

THESIS FOR THE DEGREE OF DOCTOR OF PHILOSOPHY

Hydrodynamic modelling of microbial water quality
in drinking water sources

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Gothenburg, Sweden 2013

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ISBN 978-91-7385-920-2

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Doktorsavhandlingar vid Chalmers tekniska högskola
Ny serie Nr 3601
ISSN 0346-718X

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Chalmers Reproservice
Gothenburg, Sweden 2013

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ABSTRACT

The faecal contamination of water sources can cause waterborne disease outbreaks among drinking water consumers. To design drinking water treatment and minimise consumer health risks, knowledge on source water quality is needed. The aim of this thesis was to describe the microbial water quality in water sources in order to facilitate the provision of safe drinking water. In this thesis, hydrodynamic modelling, microbial source tracking (MST), and quantitative microbial risk assessment (QMRA) were combined to study two surface drinking water sources, Lake Rådasjön and the river Göta älv in Sweden. The microbial water quality in these water sources was successfully characterised by the developed hydrodynamic models. The results demonstrated that the concentrations of faecal indicators and pathogens in these water sources vary and are event-driven. In the lake, the contaminant transport was strongly affected by wind conditions and by the vertical temperature stratification; in the river, the contaminant transport was driven by the water flow. Both for the lake and river, human faecal sources were the main contributors to the contamination at the water intakes. Based on the obtained results, recommendations for the management of the microbial risks concerning the studied water sources were formulated. It can be concluded that hydrodynamic modelling is a very useful approach to describe and predict the microbial water quality in drinking water sources. In this thesis, hydrodynamic modelling was successfully applied to study the factors that affect the contaminant spread in the water source, to capture the spatial and temporal variability of the microbial water quality, to provide short-term forecasts, and to test hypothetical scenarios. Furthermore, the results of the hydrodynamic modelling improved the interpretation of the MST data and provided input for QMRA. The novelty of this thesis lies in using hydrodynamic modelling in combination with MST and QMRA, in order to enhance the applicability and output of each individual approach, and to describe and predict the microbial water quality in drinking water sources.

Key words: *Bacteroidales*, *E. coli*, faecal contamination, faecal indicators, microbial source tracking, pathogens, QMRA, risk assessment.

LIST OF PAPERS

This thesis is based on the work contained in the following papers:

- I. Sokolova, E., Åström, J., Pettersson, T.J.R., Bergstedt, O., Hermansson, M., 2012. Decay of *Bacteroidales* genetic markers in relation to traditional fecal indicators for water quality modeling of drinking water sources. *Environmental Science & Technology* 46(2), 892-900.
- II. Sokolova, E., Åström, J., Pettersson, T.J.R., Bergstedt, O., Hermansson, M., 2012. Estimation of pathogen concentrations in a drinking water source using hydrodynamic modelling and microbial source tracking. *Journal of Water and Health* 10(3), 358-370.
- III. Sokolova, E., Pettersson, T.J.R., Bergstedt, O., Hermansson, M., 2013. Hydrodynamic modelling of the microbial water quality in a drinking water source as input for risk reduction management. *Journal of Hydrology* 497, 15-23.
- IV. Sokolova, E., Pettersson, T.J.R., Bergstedt, O., 2013. Hydrodynamic modelling and forecasting of microbial water quality in a drinking water source. *Journal of Water Supply: Research and Technology – AQUA* (doi: 10.2166/aqua.2013.216). Available online: <http://www.iwaponline.com/jws/up/default.htm>
- V. Sokolova, E., Petterson, S., Dienus, O., Nyström, F., Lindgren, P.E., Pettersson, T.J.R., 2013. Microbial risk assessment of drinking water based on hydrodynamic modelling of pathogen concentrations in source water. *Water Research*. Submitted.

Other relevant publications not included in this thesis:

- Sokolova, E., Lövstedt, C.B., Pettersson, T.J.R., 2011. Fate and Transport Modelling of Microbial Pollution in a Lake Used as a Drinking Water Source. In: Valentine, E.M., Apelt, C.J., Ball, J., Chanson, H., Cox, R., Ettema, R., Kuczera, G., Lambert, M., Melville, B.W., Sargison, J.E. Proceedings of the 34th World Congress of the International Association for Hydro-Environment Research and Engineering, 33rd Hydrology and Water Resources Symposium and 10th Conference on Hydraulics in Water Engineering. Barton, A.C.T.: Engineers Australia, 2011: 3171-3178.
- Sokolova, E., 2011. Hydrodynamic and microbiological modelling of water quality in drinking water sources. Thesis for the degree of Licentiate of Engineering. Chalmers University of Technology, Gothenburg.
- Åström, J., Bergstedt, O., Sokolova, E., Kjellberg, I., Pettersson, T.J.R., Borell Lövstedt, C., Karlsson, A., Wennberg, C., 2011. 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 (In Swedish: "Värdering av risker för en relativt opåverkad ytvattentäkt: Modellering av Rådasjön med stöd av inaktiveringsstudier och mikrobiell källspårning"). Stockholm: Svenskt Vatten Utveckling, report No 2011-18.
- Sokolova, E., Pettersson, T.J.R., Bergstedt, O., Hermansson, M., 2012. Hydrodynamic modelling of microbial water quality in a drinking water source. Accepted for publication in: Rauch, S., Morrison, G.M., Schleicher, N., Norra, S. Urban Environment. Springer. ISBN 978-94-007-7755-2.

- Sokolova, E., Pettersson, T.J.R., Åström, J., Bergstedt, O., Kjellberg, I., Hermansson, M., 2012. Water quality modelling, monitoring and microbial source tracking for microbial risk assessment of a drinking water source. Proceedings of the 8th Nordic Drinking Water Conference, 18 – 20 June 2012 in Stockholm, Sweden.

ACKNOWLEDGEMENTS

The work on this thesis has been carried out at the Division of Water Environment Technology, the Department of Civil and Environmental Engineering at the Chalmers University of Technology, within the framework programme for drinking water research, DRICKS. This project is a part of the Graduate School on Environment and Health (Forskarskolan Miljö och Hälsa) at the Chalmers University of Technology, University of Gothenburg and Västra Götaland Region, Sweden. This project has also been linked to the Rådasjön project (SVU-project 29-122) and the European Union project VISK (Interreg IV A programme). The author gratefully acknowledges the financial support from the Graduate School on Environment and Health, the Swedish Water and Wastewater Association (Svenskt Vatten), and the VISK project.

I would like to express my deep gratitude to my supervisors Thomas Pettersson (Chalmers University of Technology) and Malte Hermansson (University of Gothenburg), and my examiner Greg Morrison (Chalmers University of Technology), for their encouragement, guidance and constructive feedback.

I am grateful to Olof Bergstedt and Inger Kjellberg (City of Gothenburg), Mia Bondelind and Lars-Ove Sörman (Chalmers University of Technology), Johan Åström (Tyréns AB), and Susan Petterson (Water & Health Pty Ltd) for their contribution to my project.

I would also like to acknowledge the fruitful cooperation within the Rådasjön project and the VISK project.

I am grateful to my colleagues at the Division of Water Environment Technology and within DRICKS for their help, and for creating an inspiring atmosphere.

I would also like to thank DHI for providing the student licence for the MIKE by DHI software.

Special thanks are due to my father, Alexander Sokolov (Baltic Nest Institute, Stockholm University), for encouraging me to pursue an academic career, for all of his help, and for sharing his expertise and experience.

I would like to thank my family members for their unlimited support, motivation, patience and confidence in me.

Special thanks are due to my beloved husband, Niels Markwat, for all his help with my project, as well as his support and love.

Gothenburg, November 2013

Ekaterina Sokolova

ABBREVIATIONS

DWTP – drinking water treatment plant

E. coli – *Escherichia coli*

MST – microbial source tracking

QMRA – quantitative microbial risk assessment

WWTP – wastewater treatment plant

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1. INTRODUCTION

Gastrointestinal diseases are a major cause of death in the world (WHO 2008). These diseases are caused by microbial pathogens that are often present in faecal matter from animals and humans (Rusin et al. 2000). In developing countries gastrointestinal diseases are transmitted due to poor sanitation, through food sources and unsafe drinking water (Ashbolt 2004). However, even in the developed world, contaminated drinking water is a major source of microbial pathogens that can cause outbreaks of gastrointestinal diseases (Hrudey and Hrudey 2004). In Sweden, during two recent outbreaks (2010 – 2011) caused by faecal contamination of drinking water sources, tens of thousands of people in the cities Östersund and Skellefteå suffered from waterborne *Cryptosporidium* infections (Skellefteå Municipality 2011, SMI 2011).

