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Research papers

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

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A R T I C L E I N F O

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A B S T R A C T

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

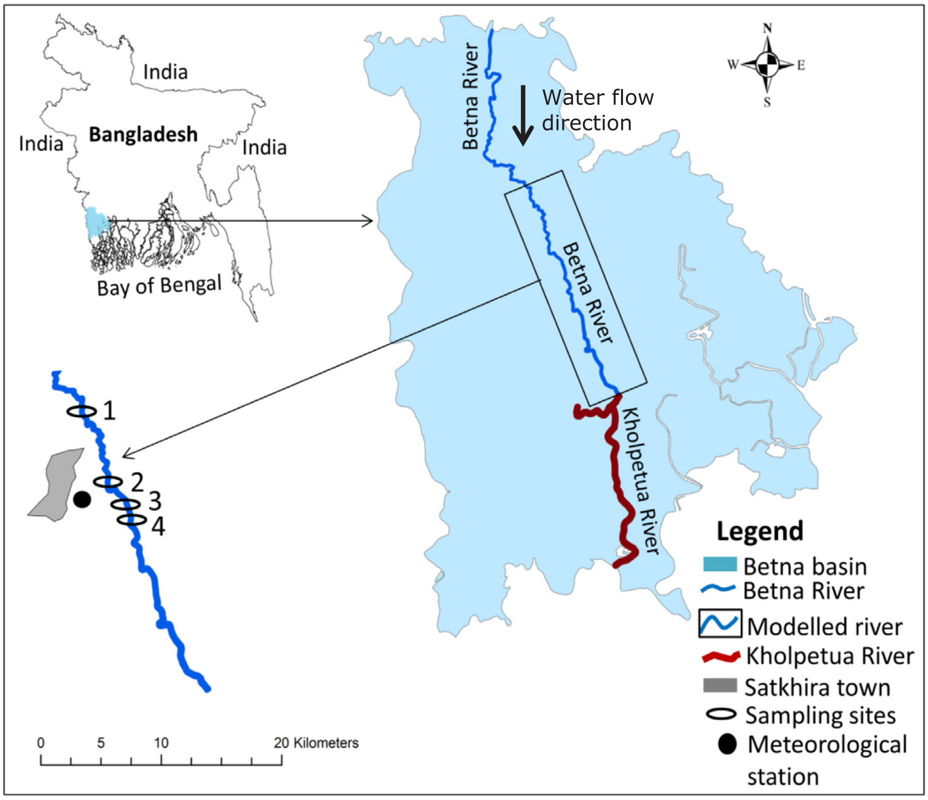

Fig. 1. Map of the study area: the Betna River basin in the southwest of Bangladesh. Sampling Site 1 receives pollutants mostly from diffuse sources; Site 2 receives wastewater from households; Site 3 receives untreated wastewater discharge from urban and industrial areas, and Site 4 receives stormwater runoff from the nearby town Satkhira. The river flows from north to south. Tidal water levels vary between 1.55 and 3.48 m in the upstream part and between −2.10 and 3.50 m in the downstream part of the river.

enterococci. The bacteria colonies were expressed as colony forming units (CFU) per 100 ml.

Water level and discharge data were gathered from the Institute of Water Modelling (IWM) in Bangladesh; and precipitation, wind speed, wind direction, air temperature and relative humidity data were collected from the Sathkira station of the Bangladesh Meterological Department (Fig. 1).

2.3. Modelling

A coupled hydrodynamic and water quality model, MIKE 21 FM with ECO Lab (DHI, 2011), was applied to simulate hydrodynamics and FIB concentrations in the Betna River. The MIKE 21 FM is a two-dimensional hydrodynamic (HD) model, which includes a water quality module (ECO Lab) for modelling bacterial spread in surface water from different contamination sources. Several process-based models have been developed to simulate the microbial concentrations or loads for a catchment and water source, examples are the Soil and Water Assessment Tool (SWAT) (Sadeghi and Arnold, 2002), ECOMSED (Blumberg and Mellor, 1987) and SENEQUE (Billen et al., 1994). In this study, the MIKE 21 FM model was chosen, because this model is suitable for tidal rivers and produces results with high temporal and spatial resolution.

2.3.1. Hydrodynamic model

The model is based on a 2D numerical solution of Reynolds averaged Navier-Stokes equations (DHI, 2011). In the model, the Boussinesq simplifying approximation is used, and hydrostatic pressure is assumed. The 2D model consists of vertically integrated momentum equations, a continuity equation, advection-diffusion equations for temperature and salinity, and an equation of state. The water density depends on temperature and salinity only (DHI, 2011).

