Dynamics of microbial pollution in aquatic systems

Matthew Richard Hipsey

B.Sc (Hons) (Environmental Science)
M.Eng.Sc (Environmental Engineering)

This thesis is presented for the degree of
Doctor of Philosophy of
The University of Adelaide

School of Earth and Environmental Sciences
May 2007

Table of Contents

List of Figures

List of Tables

Abstract

Microbial pollution of surface waters and coastal zones is one of the foremost challenges facing the water industry and regulatory authorities. Yet despite the concern and increasing pressures on water resources in both developed and developing countries, understanding of microbial pollutants in the aquatic environment is fairly scattered. There is a need for an improved ability to quantify the processes that control the fate and distribution of enteric organisms to support decision-making and risk-management activities. The aim of this thesis has been to advance the understanding of the dynamics of microbial pollution in aquatic systems through review, experimentation and numerical modelling.

Initially, a new module for simulating the protozoan pathogen, *Cryptosporidium*, was developed and implemented within a three-dimensional (3D) coupled hydrodynamic-water quality model (ELCOM-CAEDYM). The coupled 3D model was validated against a comprehensive dataset collected in Myponga Reservoir (South Australia), and without calibration, performed to a high degree of accuracy. The investigation then sought to examine the experimental dataset in more detail and found a significant difference between protozoan pathogens and the bacterial and viral indicators. To examine the role of bacterial association with particles in more detail, a second experimental campaign was carried out in Sugarloaf Reservoir (Victoria). This campaign was used to gain insights into the association of coliform bacteria with suspended sediment and to quantify their sedimentation dynamics based on *in situ* measurements. Using an inverse technique, particle profile data was used to create a simple Lagrangian model that was applied to back-calculate the sedimentation rates of the coliform bacteria and the fraction that were attached to the particles. The results indicated that 80 – 100% were associated with a small-sized clay fraction. This result was in contrast with the *Cryptosporidium* dynamics in Myponga Reservoir, where it was concluded that oocysts did not settle with the inorganic particles.

These findings indicated the current models for simulating the array of organisms of interest to regulatory authorities are inadequate to resolve the level of detail necessary for useful predictions and risk management. Large differences between the protozoa, bacteria and phages were being observed due to different particle association rates and sedimentation dynamics, order of magnitude differences in natural mortality rates, and different sensitivity to sunlight bandwidths. The original model implemented within CAEDYM was therefore rewritten to be more complete and generic for all microbial pollutants and different types of aquatic systems. The model was built using a generic set of parameterizations that describe the dynamics of most protozoan, bacterial and viral organisms of interest. The parameterizations dynamically account for sensitivities to environmental conditions, including temperature, salinity, pH, dissolved oxygen, sunlight, nutrients and turbidity, on the growth and mortality of enteric organisms.

The new model significantly advances previous studies in several areas. First, inclusion of the growth term allows for simulation of organisms in warm, nutrient rich environments, where typical die-off models tend to over-predict loss rates. Second, the natural mortality term has been extended to independently account for the effects of salinity and pH, in addition to temperature. The salinity–mediated mortality has also been adapted to account for the nutrient status of the medium to simulate the importance of nutrient starvation on the ability of an organism to survive under osmotic stress. Third, a new model for sunlight-mediated mortality is presented that differentially accounts for mortality induced through exposure to visible, UV-A and UV-B bandwidths. The new expression has capacity to simulate the photo-oxidative and photo-biological mechanisms of inactivation through included sensitivities to dissolved oxygen and pH. Fourth, the model allows for organisms to be split between free and attached pools, and sedimented organisms may become resuspended in response to high shear stress events at the water-sediment interface caused by high velocities or wind-wave action. Fifth,

the enteric organism module has been implemented within the bio-geochemical model CAEDYM, thereby giving it access to dynamically calculated concentrations of dissolved oxygen, organic carbon, and suspended solids, in addition to pH, shear stress and light climate information.

Without adjustment of the literature derived parameter values, the new model was validated against a range of microbial data from three reservoirs that differed in their climatic zone, trophic status and operation. The simulations in conjunction with the experimental data highlighted the large spatial and temporal variability in processes that control the fate and distribution of enteric organisms. Additionally, large differences between species originate from variable rates of growth, mortality and sedimentation and it is emphasized that the use of surrogates for quantifying risk is problematic. The model can be used to help design targeted monitoring programs, examine differences between species and the appropriateness of surrogate indicators, and to support management and real-time decision-making. Areas where insufficient data and understanding exist are also discussed.

