s , 0.00001 m/s were used respectively to consider the effects of particle sediment size on the removal of bacteria from the water column. The initial bacteria bed concentration was assumed to be zero, the initial sediment concentration was set to be 2 kg/m^3 and the initial bacterial concentration in the water column was set to be 100 cfu/100 ml . The decay rate in the water column was set to 1 day^{-1} , and the decay rate in the bed sediments was assumed to be zero. The partition coefficient K_D was set to 10 l/g , which gave an initial ratio of attached to total bacteria of 0.952 , which would decrease with a corresponding decrease in the sediment concentration within the water column. The equilibrium sediment concentration S_e was set to 1 kg/m^3 .

The numerical model results are shown in Fig. 5, where it can be seen that higher settling velocities reduced the total bacteria concentration level much quicker than the lower settling velocity. The concentration of free-living bacteria was not affected by the settling velocity. The reduction in the free-living bacteria in the water column was therefore purely due to decay.

6.2. Re-suspension of attached bacteria to water column

6.2.1. Effect of bed bacteria concentration

The initial bed bacteria concentration assumed in the investigations was either 100 cfu/0.1 g , or 50 cfu/0.1 g , or 10 cfu/0.1 g , with this value being used to investigate the effect of the bed concentrations on the re-suspension of the attached bacteria. The initial sediment concentration was assumed to be zero and the initial bacterial concentration in the water column was also set to zero. The decay rate in the water column was set to 1 day^{-1} . Parameters for the sediment transport model components included: $\alpha = 1$, $\gamma = 1$, fall velocity $w_s = 0.001 \text{ m/s}$, equilibrium sediment concentration $S_e = 1 \text{ kg/m}^3$ and the partition coefficient $K_D = 10 \text{ l/g}$.

The numerical model predictions are shown in Fig. 6. From these results it can be seen that higher bed bacteria concentrations gave rise to much higher bacteria concentrations in the water column. Higher bed bacteria concentrations means that more bacteria contribute to the water column under the same conditions for re-suspension, i.e. the bacteria re-

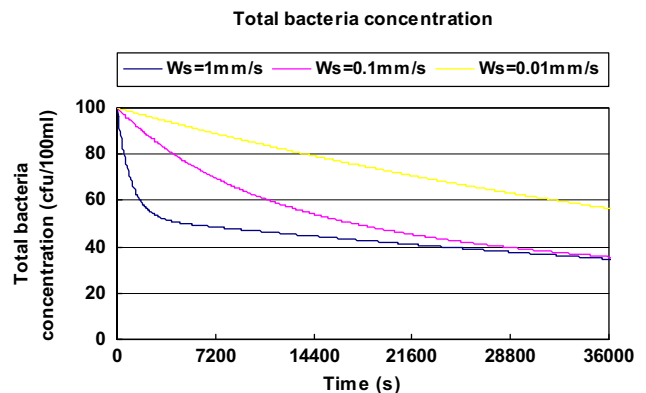


Fig. 5 – Removal of bacteria with different settling velocities.

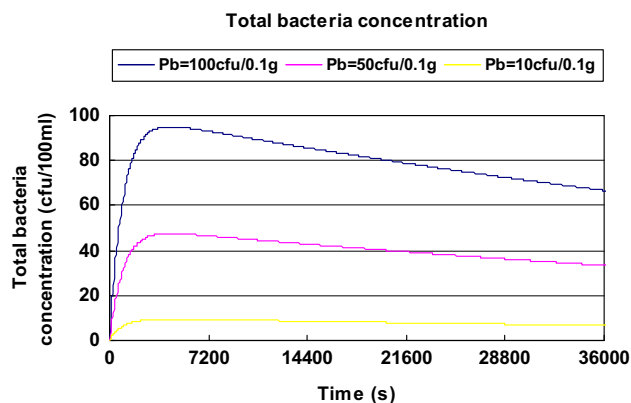


Fig. 6 – Re-suspension of bacteria with different bed bacteria concentrations.

suspended into the water column with the sediments and then re-partition into the water column.

6.2.2. Effect of partition coefficient

For this test case different partition coefficients were used to investigate the effect of the partition coefficient on the re-suspension of bacteria and the values considered included: $K_D = 10 \text{ l/g}$, 1 l/g , 0.1 l/g and 0.01 l/g respectively. The initial bed bacteria concentration was assumed to be 100 cfu/0.1 g , the initial sediment concentration was set to zero and the initial bacterial concentration in the water column was set to zero. The decay rate in the water column was set to 1 day^{-1} . The governing parameters for the sediment transport model were: $\alpha = 1$, $\gamma = 1$, the fall velocity $w_s = 0.001 \text{ m/s}$ and the equilibrium sediment concentration S_e was set to 1 kg/m^3 .