The faecal contamination of water sources used for drinking water production, in combination with insufficient treatment of raw water, can result in the microbial contamination of drinking water (WHO 2011). The faecal contamination can enter a drinking water source from a variety of point and diffuse sources. Some examples of point sources are discharges from wastewater treatment plants (WWTPs) and combined sewer overflows; some examples of diffuse sources are agricultural and cattle grazing areas, and on-site sewer systems. There are often several faecal sources present in the catchment area of a surface water source.

To design drinking water treatment and minimise consumer health risks, knowledge on source water quality is needed. However, the monitoring of microbial water quality has several limitations. One limitation is the high variability of microbial concentrations over time and in space, since the concentrations are event-driven (e.g. Brookes et al. 2004, Westrell et al. 2006, Åström et al. 2007a). In addition, the detection limits of analytical methods can be higher than the pathogen concentrations relevant to public health (Köster et al. 2003). Furthermore, in order to identify periods of increased risks, it is important to understand the factors that affect the microbial water quality in a drinking water source. Moreover, to prioritise certain mitigation measures for the protection of water sources, the relative influence of different faecal sources on the water quality needs to be quantified. Finally, monitoring cannot provide predictions concerning hypothetical or future situations.

To study the spread of faecal contamination in water sources and related health risks, (i) hydrodynamic modelling, (ii) microbial source tracking (MST) and (iii) quantitative microbial risk assessment (QMRA) can be useful. To describe the spread of faecal indicators and pathogens in water sources, hydrodynamic models can be used (Table 1). Furthermore, MST can be used to identify the origin (e.g. human or ruminant) of faecal contamination in the water source (e.g. Field and Samadpour 2007). QMRA can be used to evaluate health risks for drinking water consumers (WHO 2011).

The microbial water quality in a water source can be simulated by means of computer models, which describe the hydrodynamic situation in the water source and take the decay of microorganisms in the environment into account (see examples in Table 1). Hydrodynamic modelling can be used to describe the temporal and spatial variability of microbial

concentrations (e.g. Hipsey et al. 2008). In addition, hydrodynamic modelling can be used to quantify the concentrations that are below the detection limits of analytical methods, yet still high enough to be relevant to consumer health (McBride et al. 2013). Furthermore, hydrodynamic modelling can be used to study the influence of different processes on the microbial water quality in a water source (e.g. de Brauwere et al. 2011, Ge et al. 2010, Thupaki et al. 2010), and to quantify the relative influence of different faecal sources (e.g. Zhu et al. 2011). Moreover, modelling can be used to simulate various scenarios and situations (e.g. Ge et al. 2012b, Vijay et al. 2010), and, thus, to provide predictions and forecasts (Chan et al. 2013).

In MST, *Bacteroidales* genetic markers can be used to determine the origin of faecal contamination (Field and Samadpour 2007, Reischer et al. 2013, Roslev and Bukh 2011). *Bacteroidales* marker assays have been used to evaluate the health risks in different environments (Gourmelon et al. 2010, Reischer et al. 2011, Stapleton et al. 2009, Åström et al. 2013). Furthermore, the correlation between the presence of host-specific *Bacteroidales* markers and the presence of various pathogens has been examined in order to better understand the health risks (Fremaux et al. 2009, Savichtcheva et al. 2007, Walters et al. 2007). However, the interpretation of MST data and application of MST in surface water management is limited by several research gaps, one of which is the need for further knowledge on the decay and transport of MST markers in the environment (Field and Samadpour 2007, Roslev and Bukh 2011).

To assess the safety of drinking water, 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). For this purpose, QMRA is widely applied to assess and manage drinking water supply systems in both developing (Coulliette et al. 2013, Enger et al. 2012, Machdar et al. 2013, Razzolini et al. 2011) and developed countries (Medema and Smeets 2009, Pintar et al. 2012, Teunis et al. 1997, Åström et al. 2007a). QMRA comprises hazard identification, exposure assessment, dose-response assessment and risk characterisation (Haas et al. 1999). Generic QMRA tools have been developed (Petterson and Stenström 2007, Schijven et al. 2011) to perform QMRA for specific drinking water treatment plants (DWTPs) with different treatment trains. To perform QMRA, data on pathogen concentrations at the water intake to the DWTP are needed. Thus, a major limitation of QMRA is constituted by a common lack of proper input data on the pathogen concentrations in raw water (Petterson et al. 2007, Schmidt et al. 2013, Signor and Ashbolt 2006).

These three approaches (hydrodynamic modelling, MST and QMRA) have a great potential to complement – and address the limitations of – one another. Although this potential has been mentioned in a few recent studies (Bambic et al. 2011, McBride et al. 2012, Schijven and De Roda Husman 2011), the combination of these three approaches has not yet been widely adopted. Hydrodynamic modelling can improve the interpretation of MST data by providing information on the decay and transport of genetic markers within the water source. Furthermore, hydrodynamic modelling can be used to describe the pathogen concentrations in a water source and, thus, provide input data for (discharge-based) QMRA (McBride et al.

2013, McBride et al. 2012). Likewise, MST can play a prominent role in the hazard identification step of QMRA (Bambic et al. 2011, Schijven and De Roda Husman 2011).

In this thesis, these three approaches were used to study the microbial water quality in two surface drinking water sources, Lake Rådasjön and the river Göta älv in Sweden. The novelty of this work lies in using hydrodynamic modelling in combination with the other approaches, in order to enhance the applicability, performance and output of each individual approach.

1.1. Aim and objectives

The aim of this thesis was to describe the microbial water quality in drinking water sources in order to facilitate the provision of safe drinking water.

The objectives of this thesis are listed below.

- To describe the decay and transport of the microbial contamination in drinking water sources, by means of
 - microcosm trials (Paper I) and
 - hydrodynamic modelling (Papers I – V).
- To characterise the microbial water quality in drinking water sources. This was done by using hydrodynamic modelling in order to
 - simulate the real situation in the water source (Papers III and IV),
 - forecast the microbial water quality in the water source (Paper IV), and
 - simulate scenarios and hypothetical situations (Papers I, II and V).
- To compare the influence of different contamination sources on the microbial water quality in drinking water sources, using
 - MST (Paper I) and
 - hydrodynamic modelling (Papers I – V).
- To estimate health risks for drinking water consumers, using hydrodynamic modelling in combination with QMRA (Paper V).
- To evaluate the applicability of hydrodynamic modelling (in combination with MST and QMRA) to describe and predict the microbial water quality in drinking water sources.

1.2. Overview of the thesis and included papers

This thesis is based on the work reported in Papers I – V. The purpose of this section is to provide a short overview of the work and the papers.

The decay of faecal contamination in the water environment is an important factor to consider when studying microbial water quality. The decay of faecal indicators under local conditions was studied in microcosm trials (Paper I). The microcosms were created by inoculating water from Lake Rådasjön with bovine faecal slurry and untreated wastewater. The trials were conducted outdoors during two-week periods in different seasons. The microcosms were regularly sampled to follow the decay of total coliforms, *Escherichia coli* (*E. coli*), intestinal enterococci, somatic coliphages, and human and ruminant-specific faecal *Bacteroidales*

genetic markers (BacH and BacR). The obtained experimental data were used to describe the decay processes in the hydrodynamic model.

The MST and hydrodynamic modelling approaches were combined to identify the origin of the faecal contamination in the lake (Paper I). The concentrations of BacH and BacR markers were measured in Lake Rådasjön and in the contamination sources around the lake. The decay and transport of BacH and BacR markers within the lake were simulated using a hydrodynamic model. The modelling results and the obtained MST data suggested that mitigation measures should focus on human contamination sources. It was demonstrated that this modelling approach improves the interpretation of MST data, especially when contamination from the same host group is released from different sites in the catchment.

