Quantifying public health risks from exposure to waterborne pathogens during river bathing as a basis for reduction of disease burden

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ABSTRACT

A Quantitative Microbial Risk Assessment (QMRA) technique was applied to assess the public health risk from exposure to infectious microorganisms at bathing areas of three rivers in Bangladesh. The QMRA assessed the probability of illness due to the accidental ingestion of river water impacted by untreated sewage. The simplified QMRA was based on average concentrations of four reference pathogens *Escherichia coli* (*E. coli*) O157:H7, *Cryptosporidium* spp, norovirus and rotavirus relative to indicator bacterium *E. coli*. Public health risk was estimated as the probability of infection and illness from a single exposure of bathers. The risks of illness were ranged from 7 to 10% for *E. coli* O157:H7, 13 to 19% for *Cryptosporidium*, 7 to 10% for norovirus and 12 to 17% for rotavirus. The overall risk of illness at the rivers was slightly higher in children (9–19%) compared to adults (7–16%). The risks of illness in individuals exposed to the river bathing were unacceptably high, exceeding the USEPA acceptable risk of 3–6 illnesses per hundred bathing events. This study gives a basis for reducing the burden of disease in the population by applying appropriate risk management. Findings and methods of this study will be helpful for other countries with similar socio-economic and geographic settings.

Key words | *Cryptosporidium*, *E. coli* O157:H7, norovirus, quantitative microbial risk assessment, risk of infection, rotavirus

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HIGHLIGHTS

- The study estimates risks of illness due to the accidental ingestion of contaminated river water.
- Waterborne pathogens in the river water pose unacceptably high risks to human health.
- Risk of illness from the river bathing is higher in children compared to adults.
- A simplified QMRA can be effectively applied in areas with limited data.

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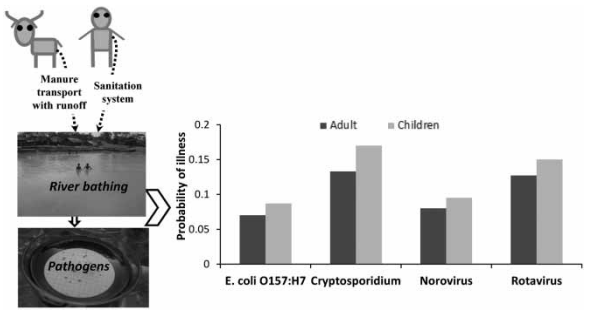
GRAPHICAL ABSTRACT



INTRODUCTION

As a consequence of population growth and economic development, large amounts of wastewater are being generated in developing countries. In most developing countries, there is a lack of effective water management infrastructure and a large portion of their population relies on untreated and highly contaminated surface water (Van Abel & Taylor 2018). Also in Bangladesh, despite recent improvements, access to clean water and improved sanitation remains a major problem (Islam *et al.* 2018a). Wastewater treatment facilities are lacking and wastewater thus enters directly into the rivers. The continuous discharge of untreated sewage into surface waters contributes directly to the introduction of waterborne pathogens in the water sources (Bosch *et al.* 2008; Islam *et al.* 2018a). This contaminated river water is widely used, which increase the people's vulnerability to waterborne diseases. In Bangladesh, for example, diarrheal disease is very common and every year it causes around a hundred thousand deaths (Faruque 2014).

Poor microbial water quality at the surface waters poses health risk to bathers. Most people in the southwest of Bangladesh rely on highly contaminated surface waters for household purposes, agriculture, aquaculture, fishing and bathing (Islam *et al.* 2017). Moreover, this part of the country has been affected by flooding almost every year during the last two decades. Consumption of surface water and direct contact with the contaminated surface or flood water is a plausible route of primary transmission of waterborne pathogens (Van Abel & Taylor 2018; Dias *et al.* 2019). This makes the population vulnerable to waterborne diseases. Despite the high relevance for public health, studies on the surface water microbial water quality are lacking in Bangladesh. Some studies have been based on cholera diseases and urban flooding (e.g. Kunii *et al.* 2002; Qadri *et al.* 2005; Hashizume *et al.* 2010; Ali *et al.* 2013). Few studies have been conducted in the shrimp farms, those are primarily PCR-based genetical analysis for bacteria (e.g. Adhikari *et al.* 2015; Ahmed *et al.* 2010). Our previous study in the Betna river (Islam *et al.* 2017) in Satkhira is the first detail surface water microbial water quality assessment in Bangladesh. However, the health risk assessment has not been done in that study.

Assessing the risk of acquiring gastrointestinal illness (GI) due to the consumption of contaminated surface water is important because it can help to reduce the risk and ensure safety of the people (Amoueyan *et al.* 2019; Dias *et al.* 2019). These assessments are particularly important in developing countries, where microbial pathogens may be transmitted by a number of routes (Howard *et al.* 2006). However, the links between the consumption of surface water and the health risk for the population are poorly understood. The probability of acquiring GI by consumption of surface water or bathing in the river can be calculated by means of the quantitative microbial risk assessment (QMRA). The QMRA has become a popular method to estimate health risks caused by microorganisms. It is a useful tool for formulating water safety management strategies (Van Abel & Taylor 2018; Dias *et al.* 2019).

QMRA is a tool that has been developed for assessing the risk of disease from a specific pathogen. For QMRA, the main factors required are pathogen concentration in surface water, a pathogen-specific dose–response analysis and risk characterization. A QMRA for every pathogen would be time-consuming and the necessary information is currently not available for many pathogens. To overcome this difficulty, WHO (2004) recommended using 'reference pathogens', with similar nature.

