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Research papers

Modelling of river faecal indicator bacteria dynamics as a basis for faecal contamination reduction

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ABSTRACT

To improve microbial water quality and to prevent waterborne disease outbreaks, knowledge on the fate and transport of contaminants and on the contributions from different faecal sources to the total contamination is essential. The fate and transport of faecal indicators *E. coli* and enterococci within the Betna River in Bangladesh were simulated using a coupled hydrodynamic and water quality model. The hydrodynamic model for the river was set up, calibrated and validated with water level and discharge in our earlier study. In this study, the hydrodynamic model was further validated using measured water temperature and salinity and coupled with the water quality module. Bacterial load data from various faecal sources were collected and used as input in the water quality model. The model output corresponded very well with the measured *E. coli* and enterococci concentrations in the river; the Root Mean Square Error and the Nash-Sutcliffe efficiency for Log_{10}-transformed concentrations were found to be 0.23 (Log_{10} CFU/100 ml) and 0.84 for *E. coli*, and 0.19 (Log_{10} CFU/100 ml) and 0.86 for enterococci, respectively. Then, the sensitivity of the model was tested by removing one process or forcing at a time. These simulations revealed that the microbial decay, the upstream concentrations and the discharge of untreated wastewater were the primary factors controlling the concentrations in the river, while wind and the contribution from the diffuse sources (i.e. urban and agricultural runoff) were unlikely to have a major influence. Finally, the model was applied to investigate the influence of wastewater treatment on the bacteria concentrations. This revealed that wastewater treatment would result in a considerable improvement of the microbial water quality of the Betna River. This paper demonstrates the application of a comprehensive state-of-art model in a river in a data-poor tropical area. The model can potentially be applied to other watersheds and can help in formulating solutions to improve the microbial water quality.

1. Introduction

Waterborne diseases caused by faecal contamination of surface waters are a major problem worldwide, in particular in developing countries. In most developing countries, sanitation and sewage treatment systems are underdeveloped, and a large portion of the population relies on untreated and highly contaminated surface water (Kamal et al., 2008). This widespread faecal contamination of surface waters often leads to outbreaks of diarrheal diseases (Wu et al., 2016). Globally, an estimated 1.8 million people die annually from waterborne diseases and most of them are children from developing countries (WHO, 2012).

Surface waters can be contaminated by various faecal sources, including untreated wastewater discharges, septic leakage, agricultural or urban runoff, and wildlife populations (An et al., 2002). Knowledge on the dynamic distribution of faecal contamination in water bodies is lacking worldwide, especially in developing countries, like Bangladesh, where faecal contamination is not well monitored. To mitigate faecal contamination of surface waters, knowledge on the microbial fate and transport, the influence of different processes, and the contribution from different sources to the total contamination is essential (Rochelle-Newall et al., 2015, Sokolova et al., 2013).

While regular monitoring of microbial water quality of a river is expensive and time consuming, process-based mathematical modelling can save time and resources. Modelling is useful to generate spatially and temporally continuous concentrations, and helps to better understand the sources, fate and transport of the faecal contamination. Previous studies have shown that concentrations of faecal contaminants in water sources can be described using coupled hydrodynamic and water quality models (Harwood et al., 2005, Sokolova et al., 2013, Ouattara et al., 2013, Liu et al., 2006). These models describe the hydrodynamic situation in the water body and take into account the decay

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of microorganisms in the water environment (Sokolova et al., 2013, Liu et al., 2015). These models can be used for scenario analysis in order to provide a basis for water management, for example, to plan mitigation measures to reduce faecal contamination of a water body. However, process-based modelling of microbial water quality is very sparse worldwide, particularly in tropical developing countries, where diarrheal diseases are endemic (Hofstra, 2011). Most of the recent studies have been conducted in the developed countries (e.g. Schijven et al., 2015, Brauwere et al., 2014, Sokolova et al., 2013, Bedri et al., 2014, Gao et al., 2015), and the models mostly exclude contributions from diffuse sources (e.g. Sokolova et al., 2013, Schijven et al., 2015, Vijay et al., 2016).

To increase the knowledge base, in this study, we implement a coupled hydrodynamic and microbial water quality model (MIKE Powered by DHI software: MIKE 21 FM and ECO Lab, DHI, 2011) to study the faecal contamination in the tidal Betna River located in the developing country Bangladesh. Our study provides the first example of modelling the microbial water quality of a surface water source in Bangladesh. The model effectively takes into account point and diffuse faecal sources of human and animal origin, hydro-meteorological conditions and microbial decay processes.

The aim of this study was to better understand the sources, fate and transport of the faecal contamination in the Betna River. To represent the faecal contamination, we used the faecal indicator bacteria (FIB) *E. coli* and enterococci, which are the two most widely used indicators of microbial water quality (Lata et al., 2009, Ouattara et al., 2013). In this study, the previously developed hydrodynamic model of the Betna River (Islam et al., 2017b) was further developed and validated with water temperature and salinity distribution in the river. The model was then applied to simulate the fate and transport of *E. coli* and enterococci in the river, taking into account the bacterial decay. The modelling results were compared with the observed FIB concentrations in the river. Next, the processes that influence the FIB concentrations in the river were discussed, and contributions from the different faecal sources were analysed. Finally, the model was applied to predict the effect of different wastewater management scenarios on the microbial water quality in the river. This paper thus provides an enhanced understanding on the application of fate and transport modelling of faecal contamination in surface water in a developing country. The developed model can potentially be applied to other watersheds in the world with similar characteristics.

