A study to estimate the fate and transport of bacteria in river water from birds nesting under a bridge

M. M. M. Nayamatullah, S. Bin-Shafique and H. O. Sharif

ABSTRACT

To investigate the effect of input parameters, such as the number of bridge-dwelling birds, decay rate of the bacteria, flow at the river, water temperature, and settling velocity, a parametric study was conducted using a water quality model developed with QUAL2Kw. The reach of the bacterial-impaired section from the direct droppings of bridge-nesting birds at the Guadalupe River near Kerrville, Texas was estimated using the model. The concentration of *Escherichia coli* bacteria were measured upstream, below the bridge, and downstream of the river for one-and-a-half years. The decay rate of the indicator bacteria in the river water was estimated from the model using measured data, and was found to be 6.5/day. The study suggests that the number of bridge-dwelling birds, the decay rate, and flow at the river have the highest impact on the fate and transport of bacteria. The water temperature moderately affects the fate and transport of bacteria, whereas, the settling velocity of bacteria did not show any significant effect. Once the decay rates are estimated, the reach of the impaired section was predicted from the model using the average flow of the channel. Since the decay rate does not vary significantly in the ambient environment at this location, the length of the impaired section primarily depends on flow.

Key words | decay rate, indicator bacteria, QUAL2Kw, settling velocity, water quality model

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INTRODUCTION

Predicting the fate and transport of enteric bacteria in surface water is important for assessing and managing the risk that these organisms may pose to public health. To investigate the sources, distribution, and the fate and transport of fecal bacteria populations in surface water, computer modeling is used extensively these days. In general, collection, storage, and analyses of field data involve expensive and labor-intensive operations (Scarlatos 2001). In order to reduce the amount of field data, water quality modeling simulation is incorporated into the natural system. Numerical simulations of a model complement field investigations by being able to fill in missing data, extrapolate data series, run sensitivity analyses, and simulate different physical scenarios, including those where field sampling is hard to accomplish, i.e. severe weather conditions, late night measurements, etc. (Scarlatos 2001).

The primary sources of bacteria that enter surface waters include sanitary, storm and combined sewer discharges, direct runoff, and others (e.g., birds and boats). However, for the evaluation of some surface water bodies, direct droppings from bridge-nesting birds are identified as a potential source of bacterial contamination (TCEQ 2007). Several studies suggest that the potential for underlying water pollution from the direct droppings of bridge-nesting birds is significant (Palmer 1982; Smith *et al.* 1993; Bashar *et al.* 2010).

The prediction of the extent of contamination using a water quality model and the parameters involved for the fate and transport of bacteria from the direct droppings of bridge-nesting birds is discussed in depth in an other article published by the authors (Nayamatullah *et al.* 2012). The primary objective of the parametric study is to investigate the effect of different model parameters that have been used in a surface water model to simulate the fate and transport of bacteria from the direct droppings of bridge-dwelling birds. In this study, sources of bacteria other than direct droppings from bridge-nesting birds, such as runoff, storm discharge etc. have not been considered.

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BACKGROUND

'One Total Maximum Daily Load (TMDL) for Bacteria in the Guadalupe River above Canyon Lake', for Segment 1806 was adapted on July 25, 2007 by the Texas Commission on Environmental Quality (TCEQ). The TMDL examined water quality data and observed a considerable increase in *Escherichia coli* concentration at station 12617, which is located in the Guadalupe River at Louise Hays Park, below the bridge at SH16. This bridge is a nesting location for hundreds of migratory cliff swallows. A thorough investigation was conducted at this site and the effect of bridge-dwelling birds on water quality, the fate and transport of bacteria, and the reach of contamination is discussed elsewhere (Bashar *et al.* 2010; Nayamatullah *et al.* 2012). The surface water quality model that has been developed to simulate that site requires several inputs, which have been measured at the field site. The sensitivity of each parameter is extremely important in order to understand the fate and transport of bacteria that have been studied here.

Site selection

In order to understand whether the direct droppings from bridge-nesting birds are the primary reason for the elevated bacterial loading in station 12617, this site was selected for the experiment (Figure 1).

The maximum number of active nests was counted in May 2009, when the number of active nests was approximately 163 over the water and approximately 335 over the ground surface. Similar numbers of nests were also found in May 2010. In winter, only a few pigeons and sparrows were seen under the bridge.