The scarcity of pathogen data in developing countries requires that a QMRA can be based on faecal indicator bacteria (Dias *et al.* 2019). Despite the weaknesses of using indicator organisms, many initial QMRAs will have to be performed using data on indicator organisms due to inadequate data for the occurrence of pathogens. The use of indicator organisms does, however, require assumptions to be made about the relationship between pathogens and indicators that introduces an additional level of uncertainty into the risk assessment (Howard *et al.* 2006).

There are challenges to applying the method particularly in developing countries where data and resources are very limited. In the 3rd edition of its Guidelines for Drinking-Water Quality (2004), WHO promotes the use of risk assessment coupled with risk management for the control of water safety in water sources. QMRA is a technique to estimate the disease burden from waterborne pathogens using the level of pathogen or an appropriate surrogate. This information may then be used to formulate appropriate management strategies of the water supply system. Although QMRA has been applied in developed countries, the technique has not been evaluated in developing regions where relevant data are very limited. So far, one study focused on modelling Dhaka city flooding and cholera risk assessment (Mark *et al.* 2015), but no such QMRA study has been performed for surface waters in Bangladesh.

In this study, we aim to apply a simplified risk assessment procedure to calculate the probability of illness from four reference pathogens (pathogenic *Escherichia coli* (*E. coli*) (O157:H7), *Cryptosporidium* spp, norovirus and rotavirus) in the surface water in southwest of Bangladesh, where waterborne diseases are endemic (Islam *et al.* 2018b). The data on pathogens were collected from literature, because the laboratory facilities to measure a variety of viruses are not available in Bangladesh. If QMRA is to gain acceptance and be used in developing countries, it must be offered in a workable and simple form. This is the first QMRA study in Bangladesh that provides useful information for river water quality management in the country. The study will inform policy makers and help to identify interventions to reduce the burden of disease on the population. The study demonstrates the potential of a simplified QMRA as a tool in the context of a developing country with limited data to evaluate public health risk and regulate river bathing.

METHODS

Study area

The study sites are located in the Rupsha and Bhairab rivers near Khulna city and the Betna river near Satkhira town. Water samples were obtained from several sewer drains and the selected three rivers to measure concentrations of *E. coli*. Sampling was done bi-weekly during a wet season (July–September 2018) and a dry season (November 2018–January 2019). Six important industrial and populous sites (Figure 1) near Khulna city were selected, five from the Rupsha and one from the Bhairab rivers. All the sites near Khulna city receive untreated sewage through sewer drains. The measured *E. coli* data from four sites of the Betna river in Satkhira during our previous study (Islam *et al.* 2017) were used in this study. The sites in the Betna river receive contaminations from mixed sources including inputs from sewer networks, urban and agricultural runoffs.

Sampling and analysis of *E. coli*

Water samples from several sewer drains and the selected sites were collected at a depth of 50 cm from one river bank into sterile nalgene plastic bottles facing the mouths of the bottles upstream. Three replicates were collected at each sampling site. All samples were collected with the care required for indicator bacteria analysis. Sampling bottles were sterilized according to the procedures described in standard methods (APHA 2005). All samples were placed in an insulated box filled with ice packs, transported to the laboratory of Environmental Science Discipline,