2. Materials and methods

2.1. Study area

The study area covers an area of approximately 107 km^2 in the Betna River catchment in the southwest of Bangladesh (Fig. 1). This catchment is located in the Ganges-Brahmaputra delta. The total length of the Betna River is about 192 km; the average width is 125 m; and the maximum water depth is 9 m. The present modelling study focuses on the downstream 30 km of the Betna River. This river is hydrologically connected with the Bhairab River near the Jessore district in the north and the Kholpetua River near Assasuni of the Satkhira district in the south. The Bay of Bengal is located approximately 60 km south of the study area. The river has a tidal influence that contributes to the river's sustainability, because during the dry season, the inflow of fresh water from upstream areas becomes very limited. Tide generates from the Bay of Bengal and propagates to the north to the upstream boundary of the study area. The observed tidal water levels in the Betna River vary between −2.10 and 3.50 m. The observed maximum discharge in 2012 was 277 and 392 m^3/s at the time of ebbing and flooding respectively (IWM, 2014).

The study area has a typical monsoon climate with a hot season March – May, followed by a rainy season June – October and a cool period November – February. The mean annual rainfall in the area is about 1800 mm, of which approximately 70% occurs during the monsoon season. This area is affected by flooding during the monsoon in July – September and during the cyclone season (pre-monsoon) in April – May (CEGIS, 2013). Relative humidity of the area varies from about 70% in March to 90% in July. Mean annual air temperature is 26 °C with peaks of around 35 °C in May – June; the temperature in winter may fall to 10 °C in January. Wind in the region shows two dominant patterns, i.e. south westerly monsoon wind during July – September and north easterly wind during November – February.

The study area consists of flat terrain with low-lying depressed areas and many tidal channels and creeks criss-crossing the area. The soils are mostly clay and loam. The land use of the study area is dominated by paddy rice cultivation and integrated paddy rice-shrimp culture. About 8% of the total area is used for homestead and settlements, about 10% is water body, 0.5% is forest, 61% is used for agriculture/paddy rice cultivation, and the remaining 20.5% is wetland (also used for aquaculture or integrated paddy rice-shrimp culture). In winter, due to a lack of upstream flow, salinity increases, and as a result agriculture is hindered in this season. Water salinity reaches the highest level during March – April (up to 15 parts per thousand (ppt)) and the lowest level (near 0 ppt) in the rainy season during August – September (IWM, 2014).

The study area has a high population density of 1050 people per km^2 (BBS, 2011). Wastewater and manure are the main sources of faecal contamination in this catchment. Wastewater treatment facilities are very limited in Bangladesh; in the study area, domestic, municipal and industrial wastewater is discharged into the river without treatment. The manure sources include manure applied to the agricultural lands as organic fertilizer and direct deposition of manure in to the river and canals. Various waterborne diseases, including gastrointestinal and skin diseases, are observed in this area during and after flooding (CEGIS, 2013). The observed FIB concentrations in the river were 1.3–4.5 Log_{10} CFU/100 ml for *E. coli* and 2.4–4.8 Log_{10} CFU/100 ml for enterococci (Islam et al., 2017a).

2.2. Data collection and analysis

To validate the microbial water quality model, water temperature, salinity and FIB (*E. coli* and enterococci) concentrations were measured in samples collected at four sites along the Betna River (Fig. 1). The sampling sites were selected to ensure representation of the various wastewater sources (including wastewater input from the nearby city Satkhira) and manure discharge into the river. The sampling sites were: an upstream site that receives contamination mostly from diffuse sources (Site 1), a site adjacent to households (Site 2), a site that receives untreated wastewater discharge from urban and industrial areas (Site 3), and a site adjacent to a creek that receives stormwater runoff from the nearby town Satkhira (Site 4).

The samples were collected on 30 occasions: monthly between April 2014 and November 2015 and during heavy rainfall events. The sampling methods and data were discussed in detail in Islam et al. (2017a). In brief: water temperature and salinity were measured on the spot, and the water samples for bacterial analysis were collected into sterile nalgene plastic bottles with the care required for FIB analysis. All samples were placed in an insulated box filled with ice packs and transported to the laboratory of Environmental Science Discipline, Khulna University; the analyses were started within six hours of collecting the first sample. Enumeration of *E. coli* and enterococci was performed by the membrane filtration (MF) technique (USEPA, 2002, USEPA, 2009). Diluted water samples were filtered through 0.45 µm membrane filter. For enumeration of *E. coli,* the mTEC agar plates were incubated at 35 ± 0.5 °C for 2 h followed by further incubation at 44.5 ± 0.2 °C for 22–24 h. For enumeration of enterococci, the mE agar plates were incubated at 41 ± 0.5 °C for 48 h followed by further incubation on Esculin Iron agar plate at 41 ± 0.5 °C for 20–30 min. After incubation, black or reddish-brown colonies were counted as