Water quality modelling, monitoring and microbial source tracking for microbial risk assessment of a drinking water source

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Abstract. To prevent waterborne disease outbreaks, mitigation of faecal contamination of drinking water sources and sufficient treatment of water at the drinking water treatment plant (DWTP) are required. The aim of this study was to combine and apply several tools to investigate the raw water quality and determine the risk for waterborne infections in a drinking water source for the cities of Mölndal and Gothenburg in Sweden, Lake Rådasjön.

To identify the major contamination sources around the lake and their contribution to the faecal contamination at the water intakes of DWTPs, monitoring of faecal indicators and pathogens was combined with microbial source tracking and water quality modelling. The microbial source tracking was performed to determine the human or ruminant origin of faecal contamination using host-specific *Bacteroidales* genetic markers. The decay of these genetic markers in relation to the decay of traditional faecal indicators in water environment was investigated in outdoor microcosm trials performed in different seasons. Using measured concentrations of *Bacteroidales* genetic markers the pathogen (norovirus and *Cryptosporidium*) concentrations in faecal contamination sources around the lake were estimated for endemic and epidemic conditions. Afterwards, the fate and transport of faecal indicators and pathogens within the lake were simulated using a three-dimensional coupled hydrodynamic and microbiological model, which was calibrated based on the decay data from the microcosm trials. Based on the obtained results a microbial risk assessment of a conventional DWTP was conducted using two different approaches – optimal disinfection practices (ODP) and quantitative microbial risk assessment (QMRA).

The results showed that the on-site sewers were the source that contributed the most to the pathogen concentrations at the water intakes under both endemic and epidemic conditions. The results from both the ODP and QMRA risk assessments indicated that the barrier efficiency against *Cryptosporidium* and possibly viruses may be too low at a conventional DWTP. This study demonstrated how different approaches and tools can be applied to evaluate the risks for waterborne infections and prioritise mitigation measures related to faecal contamination of surface drinking water sources.

Introduction

The faecal contamination of drinking water sources can lead to waterborne disease outbreaks among consumers, as recently happened in the Swedish cities Östersund and Skellefteå in 2010/2011 (Skellefteå Municipality 2011, SMI 2011). To prevent waterborne disease outbreaks, mitigation of faecal contamination of drinking water sources and sufficient treatment at the drinking water treatment plant (DWTP) are required.

To mitigate faecal contamination of drinking water sources, knowledge on the faecal sources in the catchment and their contribution to the contamination at the water intakes is required. Faecal contamination can enter a drinking water source through wastewater discharges from various sources and surface runoff. Therefore, it may be difficult to estimate the relative contribution from different sources to the total contamination at the water intakes. Moreover, the presence of pathogens from faecal contamination in a water source may remain undetected due to limitations of the commonly used monitoring techniques (Brookes et al. 2005).

To ensure sufficient drinking water treatment in terms of pathogen removal at the DWTP, a microbial risk assessment needs to be performed. Microbial risk assessment is mainly based on the information about the quality of the raw water and the performance of the treatment steps at the DWTP. A correct representation of pathogen concentrations in the raw water is crucial for estimation of the infection risks among consumers. However, the variations in the pathogen concentrations in the raw water over time, caused by the variations in the hydrodynamic conditions and the level of infection in different hosts, are often unknown or poorly understood.

This article provides a short overview of the work performed within a project "Evaluation of the microbial risks in a relatively unaffected surface drinking water source: water quality modelling, decay trials and microbial source tracking in Lake Rådasjön" (Åström et al. 2011). The aim of this project was to evaluate and implement several tools to determine the risks for waterborne infections posed by different contamination sources. The microbial water quality in a drinking water source for the cities of Mölndal and Gothenburg in Sweden, Lake Rådasjön, was investigated using monitoring, microbial source tracking, a microcosm study of the faecal indicator decay in raw water and coupled hydrodynamic and microbiological modelling. Based on the obtained results a microbial risk assessment of a conventional DWTP was conducted using two different approaches – optimal disinfection practices and quantitative microbial risk assessment.