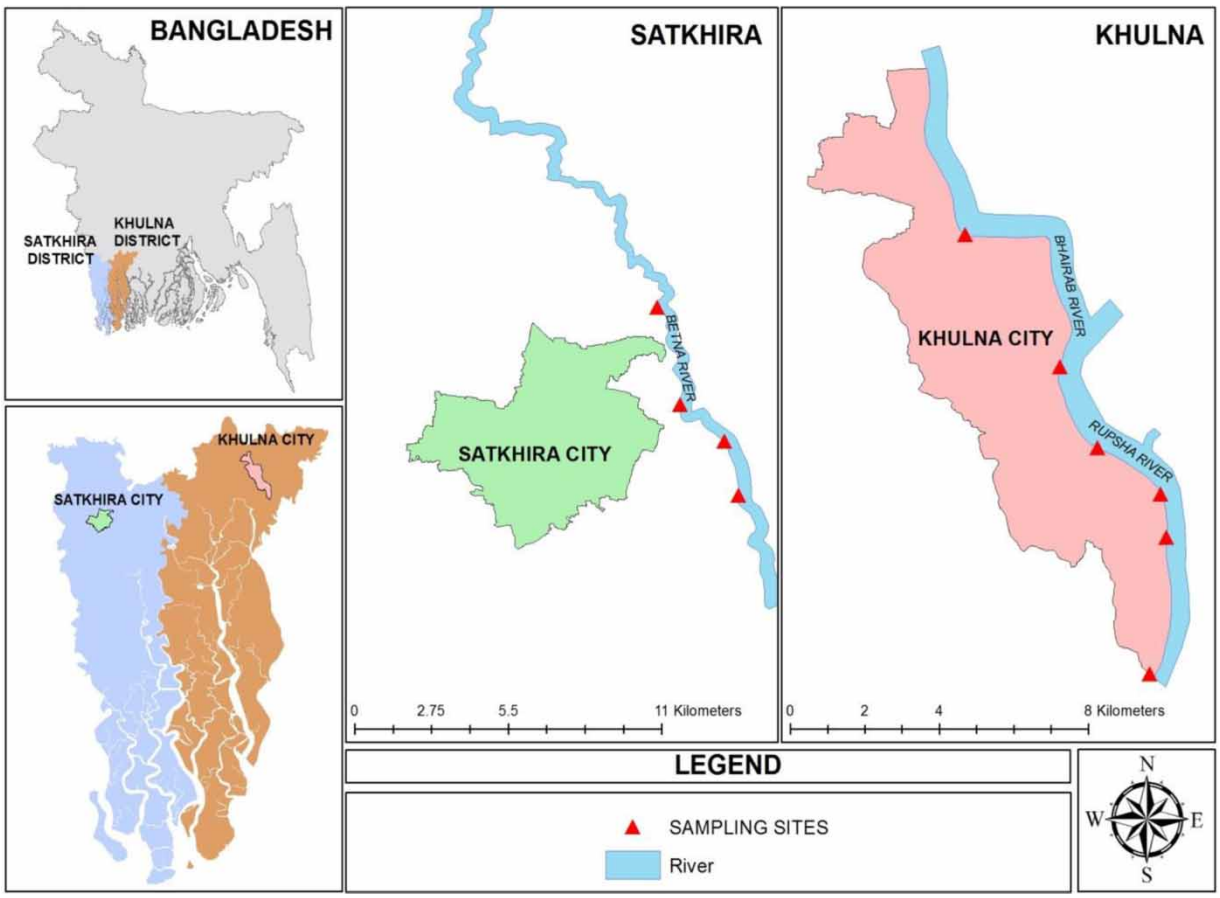


Figure 1 | Sampling sites in the Betna, Rupsha and Bhairab rivers near Satkhira and Khulna city.

Khulna University and the analyses were started within six hours of collecting the first sample.

Enumeration of *E. coli* was performed by the membrane filtration (MF) technique (USEPA 2002) method number 1103.1. The detail of the analysis is described in our previous study (Islam *et al.* 2017). In brief, the water samples were filtered by using a Whatman 1 and 40 (according to requirement) filter paper to remove suspended matter from the samples. Several dilutions of samples and triplicate plates for each dilution were considered to determine the number of *E. coli*. Diluted water samples were filtered through 0.45 μm membrane filters (Millipore Corp., Bedford, MA, USA). To ensure proper sterilization and to prevent cross contamination among samples, a burner was used in the treatment of the filtration devices. The membrane thermotolerant *E. coli* (m-TEC) agar media was used and the agar plates were incubated at 35 ± 0.5 °C for two hours followed by further incubation at 44.5 ± 0.2 °C for 22–24 hours. The filters were then transferred to a pad saturated with urea substrate and kept for 15–20 min. After incubation at room temperature on the urea substrate, yellow, yellow–green, or yellow–brown colonies were counted as *E. coli*.

Quantitative microbial risk assessment

To estimate the health impact of river water utilization, a simplified QMRA was conducted using the example of the Rupsha, Bhairab and Betna rivers in the southwest of Bangladesh. The probability of illness was estimated as a person contracting illness from the direct contact of contaminated river water during bathing or fishing. The probability of illness was estimated separately for sewage sources (for the Rupsha and the Bhairab rivers) and mixed

sources (for the Betna river). For QMRA, the main factors required are pathogen concentration in surface water, a pathogen-specific dose–response relationship and exposure assessment (the consumed amount of water) to forecast the probability of infection due to exposure to waterborne pathogens in river surface water. This QMRA approach assumes that this indicator bacteria density has the probability to result in illness rates of 0.01–0.02 (1–2 illnesses per hundred bathing events). For QMRA, the following steps are described briefly: (i) identifying reference pathogens (hazard identification); (ii) exposure assessment; (iii) dose–response relationships; and (iv) risk characterization.

Reference pathogens

The QMRA has been estimated as the disease burden from four reference pathogens: *E. coli* O157:H7, *Cryptosporidium* spp, norovirus and rotavirus. Worldwide, these pathogens have been commonly reported in sewage and these are the important agents of acute gastroenteritis (Prez *et al.* 2015). Rotavirus is the most important causative factor of acute gastroenteritis and the main cause of morbidity and mortality among infants and children under-5 years old in developing countries (Prez *et al.* 2015). The virus is transmitted by the faecal–oral route and infects enterocytes, this induces severe gastroenteritis and leads to about half a million human deaths each year globally (Kiulia *et al.* 2015). Norovirus are the globally significant disease-causing agents and have been associated with waterborne diseases due to recreational water exposure (Patel *et al.* 2009; Ito *et al.* 2017; Amoueyan *et al.* 2019; Simhon *et al.* 2019). *Cryptosporidium* is a protozoan parasite, which is very pathogenic and a leading causative agent of diarrhoea worldwide (Hofstra & Vermeulen 2016). Another important reason for selecting these reference pathogens is that corresponding dose–response relationships of these are available in the literature. The use of reference pathogens is a common practice in the QMRA study (Signor *et al.* 2007; Soller *et al.* 2010) to represent environmental fate and transport and infectivity of each pathogen group (WHO 2004). As pathogen data from water sources in Bangladesh are not available, in this study, indicator bacterium *E. coli* was used as surrogates. *E. coli* and faecal coliform have also been used as surrogates of pathogens in different studies (e.g. Howard *et al.* 2006; Schoen & Ashbolt 2010; Eregno *et al.* 2016). In this study, *E. coli* were measured in the surface waters of the southwest region. Additionally, *E. coli* data from our previous study (Islam *et al.* 2017) and waterborne pathogen data from the literature (e.g. Abong'o *et al.* 2008; Teunis *et al.* 2008; Timm *et al.* 2016) were collected.

Exposure assessment

The number of pathogens ingested during a single exposure depends on the volume of water consumed during the recreational activity and the concentration of pathogens in the water (Eregno *et al.* 2016). The volume of water considered here is the average volume of water consumed per individual during swimming or bathing. Water consumption rates reported in different studies varied depending on recreational versus competitive swimmers, adult versus children, occupational versus sport divers, limited contact versus full contact recreational activities (Rijal *et al.* 2011; Eregno *et al.* 2016). Chigor *et al.* (2014) used 30 mL for the estimation of risk via recreation-based exposures in South Africa. For this study, water ingestion rates of 16 mL for adults and 37 mL for children per daily recreational swimming/bathing were used based on Dufour *et al.* (2006) and Eregno *et al.* (2016).

