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Microbial risk assessment of drinking water based on hydrodynamic modelling of pathogen concentrations in source water

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HIGHLIGHTS

- Applied discharge-based QMRA and hydrodynamic modelling in drinking water context
- Simulated transport of norovirus from sewage to the drinking water intake
- Estimated required norovirus reduction by treatment to achieve health targets
- Treatment was adequate, but strongly dependent on chlorine disinfection.

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ABSTRACT

Norovirus contamination of drinking water sources is an important cause of waterborne disease outbreaks. Knowledge on pathogen concentrations in source water is needed to assess the ability of a drinking water treatment plant (DWTP) to provide safe drinking water. However, pathogen enumeration in source water samples is often not sufficient to describe the source water quality. In this study, the norovirus concentrations were characterised at the contamination source, i.e. in sewage discharges. Then, the transport of norovirus within the water source (the river Göta älv in Sweden) under different loading conditions was simulated using a hydrodynamic model. Based on the estimated concentrations in source water, the required reduction of norovirus at the DWTP was calculated using quantitative microbial risk assessment (QMRA). The required reduction was compared with the estimated treatment performance at the DWTP. The average estimated concentration in source water varied between 4.8×10^2 and 7.5×10^3 genome equivalents L^{-1}; and the average required reduction by treatment was between 7.6 and 8.8 Log_{10}. The treatment performance at the DWTP was estimated to be adequate to deal with all tested loading conditions, but was heavily dependent on chlorine disinfection, with the risk of poor reduction by conventional treatment and slow sand filtration. To our knowledge, this is the first article to employ discharge-based QMRA, combined with hydrodynamic modelling, in the context of drinking water.

1. Introduction

Gastrointestinal diseases related to the contamination of drinking water constitute a major threat to global human health (WHO, 2011). Although this problem is most dominantly present in developing countries, the microbial contamination of drinking water causes outbreaks in developed countries as well (e.g. Braeye et al., 2014; Craun et al., 2010; Larsson et al., 2014; Mac Kenzie et al., 1994). Water is an important transmission route of noroviruses, and human noroviruses are considered a significant cause of waterborne gastroenteritis (Mathijs et al., 2012).

To assess drinking water safety, the World Health Organization recommends a risk-based approach encompassing all steps of the drinking water supply system from the catchment to the consumer (WHO, 2011). In this light, Quantitative Microbial Risk Assessment (QMRA) is widely used to analyse and inform the management of the drinking water supply system (Medema and Smeets, 2009; Smeets et al., 2010). Generic QMRA tools have been developed (Petterson and Stenström, 2007; Schijven et al., 2011) to perform QMRA for specific

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drinking water treatment plants (DWTPs) with different treatment trains and varying pathogen levels in the source water.

A major limitation of QMRA is constituted by a common lack of proper input data on the pathogen levels in source water. The monitoring of pathogen concentrations in source water is often too infrequent. However, pathogen concentrations in water sources are driven by upstream loading events and are highly variable, with peaks that can occur suddenly and may disappear within only a few hours (Åström et al., 2007; Westrell et al., 2006b). Thus, monitoring processes often fail to detect potentially hazardous peaks in pathogen concentrations. In addition, detection limits of analytical methods can be higher than pathogen concentrations relevant to public health. Therefore, monitoring data could provide misleading input for QMRA. This could negatively impact the safety of the produced drinking water and the health of consumers.

In order to address the limitation regarding the lack of source water quality data, the monitoring data can be supplemented by the results of hydrodynamic modelling (McBride et al., 2012). Hydrodynamic modelling has proven to be useful in order to describe the microbial water quality in water sources and to assess the influence of different conditions and events (e.g. Liu et al., 2006; Sokolova et al., 2013). Thus, a hydrodynamic model can be used to simulate the influence of upstream loading events on the source water quality at the intake of a DWTP.

The aim of this article was to quantify the impact of upstream loading events on the health risks for drinking water consumers. For this purpose, hydrodynamic modelling and QMRA approaches were combined. The norovirus concentrations in the source water during various upstream loading conditions were quantified using hydrodynamic modelling. Based on the modelling results, the required reduction of norovirus concentrations at the DWTP was calculated and compared with the estimated performance of the DWTP. To our knowledge, this article is the first to employ discharge-based QMRA, combined with hydrodynamic modelling, in the context of drinking water management.

2. Methods

2.1. Study area

The Överby DWTP produces drinking water for approximately 49,000 consumers in the municipality of Trollhättan in Sweden. The Överby DWTP draws water from the river Göta älv and employs the following treatment steps: coagulation/flocculation, rapid sand filtration, slow sand filtration and free chlorine disinfection.

