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Enhancing Human Health through Improved Water Quality

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Table of Contents

Acknowledgements	ii
Disclaimer	ii
Details of Project Partners	iii
Executive Summary	vii
1 Background and Objectives	1
2 Research Approach, Actions and Results	3
2.1 Understanding the Dynamics of Microbial Contamination of Major Groundwater Sources and River Catchments	3
2.2 Understanding the Extent and Frequency of Contamination of Rural Group Water Supplies	9
2.3 The Application of Geographical Information Systems and Mathematical Modelling to Improve Understanding of Cryptosporidium Infection	10
2.4 Emerging Technologies for Detection and Tracking of Microbial Contamination of Water	13
2.5 Emerging Water Contaminants of Concern	14
3 Summary of Overall Project	18
3.1 Project Output	18
3.2 New Information	18
3.3 New Methods	18
3.4 Awareness	18
3.5 Capacity Building	19
3.6 Partnerships for Environmental Research	19
4 Conclusions from Research and Future Research Needs	20
5 Recommendations for Implementation and Uptake of Research Findings	21
References	23

Acronyms and Annotations	24
Appendix 1 Names of those Involved Directly in Project	25
Appendix 2 Selected Outputs of Project	26
Research Outputs	26
Conference Presentations (International Meetings)	27
Recognition/Acclaim for Research Work	29
Thesis Submissions	29
Outreach Programmes Delivered to Schools, General Public and Organisations	29
Media/Publicity	29

Executive Summary

Ireland's water resources are important from the perspective of amenity value, agriculture, industry and environmental sustainability, but most fundamentally they are an essential prerequisite for good health and well-being. Awareness that water quality and the general environment are central to the agenda of sustainability and equity in the health of the population was central to the design of the project, *Enhancing Human Health through Improved Water Quality*, which commenced in 2006. It is estimated that between 10 and 30% of the surface water and 15% of groundwater bodies in Ireland are at risk of failing to meet European Union Water Quality objectives; this is a major challenge for government.

Microbial parameters are the most important indicators of drinking water quality. The extent of microbial contamination of water sources, including groundwater sources, can change rapidly. The potential for rapid changes in levels of faecal contamination of severely vulnerable aquifers after rainfall events was demonstrated by this project – indicating the need for water-quality monitoring programmes that include sampling in different weather conditions and for treatment systems that have the capacity to cope with sudden surges in contamination.

This project developed an approach for categorising the susceptibility of groundwater sources to microbial contamination in Ireland. This tool may help authorities to assess the risk of contamination in specific aquifers. Mathematical modelling of water catchments to predict the occurrence of faecal contamination was also developed. The model developed is a significant advance in the field, which shows potential but requires further refinement before routine application.

A large percentage of the population of rural Ireland are dependent on group water supplies. The project demonstrated that water delivered to homes in the West of Ireland by some group water supplies is contaminated with faecal material most of the time. This is caused by contamination of the source and the failure of effective and consistent water treatment. Molecular methods that differentiate between faeces of human and ruminant origin indicate that the source

of contamination appears to be predominantly animals (ruminants). Furthermore, many of the *E. coli* bacteria contaminating these water supplies are resistant to one or several commonly used antibiotics. The findings underscore the necessity of progressing rapidly with measures to protect sources of group water supplies and to ensure effective and consistent treatment.

Cryptosporidium spp. are protozoan parasites associated with infectious gastroenteritis. The parasites represent a particular challenge in water treatment as they are relatively resistant to chlorination. This project used geographical information system (GIS) technology to investigate the relationships between variation in notified cases of cryptosporidiosis and water supply with regard to social deprivation and environmental factors. At the basic level, the system was valuable in presenting spatial information about cases of infection during a major waterborne outbreak of cryptosporidiosis in Galway in 2007. As GIS allows for the combination of many datasets, information on other diseases can similarly be analysed with the spatial data already present in the GIS. A mathematical model for the prediction of risk of waterborne cryptosporidiosis was also developed. The model highlights a critical role for source protection in preventing waterborne cryptosporidiosis and points to microfiltration as a particularly effective measure for removing *Cryptosporidium* from contaminated water. The model also suggests that operational failure in conventional water-treatment systems represents one of the greatest risks of water contamination and hence to human health. On this basis, it is suggested that the implementation of an appropriate physical infrastructure for water treatment *should be combined with a total quality management approach* to ensure consistent high standards in the operation of water-treatment systems to protect human health.

Traditional methods for monitoring the microbiological quality of water have some limitations that may be overcome through the application of molecular methods. This project has developed and piloted molecular methods for detecting specific bacterial (Verocytotoxigenic *E. coli*) and viral (Norovirus) pathogens in water. In addition, molecular methods have

been developed and applied to differentiate between human faecal contamination and ruminant faecal contamination. These methods have the potential to assist authorities in detecting pathogens that may have previously been missed and in defining more precisely the origin of faecal contamination in water sources.

Acquired resistance to antibiotics in bacteria is a growing human health problem. This project has demonstrated the substantial extent to which antimicrobial-resistant *E. coli* are now widely disseminated in the environment. For example, in some rural water supplies systems studied, from 6% to more than 80% of *E. coli* contaminating the water were resistant to the common antibiotic, ampicillin. Also of concern was the detection of *E. coli*, belonging to the category extended spectrum beta lactamase (ESBL) *E. coli* (resistant to a very wide range of antimicrobial agents) in treated wastewater and the detection on one occasion of *Enterococcus faecium* with high-level resistance to vancomycin in a rural water supply source. This most likely reflects

decades of overuse of antibiotics in human and animal health care. The project draws attention to the detection of *E. coli* and Enterococci with resistance to more recently introduced antibiotics, associated in particular with effluent related to major hospitals. In addition to the presence of antibiotic-resistant bacteria, the project showed evidence of residual antimicrobial activity in hospital effluent. This antibiotic activity may have implications for microbial biodiversity because it may inhibit the growth of some microbes and favour growth of other antibiotic-resistant bacteria in the environment.

This project provides new information that has informed a series of recommendations (across a broad range of areas) that can improve our aquatic environment and improve human health. This report represents one step towards the translation of this research into action for improved health. The researchers engaged in the project are happy to engage with partners to find ways to support such actions.

1 Background and Objectives

The flow of water into, through and out of our bodies is indispensable to life. As it flows, it can carry along with it chemicals and organisms that have a profound impact on our health. Through the course of evolution this flow of water between humans, animals and environment has become a critical mechanism for the transmission of many organisms. Much of the health gain of human populations in the twentieth century was achieved by control of this flow of water through the technologies of sanitation and water treatment. However, even now, the *Global Annual Assessment of Sanitation and Drinking Water* (World Health Organisation [WHO] 2012) reminds us that, on current projections for 2015, worldwide '605 million people would remain without access to an improved drinking-water source, and 2.4 billion people would be without access to improved sanitation facilities' and that 'billions will remain at risk or water, sanitation and hygiene related disease'.