At the onset of the modelling process, to describe the bathymetry of the river, a digital representation of the modelling domain was created. The modelling domain was divided into elements to create the computational mesh. The mesh was generated in the MIKE Zero Mesh Generator tool using a flexible mesh approach with triangular elements in the horizontal plane, using Delaunay triangulation (DHI, 2011). The mesh resolution was finer in the areas where the river is narrow. The mesh consisted of 4089 nodes and 6628 elements; the mesh element area varied from approximately 43–498 m^2. The model accounted for wind forces and the net precipitation on the river surface, and calculated the heat exchange between the atmosphere and the river. A flooding depth of 0.05 m, drying depth of 0.005 m and wetting depth of 0.1 m were set in the model. The water density was formulated as a function of temperature and salinity. The horizontal eddy viscosity was simulated using the Smagorinsky formulation. The bed resistance was described by a constant Manning number of 60 $m^{1/3}/s$. The conditions on the upstream and downstream open boundaries were described using time-series for discharge and water level respectively; the land boundary was set to zero normal velocity. The initial conditions were specified using the measured water level, and initial water velocity was set to zero. The initial and boundary conditions for the water temperature and salinity were described using measured and interpolated data. For heat exchange, the measured data for air temperature and relative humidity were used, and a constant clearness coefficient (70%) was assigned; the default parameterisation was used (DHI, 2011). Heat exchange with the atmosphere was applied to simulate the water temperature, which determines microbial decay.

In our previous study, the hydrodynamic model for the Betna River was set up, and then calibrated and validated using the measured data for water level and discharge. The calibration and validation were performed for the periods 26 August – 15 September 2012 and October 2014 – September 2015, respectively. The model performance was assessed using the coefficient of determination (R^2) and Nash-Sutcliffe efficiency (NSE). The model performed well both for calibration (water level: R^2 = 0.92, NSE = 0.81; discharge: R^2 = 0.83; NSE = 0.66) and validation (water level: R^2 = 0.89, NSE = 0.76; discharge: R^2 = 0.84; NSE = 0.72). The good model performance for water level and river discharge signifies the potential of the model to simulate microbial water quality. The details regarding the model development, input data, calibration and validation are described in our previous study (Islam et al., 2017b). In the present study, the model was further validated using the water temperature and salinity data for the period October 2014 – September 2015, because water temperature and salinity have a major influence on microbial processes.

2.3.2. Microbial water quality model

In the present study, the transport and fate of FIB in the Betna River were simulated for the period October 2014 – September 2015. The microbial water quality module ECO Lab utilizes the output (e.g., the velocity field, water temperature, salinity) from the hydrodynamic model to calculate the fate of FIB in the river. In our study, the modified ECO Lab template contained two state variables: *E. coli* and enterococci.

Faecal contamination can enter the river through wastewater discharges from the nearby urban areas and households through sewer drains. The wastewater discharges from drains were described as sources of faecal contamination in the model. The input flows from the drains were estimated based on the number of people connected to the sewer network and water consumption per person of 90 L/day (WSP, 2009). The *E. coli* concentration in untreated wastewater was set to 1.5×10^6 CFU/100 ml based on the concentrations reported by Payment et al. (2001), Carlos et al. (2013) and Sokolova et al. (2013). The enterococci concentration in untreated wastewater was set to 1.0×10^6 CFU/100 ml, which is comparable to the value reported by Ahmed et al. (2008).

In addition, faecal contamination can enter the river with stormwater runoff from the nearby town Satkhira (Fig. 1). The runoff volume was estimated using the curve number method. The runoff curve number developed by the US Department of Agriculture (USDA, 1986) is an empirical hydrological parameter to predict the approximate amount of direct runoff from a rainfall event (Balvanshi and Tiwari, 2014). The curve number is based on the soil type, land use and hydrologic conditions. Stormwater is not treated and is likely to carry faecal contamination from cats and dogs that live in the urban area. The FIB concentration in urban stormwater ranges between 10^3 and 10^4 CFU/100 ml (Marsalek and Rochfort, 2004). In this study, a concentration of 5×10^3 CFU/100 ml was used for both *E. coli* and enterococci.