Indicator bacteria

The probable presence of pathogens can be identified by using indicator bacteria of which *E. coli*, fecal coliform, and enterococci are most widely used (EPA 1986). These microorganisms are typically found in the presence of pathogens but are much easier to detect and quantify. The presence of indicator bacteria would not necessarily mean that pathogens were present, it only suggests that there is a strong possibility of their presence (Schroeder *et al.* 2002).

TCEQ provides numeric and narrative criteria to evaluate attainment of designated uses. The numeric criteria for *E. coli*, fecal coliform, and enterococci defined in the standards for support of the contact recreation use are delineated in Table 1.

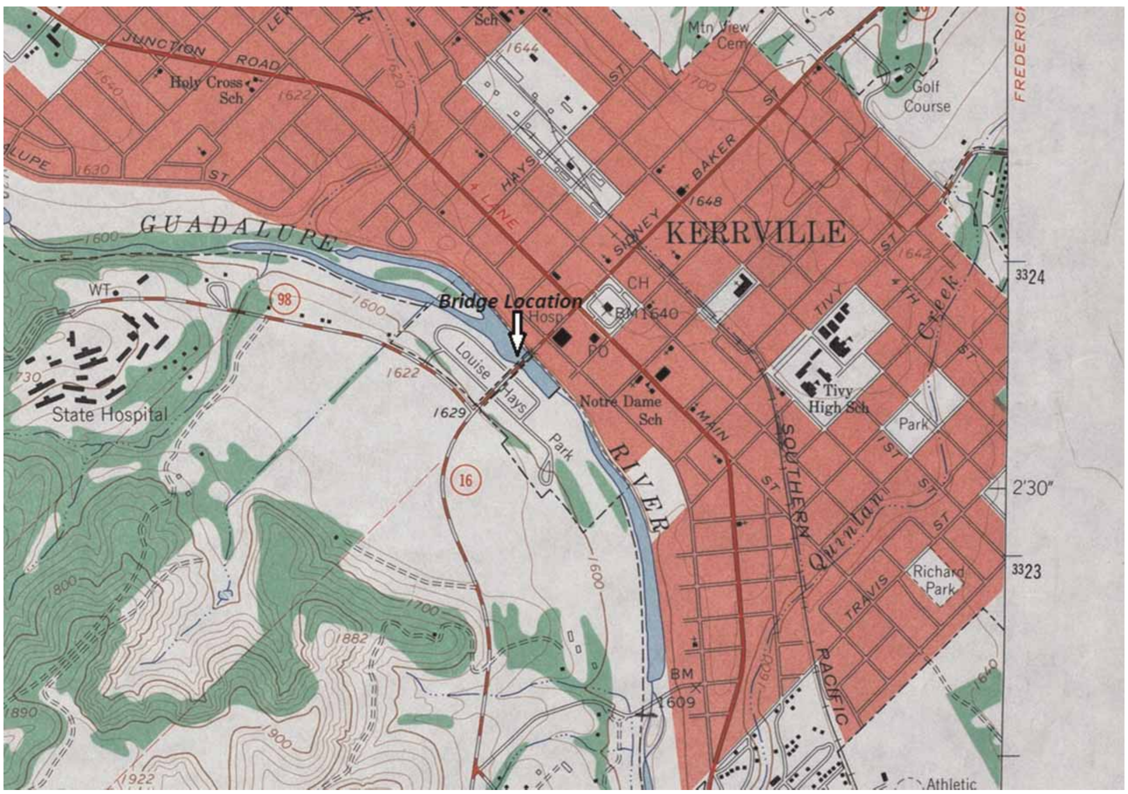

Figure 1 | Experimental sites over Guadalupe River at Kerrville, TX. Adapted from United States Geological Survey (USGS).

Table 1 | TCEQ standards for indicator bacteria in contact recreation

Parameter	*E. coli* (# per 100 ml)	Fecal coliform (# per 100 ml)	Enterococci (# per 100 ml)
Geometric mean	126	200	35
Single sample max	394	400	89

METHODS

Sampling

The samples were collected from the surface of the water body from three locations: (1) just below the centerline of the bridge, (2) 22.86 m upstream, and (3) 22.86 m downstream of the bridge. The samples were collected two to three times in each of the months during nesting seasons (March to August) and once in months when migratory birds were not present.