The situation in Ireland is much more favourable than in many other parts of the world. Ireland's relatively abundant supply of fresh water constitutes a key resource in terms of its human health, economic, amenity and aesthetic value. Most people in Ireland have access to sanitation and to safe drinking water. The situation with respect to drinking water has shown progressive improvement in recent years as reflected in the Environmental Protection Agency (EPA) report, *The Provision and Quality of Drinking Water in Ireland A Report for the Year 2010* (EPA, 2010). Waterborne disease, when it occurs, is less likely to result in long-term health impacts or death because of better access to health care. Nevertheless, the situation is far from ideal both in terms of the protection of water sources from contamination and in ensuring safe drinking water for all.

Obligations with respect to protecting water quality in Ireland are specified in the European Commission (Water Policy) Regulations 2003 (S.I.722 of 233), which transposed the requirements of Directive 2000/60/EC into Irish law. This directive has established a Europe-wide framework for community action in the field of water policy (the Water Framework Directive [WFD]). The need for continuing action on water quality for

human health at the European level is reaffirmed in the Parma Declaration adopted in March 2010 in which Regional Priority Goal 1 is identified as 'Ensuring public health by improving access to safe water and sanitation' (Ministers and Representatives of Member States in the European Region of the World Health Organisation, 2010).

Available data indicate significant challenges in meeting Ireland's obligations to protect water sources. The EPA's *Ireland's Environment 2008* report (EPA, 2008) states that, of 972 instances of slight and moderate pollution, 360 were related to municipal sources including sewage and septic tanks (McGarrigle et al., 2008). Of 39 locations affected by serious pollution, municipal (mostly sewage) discharges are suspected to account for 21 instances and agricultural activities for 9 instances. Therefore, municipal sewage and diffuse agricultural sources continue to be the main threat to the quality of Ireland's surface waters. The *Water Quality in Ireland Report 2007–2009* again highlights the importance of these as sources of pollution in rivers and lakes in Ireland (EPA, 2010).

Drinking water quality in Ireland is regulated by the European Communities Drinking Water Regulations, 2007. The European Directive on the quality of water intended for human consumption (98/83/EC) was transposed into Irish law on 8 March 2007, and took effect on the same day. Although a large proportion of the urban population is supplied from public supplies delivering treated water, in rural areas many people depend on small, often voluntary, rural group water supplies or private wells. These supplies frequently draw on sources that are inadequately protected from contamination: the water entering the distribution system is often either not treated or is inadequately or inconsistently treated. It is encouraging to note that in the EPA report (EPA, 2010) *The Provision and Quality of Drinking Water in Ireland: A Report for the Years 2010* the number of private group water schemes where *E. coli* was detected dropped from 87 in 2009 to 56 in 2010. Nevertheless, 12% of private group water schemes were contaminated at least once in 2010.

The continuing vulnerability of the Irish population, even in urban areas, to the health impacts of microbial contamination of water sources was demonstrated dramatically during the period of this research project by a major waterborne outbreak of cryptosporidiosis in Galway in 2007. More generally, the continuing problems are reflected in the 2009 *Health Protection Surveillance Centre Annual Report*, which describes 10.5 notified cases of cryptosporidiosis per 100,000 population, 5.7 per 100,000 for Verotoxigenic *E. coli* and 42.6 per 100,000 for campylobacteriosis (Health Protection Surveillance Centre, 2010). Although drinking water is certainly not the only source of infection with these organisms, it is likely to be a significant contributor, as evident in the case of Verotoxigenic *E. coli*, with 12 outbreaks of this infection in 2009 attributed to drinking water. Furthermore, the number of notified cases is a very significant underestimation of the burden of disease given that the great majority of cases of acute gastrointestinal disease go undocumented and undiagnosed.

This report provides an overview of a large-scale project with the objective of providing evidence and developing methods to guide policy to improve human

health through improved water quality. This project also aimed to develop a partnership between academic researchers, local authorities and health care providers to enhance the capacity for research on environment and health. The establishment of a Centre for Health from Environment at the Ryan Institute, National University of Ireland (NUI) Galway represents an important expression of that developing capacity.

The major themes of the project were:

- 1 Understanding the dynamics of microbial contamination of major groundwater sources and river catchments.
- 2 Understanding the extent and frequency of contamination of rural group water supplies.
- 3 The application of GIS and mathematical modelling to improve understanding of *Cryptosporidium* infection.
- 4 The examination of the potential application of emerging technologies for detection and tracking of microbial contamination of water.
- 5 The study of specific emerging water contaminants of concern.

2 Research Approach, Actions and Results

The project was designed as a series of linked work-packages. The key challenges of this design were to ensure that:

- The research in the work-packages was integrated and cross-functional.
- The multi-disciplinary group of researchers maintained regular communication.
- Stakeholders in the local authorities, health care systems (health care providers, Department of Public Health Medicine, Environmental Health Officers), the wider public and the funding agency could see the value of the project and feel able to support it.

Communication among researchers and between researchers and the project management team was maintained through regular e-mail contact and face-to-face meetings. The provision of feedback on outcomes to partners outside of the academic community helped to ensure that support was available throughout the duration of the project.

2.1 Understanding the Dynamics of Microbial Contamination of Major Groundwater Sources and River Catchments

Groundwater is an important source of drinking water. Although generally at lower risk for contamination than surface water sources, the risk of contamination is significant.

2.1.1 Groundwater Susceptibility Matrix

Professor Vincent O'Flaherty and his group developed a Groundwater Susceptibility Matrix ([Table 2.1](#)) to facilitate nationwide monitoring and a comprehensive study of the microbiological quality of Irish groundwater systems. Nine test sites were chosen from a list of 108 sites broadly representative of public and private groundwater sources, from 15 counties, based on available historical data, site descriptions, maps and additional criteria. This data was entered into the matrix and each site given a vulnerability rating from 1 to 5 based on its vulnerability to contamination.

Table 2.1. Groundwater Susceptibility Matrix.

Aquifer category code ^b	Pathway susceptibility		Vulnerability ranking ^a
	Soil/subsoil depth (m)	Definition	
Rkc	0	Karst with point recharge	1 (S)
Rkd	<1	Karst with no point recharge	2 (E)
Rkd	1–3		
Rf & Lm	<1	Fissured aquifer	
LI, PI & Pu	<1	Low flow fissured	3 (H)
K	3–5	Karst with no swallow-holes	
Rf & Lm	1–3	Fissured aquifer	
LI, PI & Pu	1–3	Low flow fissured	
Lg & Rg	<1	Sand/gravel aquifers	4 (M)
Lg & Rg	1–3	Sand/gravel aquifers	
Rf & Lm	3–5	Fissured aquifer	
LI, PI & Pu	3–5	Low flow fissured	
Remaining areas	>5		5 (L)

^a Aquifer vulnerability number rating increases with decreasing severity. S = severe, E = extreme, H = high, M = medium, L = low.

^b R = regionally important (R) aquifers, locally important (L) aquifers, poor (P) aquifers, k = karstified bedrock, c = dominated by conduit, d = dominated by diffuse flow, f = fissured bedrock, g = extensive sand & gravel (Rg), m = bedrock which is generally moderately productive, l = bedrock which is generally unproductive except for local zones, u = bedrock which is generally unproductive.

The matrix showed that two supplies (one in Co. Clare and one in Co. Roscommon) were severely vulnerable to contamination: these were chosen for detailed monitoring during the project. An additional seven supplies (five private and two public) were chosen for monitoring from the other vulnerability categories in the matrix.