Material and Methods

Lake Rådasjön (Figure 1) is located on the west coast of Sweden and constitutes the main water source for the city of Mölndal (60 000 consumers) and a reserve water supply for the city of Gothenburg (500 000 consumers). The surface area of the lake is approximately 2.0 km^2 and the maximum water depth is 23 m. The main inflow to the lake is the river Mölndalsån with a water flow in the range from 1 to 20 m^3/s. The river Mölndalsån enters the lake in the southeast and drains the lake in the west to Lake Stensjön (Figure 1). The water intakes for the cities of Gothenburg and Mölndal are located in the north-western part of the lake at 8 m and 15 m depth respectively (Figure 1). Lake Rådasjön is potentially subjected to faecal contamination from various sources located in the catchment of the lake. In terms of the risks for waterborne disease outbreaks the sources of human and ruminant faecal contamination are assumed to be the most relevant. Some examples of such sources in the catchment of Lake Rådasjön are: discharges from on-site sewers, emergency sewer overflows, surface runoff from urban areas and grazing areas for cattle and horses.

A monitoring program commenced in 2008 to identify the major contamination sources around the lake and to evaluate the water quality at the water intakes. The program included analyses of various faecal indicators in grab samples repeatedly collected at the contamination sources and the water intakes, as well as at-line monitoring (measurements once a day) of *E. coli* at the water intakes using Colifast® equipment (www.colifast.no). Moreover, analyses of *Giardia* and *Cryptosporidium* were performed on samples collected regularly at the water intakes and sporadically at a contamination source close to the water intakes.

To determine the human or ruminant origin of the faecal discharges from the contamination sources around the lake, a microbial source tracking method using host-specific *Bacteroidales* genetic markers was applied. The concentrations of human (BacH) and ruminant (BacR) *Bacteroidales* 16S rRNA markers in the samples collected at the contamination sources and the water intakes were analysed using qPCR assays (Reischer et al. 2006, Reischer et al. 2007). To account for the uncertainties and provide a reliability measure for interpreting microbial source tracking data, a Bayesian approach was used to combine the *Bacteroidales* qPCR assay performances with expert judgements based on the knowledge of the study area (Åström et al. 2012).

The decay of human and ruminant *Bacteroidales* markers in relation to the decay of traditional faecal indicators in the conditions of Lake Rådasjön was investigated in outdoor microcosm trials. Microcosm trials were conducted in March, August and November 2010 in order to capture the varying light and temperature conditions in different seasons. Two microcosms were constructed, one exposed to natural light and another protected from light. Microcosms were constructed in aquaria filled with raw water from Lake Rådasjön and inoculated with untreated wastewater and bovine faecal matter. The concentrations of *Bacteroidales* markers, total coliforms, *E. coli*, intestinal enterococci and somatic coliphages were analysed during two-week periods to follow the decay of faecal indicators (Sokolova et al. 2012a).

To quantify the contribution from different contamination sources to the microbial concentrations at the water intakes, the decay and transport of *E. coli* and pathogens within the lake were simulated using a microbiological model (ECO Lab by DHI) coupled to a three-dimensional hydrodynamic model (MIKE 3 by DHI). The input data for the model regarding the *E. coli* concentrations in the contamination sources around the lake were obtained from the monitoring campaign. The possible pathogen (*Cryptosporidium*, norovirus and *E. coli* O157/H7) concentrations in the contamination sources around the lake were estimated for endemic and epidemic conditions using the obtained microbial source tracking data (Sokolova et al. 2012b). The microbiological model was calibrated using the faecal indicator decay data from the microcosm experiment. The modelling results regarding the *E. coli* concentrations at the water intakes were validated using the measured data.