The obtained MST data and hydrodynamic modelling were also used to estimate the pathogen concentrations in the lake (Paper II). The concentrations of norovirus, *Cryptosporidium* and *E. coli* O157/H7 in the contamination sources around the lake were estimated using the measured concentrations of *E. coli*, and BacH and BacR markers. Then, the decay and transport of pathogens within the lake were simulated using the hydrodynamic model. The results provided input for the QMRA and showed how much different contamination sources contributed to the pathogen concentrations at the water intake of a DWTP.

The relative contribution of different contamination sources was further studied by simulating the decay and transport of *E. coli* within the lake (Papers III and IV). The hydrodynamic model was calibrated using measured data on vertical temperature distribution. The model illustrated that wind conditions as well as seasonal stratification and mixing processes influence the contaminant spread within the lake. Based on the modelling results, the contamination sources that contributed the most to the concentrations at the water intake were identified. The developed hydrodynamic model of the lake was also used to obtain a short-term forecast of the microbial water quality at the water intake (Paper IV). As an outcome of these modelling studies, recommendations for water producers regarding risk reduction management were formulated.

For the river Göta älv, hydrodynamic modelling was used to provide input for discharge-based QMRA (Paper V). The concentrations of norovirus were characterised in wastewater discharges from a WWTP. Then, the transport of norovirus within the river was simulated using a hydrodynamic model. Based on the predicted concentrations at the water intake and the health targets, the required norovirus reduction by a DWTP was calculated using QMRA. The required reduction was compared with the estimated treatment performance of this DWTP. It was concluded that the treatment performance was adequate to produce safe drinking water, but depended strongly on the chlorine disinfection of the water.

2. BACKGROUND

2.1. Drinking water supply system

The drinking water supply system in the developed world usually consists of a water source, a DWTP and a piped distribution system (Fig. 1). Raw water is abstracted from a water source, treated at the DWTP and then transported in the distribution system to the consumer. Raw water can be abstracted from surface (rivers, streams, lakes) and groundwater (underground aquifers) sources. The selection of the best protected water source is a key step in providing safe drinking water since the most protected source waters will be the easiest and the cheapest to transform into safe drinking water (Medema et al. 2003).

The treatment of raw water usually consists of a number of microbial barriers that are designed to remove or inactivate microbial pathogens. The number of microbial barriers depends primarily on the quality of the raw water (Stanfield et al. 2003). Processes for the removal of microbes from water include: pre-treatment (any process to modify microbial water quality before, or at the entry to, a DWTP); coagulation, flocculation and sedimentation/flotation; granular filtration; slow sand filtration (LeChevallier and Au 2004). Disinfection processes used in drinking water treatment to inactivate microbes are: pre-treatment oxidation, in which oxidants are added to water early in the treatment process; primary disinfection, which is important because granular filter media do not remove all microbial pathogens from water; secondary disinfection used to maintain the water quality achieved at the DWTP throughout the distribution system up to the tap (LeChevallier and Au 2004).

The distribution system must provide a secure barrier to post-treatment contamination of drinking water during its transport to the consumer. Recontamination of microbiologically safe drinking water in the distribution system may occur due to damage of the integrity of the distribution system and the resulting penetration of faecal contamination. Penetration of faecal contamination can occur through: infiltration of contaminated sub-surface water; backflow of contaminated surface water; contamination of open drinking water storage reservoirs; line construction and repair (Robertson et al. 2003). In addition, microbial quality of the water in the distribution system can deteriorate when the bacteria remaining after treatment grow on residual nutrients and form biofilms (Robertson et al. 2003).

2.2. Pathogens and faecal indicators

Potential pathogens in drinking water systems include bacteria, viruses, protozoa and helminths. The effects of these pathogens on human health vary in severity from mild gastroenteritis to severe and sometimes fatal diarrhoea, dysentery, hepatitis and typhoid fever (WHO 2011). The main known causative agents of waterborne disease outbreaks in the developed world are: the bacterial pathogens *Shigella*, *Legionella*, *E. coli* O157/H7, *Campylobacter*, *Salmonella*; the viral pathogens norovirus and hepatitis A virus; protozoan pathogens *Giardia* and *Cryptosporidium* (Blasi et al. 2008, Craun et al. 2006, Schuster et al. 2005). However, despite thorough investigations the agent is often not identified, even though laboratory analyses are available (Craun et al. 2006). Most of the pathogens that can cause

waterborne disease outbreaks are introduced into the drinking water systems by human or animal faeces (WHO 2011).

Since the testing of water for pathogens is limited due to its complexity and cost, faecal indicators are usually used to detect the presence of faecal contamination in water. The criteria for faecal indicators are that they should not be pathogens themselves and should: be universally present in faeces of humans and animals in large numbers; not multiply in natural waters; persist in water in a similar manner to faecal pathogens; be present in higher numbers than faecal pathogens; respond to treatment processes in a similar way to faecal pathogens; and be readily detected by simple, inexpensive methods (WHO 2011).

Faecal indicators that are used in drinking water systems include total coliforms, *E. coli* and thermotolerant coliforms, intestinal enterococci, *Clostridium perfringens*, and coliphages (somatic and F-RNA) (WHO 2011). Since total coliforms include species that can grow in water environments, they are not useful as an indicator of faecal contamination in natural waters. *E. coli* and thermotolerant coliforms are a subset of the total coliform group. *E. coli* is considered to be the most suitable indicator of faecal contamination, since it is present in human and animal faeces in high numbers and is rarely found in the absence of faecal contamination. Although thermotolerant coliform species other than *E. coli* can include environmental organisms, in most circumstances, thermotolerant coliforms are composed predominantly of *E. coli*. Therefore, thermotolerant coliforms are regarded as acceptable but a less reliable indicator of faecal contamination. Intestinal enterococci can also be used for indication of faecal contamination, since they are typically excreted in the faeces of humans and other warm blooded animals, and most species do not multiply in water environments. *C. perfringens* has been proposed as an indicator of enteric viruses and protozoa, since it produces spores that are exceptionally resistant in water environments. Coliphages have been reported as a useful indicator to assess the behaviour of enteric viruses in water environments, since they share many properties, such as composition, morphology, structure and mode of replication, with human viruses (WHO 2011).

While traditional faecal indicators, such as total coliforms, *E. coli* and intestinal enterococci, give a general indication of fresh faecal contamination, *Bacteroidales* genetic markers can be used to indicate the human or ruminant origin of faecal contamination. Several *Bacteroidales* assays have been proposed and compared for the identification of host-specific human and ruminant faecal matter (e.g. Bernhard and Field 2000, Converse et al. 2009, Kildare et al. 2007, Layton et al. 2006, Layton et al. 2013, Raith et al. 2013, Reischer et al. 2013, Reischer et al. 2007, Reischer et al. 2006, Stricker et al. 2008). These assays are based on the detection of *Bacteroidales* 16S rRNA host-specific genetic markers.

As indicated by the criteria for faecal indicators, an understanding of the decay processes in the water environment is required for the proper use of faecal indicators, including the *Bacteroidales* markers (Field and Samadpour 2007). The decay of traditional faecal indicators has been extensively studied during the past decades (e.g. Crane and Moore 1986, Davies and Evison 1991, Kim and Hur 2010, Medema et al. 1997, Noble et al. 2004). However, MST using faecal *Bacteroidales* markers is a fairly new approach, and relatively few experiments

have been carried out to determine their decay (e.g. Bell et al. 2009, Dick et al. 2010, Okabe and Shimazu 2007, Walters and Field 2009). The fact that the decay of these markers in relation to standard indicators is poorly known is a major limitation in the interpretation of MST data from field studies (Field and Samadpour 2007).

The decay of *Bacteroidales* markers, as well as of faecal indicators in general, is expected to be site-specific and depends strongly on environmental conditions, such as temperature, salinity, exposure to sunlight, predation, and physical and chemical water properties (e.g. Bell et al. 2009, Dick et al. 2010, Okabe and Shimazu 2007). In this study the term decay refers to the loss of culturability of faecal indicators or the degradation of their genetic matter depending on the measurement technique.

2.3. Hydrodynamic modelling of microbial water quality

There are two major types of modelling approaches in the field of water quality: empirical models and complex mechanistic models. Empirical models tend to be site-specific, since they rely on the statistical relationship between observed parameters and pathogen concentrations. Mechanistic models link a hydrodynamic model with a mathematical model describing microbial dynamics. Mechanistic models are often adaptable for different locations and changing environmental factors, but have high data requirements (Dyble et al. 2008). This thesis focuses on the mechanistic models that simulate hydrodynamics and microbial water quality in the water source.