Göta älv is a river that drains Lake Vänern into the strait Kattegat. The length of the river between the outflow from Lake Vänern and the mouth of the river is 93 km. The water flow in the river Göta älv is regulated by several hydropower stations. In this study we focus on the 11 km stretch of the river between the Vargön and Trollhättan hydropower stations. In 2011, the water flow in the studied part of the river varied between 138 and 898 m^3/s, with an average of 575 m^3/s.

The virus contamination at the intake can be caused by sewage discharges into the river from faecal sources located upstream the Överby DWTP: the Holmängen wastewater treatment plant (WWTP) and the sewage pumping stations. The Holmängen WWTP treats sewage from approximately 27 000 persons. The treatment at the Holmängen WWTP consists of the following treatment steps: rotating screens, aerated grit chambers, aeration tank, primary sedimentation tank, trickling filter, denitrification, flocculation tanks and sedimentation tanks. By-passes of untreated sewage are possible, but occur relatively seldom–approximately once a year. Untreated sewage often enters the river during the periods of heavy rain through emergency discharges from the pumping stations.

2.2. Quantification of norovirus concentrations in sewage

A norovirus monitoring campaign was undertaken as a part of the European Union project VISK (visk.nu). During the monitoring campaign, the sewage from the inflow and outflow of the Holmängen WWTP was sampled daily from 15 to 29 February 2012 (n = 15). Each of these days, the sewage was collected over 24 h using an automated sampler, which was flow rate driven. The sewage volume used for analysis was 50 mL. The sewage was analysed for norovirus genogroups I and II (GGI and GGII) using quantitative real-time PCR (qPCR) based on reported methods (Dienus et al., 2015; Kageyama et al., 2003; Nordgren et al., 2009; Shieh et al., 1995) as described in Appendix A. The GGI and GGII were chosen, since they constitute the most important norovirus genogroups in terms of human infection (Matthews et al., 2012). The qPCR analysis determined the concentration of norovirus genome equivalents.

The obtained qPCR data (Table 1) (Dienus et al., 2015) were used to characterise the probability density functions for norovirus GGI and GGII in raw and treated sewage from the Holmängen WWTP. The virus concentrations were assumed to follow a gamma distribution with parameters ρ (shape) and λ (scale):

$$f(c|\lambda,\rho) = \frac{e^{-\frac{c}{\lambda}}\lambda^{-\rho}c^{-1+\rho}}{\Gamma[\rho]}. \quad (1)$$

The gamma distribution was then used to calculate the likelihood function for each dataset of reported concentrations ($c_1, c_2 \ldots c_{15}$):

$$L(\lambda,\rho|c_i) = \prod_{i=1}^{15} f(\lambda,\rho|c_i). \quad (2)$$

The likelihood functions were optimised (in Mathematica 8.0) to obtain maximum likelihood estimators of ρ and λ for each of the four datasets.

2.3. Hydrodynamic modelling

To simulate the transport of norovirus within the river Göta älv, a hydrodynamic model was set up. A three-dimensional time-dependent hydrodynamic model was used — MIKE 3 FM (MIKE Powered by DHI software package). This hydrodynamic model is based on the numerical solution of three-dimensional incompressible Reynolds averaged Navier–Stokes equations invoking the assumptions of Boussinesq and of hydrostatic pressure (DHI, 2011). The model consists of continuity and momentum equations and is closed by a turbulent closure scheme (DHI, 2011). The water density was assumed to be homogenous (barotropic formulation).

The modelling domain was approximated with prisms (triangles in horizontal plane) using a flexible mesh approach. The length of the triangles' sides varied from approximately 40 to 90 m. In vertical direction, the river was divided into 10 layers with a thickness that could vary depending on the depth and water surface elevation in the river (sigma-layers).

The initial conditions in the river were defined by the water surface elevation. The upstream and downstream boundary conditions were defined by the water flow through the Vargön hydropower station

Table 1
Summary of reported norovirus GGI and GGII concentrations (genome equivalents L^{-1}) in raw and treated sewage from the Holmängen WWTP during daily sampling in February 2012.

	Sewage	n (detects)	Min	Max	Mean
GGI	Raw	15 (15)	8.0×10^4	1.7×10^6	6.9×10^5
	Treated	15 (15)	1.2×10^5	4.5×10^5	2.8×10^5
GGII	Raw	15 (15)	4.2×10^5	4.8×10^6	2.7×10^6
	Treated	15 (15)	8.9×10^4	1.7×10^6	1.0×10^6