The numerical model results are shown in Fig. 7, where it can be seen that the partition coefficient does not significantly affect the total bacteria concentration in the water column in the re-suspension mode.

7. Model application: artificial flooding case study

The numerical model was applied to a published artificial flooding study. Muirhead et al. (2004) conducted a study in

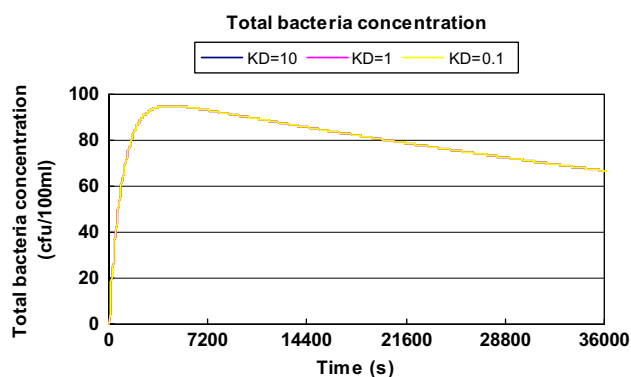


Fig. 7 – Re-suspension of bacteria with different partition coefficients.

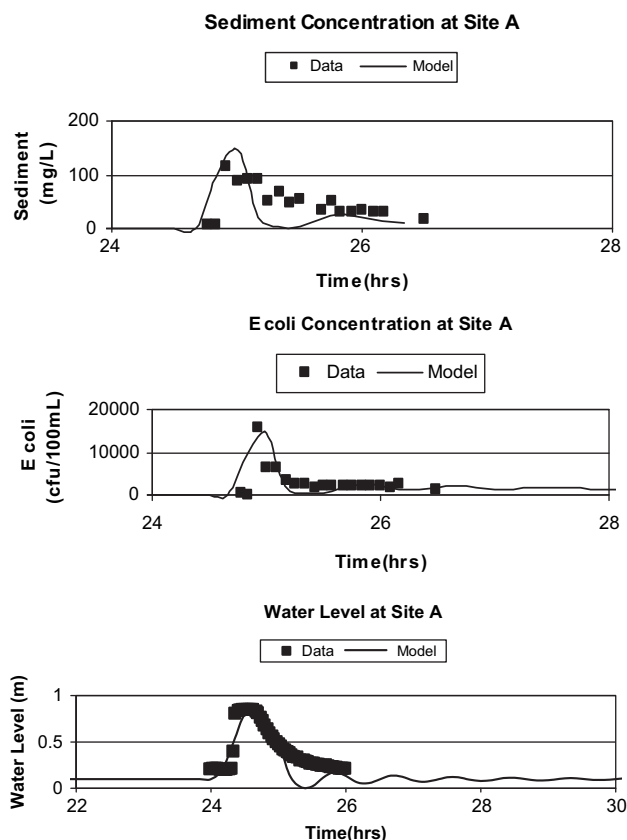


Fig. 8 – Comparison of model results and site data at Site A.

Topehaehae Stream in the Waikato Region, New Zealand, to investigate faecal bacteria transport during floods. This study was reproduced numerically by Bai and Lung (2005). The median flow rate was 260 l/s and the average stream width was 5.8 m . The relatively straight stream was simplified to a straight and uniform river. A water supply reservoir, located at the upstream end of the river, was used as the source of water for the artificial flooding. The reservoir was the only source of water supply during the artificial flooding experiment. The artificial floods were created by opening the valve of a dam for over 30 min, holding the valve for 20 min, and then closing the valve over 10 min for three successive days and with the peak flow reaching 4300 l/s . Faecal bacteria and turbidity were sampled at sites A and B, located at 1.3 and 2.5 km downstream of the reservoir respectively. A weir equation was used at the downstream boundary. A detailed account of the artificial flooding procedure is given in Muirhead et al. (2004) and Bai and Lung (2005).

The hydrodynamic modelling was carried out by using time series flow rates of the artificial flood as the upstream boundary condition and a weir equation was assigned at 3.0 km downstream of the reservoir as the downstream boundary condition. The roughness height was set to 10 mm .