Dose–response equation

The reference pathogen (rp) doses were derived from the concentration of *E. coli* in the water from a specific source as described by Schoen & Ashbolt (2010). The calculation of the pathogen dose is based on the observed ranges of pathogen and faecal indicator densities in faecal waste. The dose μ_{rp}^{s} of each reference pathogen in the units of cfu, genomes or (oo)cysts, from each source (S) was calculated as:

$$\mu_{rp}^{s} = \frac{C_{EC}}{F_{EC}^{S} \times 100} \times R_{rp}^{S} \times p_{rp}^{S} \times V \quad (1)$$

where S is the faecal contamination source;

C_{EC} is the average concentrations of *E. coli* (cfu/100 mL) in a river water;

F_{EC}^{S} is the density of *E. coli* in sewage (cfu/L);
R_{rp}^{S} is the density of pathogen species in sewage (number of pathogens or genomes L^{-1});
p_{rp}^{S} is the fraction of infectious pathogenic strains from source *S*; and
V is the volume of water ingested (mL).

A detailed literature search was conducted to find appropriate values for each of the model parameters shown in Equation (1).

Risk characterization

Risk characterization is the final step and the main output of the QMRA study that estimates the probability of public health risk associated with the exposure to the river waterborne pathogens. The risk from each source was characterized as the total probability of GI illness after one exposure to recreational water through accidental ingestion of water while swimming. The risk estimations were done according to age categories (adult and children), based on differences in the amount of accidental water ingestion during bathing or swimming. The risk of infection (P_{inf}) and subsequent illness (P_{ill}) for individuals were estimated by using the beta-Poisson models (Eregno *et al.* 2016) for viruses and exponential dose–response relationships (Haas 1984) for *Cryptosporidium*. The beta-Poisson curve calculates the probability of infection using the formula, $P_{inf} = 1 - (1 + d/\beta)^{-\alpha}$. The exponential dose–response curve, $P_{inf} = 1 - e^{-r\mu}$, where r, α, and β are dose–response parameters, the values of which are presented in Table 2. The dose μ or $d = CV$, where C is the estimated concentration of pathogens in the water samples (n/L) and V is the individual consumption of water (L) as estimated using the above Equation (1). The total probability of illness from a specific source was calculated using the probability of illness from each source-specific reference pathogen as $P_{ill}^{S} = 1 - \prod_{rp}(1 - P_{illrp}^{S})$.

RESULTS

Quantifying probabilities of GI illness

The probability of microbial infection and illness from river bathing was calculated using the dose input presented in Table 1 and the dose–response parameters in Table 2. The analysis revealed that the possible range of infection risk varied between 14% and 29% for viruses, between 25% and 34% for *E. coli* O157:H7 and between 19% and 28% for *Cryptosporidium* as shown in Figure 2. The estimated daily risks of infection were varied with the pathogens ingested and exposure scenarios.

The resulting probabilities of illness varied between 7% and 17% for viruses, between 7% and 10% for *E. coli* O157:H7 and between 13% and 19% for *Cryptosporidium* (Figure 3). The highest risk of illness was observed due to *Cryptosporidium* (Figure 3). Whereas *E. coli* O157:H7 was found to cause a higher rate of infection in all the three rivers (Figure 2). The overall risk of illness for a single exposure of pathogens during bathing was substantially higher for children (9–19%), compared to adult (7–16%). The risk of infection and illness (both in the adults and children) was slightly higher (1–3%) during the wet season, compared to the dry season. No substantial differences in the probabilities of gastrointestinal infection and illness were observed among the rivers.

Table 1 | Parameter values used in the QMRA model

E. coli/pathogen	Average concentrations in sewage	Units	References
E. coli	3.2×10^{6}	cfu 100 mL^{-1}	Measured in this study
E. coli O157:H7	50	cfu 100 mL^{-1}	Abong'o *et al.* (2008)
Cryptosporidium	678.1	oocysts L^{-1}	Robertson & Gjerde (2006)
Norovirus	5.0×10^{4}	genomes L^{-1}	Teunis *et al.* (2008)
Rotavirus	1.9×10^{3}	genomes L^{-1}	Timm *et al.* (2016)

Table 2 | Dose–response parameter values used in the QMRA model

Pathogen	Models	Parameters	References
E. coli O157:H7	Beta-Poisson	$\alpha = 0.49, \beta = 45.9$	Teunis *et al.* (2008)
Cryptosporidium	Exponential	$r = 0.2$	WHO (2011)
Norovirus	Beta-Poisson	$\alpha = 0.04, \beta = 0.055$	Teunis *et al.* (2008)
Rotavirus	Beta-Poisson	$\alpha = 0.253, \beta = 0.427$	Chigor *et al.* (2014)

Uncertainty and sensitivity analysis

Uncertainty analysis is an important part of the risk characterization to assess limitations and determine the degree of confidence of the risk assessment. Sensitivity analysis was performed to estimate the rate of change in the output with respect to change in different input variables. QMRA modelling involves different sources of inputs that can cause uncertainty in the output. In this study, the uncertainty analysis was based on some of these input variables consisting of three types: (1) Uncertainties associated with the volume of water ingestion during swimming or bathing in the rivers, (2) Uncertainties associated with the estimated concentration of pathogen at the rivers and (3) Uncertainties related to the dose–response model parameters.

Figure 4 shows the effect of variation in dose–response parameter value on daily risk of *E. coli* O157:H7 and enteric virus infection, while the volume of water ingested was kept constant at 16 mL for adults and 37 mL for children. For the beta-Poisson model, the risk of infection increased with the increase in dose–response parameter in all rivers. A similar trend was observed for the parasite *Cryptosporidium*. The risk of viral infection was also increased with the volume of water ingestion (Figure 5) in the rivers. A strong positive correlation of 0.86 was found between the rate of enteric virus infection and the volume of water ingestion. A positive correlation of 0.77 was also found between the rate of enteric virus infection and the dose–response parameter.