The loadings of bacteria from the paddy fields were estimated based on the estimated discharge from the paddy fields and the FIB concentrations in the water of the paddy fields. At first, the *E. coli* concentration in the paddy fields of the study area was estimated from the manure application rate of 420 kg/ha/yr (Hasanuzzaman et al., 2011), the *E. coli* concentration in manure of 4.2×10^5 CFU/g (Coffey et al., 2010) and the average water height of the farm of 21 cm; all *E. coli* in manure was assumed to enter the water column. The resulting theoretically calculated concentration was 4.1×10^3 CFU/100 ml, which was similar to the average *E. coli* concentration of 4.6×10^3 CFU/100 ml reported by Kim et al. (2006) for the paddy fields in South Korea. For confirmation and to get accurate concentrations for both *E. coli* and enterococci, sampling was performed in five paddy fields around the Betna River in 2016 in August, when most discharges from the paddy fields occur. The measured average *E. coli* and enterococci concentrations in the paddy fields were 3.6×10^3 and 7.4×10^3 CFU/100 ml respectively; these values were in the same order of magnitude as the theoretical calculations. These measured values were applied in the model.

Another source of faecal contamination is the inflowing bacterial load from the upstream part of the river. The daily concentrations at the upstream boundary were estimated by interpolating the concentrations measured at Sampling Site 1 (Fig. 1). The concentration at the downstream boundary was assumed to be 0 CFU/100 ml due to a limited anthropogenic impact on the water quality, since very few people live in this forested area. The model sensitivity analysis also showed that the concentration at the downstream boundary does not have an impact on the location of interest, because it is far away. Bedri et al. (2014) in their modelling study also used zero concentrations for open boundaries and indicated that the far distance from the shoreline is sufficient to negate the effect of boundary conditions on the location of interest.

Occasional leakage of septic tanks and open defaecation from humans can also contaminate the river water (An et al., 2002). However, the lack of sufficient data (e.g., corresponding amount of faecal matter and bacterial concentrations) prevented inclusion of the leakage and open defaecation in the model. Direct defaecation from cattle was also ignored in this study due to the difficulties in estimation of the coincident amount of deposited manure. We have found no correlation between the measured turbidity and the FIB concentrations; this may indicate that the influence of bacterial resuspension from sediments on the FIB concentrations is not strong in case of this river. For this reason and the lack of sediment data, resuspension of bacteria from sediments was not taken into account in the model.

FIB were assumed to be inactivated in the river water following first order decay kinetics; the decay was described as a function of temperature, salinity and solar radiation (Mancini, 1978):

$$\frac{dC}{dt} = -k_0 \cdot \theta_S{}^{Sal} \cdot \theta_I{}^{Int} \cdot \theta_T{}^{(Temp-20)} \cdot C \tag{1}$$

In Eq. (1), C is the concentration of bacteria; t is the time; k_0 is the decay rate (1/day) at 20 °C for a salinity of 0‰ and in a dark condition; θ_S is the salinity coefficient for the decay rate; *Sal* is the salinity (‰); θ_I is the light coefficient for the decay rate; *Int* is the light intensity (kW/m^2); θ_T is the temperature coefficient for the decay rate; *Temp* (°C) is the water temperature.

The temperature (θ_T) and the decay rate (k_0) constants for *E. coli* were set to 1.07 and 0.80 respectively; these values are consistent to the values used by Hellweger and Masopust (2008), Mancini (1978) and Liu et al. (2006). As enterococci survive longer than *E. coli* in natural waters (Liu et al., 2006), the θ_T and k_0 constants for enterococci were set to 1.04 and 0.50 respectively; these values are also consistent with the values used by Liu et al. (2006). The salinity coefficient (θ_S) was set to 1.006 for both bacteria based on the values reported in the literature (Canteras et al., 1995, McCorquodale et al., 2004, Brauwere et al., 2014). A constant light intensity of 0.14 kW/m^2 was assigned in the model; this was based on the daily average light intensity and daily sunshine hours data for the study area (collected from NASA's satellite derived data centre and the Bangladesh Meteorological Department, respectively). The light coefficient (θ_I) was set to 7.4, which is the default value and is comparable to the value used by Gao et al. (2015).

2.3.3. Model performance

In this study, the previously validated hydrodynamic model was further validated with measured water temperature and salinity for the period October 2014 – September 2015. The model was then applied to simulate the FIB concentrations for the period October 2014 – September 2015, and the results were compared with the measured FIB data. The model performance was assessed using the following statistical parameters: the coefficient of determination (R^2), the Root Mean Square Error (RMSE), and the Nash-Sutcliffe efficiency (NSE). NSE ranges between $-\infty$ and 1.0; values between 0.0 and 1.0 are usually viewed as acceptable. The closer NSE is to 1.0, the more accurate the model is; NSE > 0.90 is excellent, 0.75–0.89 is very good, and 0.50–0.74 is good (Moriasi et al., 2007). The Log_{10}-transformed values of the FIB concentrations were used to calculate the RMSE and NSE, because the concentrations were highly variable (e.g., measured *E. coli*: 120–3.6×10^4 CFU/100 ml), and other studies also used Log_{10}-transformed values (e.g. Ouattara et al., 2013, Thupaki et al., 2010).