In addition, a series of control field sites, located at the Teagasc Environmental Research Centre, Johnstown Castle, Co. Wexford, were selected by the project team to evaluate the impact of soil type and the spreading of animal slurries on the breakthrough of bacterial indicators and phage to groundwater. This was to provide highly controlled data that supported the work of the overall project.

The nine supplies sites were monitored by both occasional (e.g. daily or weekly sampling) and intensive (hourly sampling) analysis for the presence of bacterial indicators of faecal pollution (Coliforms and *E. coli*).

The development and deployment of the Groundwater Susceptibility Matrix to monitor factors influencing the susceptibility of aquifers to contamination yielded several important findings. Firstly, the importance of factors (soil depth and properties of bedrock), which had been highlighted in the design of the matrix, for protecting underlying groundwater supplies from contamination was confirmed. For example, although evidence of faecal contamination was detected at least once in all aquifers tested, those with little overlying protection from soil cover were more vulnerable to contamination ([Fig. 2.1](#)). Local authorities can use source protection area boundaries as delineated by the Geological Survey of Ireland (GSI) and the EPA to monitor and assess local practices within protection zones that could potentially contribute to groundwater contamination.

The Groundwater Susceptibility Matrix may be of value to local authorities in highlighting the importance of specific factors in protecting underlying groundwater supplies. Faecal contamination was detected most commonly in those aquifers with little overlying soil protection. Use of source protection area boundaries would provide local authorities with a tool to monitor and assess local practices that could potentially contribute to groundwater contamination.

While the matrix can assist in assessing the vulnerability of a supply to contamination, it is not sufficient. This is because the results generated from this study highlighted not only key differences in the occurrence of faecal indicator organisms across aquifer vulnerability categories, but also the dynamic nature of the microbiological properties of water sources. Rapid pulses of *E. coli* and other faecal bacteria in groundwater can and do occur following heavy rainfall events in vulnerable groundwater supplies. This is because rainfall contributes to surface runoff and rapid infiltration into these supplies. This is highlighted clearly by coliform and *E. coli* data generated during the project's intensive monitoring study at Drumcliff ([Fig. 2.2a and b](#)). The spike in *E. coli* and coliform numbers shortly after rainfall is worthy of note. However, water-treatment plants generally monitor the microbial content of source and treated water on a daily, or less frequent, basis. Currently, turbidity is the main indicator of changes in water quality used by water-treatment facilities. Turbidity correlates well, but not absolutely, with microbial breakthrough: therefore, these rapid pulses of *E. coli*, which could represent a threat to public health, might not be detected using occasional unstructured microbiological sampling.

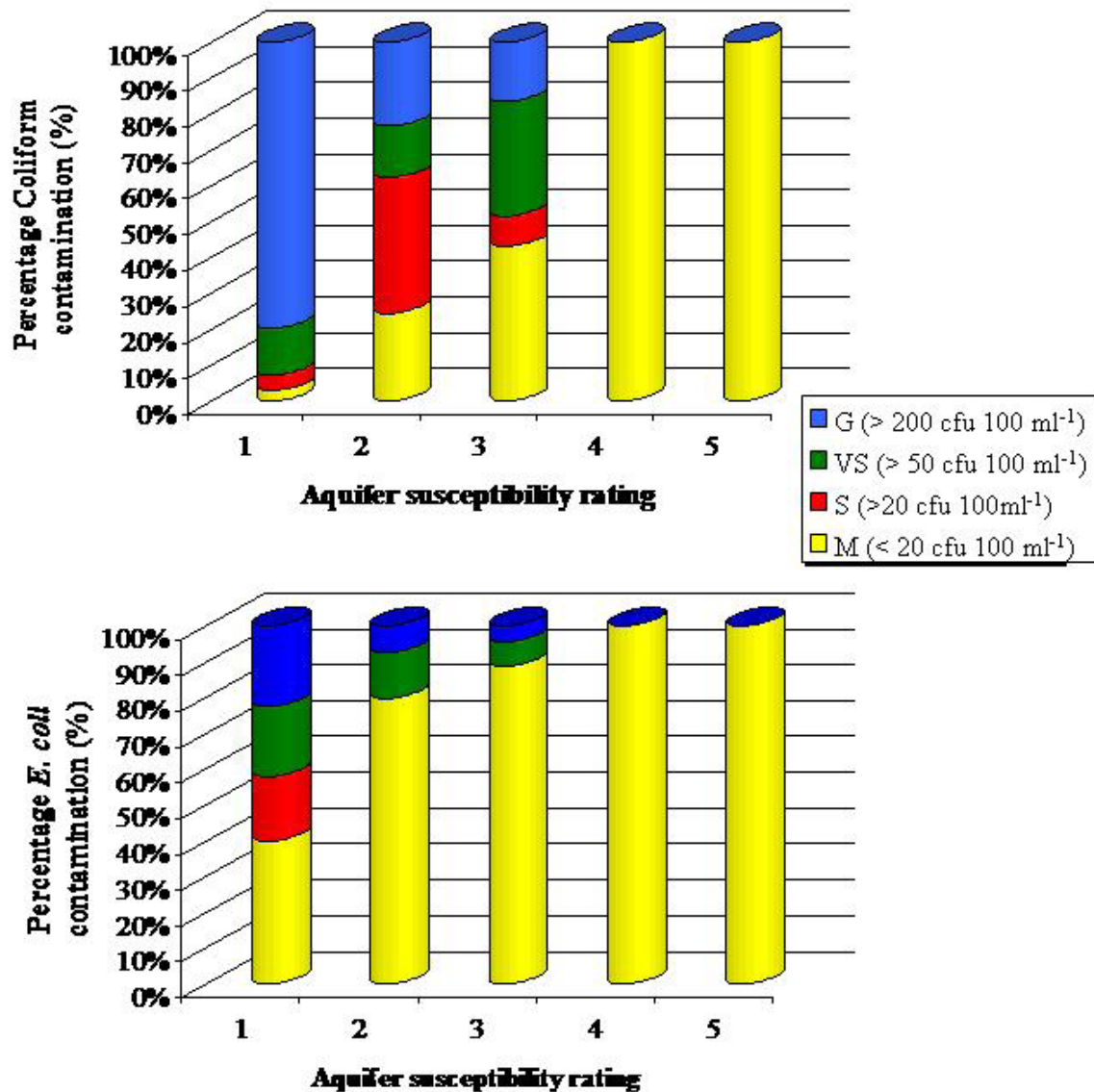


Figure 2.1. Level of groundwater contamination with (a) coliforms and (b) *E. coli* across the five aquifer vulnerability ratings assigned in the Groundwater Susceptibility Matrix.

Aquifer susceptibility ratings (1–5 where 1 is severe vulnerability and 5 is low vulnerability) are reported on the x-axis in both graphs. In the inset box M = moderate, S = serious, VS = very serious and G = gross pollution. CFU = colony forming units. Number of samples tested for each category are as follows S: n = 552; E: n = 120; H: n = 96; M: n = 24; L: n = 72.