Further sensitivity analysis was performed by using a set of input values above and below the reference parameter value to estimate the corresponding change in the output. In Figure 6, the change of probability of rotavirus infection was visualized (as an example) in response to change in different input values. This analysis also revealed that the probability of rotavirus infection increases with an increase in the volume of water ingested, concentration of the virus and dose–response parameter value.

DISCUSSION

The risk of GI to bathers from waterborne pathogens at different rivers was estimated using a QMRA technique. According to the European Commission (2002) and USEPA (2012), the acceptable risk of illness is 3–5% and 3–6%, respectively. The present study results show that the calculated risk of illness (7–19%) is substantially higher than both Europe and U.S. bathing water guidelines, but similar with the studies of Chigor *et al.* (2014) and Eregno *et al.* (2016).

The QMRA estimation is based on assumptions and there are limitations that might impact the accuracy of the risk assessment. In the present study, the dose–response data were not taken from direct clinical trials. Instead, the data were obtained from previous studies, which were based on young and healthy adults (Soller 2006). However, the susceptibility of various individuals to exposure to waterborne viral pathogens may differ depending on various factors, including the immune status and age of an individual as well as the virulence, serotype and infection pathways of the virus (Chigor *et al.* 2014; Van Abel & Taylor 2018). Therefore, certain population groups including children, the elderly, sick people and individuals with compromised immune systems are not considered during obtaining such data (Chigor *et al.* 2014).

A discussion of uncertainties is an important part of the risk characterization to estimate the degree of confidence and to evaluate the implications and limitations of the risk assessment. Sensitivity analysis was performed to investigate how variation in the input can influence the different sources of variation in the output. QMRA modelling involves different input variables that can be a potential source of uncertainty in the output and the analysis was based on some of these input variables. The study revealed that the dose–response parameter value and volume of water ingestion have a stronger influence on the risk of infection and illness, which agrees with Eregno *et al.* (2016). This is also

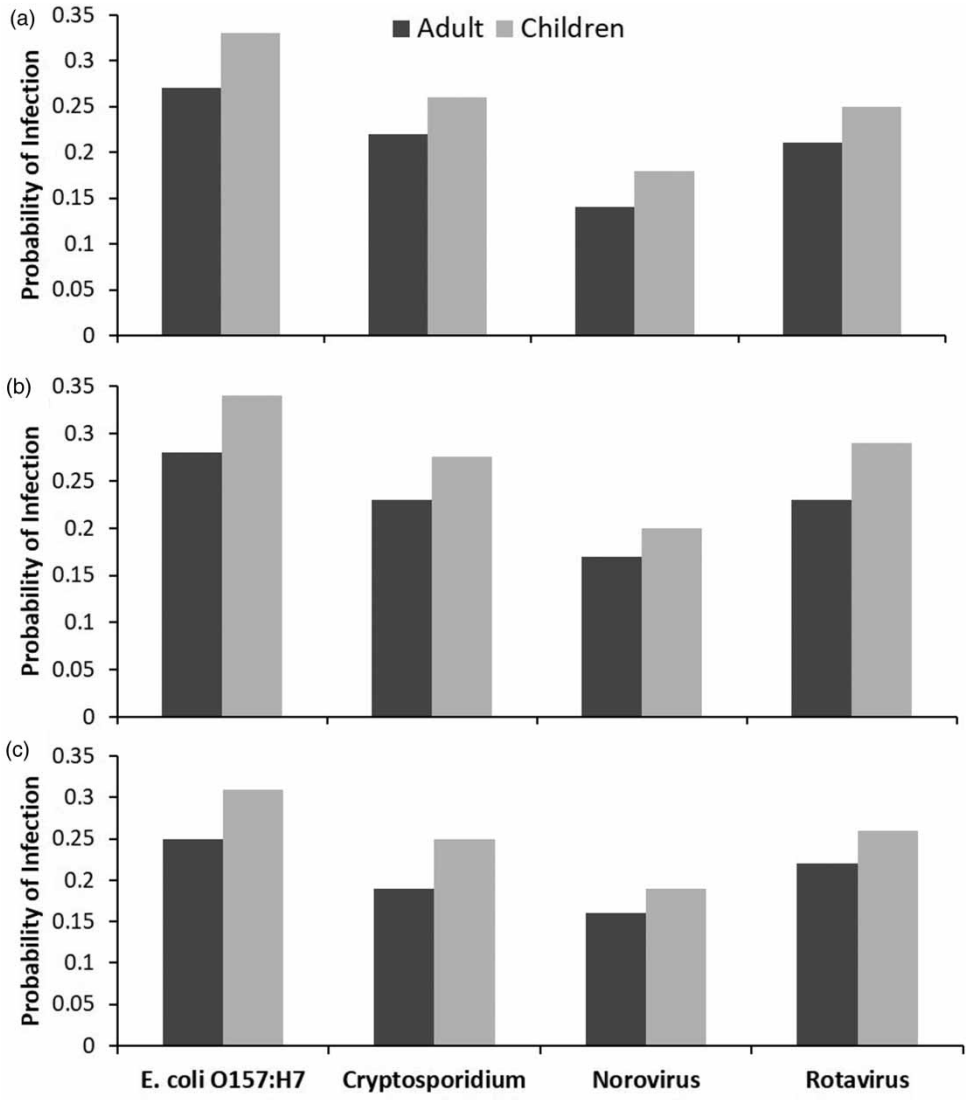


Figure 2 | Probabilities of infection of adults and children by exposure to various pathogens in the Rupsha (a), Bhairab (b) and Betna (c) rivers.