Hydrodynamic modelling has been applied to simulate the microbial water quality in various types of water sources, including rivers, estuaries, lakes and coastal areas (some examples are mentioned in Table 1). However, this type of modelling has mainly been used to study the (bathing) water quality of recreation sites (Table 1). There are also several examples of using this type of modelling in the context of shellfish harvesting and drinking water production (Table 1). However, hydrodynamic modelling is by far not as widely applied in the context of drinking water research (yet), as it is in studies on recreational water quality.

Hydrodynamic modelling has been widely applied to simulate the fate and transport of traditional faecal indicators (Table 1). However, relatively few studies have focused on modelling the spread of pathogens within water sources (Table 1), mainly due to a lack of data on pathogen concentrations.

Table 1 Applications of hydrodynamic modelling to simulate microbial water quality

Model	Indicator/Pathogen ^a	Study area	Reference
3D & fate	<i>E. coli</i>	Tsuen Wan beaches, Hong Kong	Chan et al. (2013) ^b
1/2D & fate	ENT	Severn Estuary, Bristol Channel, UK	Gao et al. (2013) ^b
3D & fate	rotavirus	Estuaries in New Zealand	McBride et al. (2012) ^{b,c}
2D & fate	FC	Danshui Estuary, Taiwan	Liu and Huang (2012) ^e
1D & fate	<i>E. coli</i>	Sonora River, Mexico	Robles-Morua et al. (2012) ^b
3D & fate	<i>E. coli</i>	Lake Michigan, US	Ge et al. (2010, 2012a, 2012b) ^b
2D & fate	ENT	Beach in Miami, Florida, US	Zhu et al. (2011) ^b
3D & fate	<i>E. coli</i>	Lake Michigan, US	Thupaki et al. (2010) ^b
2D & fate	FC	Malad Creek, Mumbai, India	Vijay et al. (2010) ^e
3D & fate	<i>E. coli</i>	Charles River, US	Hellweger and Masopust (2008) ^b
3D & fate	<i>Cryptosporidium</i> , TC, FC, <i>E. coli</i> , ENT, coliphages	Myponga Reservoir and Sugarloaf Reservoir, Australia; Billings Reservoir, Brazil	Hipsey et al. (2008) ^d
3D & fate & empirical	<i>E. coli</i>	Charles River, US	Hellweger (2007) ^b
2D & fate	<i>E. coli</i> , coliphages	Cotentin Peninsula, France	Riou et al. (2007) ^c
3D & fate	FC	Seine Estuary, France	Garcia-Armisen et al. (2006) ^e
2D & fate	FC, TC	Irvine Bay, UK	Kashefipour et al. (2006) ^b
2D & fate	<i>E. coli</i> , ENT	Lake Michigan, US	Liu et al. (2006) ^b
3D & fate	<i>Cryptosporidium</i>	Myponga Reservoir, Australia	Brookes et al. (2006), Hipsey et al. (2004) ^d
2D & fate	TC, <i>E. coli</i> , ENT	Talbert Marsh, Huntington Beach, US	Sanders et al. (2005) ^b
2/3D & fate	FC	South Wales coast, UK	Harris et al. (2004) ^b
3D & fate	FC	Quincy Bay, US	Li et al. (2003) ^b
3D & fate	FC, ENT, <i>C. perfringens</i> , <i>Salmonella</i> , <i>Cryptosporidium</i> , <i>Giardia lamblia</i> , enterovirus	Island of Oahu, US	Connolly et al. (1999) ^b

^a Abbreviations used in the table are: FC – faecal coliforms, TC – total coliforms, ENT – intestinal enterococci. ^b Recreational water quality. ^c Shellfish harvesting. ^d Drinking water production. ^e Environmental water quality.

3. METHODOLOGY

3.1. Study area

3.1.1. Lake Rådasjön

Lake Rådasjön is located on the west coast of Sweden. The surface area of the lake is approximately 2 km² and the catchment area of the lake is 268 km². The maximum water depth in the lake is 24 m. The main inflow into the lake is the river Mölndalsån (Figure 1). The water flow in the river Mölndalsån varies from 1 to 20 m³/s and the average water flow is approximately 4 m³/s.

Lake Rådasjön constitutes the main water source for the city of Mölndal (60 000 consumers) and a reserve water source for the city of Gothenburg (500 000 consumers). The raw water intakes for the city of Mölndal and the city of Gothenburg are located in the north-western part of the lake (Figure 1) at 15 m and 8 m depths, respectively.

Lake Rådasjön is subject to contamination from various faecal sources (Figure 1). Faecal contamination enters the lake through emergency wastewater discharges from the pumping station Pixbo Päls and from a pumping station located near the stream Vällbäcken, which enters the lake. These emergency discharges occur several times a year, due to hydraulic overloads or technical failures within the sewer network. The faecal contamination in the lake can also originate from the on-site sewers, which were designed for sludge removal. These on-site sewers do not meet legal requirements regarding treatment performance and provide little to no microbial reduction. The effluent from these on-site sewers is continuously released into a stream that enters the lake close to the water intakes. Moreover, faecal contamination can enter the lake through the inflow from the river Mölndalsån, which transports contamination from various sources, mainly emergency sewer overflows and on-site sewers, located in its upstream catchment area. In addition, faecal contamination can enter the lake with stormwater runoff from an urban area located close to the lake. Furthermore, faecal matter can be released from a cattle grazing area and can reach the lake after a short transport in a small stream.