This may have important implications for authorities responsible for water supply. Although turbidity does not correlate absolutely with microbial contamination, nevertheless, automated hourly turbidity monitoring systems may detect evidence of sudden surges in faecal contamination. In addition, routine microbiological sampling of groundwater sources

should be based on a structured plan that includes sampling after periods of heavy rainfall to ensure that relevant authorities have a clear picture of how heavy rainfall events influence the microbiological properties of the source. This is particularly true for those groundwater supplies that are categorised as severely vulnerable to contamination.

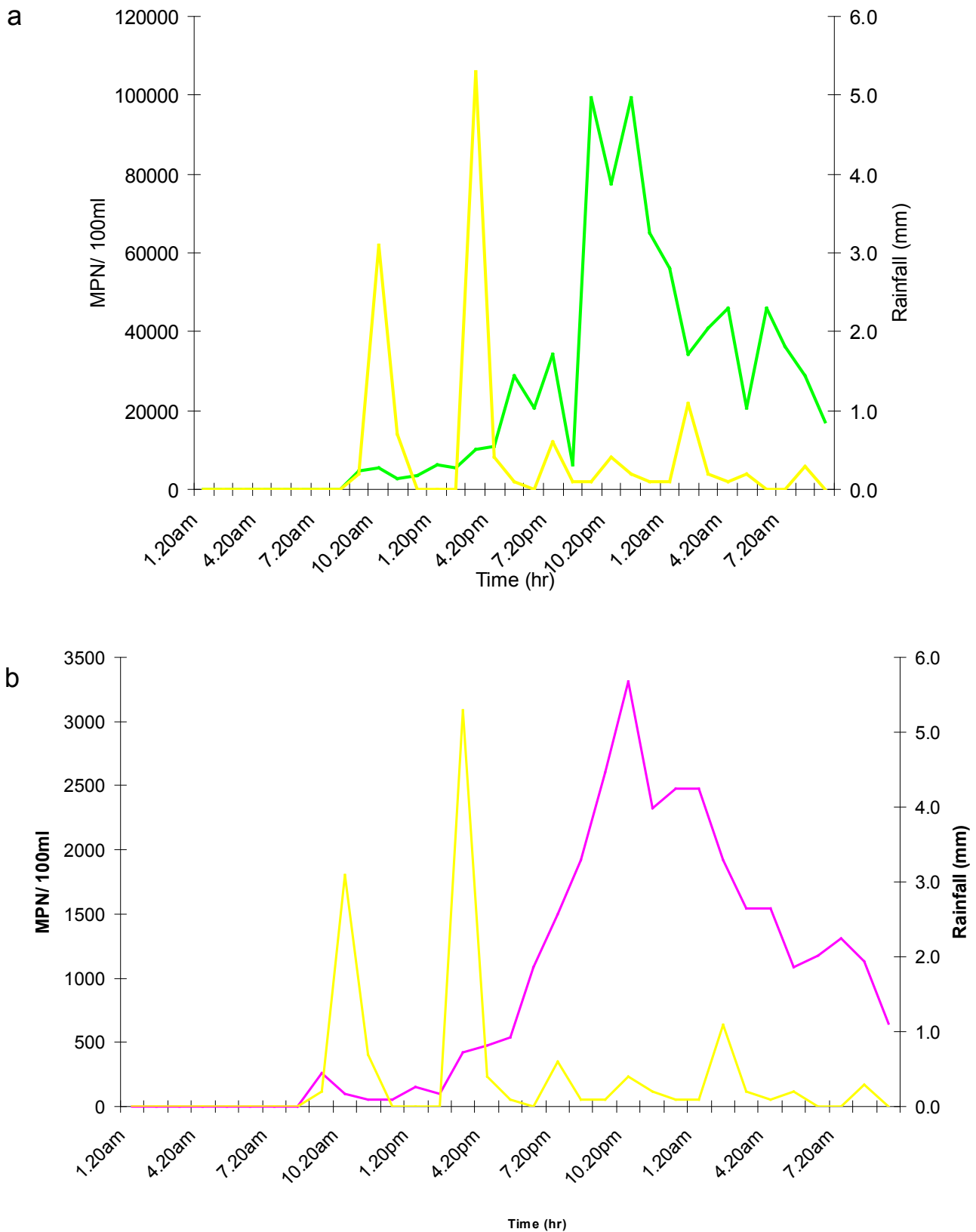


Figure 2.2a and b. Faecal microbial contamination in response to rainfall in Drumcliff.

MPN = Most probable number (of coliforms or *E. coli*). (a) *E. coli* (hourly MPN/100ml) and 2 (b) coliforms (hourly MPN/100ml). Yellow: Rainfall; Green: total coliforms; Pink: *E. coli*.

Most probable number refers to the estimated number of colony forming units/100ml based on the multiple tube method for enumeration.

Microbiological sampling of groundwater sources should be based on a structured plan that includes sampling after periods of heavy rainfall. This is particularly true for those groundwater supplies that are categorised as severely vulnerable to contamination. Systems for treatment of water from identified vulnerable supplies should be designed, assessed and operated so as to ensure that they have the capacity to cope effectively with transient surges in microbial contamination.

2.1.2 Mathematical Modelling

Another approach to managing the dynamic nature of the microbiological properties of water sources is to develop mathematical models to describe and predict the transport of potential contaminants into groundwater as rainwater travels through soil and rock. Thirteen quantitative simulation models identified from the previously published scientific literature that could potentially be used for modelling bacterial pollutants in agricultural watersheds were assessed (see Coffey et al., 2010 for additional details). Commonly used models were examined to determine their capacity to model water pollution and provide a good reference point for the microbial risk assessment of waterborne pathogens. It was found that no single model suits all modelling criteria. Pathogen predictions with these models have proved variable, and no model currently available was capable of accounting for all geological and hydrological factors and also for modelling the physical transport of bacteria in surface runoff. The SWAT (Soil and Water Assessment Tool) indicated the greatest potential as a predictive water-catchment tool using available Irish data.

Following the review of published data, a probabilistic model to describe the variation in parameters that affect water quality and put human health at risk was developed, using SWAT and ArcGIS (ArcSWAT). The study area was based on the River Fergus catchment, located in the west of Ireland. Recorded water-flow data over a two-year period was used for hydrologic calibration (2003) and validation (2004–2005). Based on information gathered regarding agricultural practice,

demographics and hydrological parameters, the model was run to predict variations in concentrations of *E. coli* at different times. The levels of *E. coli* predicted were then compared with the levels of *E. coli* actually measured from September 2005 to September 2006. The values for flow rates predicted using the models agree closely with the measured values (Fig. 2.3) (Coefficient of determination [R²] = 0.83, Nash-Sutcliffe efficiency [E] = 0.78) and indicate that the model provides satisfactory simulation of hydrologic processes within the catchment.

The correlation between observed and predicted *E. coli* numbers in the Drumcliff catchment area for the simulation period is illustrated in Fig. 2.4. The mathematical models developed to predict *E. coli* levels in water may be described as acceptable and satisfactory (based on criteria recommended by Moriasi et al., 2007); therefore, the project demonstrated the potential of this approach successfully. However, the extensive additional refinement and validation of the models required to ensure reliability in day-to-day use in water-quality management was beyond the scope of this project.

The same model was also used to model likely *Cryptosporidium* contamination events. The model indicated potential periods of high risk; however, unlike the *E. coli* model, validation data for *Cryptosporidium* estimates were not available.