reflected in the results of the present study. Although the sampling sites of the Rupsha and Bhairab rivers receive untreated sewage mainly through sewer drains, and the sites in the Betna river receive contaminations from mixed sources (e.g., inputs from sewer networks, urban and agricultural runoffs), the resulting risk of infection and illness were similar for all three rivers. It indicates that the sources of contamination have a minor influence on the risk of infection and illness compared to dose–response parameter value and volume of water ingestion. Thus, the overall risk of infection and illness was found higher for children compared to adults, because the amount of water consumed by children was higher. The comparatively higher infection and illness risk in the wet season are due to the observed higher concentrations of *E. coli* during the wet season. During the wet season, the rivers receive untreated wastewater discharges from point sources in the urban area and non-point/diffuse sources (e.g. urban and agricultural runoff) in the surrounding river catchment and upstream areas. In the dry season, the rivers received contamination only from the point sources near the sampling sites. This is in agreement with our previous studies in Betna river (Islam *et al.* 2017, 2018b), where

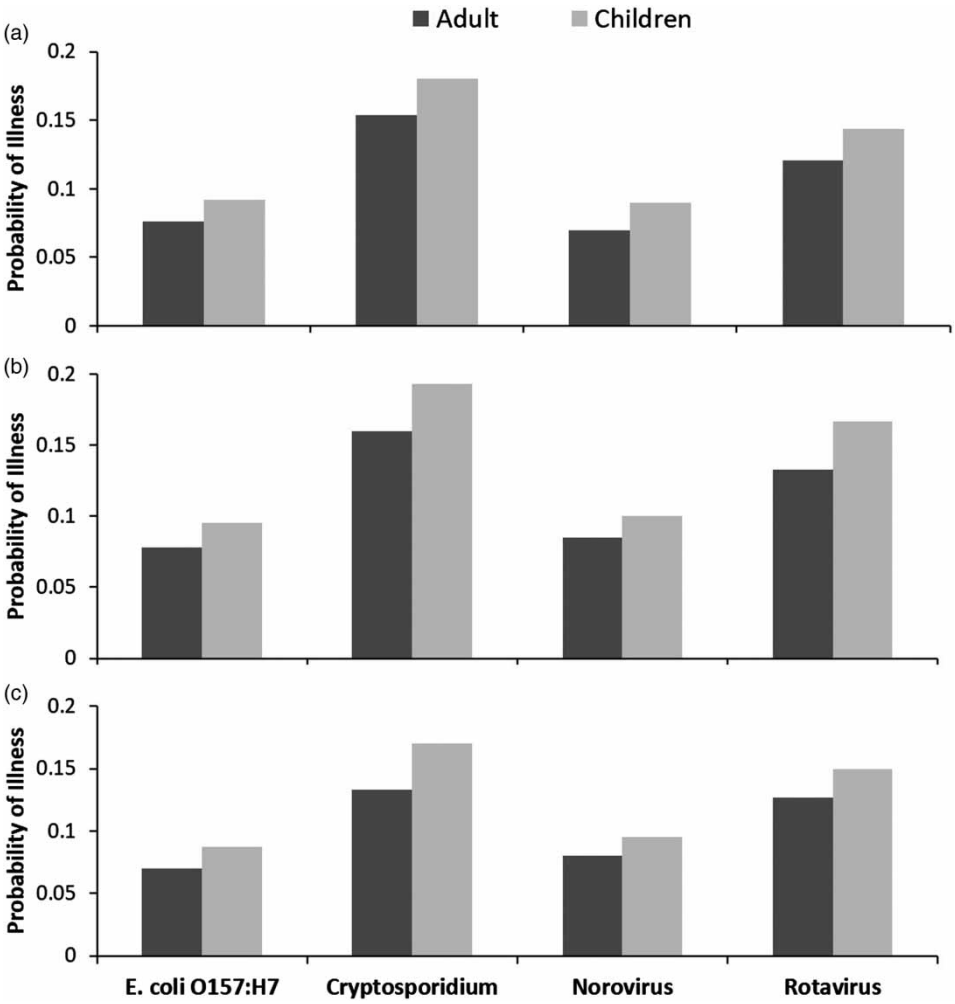


Figure 3 | Probabilities of illness of adults and children by exposure to various pathogens in the Rupsha (a), Bhairab (b) and Betna (c) rivers.

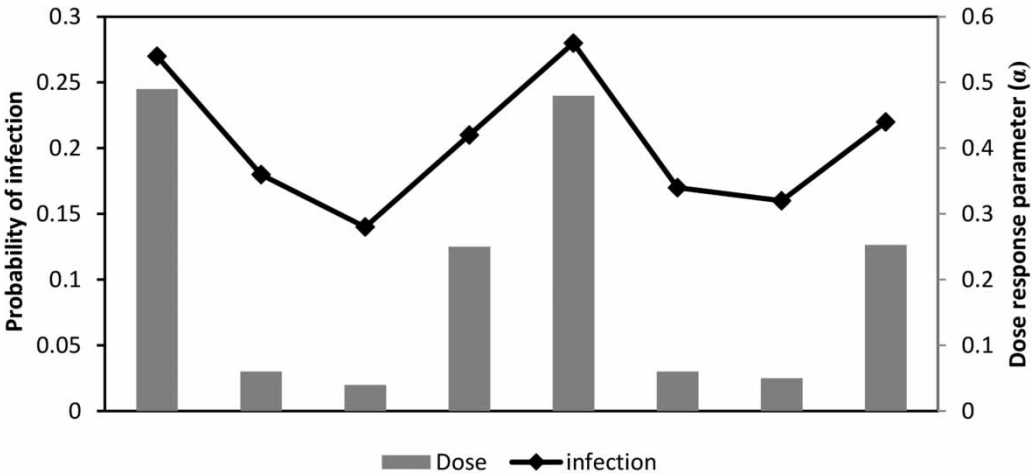


Figure 4 | Influence of the dose–response parameter on the probability of infection of bathers in the Rupsha, Bhairab and Betna rivers as determined by means of the beta-Poisson model for *E. coli* O157:H7, norovirus and rotavirus.