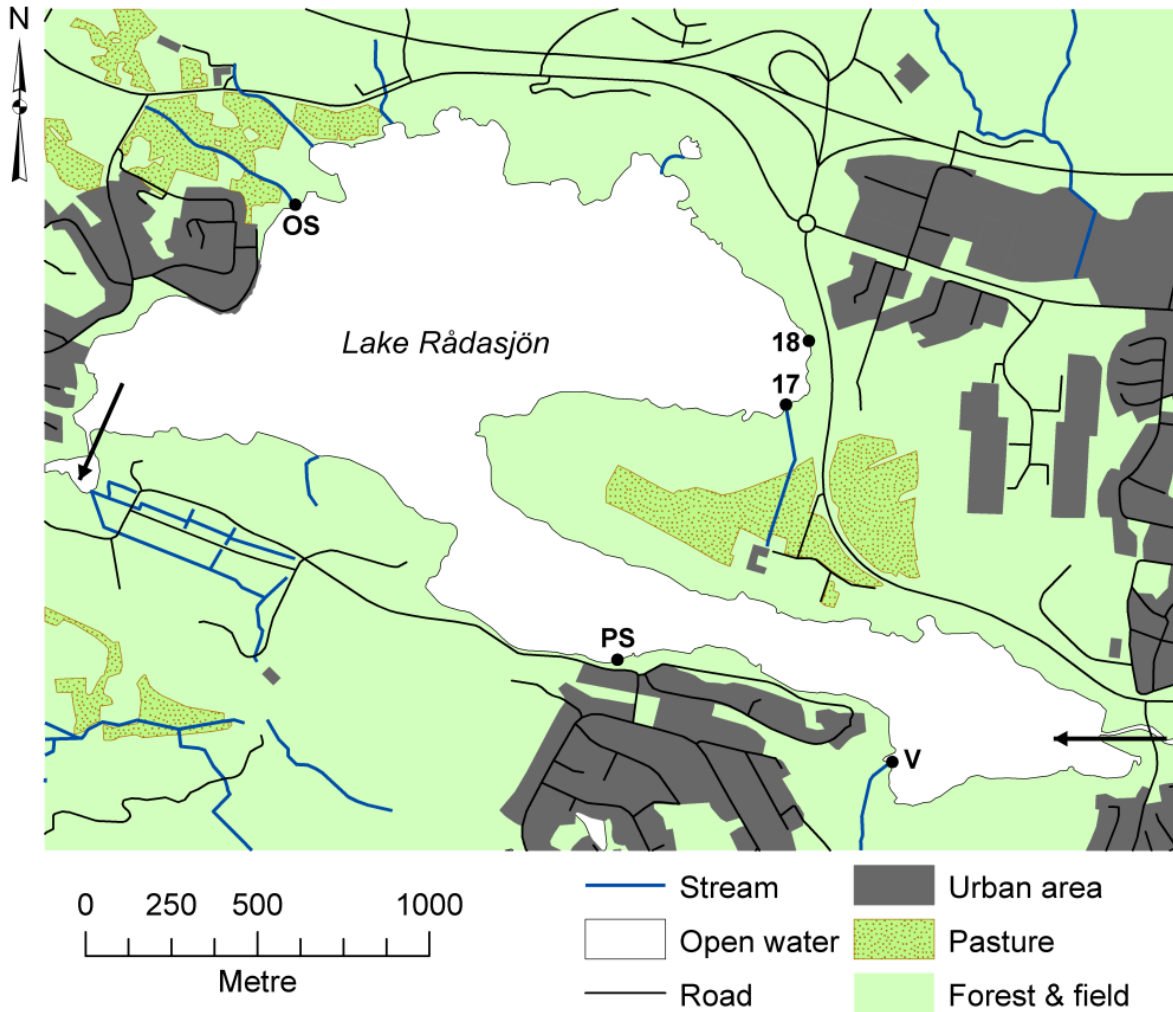


Figure 1 Map of Lake Rådasjön. Contamination sources around the lake are: on-site sewers (OS), stormwater runoff from an urban area (18), stormwater runoff from a cattle grazing area (17), Pixbo Päls wastewater pumping station (PS), the stream Vällbäcken that transports discharges from a wastewater pumping station (V). Arrows show inflow from the river Mölndalsån and outflow to Lake Stensjön.

3.1.2. The river Göta älv

Göta älv is a river that drains Lake Vänern into the strait Kattegat at the city of Gothenburg on the west coast of Sweden (Figure 2). The total catchment area of the river Göta älv is approximately 50 000 km², which constitutes approximately 10 % of the area of Sweden. The part of the catchment area that is located downstream of Lake Vänern is approximately 3500 km². The length of the river between the outflow from Lake Vänern and the mouth of the river is 93 km. The vertical drop of the river is approximately 44 m. The water flow in the river Göta älv is regulated by several hydropower stations (Figure 2) and varies strongly; the average and the maximum water flows are approximately 550 and 1000 m³/s, respectively. Upstream of the island Hisingen, the river splits into two branches; the northern branch – Nordre älv – transports from 2/3 to 3/4 of the total water flow, the southern branch keeps the name Göta älv and runs towards the city of Gothenburg (GÄVVF 2006).

The river Göta älv is used for many purposes, among which are drinking water production, transportation, hydropower, fish farming and sport fishing. The river is used as a water source for the drinking water supply of approximately 700 000 consumers in several municipalities, among which Gothenburg with approximately 500 000 consumers. Along the river there are five raw water intakes. The water intake for the city of Gothenburg is located the most downstream (Figure 2).

Between Lake Vänern and the Gothenburg water intake, the river Göta älv receives wastewater from approximately 100 000 persons. Approximately 95 % of this wastewater is treated at municipal WWTPs, while 5 % is treated by on-site sewer systems (GÄVVF 2006). On the stretch between Lake Vänern and the Gothenburg water intake, there are eight WWTPs that use the river for the disposal of treated wastewater (Figure 2).

In this project, the river Göta älv was studied with respect to the water quality at the Överby water intake in Trollhättan (Paper V) and the Lärjeholm water intake in Gothenburg (Sokolova et al. 2012) (Figure 2).

The Överby DWTP produces drinking water for approximately 49 000 consumers in the municipality of Trollhättan. The Överby DWTP employs the following treatment steps: coagulation/flocculation, rapid sand filtration, slow sand filtration and free chlorine disinfection. The virus contamination at the intake can be caused by discharges into the river from faecal sources located upstream the Överby DWTP: the Holmängen WWTP and the wastewater pumping stations.

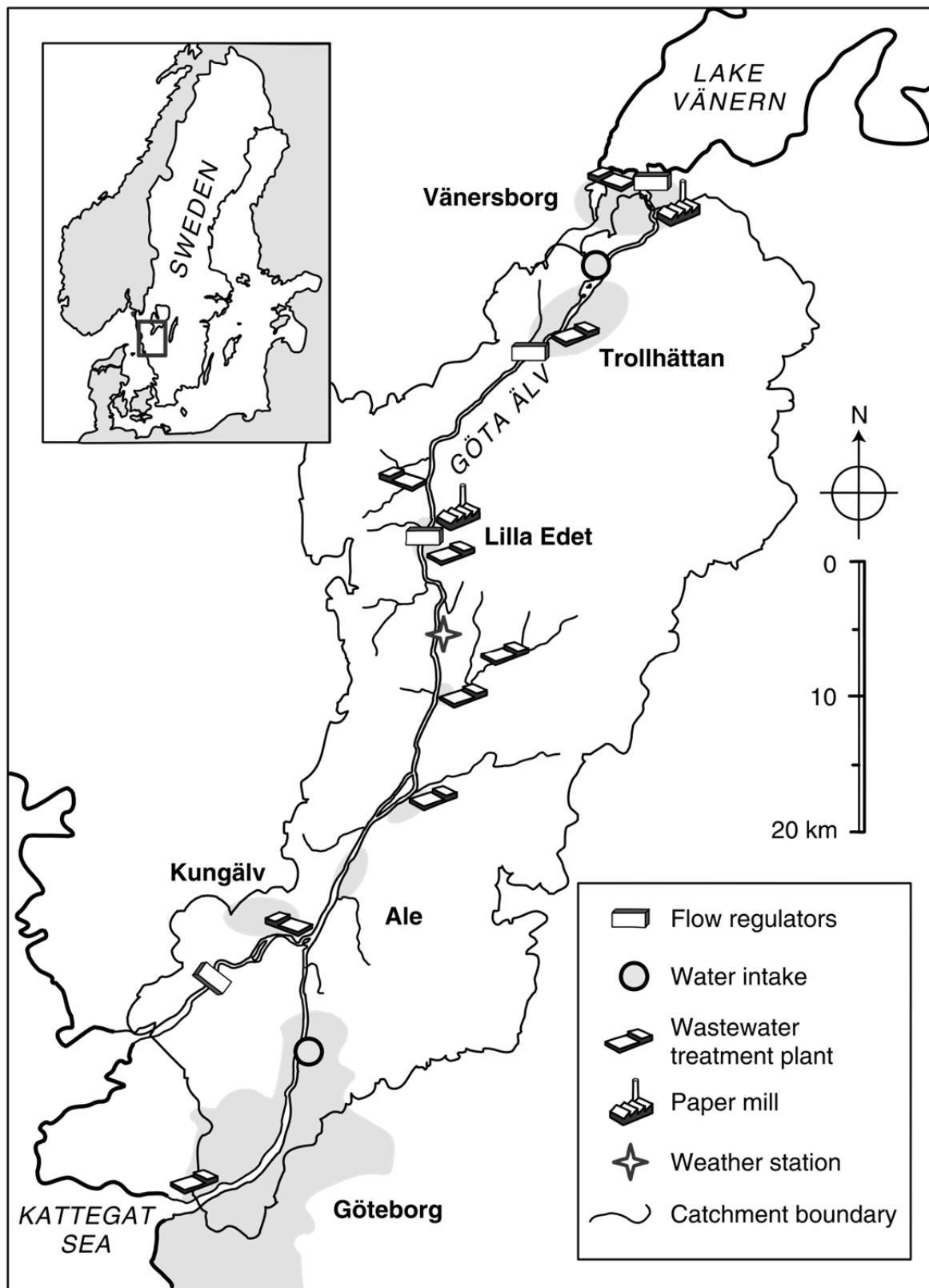


Figure 2 Map of the river Göta älv. Reproduced from (Åström et al. 2007b).

3.2. Microcosm experiment

In order to describe the spread of faecal contamination in a water source, data about the decay of faecal indicators are necessary. The decay of faecal indicators is expected to be site-specific and depends strongly on environmental conditions (Bell et al. 2009, Dick et al. 2010, Okabe and Shimazu 2007). Therefore, a microcosm experiment (Paper I) was performed to study the decay of total coliforms, *E. coli*, intestinal enterococci, somatic coliphages and *Bacteroidales* host-specific genetic markers (BacH and BacR) in water samples taken from Lake Rådasjön.