Analyses of the samples

The samples were analyzed in the certified Environmental Sciences Department Laboratory of San Antonio River Authority (SARA). For the analysis of *E. coli* and fecal coliform, MF partition method SM 9222G was used (APHA 1998 Membrane Filter Technique) and SM 9230C was used for the verification and quantification of enterococci (APHA 1998).

Numerical modeling

A water quality model was developed using QUAL2Kw (version 5.1) to estimate the reach of the section impaired due to direct droppings of birds from that particular bridge. QUAL2Kw is a comprehensive, advection-dispersion mass transport water quality model that can simulate the fate and transport of a number of constituents such as temperature, biological oxygen demand, phytoplankton, pH, alkalinity, pathogenic bacteria and bottom algae (Chapra & Pelletier 2003). A general mass balance equation for a constituent concentration (c) in the water column of a reach can be written as (Pelletier *et al.* 2006):

$$\frac{dc_i}{dt} = \frac{Q_{i-1}}{V_i}c_{i-1} - \frac{Q_i}{V_i}c_i - \frac{Q_{ab,i}}{V_i}c_i + \frac{E'_{i-1}}{V_i}(c_{i-1} - c_i) + \frac{E'_i}{V_i}(c_{i+1} - c_i) + \frac{W_i}{V_i} + S_i + \frac{E'_{hyp,i}}{V_i}(c_{2,i} - c_i)$$

where $Q_i =$ flow at segment i (L/day), $Q_{ab,i} =$ abstraction flow at segment i (L/day), $V_i =$ volume of segment i (L), $S_i =$ sources and sinks due to reactions and mass transfer mechanisms (mg/L/day), $W_i =$ the external loading (mg/day), $E =$ bulk dispersion coefficient (L/day), and $t =$ time (day). Not all of the terms in the above equation have been used in this simulation. For example, external loading (i.e., runoff), abstraction flow has been avoided in this case.

For the purpose of this numerical modeling, the experimental site was divided into twelve segments with an equal length of 22.86 m (75 ft) (Figure 2). R1 and R3 are upstream and downstream sampling locations, respectively, whereas R2 is the location of the bridge that was considered as the point source of bacterial loading. The remainder of the segments are further downstream locations for predicting bacterial concentration from numerical simulation. The measured geometry of the channel such as width, cross-sectional area, and longitudinal slope at each region was used for the model. The flow and water temperature were collected from the United States Geological Survey (USGS) station 12617 near the site. The model had the ability to self-calculate the longitudinal dispersion co-efficient.

The measured concentration of bacteria from the upstream location (R1) was used as the upstream boundary condition (continuous source) as well as the background concentration for the entire domain. It was observed that when the migratory birds are not present in the bridge, the bacteria concentration does not change significantly from location R1 to R3. Perhaps the decay of the bacteria as the water flows from R1 to R3 is compensated by the bacteria discharge from the local habitat such as ducks residing in this region in all seasons. Based on that observation, the

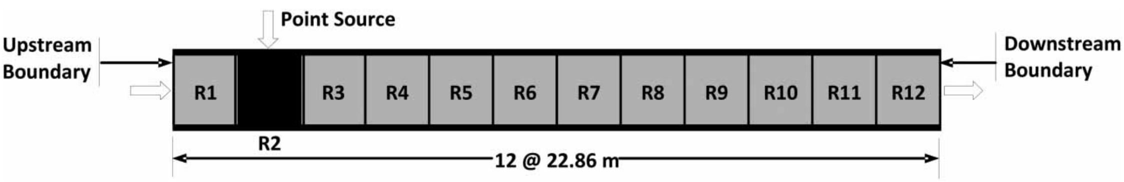

Figure 2 | QUAL2Kw segmentation scheme.

measured concentration of bacteria from the upstream location is considered as the background concentration.

The measured bacteria loading from the direct droppings of the bridge-dwelling birds was applied as a point source at R2. Having known the background bacterial concentration, the concentration at the upstream location, and the point source below the bridge, the decay rate for a particular indicator bacterium was calibrated by trial and error to determine for which decay rate the simulated concentration is equal to the measured concentration at the downstream sample location. The decay rate presented in this paper is the average of predicted decay rates obtained from the 12 sets of data that were measured at the field site.