2.3.4. Model sensitivity analysis

To better understand the influence of the different processes and faecal sources on the FIB concentration and its variability in the Betna River, a sensitivity analysis was performed. The model was run to generate the output with 15 min resolution for ten days during the wet season (8–17 July 2015) and ten days during the dry season (21–30 January 2015). The major processes (wind, decay, different faecal sources) were removed one at a time. For example, to evaluate the influence of wind, the model was run without the wind force in the model, while all other forcings and processes were kept the same. In addition, to determine the contribution of the different faecal sources to the total concentration, the model was run with and without (i) the concentrations at the upstream boundary, (ii) the wastewater discharges, and (iii) the diffuse faecal sources.

2.3.5. Scenario analysis

The response of the system to the changes in FIB loading from the sewer drains was studied during ten days in the dry season (21–30 January 2015). The dry season was studied, because during this period the wastewater discharge from the drains is the primary source of faecal contamination in the river. We considered a scenario in which (a) wastewater treatment plants (WWTPs) are constructed with the required capacity, (b) the sewer network is built to collect and transport the entire volume of wastewater to the WWTPs, and (c) primary and secondary levels of treatment are applied to treat the entire volume reaching the WWTPs. We assume that with the application of the primary and secondary levels of treatment, the concentration of FIB in wastewater will be reduced by two orders of magnitude based on Saleem et al. (2000) and George et al. (2002).

3. Results

The simulated and measured water temperature and salinity were compared for Sampling Sites 1, 2, 3 and 4 (see an example in Fig. 2). Combined for the four sampling sites, the RMSE was 0.51 °C and 0.38 ppt, and the NSE was 0.93 and 0.94, respectively, suggesting an excellent agreement between the modelling results and the measured data. The results show temporal variability of the system due to the seasonal changes in temperature and salinity. Water temperature remains high, around 30 °C, except for the winter months (Fig. 2). Salinity starts reducing at the onset of the rainy season in mid-June and reaches near zero ppt during July (Fig. 2).

The simulated and measured FIB concentrations were compared for Sampling Sites 2, 3 and 4 (Fig. 3). Combined for the three sampling sites, the RMSE and NSE for the Log_{10}-transformed concentrations of *E. coli* and enterococci were 0.23 Log_{10} CFU/100 ml and 0.19 Log_{10} CFU/100 ml, and 0.84 and 0.86, respectively, suggesting a very good model performance. The concentrations in the rainy season (July – September, mean concentration 1.2×10^4 CFU/100 ml) were higher than during the dry months (November – February, mean concentration 9.7×10^2 CFU/100 ml). The simulated and measured concentrations of enterococci were most of the time higher (on average by 0.5 Log_{10} CFU/100 ml) than the concentrations of *E. coli.*

The sensitivity analysis showed that wind does not have a major impact on the FIB concentrations in the river, since for the simulations without wind, the concentrations were 1.6–3.5% lower than the reference concentrations (the mean concentrations for the different studied periods, when the model is run with all model inputs, Table 1). However, the results showed that the decay process is very important, since for the simulations without the decay process, the concentrations were found to be one to two orders of magnitude higher than the reference concentrations (Table 1).

The results revealed that, during the wet period, the upstream boundary concentrations and the wastewater discharges through drains had the largest contribution to the total concentration (up to 55% and 42% respectively), while the diffuse sources (urban and agricultural runoff) contributed less (up to 9.3% for *E. coli* and 12.6% for enterococci; Table 1 and Fig. 4). During the dry period, the wastewater discharges contributed the most (up to 89%), the contribution from the upstream boundary was lower (11–36%), and no contribution from the diffuse sources was observed (Table 1 and Fig. 4). The scenario analysis results revealed that the faecal contamination in the river system could largely be reduced by introducing primary and secondary wastewater treatment (Fig. 5).

4. Discussion

This modelling study of the microbial water quality in the Betna River provided insights in the faecal contamination sources and the microbial fate and transport processes in the context of a subtropical developing country. Processed-based models can generate useful data for microbial risk assessment and inform mitigation measures to reduce microbial contamination of water sources. However, the models should be validated using observed microbial data that generally are hardly available, particularly in the data-poor tropical or developing countries (Hofstra, 2011). The full evaluation of the model performance in this study was limited by the lack of the FIB data measured with high temporal resolution. Comparison with the available data, however, did show that the model performed well.