The microcosm experiment consisted of three trials that were conducted outdoors during two-week periods in March, August and November 2010. The time periods were chosen in order to capture the varying light and temperature conditions during the early spring, summer and winter in Sweden. Two microcosms were set up, one exposed to natural light (light microcosm) and another protected from light (dark microcosm) (Figure 3).

Microcosms were constructed in aquaria filled with water from Lake Rådasjön and inoculated with untreated wastewater and bovine faecal matter. Water from Lake Rådasjön was collected from a landing stage (20 m distance from the shore) at 1.5 m water depth. Untreated wastewater was collected from the wastewater pumping station Pixbo Päls, from which emergency overflows to the lake can occur. Ten samples of bovine faecal matter were collected from ten animals of different age and sex. Bovine faecal slurry was prepared by mixing 60 g of faecal matter (6 g from every sample) in 300 mL sterile deionised water. Each microcosm was constructed by adding 2.5 L of untreated wastewater and 100 mL of faecal slurry to the aquarium, followed by filling up with lake water (approximately 20 L). The volumes of inocula for the microcosms were chosen to provide high initial concentrations of all studied indicators (Walters and Field 2009), including somatic coliphages.

The experimental arrangement was placed in the vicinity of Lake Rådasjön, next to one of the DWTPs of Gothenburg. The experimental site was partly shadowed, but exposed to sunlight during several hours in the middle of the day. The temperature, oxygen content and circulation in the microcosms were regulated.

The three trials commenced on 15 March, 16 August and 15 November 2010 and lasted 14 days each. One sample was taken from each microcosm at around noon on days 0, 1, 2, 3, 4, 7, 10 and 14. The samples were analysed for total coliforms, *E. coli* bacteria, intestinal enterococci, somatic coliphages, BacH and BacR.



Figure 3 Microcosm experiment arrangement. Left – microcosms without lids; right – the microcosms covered with lids.

Furthermore, the water temperature in the microcosms was monitored at 10 minute intervals during each experimental period. Time series of total solar radiation in Gothenburg during each experimental period were obtained from official environmental measurements performed by the city of Gothenburg.

The detailed description of the microcosm arrangement, performed microbial analyses, as well as data analyses, can be found in Paper I.

3.3. Hydrodynamic modelling

To simulate the water flows in Lake Rådasjön (Papers I – IV) and the river Göta älv (Paper V), a three-dimensional time-dependent hydrodynamic model MIKE 3 FM (DHI 2011a) was used. The MIKE 3 FM model is based on the numerical solution of three-dimensional incompressible Reynolds averaged Navier-Stokes equations using Boussinesq and hydrostatic assumptions (DHI 2011a). The model consists of continuity, momentum, temperature, salinity and density equations, and is closed using a turbulent closure scheme (DHI 2011a).

In order to simulate the decay and transport of the faecal contamination, the microbial water quality model ECO Lab (DHI 2011b) was coupled to the hydrodynamic model. ECO Lab uses flow fields from the hydrodynamic model to calculate the concentrations of the faecal indicators and pathogens in the water source.

The modelling domains were approximated with prisms (triangles in the horizontal plane) using a flexible mesh approach. The length of the triangles' sides varied from approximately 40 to 90 m, and was adjusted to describe the coastline and bathymetry. Vertically, the water sources were approximated with layers of varying thickness. This thickness was adjusted to describe the physical processes in the water sources, taking into account that a greater number of layers increases the computational time.

In the ECO Lab model, the decay in the water source due to temperature and sunlight is described by Equation 1 (Mancini 1978):

$$\frac{dC}{dt} = -k_0 \cdot \theta_s^{Sal} \cdot \theta_l^{Int} \cdot \theta_T^{(Temp-20)} \cdot C \quad (\text{Equation 1})$$

where t is the time; C is the concentration of faecal indicator or pathogens; k_0 (1/day) is the decay rate at 20°C for a salinity of 0 ‰ and darkness; θ_s is the salinity coefficient for the decay rate; Sal (‰) is the salinity; θ_l is the light coefficient; Int (kW/m²) is the light intensity integrated over depth; θ_T is the temperature coefficient for the decay rate; $Temp$ (°C) is the water temperature. The coefficients in Equation 1 were estimated based on the results of the microcosm experiment (Paper I) and the literature data.

To distinguish between the influences of different contamination sources on the water quality at the intake, the contamination spread from every source was modelled separately.

The model setup is summarised in Table 2. The detailed descriptions of the models for Lake Rådasjön and the river Göta älv can be found in Papers I – IV and Paper V, respectively.

Table 2 Model setup for Lake Rådasjön and the river Göta älv

Model setup	Lake Rådasjön (Papers I – IV)	The river Göta älv (Paper V)
Simulations	real situations, forecast, scenarios	scenarios
Simulation time periods	months, years	days
Density formulation	function of temperature	barotropic
Horizontal eddy viscosity	Smagorinsky formulation	Smagorinsky formulation
Vertical eddy viscosity	k-epsilon formulation	k-epsilon formulation
Boundary conditions	water flow, surface elevation	water flow, surface elevation
Initial conditions	surface elevation	surface elevation
Driving forces	meteorological conditions	none
Microbial water quality	<i>E. coli</i> , BacH/BacR, norovirus, <i>Cryptosporidium</i> , <i>E. coli</i> O157/H7	norovirus
Microbial decay	microcosm experiment, literature values	none (conservative approach)
Calibration/validation, hydrodynamics	using measured temperature profiles	using measured surface elevation ^a
Validation, microbial water quality	using measured <i>E. coli</i> concentrations	none

^a The hydrodynamic model of the river Göta älv downstream the Lilla Edet hydropower station was validated using the measured water surface elevation in the river (Sokolova et al. 2012).

4. RESULTS AND DISCUSSION

4.1. Decay and transport of faecal contamination in drinking water sources

The decay of faecal indicators, and BacH/BacR genetic markers, in the water environment was investigated in the outdoor microcosm trials performed in March, August and November (Paper I). No statistically significant differences were observed between the persistence of the genetic markers and the other faecal indicators. It was concluded that the persistence of BacH and BacR genetic markers equals or even exceeds the reported persistence of bacterial and viral pathogens, but is below the reported persistence of *Cryptosporidium* (Allwood et al. 2003, Medema et al. 1997, Obiri-Danso et al. 2001, Walters and Field 2009).

During the August trial, the persistence of the faecal indicators was significantly shorter than during the March and November trials. No statistically significant differences in persistence were registered between the March and November trials. Moreover, no statistically significant differences in persistence were observed between dark and light microcosms; this is consistent with several earlier studies (Bae and Wuertz 2009, Boehm et al. 2009, Dick et al. 2010, Walters and Field 2009). However, temperature was significantly correlated with persistence levels; this was also confirmed by earlier studies (Ballesté and Blanch 2010, Bell et al. 2009, Crane and Moore 1986, Dick et al. 2010, Mancini 1978, Medema et al. 1997, Okabe and Shimazu 2007). The persistence of microbial contamination in the lake is shorter during summer months, when the water temperature is higher.

The modelling results showed that the contaminant transport in Lake Rådasjön is affected by wind conditions (Papers I, III and IV). Wind speed and direction influenced the time it takes for contamination to reach the water intakes (Paper III). Southeast winds caused higher contaminant concentrations at the water intakes than southwest winds (Paper I). In the absence of wind or when the lake is covered by ice, contaminant transport occurs very slowly (Paper III).

The contaminant transport is also affected by the vertical temperature stratification of the lake (Papers I and III). A thermocline, which separates the epilimnion and hypolimnion, is present in the lake from May until September (Paper III). During this time, the contamination stays above the thermocline, in the epilimnion. Starting from October, the lake is well mixed from top to bottom. The winter stratification is weak and is unlikely to have a major impact on transport processes (Paper III).

In the river Göta älv, in the studied part between the Vargön (Vänernborg) and Trollhättan hydropower stations (Figure 2), the contaminant transport is driven by the water flow in the river (Paper V). According to the hydrodynamic model, the transport time in this part of the river is short. It took between 2 and 40 hours before the peak concentration arrived at the water intake, depending on the flow conditions in the river (Paper V).