Once the decay rate was determined, a parametric study was conducted in order to understand the sensitivity of the input parameters, such as bacterial loading in terms of number of dwelling birds or active nests, settling velocity, water temperature, decay rate of the bacteria in ambient environment, and channel flow. Each of the input parameters was varied within the possible ranges that can be encountered in the field site while all other parameters were kept constant as shown in Table 2.

RESULTS AND DISCUSSION

Effect of the number of birds

The effect of the number of birds on the bacterial contamination of the river water at different distances from the bridge is shown in Figure 3(a). Since the migratory birds nesting under the bridge are the major source of bacterial contamination, the bacterial loading increases as the number of birds increases. As a result, the bacterial concentration increases below the bridge as well as in the downstream. Since dilution and decay are constant, the bacterial concentration decreases at a constant rate toward the downstream. The number of active nests is varied, based on the maximum (163), minimum (50) and the average (100) count throughout the monitoring period.

Table 2 | Model input parameters

Parameter	Value
Number of active nests	163
Flow of the channel (m^3/sec)	2
Decay rate (/day)	5.5
Light extinction coefficient (/m^2)	0.2
Alpha constant for light mortality (/day/hr)	1.0
Settling velocity (m/day)	1
Water temperature (°C)	20
Temperature co-efficient	1.047

Effect of the decay rate of bacteria

Natural die-off or decay rate in the ambient environment imposes the potential effects on the fate and transport of bacteria. The effect of the decay rate on the bacterial contamination of river water at different distances from the bridge is shown in Figure 3(b). The maximum concentration (below the bridge) does not change with the change of the decay rate. However, the attenuation of the bacterial concentration towards downstream is significantly dependent on the decay rate. As the decay rate increases, the attenuation of bacterial concentration occurs in a faster rate toward downstream. Since the decay rate is a function of time, the effect of the decay rate is more pronounced as it moves further downward.

Effect of the flow rate

The effect of the flow rate of water on the bacterial contamination of the river water at different distances from the bridge is shown in Figure 3(c). The flow is varied from 0.6 to 4.3 m^3/s, which represent the minimum and maximum flow, respectively measured throughout the monitoring period. The average flow was 2 m^3/s. Similar to the decay rate, the channel flow does not have any significant effect on maximum concentration near the loading source (below the bridge), but the effect is more indicative further downstream. Figure 3(c) shows that bacterial concentration decreases significantly downstream as the flow decreases. As the flow increases, the velocity of water increases too. Thus, the water moves faster and needs less time to move a certain distance.

Since the point source is considered continuous, attenuation is expected to be lower at higher flow because the decay is only a function of time in any particular environment.

Effect of water temperature

Water temperature significantly impacts bacterial growth or death in a surface water system. Therefore, in order to explore the effect of water temperature on the attenuation of bacteria from the surface water, water temperature was varied in the