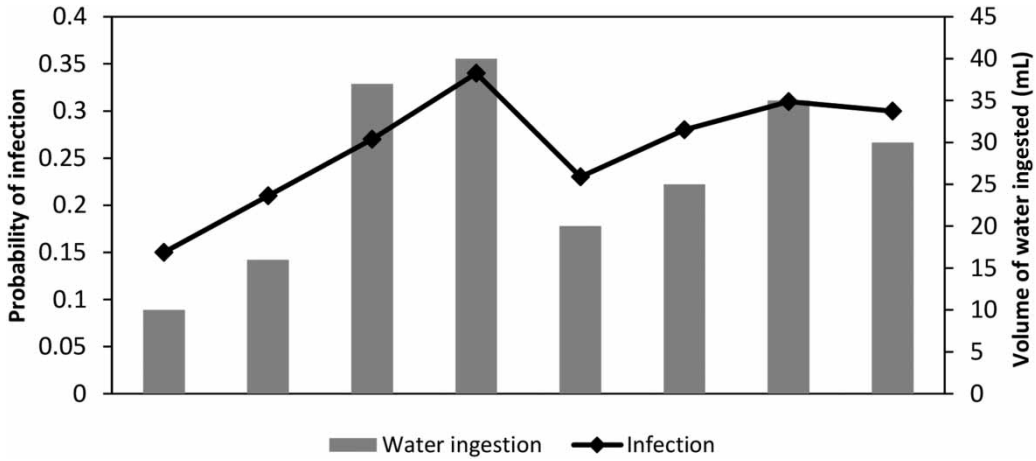


Figure 5 | Probability of rotavirus and norovirus infection of bathers in the rivers when ingesting different volumes of water.

we found that *E. coli* concentrations became very high after a heavy rainfall event and decreased after three to four days. Therefore, we suggest that swimming in the rivers should be avoided for at least four days after a heavy rainfall event until adequate wastewater treatments are not ensured.

Since dose–response parameters do not exist for all pathogens, previously reported dose–response parameters are typically used in risk assessment studies on those pathogens for which dose–response data have not been generated from clinical trials (Pinto *et al.* 2009). The implication is that different dose–response parameter values have been applied in QMRA for a single pathogen. Venter *et al.* (2007) used the exponential model and used a dose–response parameter (r) value of 0.549 to assess the risk of rotavirus infection in surface water in South Africa. Whereas Chigor *et al.* (2014) used the dose–response parameters α (0.253) and β (0.427) for rotavirus to assess the potential risks of infection associated with exposure to human enteric viruses in the Buffalo River, South Africa. To avoid this type of inconsistency, in the present study, we have used b-Poisson models for viruses and exponential models for the parasite *Cryptosporidium*.

One of the major sources of uncertainty is the concentration of pathogen in the sewer system and the proportion of infective viruses to the total viruses. The infectivity of viruses was not included in the calculations because data on the concentration of viruses were collected from literature, where the virus detection and measurement were based on the molecular method (RT-qPCR). In the subsequent calculations, certain factors (Table 3) for converting from infection to illness were collected from previous studies and used as input to QMRA. The consequence of this is that these assumptions can cause additional uncertainties in the QMRA estimation. Thus, the risk of infection caused by exposure to the viral pathogens in the river water could have been either under-estimated or over-estimated. To characterize this, a frequency distribution graph showing the influence of a set of different input values as an example was presented (Figure 6). From the graph, it can be seen that the risk of rotavirus infection was very sensitive to the change in virus concentrations, amount of water ingested and dose–response parameter value, which is in agreement with previous studies (Chigor *et al.* 2014; Eregno *et al.* 2016).

Many people swim/bathe and fish in the selected rivers. In this study, the health risks have been assessed for the utilization of water for swimming or bathing only. However, the rivers are also extensively utilized for domestic purposes (e.g. washing cloths and utensils), fish farming and irrigation.

Table 3 | Factors for converting from infection (P_{Inf}) to illness (P_{Ill})

Pathogen	Factor	References
E. coli O157:H7	0.28	Soller *et al.* (2010)
Cryptosporidium	0.7	WHO (2011)
Norovirus	0.5	Teunis *et al.* (2008)
Rotavirus	0.5769	Hurst (2016)