The results of monitoring and modelling provided raw water quality data needed to assess the health risks for consumers. A risk assessment was performed using the optimum disinfection practices (ODP) and quantitative microbial risk assessment (QMRA) tools (a description of these tools is available at www.svensktvatten.se). The ODP tool requires historical data on faecal indicator concentrations in raw water, while QMRA is based on pathogen concentrations in a water source.

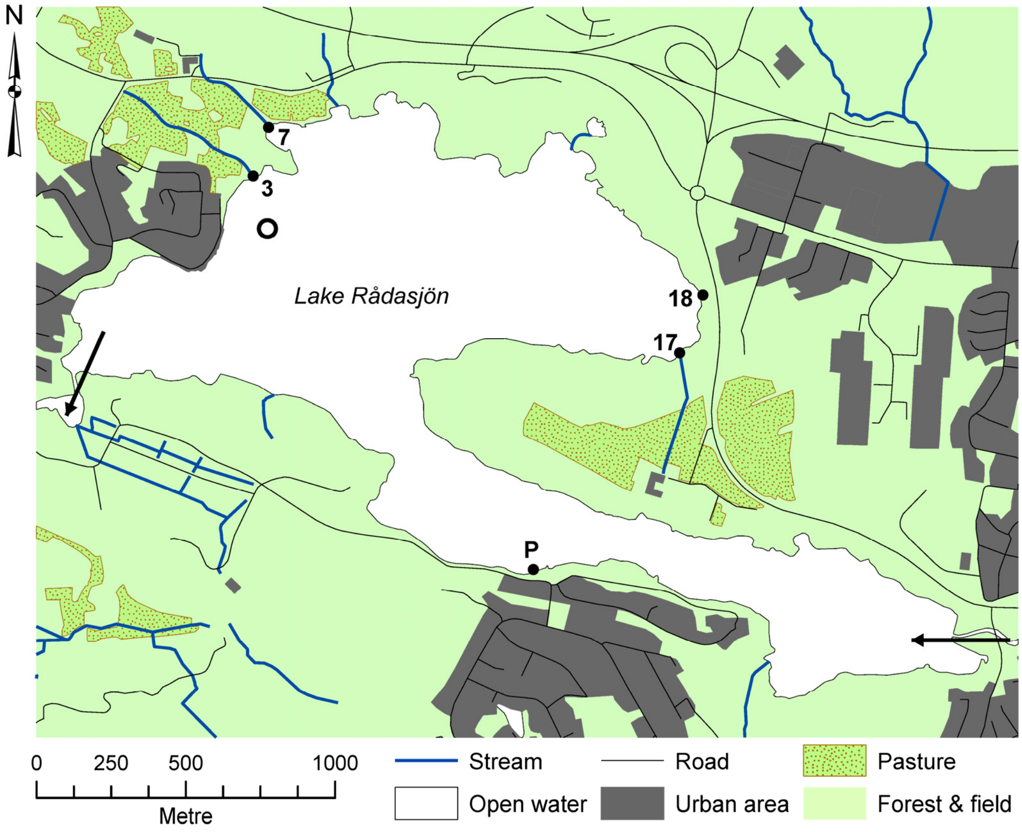

Figure 1 Map of Lake Rådasjön. The circle indicates the location of the water intakes. The dots represent the location of the major faecal contamination sources: on-site sewers (3 and 7), untreated stormwater (18), cattle grazing area (17) and emergency sewer overflow (P). The arrows represent the inflow to the lake from the river Mölndalsån and the outflow from the lake.

Results and Discussion

The monitoring campaign in combination with the microbial source tracking helped to identify the major contamination sources, which included the discharges from the on-site sewers (Figure 1, sites 3 and 7), urban stormwater runoff (Figure 1, site 18), the cattle grazing area (Figure 1, site 17), the emergency sewer overflow (Figure 1, site P), and the main inflow to the lake – the river Mölndalsån (Figure 1).