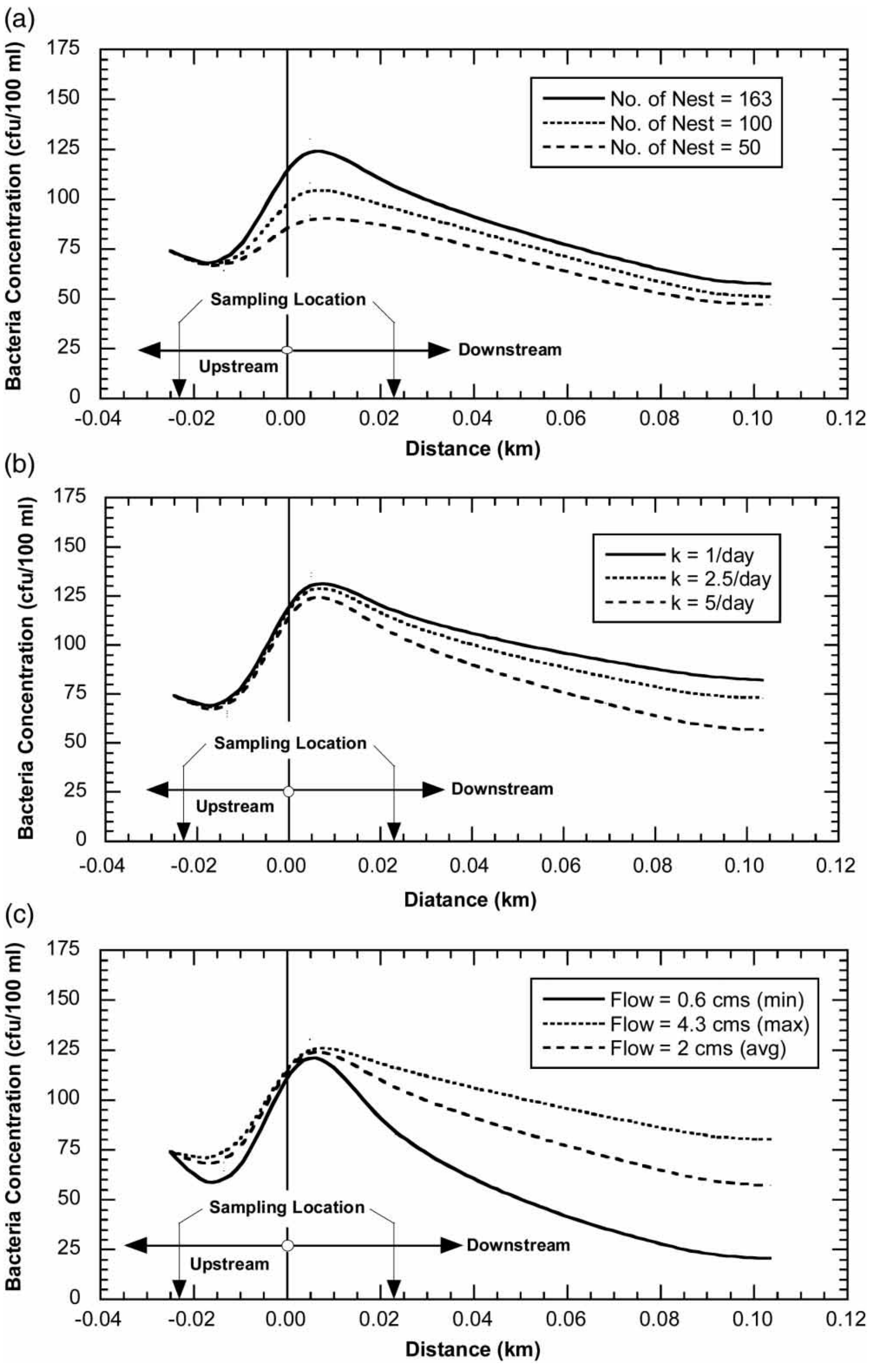

Figure 3 | Effect of (a) number of bridge-dwelling birds, (b) decay rate and (c) channel flow on *E. coli* concentration in downstream.

model. In general, fecal indicator bacteria are more likely adapted to live in the gastrointestinal tract rather in the natural environment. Studies have shown that they do not grow in surface water at ambient temperature, and can survive only from a few hours to a few days (Darakas 2002). Hence, in surface water, temperature only affects the survival kinetics of indicator bacteria by prolonging survival or expediting death. The effect of water temperature is shown in Figure 4(a), which shows that attenuation decreases for a temperature increase from 10 to 20 °C. Usually, the death of bacteria decreases with increasing surface water temperature, which might be the reason for lower attenuation at higher