4.2. Microbial water quality in drinking water sources

The concentrations of faecal indicators and pathogens at the water intakes in Lake Rådasjön varied strongly over time (Papers II, III and IV). Both the modelling results and the measured data showed that the highest concentrations were observed during October – March, while the lowest concentrations were observed during summer (Papers II and III). The concentrations at the water intakes are lower during summer due to (i) a faster decay caused by increased water temperatures (Paper I) (Ballesté and Blanch 2010, Bell et al. 2009, Crane and Moore 1986, Dick et al. 2010, Mancini 1978, Medema et al. 1997, Okabe and Shimazu 2007), (ii) stratified conditions in the lake (Paper III) and (iii) generally lower contaminant loads from the faecal sources (Paper III). During summer months, the concentrations at the 15 m intake are lower than at the 8 m intake, due to the temperature stratification of the lake (Paper I).

The results provided information on the relative contribution of different faecal sources to the concentrations at the water intakes in Lake Rådasjön. MST and hydrodynamic modelling suggested that mitigation measures should focus on faecal sources of human origin (Paper I). The main contributors to the *E. coli* concentrations at the water intakes were the on-site sewers and the river Mölndalsån (Figure 1, Papers I – IV). Other important sources were the emergency discharges from the wastewater pumping stations (Figure 1, Papers I – IV).

Furthermore, the contamination sources (on-site sewers, emergency discharges from the Pixbo Päls pumping station, stormwater runoff from the urban and the cattle grazing areas) were compared in terms of their contribution to the pathogen concentrations at the water intake in Lake Rådasjön (Paper II). The modelling results showed that, under endemic conditions, the on-site sewers were the source that contributed the most to the norovirus concentrations at the water intake. Under epidemic conditions, the on-site sewers contributed the most to both the norovirus and *Cryptosporidium* concentrations at the intake.

The contributions from the diffuse sources (the urban and the cattle grazing areas) to the concentrations at the water intakes in the lake were generally much smaller than from the identified point sources (Papers I and II).

In the river Göta älv, regular (continuous) discharges of treated wastewater from the Holmängen WWTP were an important source of norovirus at the Överby water intake (Paper V). The predicted concentrations at the water intake caused by these regular discharges were similar to the concentrations caused by discharges of untreated wastewater during loading (overflow) events. These results are consistent with the results of an earlier study on the loads of faecal contamination to the river Göta älv (Åström et al. 2009). This situation is partly explained by the high norovirus concentrations in treated wastewater, caused by low (below 0.5 Log₁₀) norovirus reduction at the Holmängen WWTP. Earlier studies of Swedish WWTPs have also shown low norovirus reduction (Nordgren et al. 2009, Ottoson et al. 2006).

The QMRA results indicated that the performance of the Överby DWTP was adequate to produce safe drinking water (Paper V). However, the norovirus reduction by the DWTP was heavily dependent on the effective chlorine disinfection treatment step. The results showed

that there is a risk for poor norovirus reduction by the other treatment steps at the DWTP (coagulation/flocculation, rapid sand filtration and slow sand filtration).

4.3. Applicability of hydrodynamic modelling

The hydrodynamic model of Lake Rådasjön was calibrated and validated using measured data on the temperature distribution in the lake (Paper III). The calibrated model described the vertical temperature profiles in the lake adequately. The Pearson correlation coefficient was 0.99 ($p < 0.001$). The absolute mean difference between the simulated and measured temperature was 0.3 °C.

The hydrodynamic model of the river Göta älv downstream the Lilla Edet hydropower station, was validated using the measured data on the water surface elevation (Sokolova et al. 2012). The validation showed that the model described the measured data adequately. The Pearson correlation coefficient was 0.99 ($p < 0.001$). The absolute mean difference between the simulated and measured water surface elevation was 0.03 m.

The modelling output in terms of time series of *E. coli* concentrations in the lake were compared to the measured data (Papers III and IV). On some occasions, the results corresponded with the measured *E. coli* concentrations (Papers III and IV). However, on some occasions the model failed to describe registered peaks in *E. coli* concentrations at the water intake (Paper III). The underestimation of the *E. coli* concentrations at the intake is likely to be caused by an underestimation of the *E. coli* load to the lake, and not by the limitations of the model. The modelling results were linearly dependent on the assumptions regarding the contaminant load.

When scenarios are simulated (Papers I, II and V), validation of the modelling results is, strictly speaking, not possible. However, the simulated BacH and BacR (Paper I) and *Cryptosporidium* (Paper II) concentrations were in agreement with field observations.

Often calibration and validation are limited by a lack of measured data on microbial water quality. Levels of microbial contamination are event-driven and, thus, highly variable over time (e.g. Brookes et al. 2004, Westrell et al. 2006, Åström et al. 2007a). However, due to the limitations of analytical methods, the temporal resolution of measured microbial data is often low, and the measurement uncertainty is often high (Köster et al. 2003). Furthermore, when hypothetical scenarios are simulated, the modelling results, by definition, cannot be compared with observed data.

The model's ability to provide short-term forecasts was evaluated by comparing the results of forecast and hindcast simulations (Paper IV). The comparison showed that the magnitude of the simulated concentrations was similar, but there were discrepancies in terms of temporal variations. These discrepancies were caused by the differences between the forecasted and observed meteorological data.

The model proved to be applicable to simulate the decay and transport of the microbial contamination in drinking water sources (Papers I – V). The model can be used to study the factors that affect the contaminant decay and transport. Understanding contaminant dynamics

helps to identify periods of increased risks and provides information on the transport time before the contamination arrives at the water intake.

The model proved to be very useful to characterise the microbial water quality at the water intake (Papers I – V). Information on the microbial water quality at the intake is needed to estimate and manage the risks for consumer health. This thesis illustrated that this modelling approach can be used to:

- capture the spatial and temporal variability in microbial concentrations and, thus, address the limitations of monitoring;
- estimate the concentrations at the water intake in the absence of measurements, or when the concentrations are below the detection limits;
- perform short-term forecasts of the microbial water quality in drinking water sources;
- test scenarios, in order to describe the effects of hypothetical conditions.

The model was also useful to assess the relative influence of various contamination sources on the microbial water quality at the water intake (Papers I – V). Moreover, the model improved the interpretation of MST data. Information on the relative contributions from various contamination sources is needed in order to prioritise mitigation measures.

The model provided useful input for the QMRA of health risks and water treatment requirements.

5. CONCLUSIONS

In this chapter, the conclusions are presented in relation to the objectives of the thesis.

Objective: To describe the decay and transport of the microbial contamination in drinking water sources

Microcosm experiments showed that the decay of BacH and BacR genetic markers was dependent on water temperature and similar to the decay of other faecal indicators (Paper I). It was concluded that the persistence of BacH and BacR equals or exceeds the persistence of bacterial and viral pathogens, but is below the persistence of protozoan pathogens (Paper I).

The hydrodynamic modelling results showed that the contaminant transport in Lake Rådasjön is strongly affected by wind conditions and by the vertical temperature stratification of the lake (Papers I – IV). In the river Göta älv, the contaminant transport is driven by the water flow in the river (Paper V).

Objective: To characterise the microbial water quality in drinking water sources

The microbial water quality in Lake Rådasjön and the river Göta älv was successfully characterised by the developed hydrodynamic models (Papers I – V). The concentrations of faecal indicators and pathogens at the water intakes in these drinking water sources were estimated. The estimates showed that the microbial water quality in the studied water sources is variable and event-driven.

Objective: To compare the influence of different contamination sources on the microbial water quality in drinking water sources

Both for Lake Rådasjön and the river Göta älv, human faecal sources were the main contributors to the contamination at the respective water intakes. For Lake Rådasjön, the hydrodynamic model showed that on-site sewers and the river Mölndalsån are the most important contamination sources (Papers I – IV). The modelling results for the river Göta älv indicated that discharges of treated wastewater from the Holmängen WWTP are an important source of norovirus at the Överby water intake (Paper V).

Objective: To estimate health risks for drinking water consumers, using hydrodynamic modelling in combination with QMRA

The QMRA based on the results of the hydrodynamic modelling indicated that the Överby DWTP produces safe drinking water with respect to norovirus (Paper V). However, the norovirus reduction was heavily dependent on effective chlorine disinfection, with a risk for poor reduction by other treatment steps. Thus, to limit health risks, it is highly important to ensure effective chlorine disinfection at all times.