Moreover, a fundamental problem with bacterial fate and transport modelling is the inherent uncertainty in some essential inputs, such as faecal loads from wildlife, failing septic tanks, livestock waste deposition to streams, and FIB concentrations in livestock waste and manure

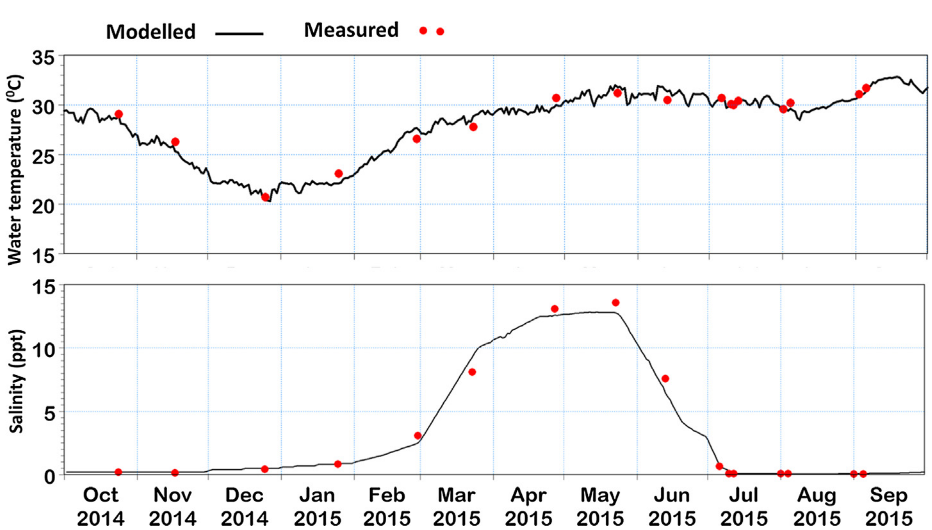

Fig. 2. The daily simulated and observed water temperature (upper panel) and salinity (lower panel) at Sampling Site 3 in the Betna River. March – May is the dry season, and June – October is the wet season. The results for the other sampling sites (Sampling Sites 1, 2 and 4) were similar.