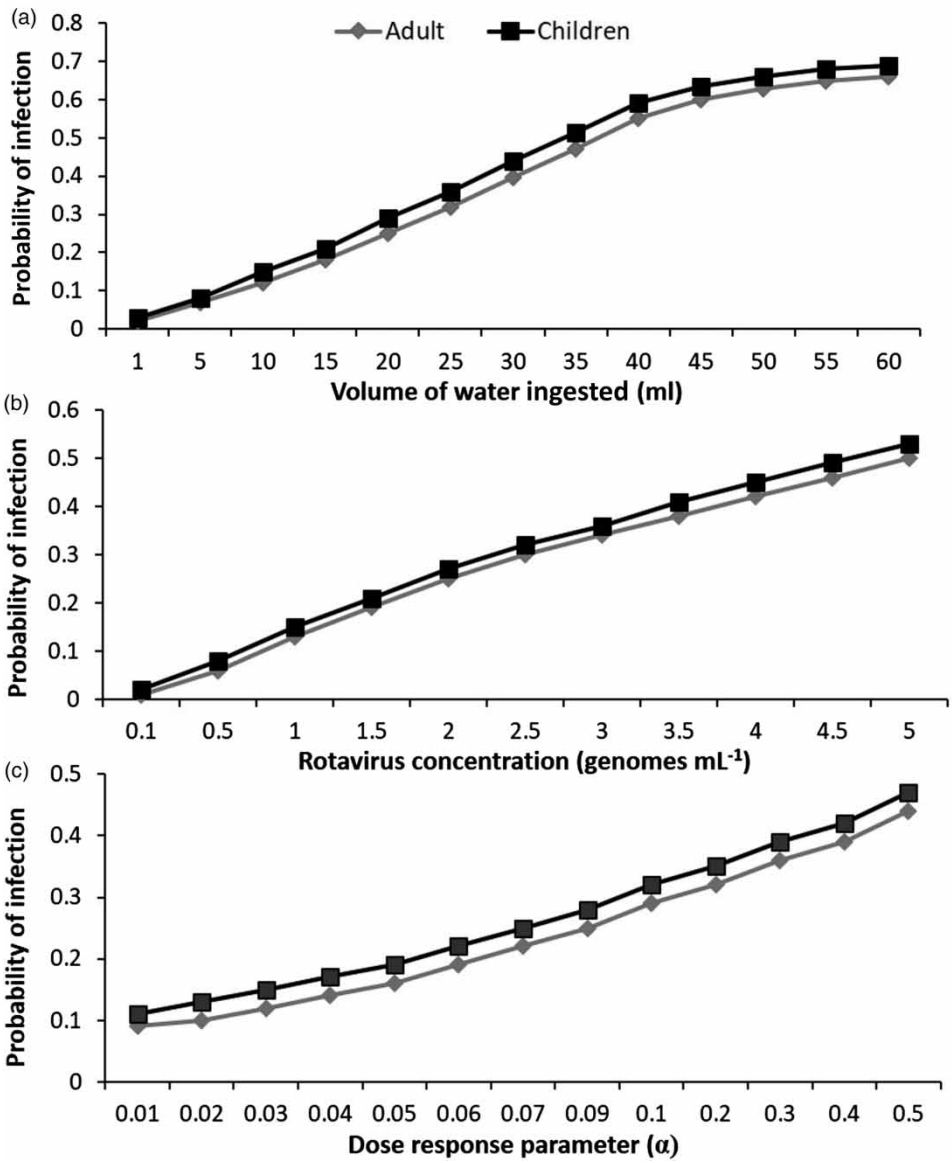


Figure 6 | The sensitivity of the probability of rotavirus infection for single exposure at the rivers for input variable of (a) volume of water ingested, (b) concentrations of rotavirus and (c) dose–response model parameter (α).

Due to the lack of data on the volume of contaminated water ingestion during other forms of water use, we were unable to quantify the risks associated with the other water uses. However, such unquantified risks might be also substantial, because even a few viral particles if ingested accidentally in our body, can infect us (La Rosa *et al.* 2012). Since the water of these rivers is not treated at all, people use water from the studied sites may be exposed to unacceptable risk of infection. Our previous study (Islam *et al.* 2017) found a higher level of indicator bacteria and the communities with high GI incidence after flooding events. However, data regarding the burden of pathogenic virus infections and diseases in Bangladesh are inadequate, and the current viral prevalence remains largely unknown. The use of contaminated river water for fish farming and agriculture represents potential health risks not only to the farmers that may accidentally ingest the water but also to the consumers (Bosch *et al.* 2008). Irrigation for vegetable cultivation

is widespread in the river catchments. Viruses on the surface of the lettuce leaf need to be inactivated fast due to the exposure to sunlight and high temperatures. If adequate time is allowed between final irrigation and consumption, the exposure of the consumer to infectious viruses would have been very low (Hamilton *et al.* 2006). Nevertheless, it is assumed that a reduction in enteric viruses in the agriculture farms is unlikely. Because farmers do not stop irrigation for some period before harvesting as they want their vegetables looking fresh during harvest (Seidu *et al.* 2008).

This study has demonstrated the successful use of a simplified QMRA. Most QMRA studies to predict the human health risks from exposure to recreational waters have been focused on surface waters impacted by human sources of contamination (Van Abel & Taylor 2018). This study has considered mixed sources of contamination along with sewage dominated human sources to predict the health risks from bathing in rivers of a developing country Bangladesh impacted by both sewage and mixture of sources. This QMRA study would act as a basis for microbial contamination reduction and provides valuable information for policy makers and water managers in reducing the widespread microbial contamination of the surface waters of Bangladesh and risks of waterborne disease outbreaks. The study hopefully would also create awareness, help in formulation of the proposed water safety plan for southwest Bangladesh and contribute to achieve the Sustainable Development Goal (SDG) 6, clean water and sanitation for all. The method can potentially be applied to other watersheds of the world with similar characteristics and can help in formulating solutions to improve the microbial water quality.

CONCLUSIONS

The potential risks of illness associated with the exposure to major waterborne pathogens in the three rivers in southwest Bangladesh were assessed using a QMRA technique. The QMRA assessed the probability of infection and illness due to the accidental ingestion of river water impacted by untreated sewage and urban and agricultural runoffs. The assessment results revealed that the risks of illness are unacceptably higher than the accepted probability of illness. The study confirms that the viral infection constitutes the predominant risk from exposure to bathing water in urban rivers. However, many assumptions are made and there are uncertainties in this risk assessment. Further studies are needed regarding the determination of the infectivity of viruses to assess the risk more precisely. The high infection and illness risk at the rivers suggest specific attention for mitigation measures and further in-depth risk assessment at the local level. This study provides a unique possibility for understanding the link between the ingestion of contaminated water and health risk and hence gives an option for reducing the burden of disease in the population by application of appropriate risk management. The study also demonstrates how QMRA can be applied in countries with limited data and that the results can provide valuable information for the management of surface water sources.

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