The model developed in this study is a significant advance in the field and represents the first published attempt to model microbial contaminants in an Irish catchment. The model provides a basis for further development of catchment models, specifically for the prediction of *cryptosporidium* contamination in Irish watersheds.

Mathematical models may currently be of value in highlighting high-risk periods and regions, in enabling the selection and testing of risk-reduction strategies and in targeting sampling – thus helping to manage potential human exposure to pathogens. The study of the model allowed identification of areas in which

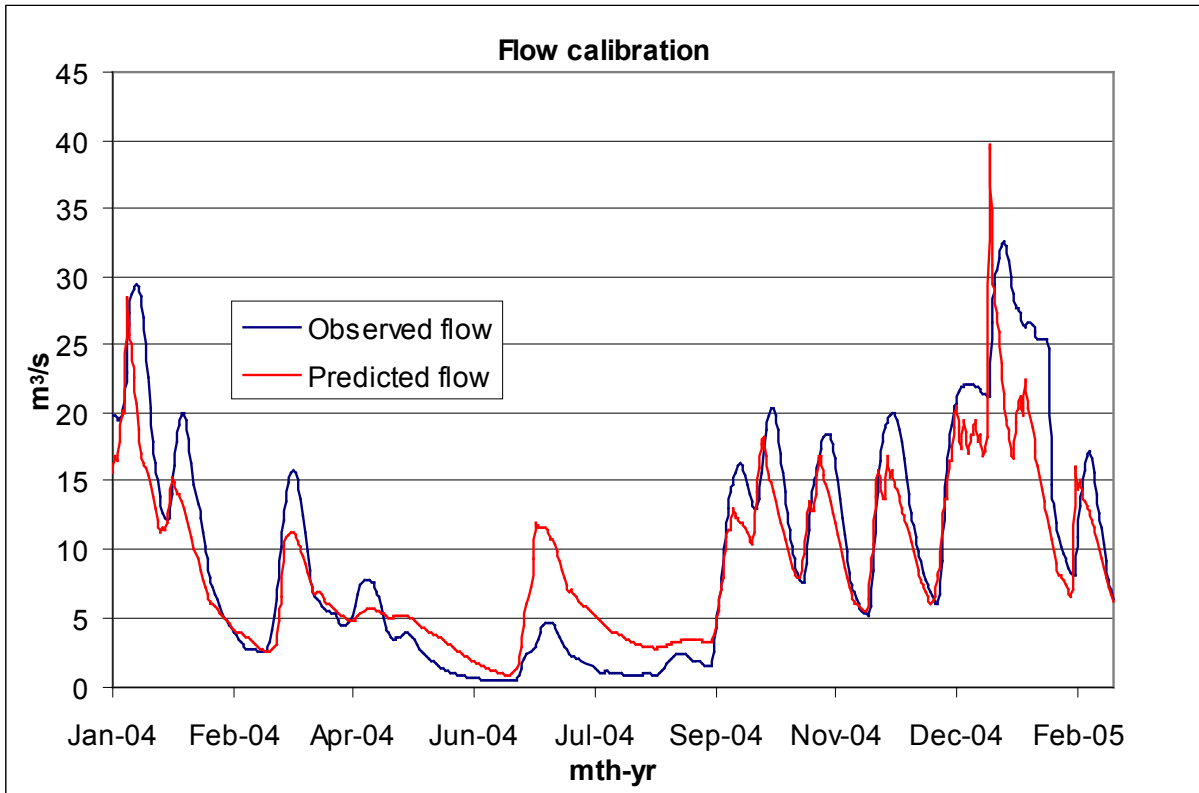


Figure 2.3. Observed flow and predicted flow of water in the River Fergus catchment for model validation period (January 2004–February 2005).

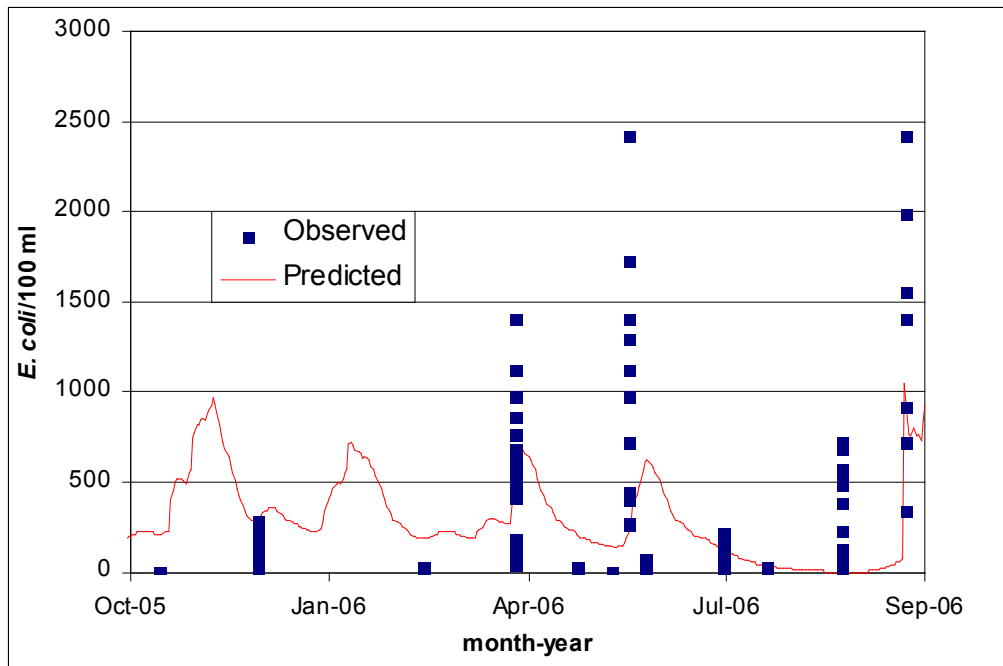


Figure 2.4. Observed and predicted most probable number of *E. coli* for the simulation period at the Drumcliff site. The correlation indicated only a general correlation and further refinement of the mathematical model is required.

further research is required to facilitate the refinement of such mathematical models, particularly for assessing the initial concentration of *E. coli* in human/animal waste. Extensive information from the monitoring of *E. coli* levels is required to ensure the best possible performance of mathematical prediction models. Model development is an iterative process and useful progress has been made in the development of a working model. Further refinement and complete validation of the model is required in order to predict *E. coli* numbers accurately; however, this was beyond the scope of this project.

2.2 Understanding the Extent and Frequency of Contamination of Rural Group Water Supplies

Large sections of the rural population depend on group water supplies for drinking water. Available evidence from occasional sampling indicates that water from many group water supplies fails to meet drinking-water microbiological standards. The pattern of faecal contamination of three rural group water supplies in rural areas (C, K and M) was examined in detail over a full calendar year, and the results were correlated to rainfall events. Both source water and water in the distribution system were monitored for *E. coli* and Coliform bacteria at two-week intervals over the year. Results were made available to the designated contact person for the water supply. The results indicated that faecal contamination of both the source water and the water delivered to homes through the distribution systems is the norm in these rural water supplies throughout the year. For water supply C, 69% of samples from the distribution systems were contaminated with *E. coli*; the corresponding figure for supply K was 56% and for supply M 19%. In general, increased rainfall resulted in increased levels of *E. coli* in the source water and this was reflected in the water in the distribution system. For sources that were predominantly surface waters (supply M), rainfall close to the time of sampling (on the day of sampling or the day before) was more closely correlated with levels of *E. coli* in the water. This is thought to reflect the immediate flow of precipitation into surface waters. For groundwater sources (supply C) there was greater correlation with rainfall over a longer time period (on the day before sampling or the previous three to five

days). This is thought to reflect a more gradual transfer of rainwater through soil and rock into groundwater.