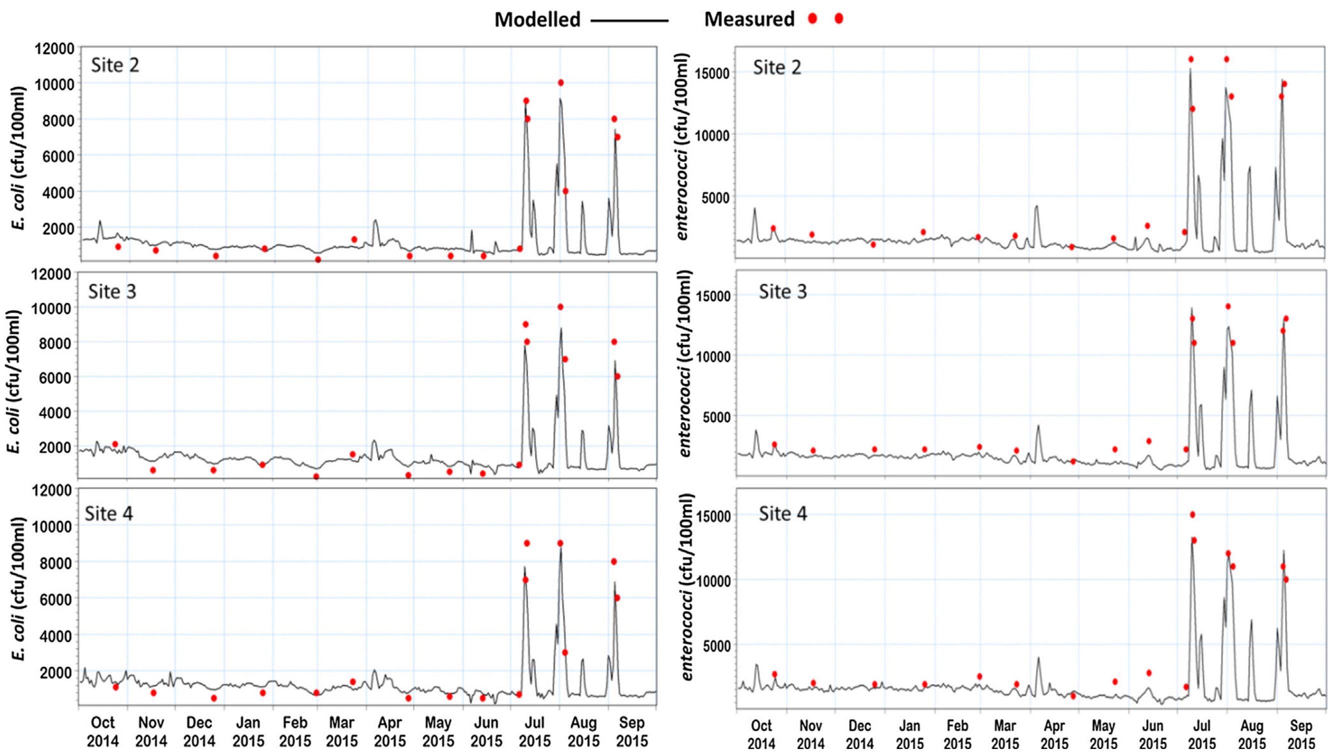

Fig. 3. Comparison of the daily simulated and measured *E. coli* (left column) and enterococci (right column) concentrations (CFU/100 ml) at Sampling Sites 2 (top), 3 (middle) and 4 (bottom) in the Betna River.

Table 1
Influence of various processes on the mean FIB concentrations (CFU/100 ml) in the Betna River. The simulations cover the wet period 8–17 July 2015 and the dry period 21–30 January 2015.

	Wet period						Dry period					
	E. coli (CFU/100 ml)			Enterococci (CFU/100 ml)			*E. coli* (CFU/100 ml)			Enterococci (CFU/100 ml)		
	Site 2	Site 3	Site 4	Site 2	Site 3	Site 4	Site 2	Site 3	Site 4	Site 2	Site 3	Site 4
*Reference concentration	3641	3176	2778	6185	5732	5341	1089	1398	1287	1492	1673	1577
Change in concentration (%) of the reference concentration												
Without wind	−1.8	−3.2	−3.5	−2.1	−2.4	−2.2	−2.0	−3.1	−3.4	−1.6	−2.2	−2.8
Without decay rate	+177	+175	+166	+ 81	+ 81	+ 78	+199	+193	+186	+158	+156	+153
Without upstream conc.	−55	−53	−49	−51	−49	−50	−15	−12	−11	−36	−35	−34
Without wastewater drains	−39	−39	−42	−38	−39	−38	−85	−88	−89	−64	−65	−66
Without urban runoff	−3.2	−4.1	−4.4	−5.2	−5.9	−6.1	0	0	0	0	0	0
Without agricultural runoff	−3.5	−4.5	−4.9	−5.9	−6.7	−6.4	0	0	0	0	0	0

* The reference concentrations are the mean FIB concentrations for the particular period, when the model is run with all model inputs.

(Niazi et al., 2015). Although in the current study the model performance was high and the model captured the measured FIB variability well, it slightly underestimated the concentrations in some of the peaks (e.g. July – August). This underestimation indicates that there is more contamination entering the river during the high discharge events than we have estimated. The underestimation in the peak concentrations can be caused by an underestimation of the load from the identified faecal sources and/or contributions from faecal sources that were not included in the model, such as septic tank leakage and open defecation. Since the model is more sensitive to the decay rate than to model inputs, such as wastewater drains, the influence of, in particular the septic tank leakage and open defecation, which are relevant for the minority of the population, are expected to be of limited importance.

The major impact of the decay process on the modelling results illustrated in this study is in agreement with the studies by Brauwere et al. (2014) and Ouattara et al. (2013). Although sunlight and temperature have a great impact on the bacterial decay (Gao et al., 2015, Liu et al., 2015, Ouattara et al., 2013), in most studies, the decay processes have been modelled using a constant decay rate due to the lack of input data (Bedri et al., 2014, Vijay et al., 2016, Menendez et al., 2013). In this study, the decay rates of FIB were estimated based on three environmental factors, i.e. temperature, salinity and sunlight intensity.