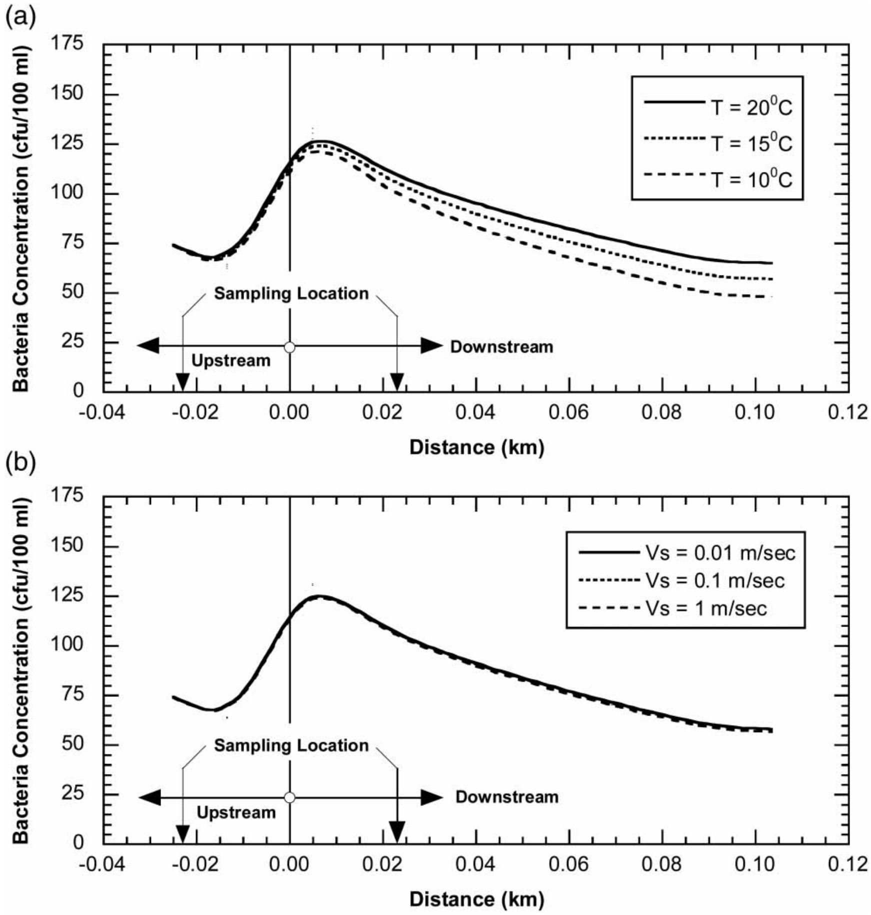

Figure 4 | Effect of (a) water temperature and (b) settling velocity on *E. coli* concentration.

water temperature. Hence, a lower attenuation in summer and a higher attenuation in winter is expected.

Effect of the settling velocity

The effect of the settling velocity of bacteria is shown in Figure 4(b), which shows that the settling velocity does not have a significant effect on the fate and transport of bacteria in surface water. Settling velocity has been increased from 0.01 to1 m/day (100 times), but did not show any effect. However, the settling velocity might have a significant effect if the water contains a considerable amount of suspended particles.

Impaired section estimation

The decay rate estimated from the model was found to be 6.5/day for *E. coli*, and 5.5/day for fecal coliform, and 3.5/day for enterococci. The decay rates are within the range of published values (Thomann & Mueller 1987). The concentration of the indicator bacteria at different distances from the point source are presented in Figure 5. The concentration of all indicator bacteria is highest below the point source and decreases as the water moves downstream due to dilution and decay. Figure 5(a) shows that the concentration of *E. coli* decreases below the TCEQ standard (394 cfu/100 ml) at a distance of 0.08 km and below the background concentration. Similarly, it can be seen from Figures 5(b) and 5(c) that the concentration decreases below the TCEQ standard at a distance of 0.12 km for fecal coliform and 0.2 km for enterococci from the point source. The concentration decreases below the upstream boundary concentration (background) at a distance of 0.14 and 0.06 km from the point source for fecal coliform and enterococci, respectively.