A novel aspect of the work of this project was the evaluation of *E. coli* contaminants in these rural water supplies for their resistance to antimicrobial agents used to treat human *E. coli* infection, such as urinary tract or bloodstream infections. Antibiotics in common use in human or animal health care are ampicillin and sulphonamides, which have been in use for 50 years of more and cefotaxime and ciprofloxacin which have been widely used for 20 to 25 years. This issue of antibiotic-resistant bacteria in water links with the theme of emerging contaminants of the aquatic environment described below.

Faecal contamination of both the source water and the water delivered to homes through the distribution systems is commonplace throughout the year in some rural water supplies.

It is apparent that the *E. coli* which contaminate the water supply to many rural homes are frequently resistant to antimicrobial agents such as ampicillin and sulphonamides. For example, over the period studied, from 6% to more than 80% of *E. coli* were resistant to ampicillin in supply C. On one occasion an *E. coli* with a resistance pattern known as extended-spectrum beta-lactamase (ESBL), which includes resistance to the relatively new antibiotic cefotaxime and related antimicrobial agents was detected in one of the three rural supplies (supply K). This supply was also positive on one occasion for vancomycin-resistant enterococcus (VRE). A further concern arose when on one occasion molecular methods detected genes that code for antimicrobial resistance (*sulI* and *strA*) in a sample of water from supply M that had been deemed compliant with drinking water standards (*E. coli* not detected). This was an isolated finding (1 of 19 water samples tested) and requires confirmation. The significance of exposure to genes coding for antibiotic resistance in the absence of viable bacteria is uncertain. It is theoretically possible that such resistance determinants present in drinking water could be taken up and expressed by resident *E. coli* in the gut of animals or people. Further research

to assess the significance of this finding for regulators and for authorities responsible for water treatment is needed.

E. coli contaminating rural group water supplies are frequently resistant to commonly used antimicrobial agents such as ampicillin. Sometimes the antibiotic-resistant *E. coli* in water are resistant even to newer antibiotics such as cefotaxime (ESBL *E. coli*).

The application of molecular microbial source tracking (MST) methods, also developed in this project, to these three rural water supplies suggests that ruminants are the principle source of faecal contamination. It appears that in the small number of supplies studied in detail farm animals are the principle source of faecal contamination. The impact of this on the occurrence of water-borne infection is likely to be influenced by the expectations of rural dwellers with respect to the quality of water piped to their homes and the use of domestic level treatments (such as filters) and/or bottled water.

Molecular biology methods suggest that ruminants are the main source of contamination of these supplies and that water that is free of viable *E. coli* may contain genes coding for antibiotic resistance. Additional research to assess the significance of genetic determinants of resistance in potable water is required.

Although anecdotal evidence suggests that some rural dwellers expect that the water may not be suitable for drinking without further treatment, this has not been researched systematically and there have been a number of incidents in which rural water supplies have been implicated in infection with Verocytotoxic *E. coli*. The risk of infection may be greatest to children and other vulnerable people who may mistakenly drink such water or use it for tooth-brushing and to occasional visitors to rural areas who may assume that tap water is potable.

Although significant progress on improving the quality of water supply to rural homes has been made in recent years, these results highlight that in some rural supplies exposure to faecal contamination is so commonplace as to be routine. This project illustrates the additional hazard that these *E. coli* frequently exhibit acquired antimicrobial resistance.

2.3 The Application of Geographical Information Systems and Mathematical Modelling to Improve Understanding of Cryptosporidium Infection

Cryptosporidium spp. are protozoan parasites associated with gastrointestinal infection. The infection is generally self-limiting although potentially life threatening in patients with impaired immune function. There are a number of different species of which *C. hominis* is essentially exclusive to people while *C. parvum* has a wider host range, including many domestic animals and humans. Cryptosporidium is shed in the faeces of infected people and animals in the form of highly resilient oocysts that can survive in the environment for extended periods. Waterborne Cryptosporidium infection represents a particular challenge because the oocysts are resistant to the action of chlorination which remains a critical component of water-treatment systems. In Ireland cryptosporidiosis is a common infection, particularly in children.

In this project GIS technology was used to examine the relationships between human cryptosporidiosis, water supplies, and environmental and social factors that may impact on this infection. In addition, a mathematical model was developed to help understand factors that contribute to Cryptosporidium contamination of drinking water.

By chance, this project coincided with the largest waterborne outbreak of cryptosporidiosis in Ireland to date, which was centred in Galway. This created an opportunity to study the methods under development in managing this major public health challenge. During