The initial faecal bacteria and sediment concentration levels in the water column were set to zero. The faecal bacteria concentration in the river bed was set to $1 \times 10^6 \text{ cfu/g}$ and the partition coefficient was set to be 10 l/g as suggested in Bai and Lung (2005). The specific weight of sediment was assumed to be

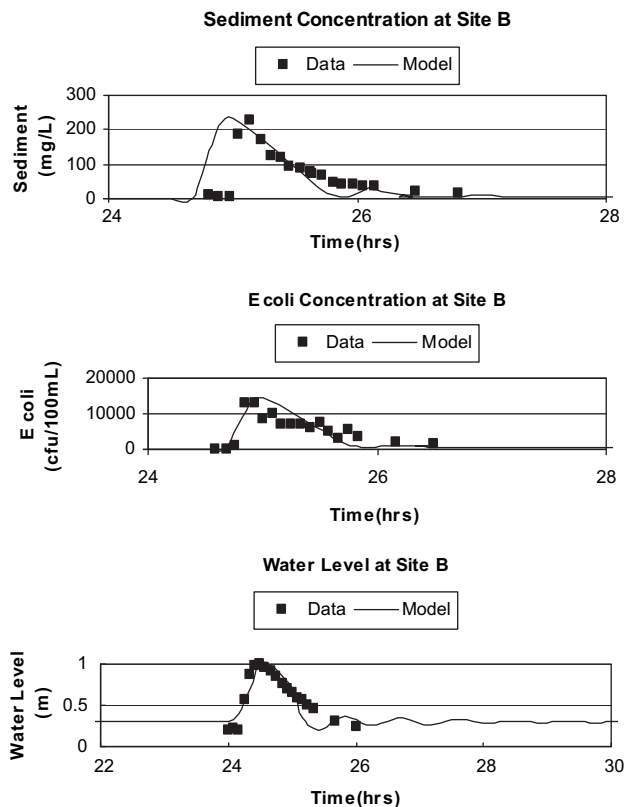


Fig. 9 – Comparison of model results and site data at Site B.

2.65. The critical shear stress for sediment re-suspension and deposition were set to 0.4 and 0.1 N/m² respectively.

The purpose of this model test study was to demonstrate the ability of the model to simulate sediment and bacteria re-suspension and deposition under artificial flooding conditions. The comparison of the model predicted results and the measurements are shown in Figs. 8 and 9. In general, the model has reproduced the re-suspension and deposition patterns of the sediment and *E. coli* levels reasonably well. The model reproduced the re-suspension pattern of sediment and *E. coli* closely. The time of the rise and peak values were predicted relatively well. The differences between the two datasets can be explained by the experimental measurements including turbidity, whereas in the numerical model sediment concentrations were predicted. This was also noted by Bai and Lung (2005).

8. Conclusions

The paper reports on the refinement of a numerical model to predict the fate and transport processes of faecal bacteria in surface waters, where sediment transport processes are significant. In this model the concentration of faecal bacteria within the water column was linked to the sediment transport processes, i.e. the faecal bacteria concentrations were affected by adsorption and desorption with sediment particles and the deposition and re-suspension of sediments.

Analytical solutions were derived for steady and uniform flow conditions for sediment–bacteria interaction processes and then the model was tested against these analytical solutions. The model predictions agreed almost perfectly with the analytical solutions and a number of observations were made from the results of these solutions, which showed that: (i) the reduction in the bacteria concentrations due to sediment deposition occurred over a fairly short time compared to the reduction due to decay; and (ii) the decay processes were effectively suppressed during re-suspension of the sediments, due to the rapid increase in the bacterial inputs arising from desorption from the re-suspended sediments.

A series of idealised test cases were then set up to study the effects of removing bacteria from the water column and the subsequent re-suspension of bacteria from the bed sediments. The main findings from these idealised model test cases were that: (i) for a higher partition coefficient then lower total bacteria concentrations were predicted in the water column during bacteria settlement, as more bacteria were transported to the bed with sediment deposition; (ii) higher settling velocities reduced the bacteria levels in the water column more rapidly; (iii) higher bed bacteria concentrations meant that more bacteria contributed to the water column load under the same conditions for re-suspension, i.e. the bacteria re-suspended into the water column with the sediments and then re-partitioned into the water column; and (iv) the partition coefficient did not significantly affect the total bacteria concentration in the water column during re-suspension, since partitioning only affected the attached and free-living bacteria levels with a higher partition coefficient, giving a higher attached bacteria ratio and a lower free-living bacteria ratio.

The model was also applied to a published artificial flooding case study. The model predictions were encouraging, with reasonably good agreement being obtained between the model predictions and the corresponding field measurements.

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