This work contains no material which has been accepted for the award of any other degree or diploma in any university or other tertiary institution and, to the best of my knowledge and belief, contains no material previously published or written by another person, except where due reference has been made in the text.

I give consent to this copy of my thesis being made available in the University Library.

The author acknowledges that copyright of published works contained within this thesis (as listed below) resides with the copyright holder(s) of those works.

Signed …………………………………………………………………………. Date…………………

Acknowledgements

Numerous people have been either directly or indirectly instrumental in enabling the completion of this thesis. This would not have been possible without the patience and help of my two main advisors Dr. Justin Brookes and Dr. Jason Antenucci. I am also grateful to Jason for the freedom he has given me, whilst juggling the dual demands of working and completing this thesis. I would also like to offer a special thanks to Assoc. Prof. George Ganf at the University of Adelaide for facilitating my candidature whilst working remotely at CWR.

Much of the work and data presented in this thesis was made possible through a grant from the American Water Works Association Research Foundation (AwwaRF), under project #2752 "Hydrodynamic distribution of pathogens in lakes and reservoirs" (view project summary online at: http://www.awwarf.org/research/topicsandprojects/execSum/2752.aspx). In addition to AwwaRF, I would like to acknowledge the contribution by the project Chief Investigator, Mike Burch, from the Australian Water Quality Centre in Adelaide for his very competent management of this ambitious research project. The project also was supported with additional cash and in-kind funding support from the following organizations:

> CRC for Water Quality and Treatment
> Melbourne Water Corporation
> Sydney Catchment Authority
> South Australian Water Corporation

The advice of the Project Advisory Committee (PAC) – including Rhea Williamson, Ronald Coss, Robin Oshiro, Thomas Mahin and particularly Linda Reekie, the AwwaRF Project Manager, is also greatly appreciated.

Although much of the thesis focuses on modelling and numerical prediction of enteric organisms, a significant component relies on field data collected during two intensive field campaigns. Both the field campaigns were logistically challenging and involved a large effort from numerous people. For their contribution in making these campaigns successful, I would like to acknowledge: Peter Hobson for input into various aspects of the project, including assistance with the preparation of the QA Plan, and during field work for the validation studies; Leon Linden who made a significant contribution to the field work at Myponga Reservoir; Melita Stevens, Kathy Cinque and Karyn Hunter from Melbourne Water were instrumental in assisting to plan and carry out field work for model verification at Sugarloaf Reservoir; Warwick Grooby, Kerry Cabaretta and the Microbiology and Protozoology Laboratories at the Australian Water Quality Centre for their efforts in processing massive numbers of microbiological samples over a short period of time collected as part of model validation exercises; Rod Boothy, Alan Brown and Viv Allan provided excellent logistical support for field work at Myponga Reservoir. Data from Billings Reservoir in Brazil was provided courtesy of Companhia de Tecnologia de Saneamento Ambiental (CETESB).

At the Centre for Water Research at the University of Western Australia, I wish to acknowledge the contribution of Prof. Jörg Imberger and Dr. José Romero for their advice and input regarding model development and application. My thanks are also given to Jörg for his seemingly endless enthusiasm and support and for helping facilitate my completion of this thesis whilst still working at CWR. I also wish to acknowledge the opportunity offered to me early in my career, which was the custodianship of the model CAEDYM - much of this thesis would not have been possible if it was not for years of experience developing such a multi-disciplinary model and daily exposure to the CAEDYM source code.

Finally, I would like to thank my family; to my parents for teaching me curiosity and commitment, to my wife, Van, who has always been supportive, patient and forgiving, and to my son Daniel, who always knows how to make me smile.

Preface

The main body of this thesis is comprised of six chapters (2-7). Chapter 2 is preliminary hydrodynamic modelling work conducted on several reservoirs proposed for use during the research program. Although it may seem somewhat peripheral to the main focus of the thesis, it forms the backbone of many of the predictions presented later on since all the systems simulated depend on the integrity of the 3D hydrodynamic predictions. Additionally, this work was performed prior to the field campaigns, and so these simulations served as virtual environmental laboratories and enabled testing of hypotheses and sampling regimes prior to committing to the field experiments.