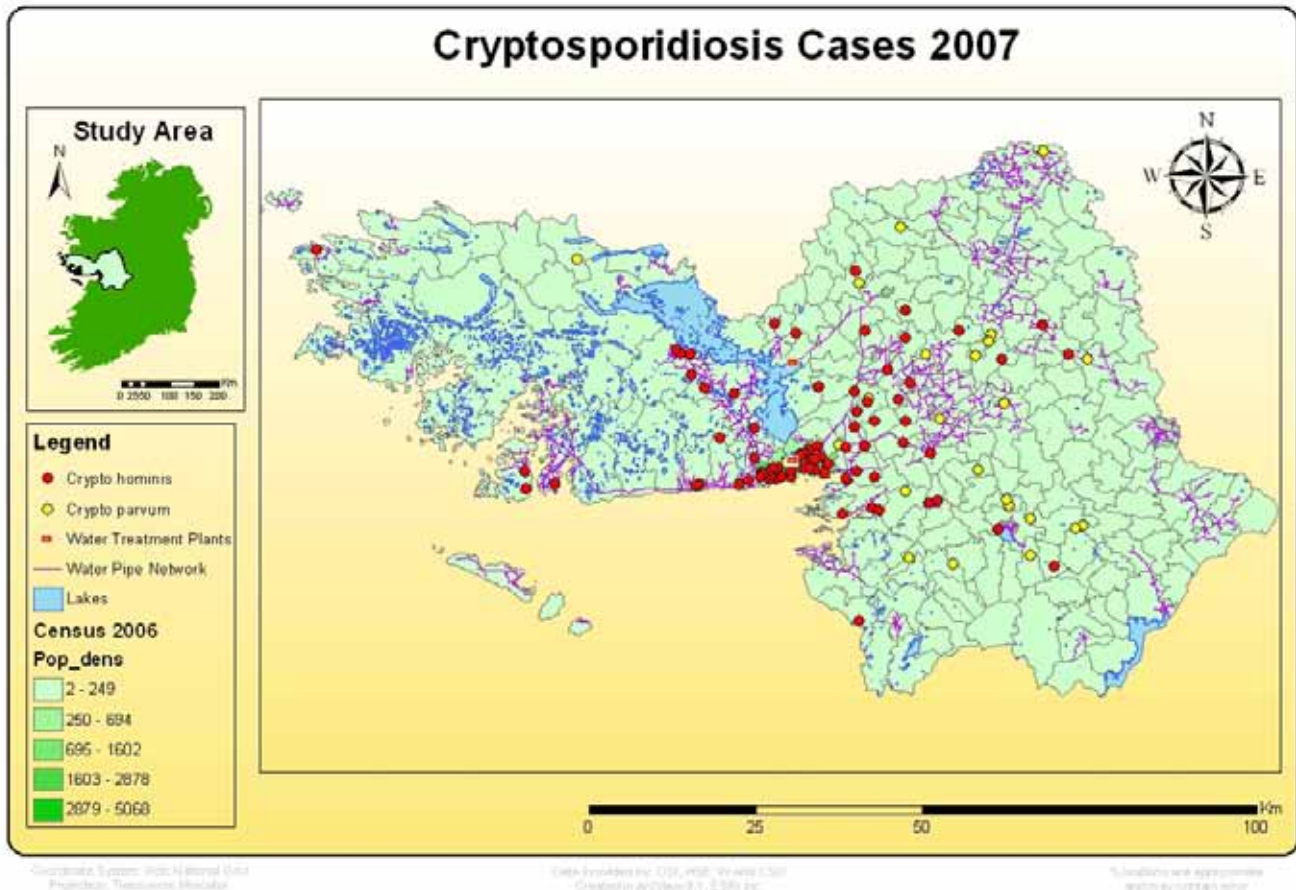


Figure 2.5. Map illustrating the spatial distribution of cases of cryptosporidiosis in Galway in 2007. Red dots correspond to case of *Cryptosporidium hominis* infection and yellow dots to cases of *Cryptosporidium parvum* infection.

Cryptosporidium hominis was associated with a discrete waterborne outbreak of infection in Galway in 2007 (red dots). In most years *Cryptosporidium parvum* (yellow dots) account for almost all locally acquired sporadic cases. The map illustrates the relative urban concentration of the *C. hominis* outbreak in contrast to the dispersed rural distribution of the *C. parvum*.

the outbreak in spring 2007 the researcher on the GIS project contributed to the management of the outbreak through providing regularly updated maps illustrating the distribution of cases (see [Fig. 2.5](#)).

The initial objective of the project, however, was to investigate the epidemiology of sporadic human cryptosporidiosis in the West of Ireland by linking health-surveillance data on human *Cryptosporidium* infection with geospatial and temporal data on water supplies, weather, farming practices and the geophysical environment. Information on cases of human *Cryptosporidium* infection (anonymised data) was obtained through microbiology and public health

systems in the HSE. Ethical approval for the study was given by the NUI Galway Research Ethics Committee. The address for each case of infection was used to generate XY coordinates representing a specific point on the map. Addresses in rural areas of Ireland may specify only a town-land and therefore do not permit the definition of a precise location; in these circumstances a point representing the geographic centre of the town-land was used.

Datasets were obtained for a range of environmental and social factors (including geology, slope, soils, water bodies, land cover, agricultural patterns, livestock density, rainfall, flooding, water supplies, lifestyle, health

facilities, and social deprivation, including occupation, unemployment, education, and medical card use) from the following sources: Central Statistics Office, Ordnance Survey Ireland, GSI, EPA, Department of Agriculture, Teagasc, Met Éireann, HSE and other sources. The datasets were converted into appropriate formats for use within a GIS.

The environmental and social information from many sources were linked to give a description of an individual electoral division (ED). Statistical analyses were then performed to explore associations at the ED level between these factors and incidences of human cases of cryptosporidiosis. With respect to sporadic cryptosporidiosis, the analysis did not identify statistically significant associations between the factors investigated and the occurrence of human disease. It is possible that the relatively low total number of sporadic cases of confirmed cryptosporidiosis in the region, the inability to develop precise XY coordinates from many rural addresses together with the aggregation of data to the ED level, impaired the ability to detect significant relationships.

The 2007 outbreak of Cryptosporidiosis in Galway highlights the potential for significant adverse consequences for human health of inadequate water treatment. The research project helped inform practical aspects of the management of the outbreak and enabled the development of new linkages with local authorities and the health service.

In addition to addressing the specific issue of *Cryptosporidium* infection, a key output of the research project is a GIS system that can be applied to investigate the spatial distribution of infection with other pathogens and to correlate data on distribution with the environmental and social factors outlined above. The application of this approach to a gastrointestinal disease, such as campylobacteriosis, with a higher incidence in the community would be a valuable way to further test the application of this approach for pinpointing the environmental and social factors that contribute to disease incidence.

A GIS containing an extensive collection of data that is applicable to the investigation of the spatial distribution of disease and its relationship to environmental and social factors was developed. The utility of the method in summarising and presenting the evolution of the spatial pattern of infection for public health purposes in an outbreak setting was demonstrated during a waterborne outbreak of Cryptosporidiosis.

To help understand the factors that contribute to the risk of such an outbreak, the mathematical model, the quantitative Monte Carlo simulation model, was developed to evaluate the annual risk of infection from *Cryptosporidium* in tap water in Ireland. The assessment considered potential initial contamination levels in raw water, oocyst removal and decontamination events following various process stages – including coagulation/flocculation, sedimentation, filtration and disinfection. A number of scenarios were analysed to represent potential risks from public water supplies, group water supplies and private wells. The simulated annual risk of illness for immunocompetent individuals was below 1×10^{-4} per year as set by the United States Environmental Protection Agency (Gale, 1998), except under extreme contamination events. The risk for an immunocompromised individual was two to three orders of magnitude greater for the scenarios analysed. The model indicates a reduced risk from tap water that has undergone microfiltration, as it is better able to cope with high contamination loads. For conventional water-treatment systems the model points to source contamination and failure/inadequacy of a specific step in water treatment (coagulation/flocculation) as contributing to the risk of human infection. The mathematical model also indicates that the frequency of operational failure of the treatment process following conventional treatment is the most important parameter influencing human risk.

Operational failure in water-treatment systems is identified as a major risk factor for human infection. This points to a requirement for quality assurance systems in all water-treatment systems to minimise the risk of operational failure.

The probabilistic model developed to examine the risk of human cryptosporidiosis related to variation in water source and treatment may be useful for local authorities, government agencies and other stakeholders to allow the evaluation of the likely risk of infection given some basic input data on source water and treatment processes used. Watershed protection should be considered a primary safeguard in the prevention of waterborne *Cryptosporidium* infection now that the contamination level in intake water into the water-treatment plant has been highlighted as a major risk. Further, the finding that the failure of conventional water systems to operate optimally poses a major risk for human infection with *Cryptosporidium* underlines the need for a quality management or continuous quality improvement approach to the routine operation of water-treatment systems to minimise the risk of systems failures.