This study showed higher bacterial concentrations during the periods of heavy rainfall and high river flow in comparison to the dry periods. Other studies (e.g. Schilling et al., 2009, Aragonés et al., 2016, Ouattara et al., 2013) also find this relationship. In the present study, in the dry period the FIB concentrations were lower than in the wet period, because in the dry period the river received contamination only from the point sources, and the bacterial decay was higher, due to higher water temperature, salinity and sunlight intensity. The comparatively higher concentrations of enterococci (which is supported by previous studies, e.g. Mishra et al., 2015, Tiefenthaler et al., 2009) can be explained by their slower decay in saline surface water in

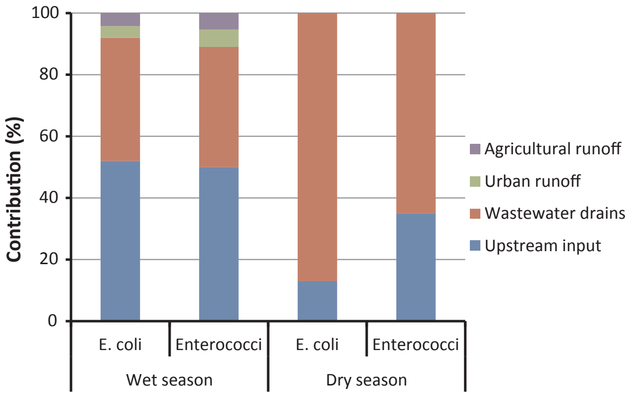

Fig. 4. Relative contribution (%) from the different sources to the mean *E. coli* and enterococci concentrations (CFU/100 ml) at Sampling Sites 2–4 (average) in the Betna River. The simulations cover the wet period 8–17 July 2015 and the dry period 21–30 January 2015.

comparison to *E. coli* (Liu et al., 2006).

The untreated wastewater from the sewer drains and the FIB inputs from the upstream boundary were the major contamination sources in the Betna River (Fig. 4, Table 1), while the contribution from the diffuse sources was comparatively lower, which is in agreement with most other studies (e.g. Ouattara et al., 2013, Sokolova et al., 2013, Gao et al., 2015, Vijay et al, 2016). In contrast, few studies (e.g. Brauwere et al. 2014, Servais, et al 2007) found that the diffuse sources were predominant compared to the point sources. This can be the case for catchments with low population density and improved sanitation and wastewater treatment. The high input from the upstream open boundary is due to untreated discharges from point sources in upstream urban areas and accumulation of small amounts from diffuse sources in the large upstream areas. This study underlines the need for establishment of wastewater treatment plants both in the studied basin and upstream urban areas.

For the Betna River catchment, the modelling results highlighted the negative impact of untreated wastewater (mostly from the Satkhira town) on the microbial water quality. The FIB concentrations were found to be higher than the US EPA bathing water quality standards (235 CFU/100 ml for *E. coli* and 104 CFU/100 ml for enterococci) most of the time, even during the dry periods (Fig. 3). The modelling results showed that introduction of primary and secondary level of wastewater treatment would result in considerable improvement of microbial water quality of the river. This is also supported by other studies (Vijay et al., 2016, Liu et al., 2015, Ouattara et al., 2013). No tertiary level of treatment was considered due to the exorbitant cost implication, where all facilities would have to be newly constructed. With the introduction of wastewater treatment, a major improvement of the water quality would be achieved in the dry season. However, noncompliance of the water quality would prevail during the wet season due to the contribution from the upstream boundary and the diffuse sources. Treatment of wastewater from the upstream urban areas will reduce the concentrations at the upstream boundary and further improve the water quality of the Betna River during the wet season.

This study confirms the applicability of the model to assess bacterial dynamics, and impact of different processes and wastewater treatment on the microbial water quality in surface waters. Although the effectiveness of wastewater treatment is known, the tendency has been to actually provide sewers/sanitation with no focus on treatment, for example, Millennium Development Goals focused on sanitation without linking it to the extent of treatment. Therefore, this paper includes a wastewater treatment scenario analysis to highlight the importance of wastewater treatment in a developing country. The presented model and approach can be applied for more complex scenario analysis, such as to determine the microbial Log_{10} reduction target values in designing WWTPs and to assess future microbial water quality under climate and socio-economic change. The developed methodology will likely be useful for water managers in mitigating faecal contamination based on local situations.

In this study, as in most studies, FIB have been used to represent faecal contamination, but FIB may not reflect the presence and behaviour of waterborne pathogens. For example, the absence of FIB does not exclude the presence of enteric viruses, which are generally more resistant to wastewater treatment than bacteria (Prez et al., 2015). The limitation of modelling pathogens is that even fewer measured data are available for pathogens than for FIB. An interesting next step would be to apply the developed model to simulate the fate and transport of waterborne pathogens and to perform quantitative microbial risk assessment (Sokolova et al., 2015, Eregno et al., 2016, Bergion et al., 2018). Also, an advanced next step could be to explicitly model the combined exposure of surface waters to multiple contaminants (nutrients, microplastics, chemicals and pathogens), as proposed by Kroeze et al. (2016).