Objective: To evaluate the applicability of hydrodynamic modelling (in combination with MST and QMRA) to describe and predict the microbial water quality in drinking water sources

Hydrodynamic modelling proved to be a very useful approach to describe and predict the microbial water quality in drinking water sources (Papers I – V). This approach was successfully applied (i) to study the factors that affect the contaminant spread in the water source (Papers I – V), (ii) to capture the spatial and temporal variability of the microbial water quality (Papers I – V), (iii) to provide short-term forecasts (Paper IV), and (iv) to test hypothetical scenarios (Paper II). Furthermore, the hydrodynamic modelling improved the interpretation of the MST data (Paper I) and provided input for QMRA (Paper V).

The comparison of the modelling results and measured data showed that the model can adequately simulate the hydrodynamic situation in water sources (Paper III and Sokolova et al. (2012)). For the microbial water quality, the model validation was somewhat limited by a lack of measured data for input and validation (Papers I – V).

Aim: To describe the microbial water quality in drinking water sources in order to facilitate the provision of safe drinking water

The aim of this thesis was fulfilled by addressing the objectives. As explained above, hydrodynamic modelling is a useful approach to describe the microbial water quality in drinking water sources. Knowledge on the microbial water quality in drinking water sources is needed to estimate and manage the risks for consumer health. Information on the contribution of different faecal sources to the contamination at the water intake is needed to implement and prioritise appropriate mitigation measures. Understanding the spatial and temporal variability of the microbial concentrations is needed in order to optimise the monitoring of raw water quality, and to optimise the treatment at the DWTP. The ability to test scenarios and provide forecasts is essential to estimate the consequences of – and prepare for – future changes. In conclusion, knowledge on the microbial water quality in drinking water sources is essential for the provision of safe drinking water.

6. RECOMMENDATIONS

6.1. Hydrodynamic modelling

The setup of the model should be derived from the research problem. The developed model needs to be suitable to simulate the processes that are relevant for the research problem. In this way, the choice of software, assumptions and simplifications, computational mesh, simulation periods, input data, as well as model parameterisation need to be adjusted to each specific research question.

Hydrodynamic modelling can be computationally expensive. The computational time is dependent on the resolution of the computational mesh and the number of dimensions (1D, 2D or 3D). The mesh resolution and the number of dimensions need to be chosen based on the research problem. In this study, a 3D model was set up for Lake Rådasjön, since the vertical stratification of the lake influences contaminant transport. For the river Göta älv, both 2D (unpublished data) and 3D (Paper V) models were set up. The choice of the number of dimensions depended on the geometry of the studied parts of the river and on the distance between the contamination sources and the water intake. The assumption of no vertical gradient in concentrations, implied by the 2D setup, is suitable when the distance between the contamination source and the water intake is long. Furthermore, the longer the periods of time that are simulated, the higher the computational time becomes.

By means of hydrodynamic modelling, it is possible to simulate situations that occurred in the past, or to test hypothetical scenarios. When situations in the past are simulated, the modelling results can be compared with measured data, in order to calibrate and validate the model. On the other hand, when hypothetical scenarios are tested, the reliability of the results cannot be properly checked, due to an inherent lack of measured data. However, these scenarios can be very useful to study the effects of individual factors, e.g. wind (Paper I) or location of contamination sources (Paper II) on microbial water quality.

6.2. Management of drinking water sources

The modelling study of Lake Rådasjön was conducted as part of a project in cooperation with water producers in the cities of Gothenburg and Mölndal, as well as representatives of the neighbouring municipality of Härryda. The results of the project have important implications for the management of Lake Rådasjön as a drinking water source (Papers I – IV).

- Since the modelling results showed that the on-site sewers located in the vicinity of the lake are an important source of contamination at the water intakes, the decision has been made to remove the on-site sewers and to connect the houses to the municipal sewer network. This process has started and, hopefully, will be completed in the near future.
- Since the modelling results showed that the river Mölndalsån strongly influences the microbial water quality in the lake, the frequency of monitoring the microbial water quality in the river Mölndalsån has been considerably increased. Nowadays, samples are collected at least on a weekly basis. When there are suspicions of malfunctions in the sewer network upstream, more frequent sampling is performed.

- Communication between water producers in Gothenburg and the upstream municipality of Härryda was established through their cooperation within this project. When water producers detect increased concentrations in the river Mölndalsån, they contact the municipality of Härryda. Then, the municipality of Härryda examines the sewer network for possible malfunctions. This has proven effective, since on different occasions several malfunctions were detected and removed. The municipality of Härryda has also established an improved reporting routine regarding the emergency discharges from the sewer network.
- The results provided decision-support data for future revisions of the extent of the water protection area around Lake Rådasjön.
- The developed model can be used to simulate the effects of various events on the water quality in the lake in near real-time regime and even provide short-term forecasts (Paper IV). This information can facilitate decisions regarding the closure and re-opening of water intakes.

Based on the obtained results, the following recommendations were formulated:

- include the catchment area of the river Mölndalsån into the water protection area;
- implement at-line monitoring of the *E. coli* concentrations in the river Mölndalsån – this will enable early detection of increased loads of faecal contamination and may indicate malfunctions in the sewer network;
- improve the maintenance of the sewer network in the vicinity of the lake and the methods for early detection of emergency discharges in the sewer network.

For the river Göta älv, the results of the hydrodynamic modelling and QMRA have important implications for understanding and managing the norovirus risks associated with the Överby DWTP (Paper V):

- The regular discharge of treated wastewater from the Holmängen WWTP is an important source of norovirus loading at the water intake. Measures to reduce the norovirus concentration in the treated wastewater could provide an effective reduction in norovirus loading to the river under baseline conditions.
- The hydrodynamic modelling results provided information regarding the response time available between an upstream event and the norovirus load reaching the water intake. Notification strategies between the WWTP and the DWTP would allow for (i) selective abstraction to avoid the most contaminated source water, and/or (ii) proactive monitoring of coagulant dosages to ensure an optimal plant operation.
- Given what is known about norovirus loading in the river Göta älv and the expected performance of the treatment, the Överby DWTP is able to produce safe drinking water.
- Meeting safe drinking water targets at the Överby DWTP is strongly dependent upon effective chlorine disinfection. Limited information was available regarding the hydraulic behaviour of the disinfection contactor. Hence, the hydraulic behaviour of the contactor needs to be characterised to ensure a suitable minimum residence time.

Based on the obtained results, the following recommendations were formulated:

- improve the norovirus reduction at the Holmängen WWTP;
- establish notification strategies between the municipalities of Vänersborg and Trollhättan regarding the upstream discharges of wastewater;
- ensure proper hydraulic behaviour of the disinfection contactor at the Överby DWTP.

7. FUTURE RESEARCH

The next step will be to simulate the decay and transport of somatic coliphages in the studied water sources. *E. coli* bacteria constitute the most commonly used indicator for the presence of faecal contamination in water. However, due to the limited persistence of *E. coli*, the time periods for which faecal contamination can be detected using *E. coli* is limited. Somatic coliphages persist longer in the water environment than *E. coli* (Paper I). Due to their high persistence, somatic coliphages can be used to detect the presence of faecal contamination for longer time periods. Somatic coliphages could thus indicate the possible presence of more persistent pathogens, such as viruses.

In order to better estimate the load from different contamination sources to the water source, a catchment-scale model can be used. The catchment-scale model can be used to simulate the spread of contamination from diffuse sources (e.g. agricultural and cattle grazing areas, and on-site sewers) within the catchment area (Coffey et al. 2010, Tang et al. 2011). Moreover, the contaminant load from emergency sewer overflows can be estimated using a model of the sewer network (Marchis et al. 2013). The output of the catchment-scale model can be used as input for the hydrodynamic model, in order to simulate the spread of contamination within the water source (Bougeard et al. 2011, de Brauwere et al. 2013, Marchis et al. 2013).

In order to prioritise mitigation measures, the modelling results could be combined with cost-benefit analysis (Benedetti et al. 2013). This would be particularly beneficial for the river Göta älv, because it is exposed to a great number of different contamination sources.

The possibilities to develop simpler hydrodynamic models (e.g. Larsen et al. 2013) for simulating the influence of contamination sources on the water quality in the studied water sources can be investigated. Simpler models, which are easier to use, less computationally expensive, less data-intensive, and do not require a software license, could be convenient to be used by water producers in their daily operation. Possibly, these models could even be used for near real-time simulations of the microbial water quality (Chan et al. 2013), which could greatly benefit the health of drinking water consumers.

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