The remaining chapters (3-7) are independent papers written for journal publication. Each of these papers contains an introduction that includes a review of the relevant literature. To avoid unnecessary duplication, Chapter 1 does not seek to provide a comprehensive review of the literature pertaining to the entire thesis, but rather to place the individual papers in the context of the overall work. Similarly, Chapter 8 draws together the conclusions from each of the individual papers and serves to synthesize the individual chapters into a single body of work.

Chapter 3 has been published in the *International Journal for River Basin Management* as "A three dimensional model of *Cryptosporidium* dynamics for lakes and reservoirs – a new tool for risk management", by M.R. Hipsey, J.P. Antenucci, J.D. Brookes, M.D. Burch, R.H. Regel and L. Linden, Volume 2(3), pp. 181-197 (2004). Copyright for this paper belongs to the International Association for Hydraulic Research.

Chapter 4 has been published in the journal *Environmental Science and Technology* as "The relative value of surrogate indicators for detecting pathogens in lakes and reservoirs", by J.D. Brookes, M.R. Hipsey, M.D. Burch, R.H. Regel, L. Linden, C.M. Ferguson and J.P. Antenucci, Volume 39(22), pp. 8614-8621 (2005). Copyright for this paper belongs to the American Chemical Society.

Chapter 5 has been published in the *Journal of Water, Air and Soil Pollution* as "*In situ* evidence for the association of Total Coliforms and *Escherichia coli* with suspended inorganic particles in an Australian reservoir" by M.R. Hipsey, J.D. Brookes, R.H. Regel, J.P. Antenucci and M.D. Burch, Volume 170(1-4), pp. 191-209 (2006). Copyright of this article belongs to Springer Publishers.

Chapter 6 is in preparation for submission to the journal *Water Research* as "A generic, process-based model of microbial pollution in aquatic systems" by M.R. Hipsey, J.P. Antenucci and J.D. Brookes.

Chapter 7 is a brief summary article aimed at lake and reservoir engineers, and outlines the tools and options available for assisting with microbial pollution problems. It appeared in the periodical *LakeLine* as "Decision support tools for managing microbial pollution in lakes and reservoirs", by M.R. Hipsey, J.P. Antenucci, and J.D. Brookes, Volume 24(4), pp. 25-28 (2004).

Various components of the work have also been presented in other papers and at conferences, but have not been included in the thesis directly. These include:

- Antenucci, J.P., Brookes, J.D. and Hipsey, M.R. A simple model for quantifying *Cryptosporidium* transport, dilution and potential risk in reservoirs. *J. AWWA*, 97(1): 86-93 (2005).

- Brookes, J.D., Antenucci, J.P., Hipsey, M.R., Burch, M.D., Ashbolt, N.J. and Ferguson, C.M. Fate and transport of pathogens in lakes and reservoirs, *Environ. Intl.*, 30: 741-759 (2004).

- Brookes, J.D., Davies, C.M., Hipsey, M.R. and Antenucci, J.P. Association of *Cryptosporidium* with bovine faecal particles and implications for risk reduction by settling within water supply reservoirs. *Water and Health*, 4(1): 87-98 (2006).

- Hipsey, M.R., Antenucci, J.P. and Brookes, J.D. Coupling a *Cryptosporidium* fate model to a 3D hydrodynamic model: results from Myponga Reservoir, SA. *Australian Water Association 20th Convention - 2003 OzWater Conf.*, Perth, Western Australia, 2003.

- Hipsey, M.R., Brookes, J.D. Antenucci, J.P. and Burch, M.D. Field and modelling evidence for pathogen behaviour in drinking water reservoirs. *Australian Society for Limnology Annual Conf.*, Warnambool, Victoria, Australia, 2003.

- Hipsey, M.R., Antenucci, J.P., Brookes, J.D., Burch, M.D. and Regel, R.H. Simulation tools for minimizing pathogen risk in drinking water reservoirs. *6th International Conf. on Hydroinformatics*, Singapore, 2004.

- Hipsey, M.R., Antenucci, J.P. and Brookes, J.D. A new process-based model of enteric organism dynamics in natural waters. *7th International Conf. on Hydroscience and Engineering*, Philadelphia, USA, 2006.