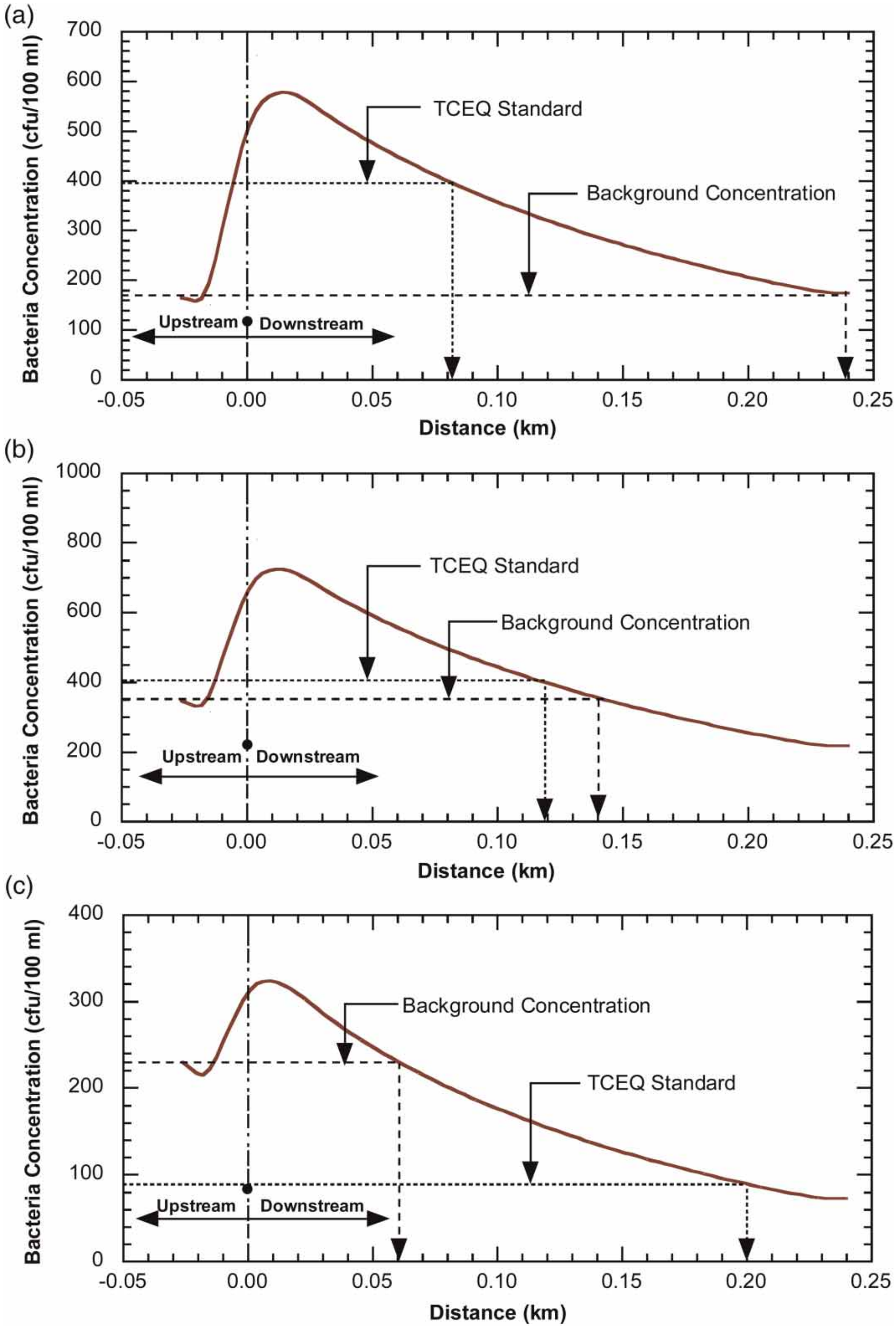

Figure 5 | Predicted Impaired Sections: (a) *E. coli,* (b) fecal coliform and (c) enterococci.

CONCLUSIONS

The water quality model that has been developed to simulate the fate and transport of bacteria in surface water from the direct droppings of bridge-dwelling birds was used for the parametric study in order to understand the sensitivity of each of the input parameters. From the parametric study, it can be suggested that the number of birds, decay rate of bacteria, and flow of the river have a significant effect on the fate and transport of bacteria in surface water. Although only *E. coli* concentration has been evaluated against those parameters, enterococci and fecal coliform also showed a similar trend of impacts. As the number of bird increases, the bacterial loading also increases, which causes higher bacterial concentration below the bridge as well as downstream. The attenuation of bacteria downstream increases as the decay rate increases or the flow decreases. The water temperature moderately affects the fate and transport of bacteria, whereas, the settling velocity of bacteria did not show any significant effect. The decay rate is highest for *E. coli* (6.5/day) and lowest for enterococci (3.5/day). Based on TCEQ standard, the length of the impaired section is 0.2 km in a normal day and enterococci is the governing bacteria in this situation. The effect of the point source will be void at a distance of 0.24 km and *E. coli* is the governing bacteria to satisfy this condition. In the real world, the findings of the length of impaired segments of a river or stream based on the TCEQ standard could be a potential tool for surface water management water organizations. Since QUAL2Kw is a one-dimensional modeling framework, for better understanding the fate and transport of bacteria in surface water, a two or three dimensional modeling program could be employed in future research.

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