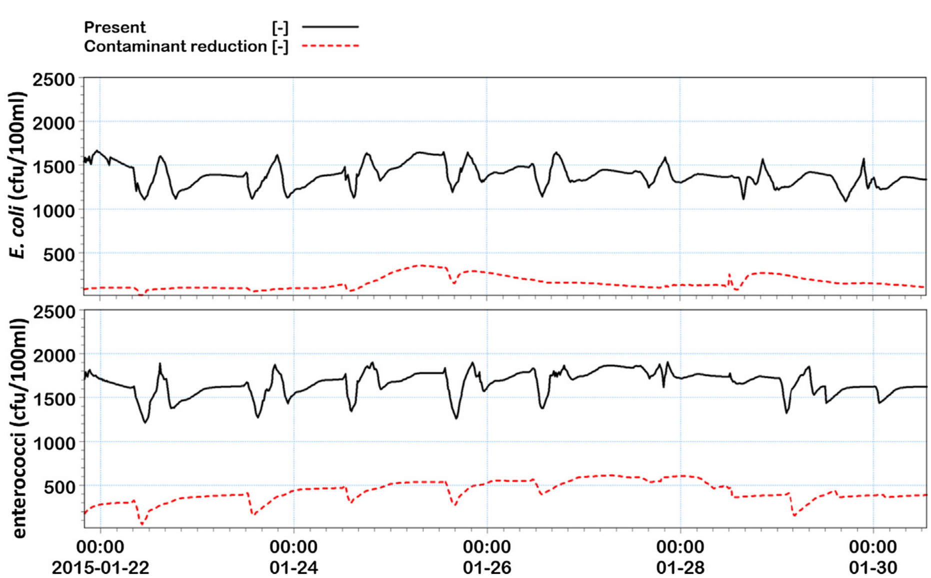

Fig. 5. The simulated *E. coli* and enterococci concentrations before and after contaminant load reduction at Sampling Site 3 in the Betna River during the period 21–30 January 2015.

In the Betna River, the FIB concentrations become very high after a heavy rainfall event and decrease after three to four days, although still remain noncompliant with the bathing water quality standards (see our previous study Islam et al., 2017a and Fig. 3). Since some people still want to bathe and fish in the river despite the poor water quality, we suggest that these activities are avoided for at least three to four days after a heavy rainfall event, as long as major improvements of wastewater treatment are not ensured in the surrounding river catchment and upstream areas. The government of Bangladesh has already made it mandatory for industries to establish effluent treatment plants. However, there is a lack of strict regulation and initiative to implement domestic wastewater treatment before disposal of wastewater into rivers. This modelling study hopefully creates awareness and provides policy support information for the government in reducing the widespread faecal contamination of the surface waters of Bangladesh. The implementation of wastewater treatment would also contribute to reaching the Sustainable Development Goal (SDG) 6 target 3 “to halve the proportion of untreated wastewater” (UN-Water, 2017).

5. Conclusions

This modelling study provides enhanced understanding on the fate and transport of FIB and the contribution of different sources to the total faecal contamination, and constitutes an example of scenario analysis for a subtropical river in a developing country. The results revealed that bacterial decay, upstream concentrations and untreated wastewater discharges were the dominant factors controlling the FIB concentrations in the river, while wind and contamination from the diffuse sources did not have a significant influence. Introduction of primary and secondary level of wastewater treatment would decrease the contamination of the river during the dry season considerably. However, due to the contribution from the upstream boundary noncompliance of the water quality would prevail during the wet season. Treatment of wastewater from the upstream urban areas would further improve the water quality during the wet season. Although, the model captured the measured FIB variability well, some of the peaks were underestimated due to the lack of data on septic tank leakage, open defaecation, and sediment resuspension. In future modelling studies, particularly in the context of developing countries, it is important to carefully consider the contributions from the diffuse sources.

This study is one of the first to model FIB in developing countries and shows that, even with limited data availability, this modelling approach can generate useful data to support implementation of mitigation measures to reduce faecal contamination of surface waters. This study serves as a test case for other river basins with similar conditions, and this modelling approach can be applied in other watersheds. The developed model can be used to provide input data for microbial risk assessment and to forecast future impacts of climate change and socioeconomic development on the microbial water quality. This modelling study provides information to support decisions by water managers in the context of reducing the widespread faecal contamination and the risks of waterborne disease outbreaks, which are the leading cause of death in developing countries. The study emphasises the need for treatment of wastewater before it is discharged into the rivers and canals, and underlines the importance for countries to achieve SDG 6.3.

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