The at-line monitoring of the *E. coli* concentrations at the water intakes corresponded well with the laboratory analyses of the *E. coli* concentrations in grab samples. At-line monitoring proved useful to relatively fast provide an overview of the raw water quality and its variations. The pathogens *Giardia* and *Cryptosporidium* were detected in 2 and 4 samples, respectively, out of 61 samples collected at the water intakes during 2005 – 2011. *Giardia* was also detected in one out of 12 samples collected during 2010 – 2011 in the stream contaminated by on-site sewers (Figure 1, site 3).

The results from the coupled hydrodynamic and microbiological modelling corresponded well with the observed *E. coli* concentrations at the water intakes (Figure 2). Both monitoring and modelling indicated that the microbial water quality can vary strongly over time and that the highest levels of faecal contamination at the water intakes can be expected in autumn, winter and early spring (Figure 2).

Based on the modelling results we can conclude that under endemic conditions the stream contaminated by on-site sewers contributed the most to the norovirus concentrations at the water intakes in Lake Rådasjön, while the cattle grazing area was the main contributor to the *Cryptosporidium* concentrations. Under epidemic conditions the stream contaminated by on-site sewers contributed the most to both norovirus and *Cryptosporidium* concentrations at the water intakes.

Integrating microbial source tracking with coupled hydrodynamic and microbiological modelling proved to be useful to evaluate the contribution of different contamination sources to the pathogen concentrations at the water intakes. Moreover, the modelling approach enables testing various scenarios, for example, future or worst-case conditions and alternative locations of the water intakes or contamination sources.

The results from both the ODP and QMRA risk assessments indicated that the barrier efficiency against *Cryptosporidium* and possibly viruses may be too low at a conventional DWTP. Although the QMRA tool was more demanding than the ODP tool in terms of input data, it presented an opportunity to test different scenarios and investigate the effects of the infection rate and the location of the contamination sources around the lake on the health risk.

This study demonstrated how different approaches and tools can be applied to evaluate the risks for waterborne infections and prioritise mitigation measures related to faecal contamination of surface drinking water sources.

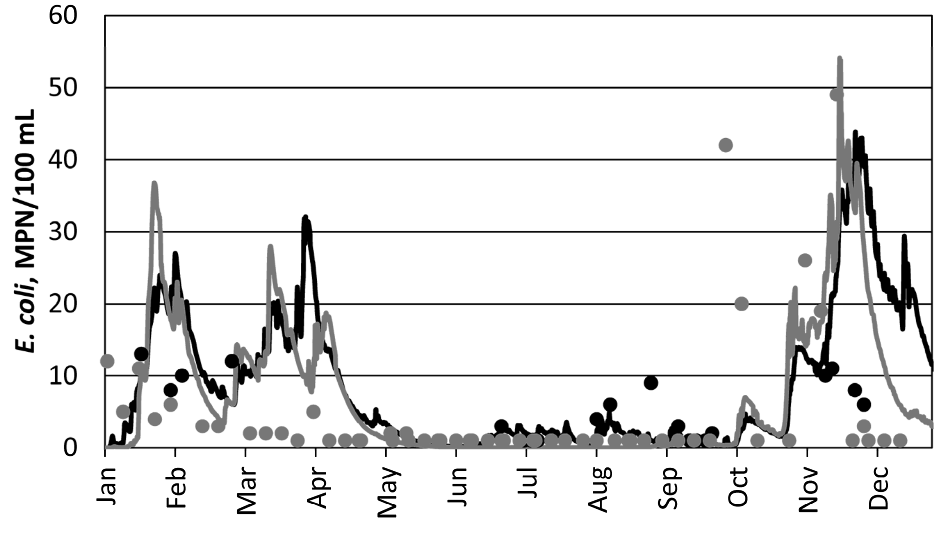

Figure 2 *E. coli* concentrations at the 8 m (black colour) and 15 m (grey colour) water intakes during the year 2008: comparison of the modelling results (line) with observed *E. coli* concentrations (dots).

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