2.4 Emerging Technologies for Detection and Tracking of Microbial Contamination of Water

Conventional microbiological monitoring of water for evidence of faecal contamination is based mainly on the detection of *E. coli* and Enterococci. This has a number of limitations. Although most *E. coli* are not associated with gastrointestinal infection, some types (for example Enterohaemorrhagic *E. coli*/Verotoxigenic *E. coli*) are associated with serious disease. However, routine methods applied to water analysis do not differentiate between pathogenic and non-pathogenic *E. coli*. It is also clear that water in which *E. coli* and Enterococci are not detected may be contaminated with pathogenic viruses such as Norovirus or protozoa. Newer molecular methods may facilitate the examination of water for specific pathogenic *E. coli* variants and for viral pathogens.

Molecular DNA-based assays were developed and employed during the project to detect specific bacterial (Verotoxigenic *E. coli*) and viral (Norovirus) pathogens in drinking-water supplies. These assays provide a rapid method for detecting key pathogens not readily uncovered using conventional approaches. The assays show potential for use on a larger scale for both public and private supplies to identify key pathogens and, subject to satisfactory performance in comprehensive validation for routine use, may be of value to water-monitoring authorities.

The detection of *E. coli* is evidence of faecal contamination, but it does not allow the differentiation between human and non-human sources of faeces. As noted above, MST allows the use of microbiological methods to identify the animal species associated with faecal contamination. This distinction will be of value in identifying sources of contamination and directing source-protection measures. The predominant bacteria in the gastrointestinal flora of humans and animals are strict anaerobic bacteria that can be difficult to culture and identify using conventional microbiological methods. For this reason, the diversity of faecal flora is not yet well characterised for humans and even less so for animals. The application of molecular methods enables the identification of species of strict anaerobic bacteria that are exclusive to – or very closely associated with – one or a small number of related animal host species (e.g. with humans or with ruminants), but which are absent or very rarely present in other host species.

Molecular methods for the detection of Verocytotoxigenic *E. coli* and Norovirus in water were developed. A molecular method to differentiate between human and ruminant faecal contamination of water was also developed.

In the course of this project nucleic acids were extracted from faeces, sewage and slurry from human, cow and sheep and analysed using a number of techniques to identify molecular markers for bacterial species specific to particular host species. The methods applied included DNA amplification, terminal

restriction fragment length polymorphism analysis, DNA sequencing and phylogenetic tree-based sequence analysis. The results generated from faecal samples of three host species were compared and DNA sequences that appeared promising for use as molecular markers for gastrointestinal contents of ruminants selected.

A series of novel DNA amplification assays based on these DNA targets was developed and evaluated relative to previously published molecular methods for microbial source tracking. The assay development and evaluation included detailed work on samples from specific animal species, and the preliminary application of the assays to water from the three rural water supplies referred to above. These results suggest that ruminants are the principle source of faecal contamination of these supplies.

The objective of this project was to develop these molecular methods (pathogen detection and MST) that show significant potential for application in identifying and characterising sources of faecal contamination of water sources. Further research and development beyond the scope of this project are required – both in terms of technical validation and in order to assess their suitability for routine use by public health agencies, local authorities and other agencies acting to protect public health and water supplies. Such a service, if provided at a reasonable cost, would be of practical value in the investigation of water-contamination incidents.

The application of molecular methods to assist in managing water quality is still in its infancy in Europe and more generally in the world and there may be significant potential to provide services in this area to relevant agencies and companies in Europe subject to comprehensive technical validation.

2.5 Emerging Water Contaminants of Concern

Changes in how we live and work can have significant impacts on the aqueous environment, in particular because of the extent to which water is used to dispose of waste. The production and consumption of pharmaceutical products, including antimicrobial

agents, has increased dramatically in recent decades. Pharmaceutical agents are specifically designed to have biological effects at low concentrations and a significant portion of many pharmaceutical agents are excreted in urine and faeces and may enter the environment.

Antimicrobial agents differ from other pharmaceutical agents in that the intended target of action is not human or animal cells, but microorganisms. Microbial populations adapt rapidly under the selective pressure of antimicrobial agents, resulting in the growing problem of *acquired antimicrobial resistance*. This term refers to the situation when members of species of bacteria that were formerly susceptible to treatment with a particular family of antimicrobial agents have become increasingly resistant to the action of the antimicrobial agent. Acquired antimicrobial resistance is a growing public health problem in Ireland and more generally across the EU and the world. Indeed, the growing recognition of the challenge of antimicrobial resistance is reflected nationally in the Strategy for Antimicrobial Resistance in Ireland (SARI) report. At a European level an annual Antibiotic Awareness Day is promoted to raise awareness and support action (European Centre for Disease Control, 2012). At a global level, WHO has identified antimicrobial resistance as a key 'Global Patient Safety Challenge'; the theme of World Health Day 2011 was 'No action today–no cure tomorrow' (Chan, 2011).

Efforts to control this growing problem have focused mainly on reducing the exposure of bacteria on or within the body (for example in the gut) to antimicrobial agents by avoiding unnecessary prescribing.

The potential for antimicrobial agents discharged into the environment in urine and faeces to contribute to the selection of acquired antimicrobial resistance in microbial populations in effluent and more generally in the environment has received less attention. In addition to any possible impact of antimicrobial residues discharged into the environment, the persistence and dissemination of antimicrobial-resistant bacteria entering the environment from human and animal faeces is also a potential problem if they subsequently enter drinking water or food. While pharmaceutical agents (including antibiotics) are used throughout the community, and bacteria with acquired antimicrobial resistance are found in both human and animal faeces, hospitals can make intensive use of relatively new

antimicrobial agents that are not yet widely used in the community. For this reason, hospitals have the specific potential to act as foci for the early dissemination of novel types of acquired antimicrobial resistance that often emerge first in the hospital setting.

During the project, water and effluent samples were examined for the presence of antimicrobial agents and for faecal indicator bacteria that had acquired resistance to antimicrobial agents. Water from a number of locations, including rivers, lakes, hospital effluent, municipal sewage and effluent from a wastewater-treatment plant was tested. There was a particular focus on effluent from hospitals and related urban sewage systems. Testing included water from rural group water supplies as previously discussed in Section 2.3.

Samples were collected from the following sites:

- 1 Hospital effluent from two hospitals and municipal sewage upstream and downstream of these institutions.
- 2 Rivers and lakes from six counties including those in the vicinity of and remote from urban areas.
- 3 Source and piped water from three rural group water supplies.

- 4 Seawater into which treated and untreated sewage was emitted.
- 5 Soil and/or slurry samples from intensive farms.
- 6 River samples upstream and downstream of these farms.
- 7 Samples from different stages of the secondary wastewater-treatment process at a secondary wastewater-treatment plant; to determine the impact of each stage of treatment on the presence of antimicrobial-resistant bacteria and antimicrobial agents.

All samples collected were examined for the presence of bacterial indicators of faecal pollution, i.e. total coliforms, *E. coli* and *Enterococci*. The presence of and the percentage of antimicrobial-resistant bacteria present was determined for each sample using a novel method developed and successfully validated during the project. This method is a modification of the Most Probable Number (MPN) method routinely used in water analysis and provides a rapid, facile and inexpensive method for determining the presence and proportion of antimicrobial-resistant bacteria in aqueous samples within 24 hours as opposed to a minimum of 48 hours using current methods ([Fig. 2.6](#)).



Figure 2.6. A water sample tested concurrently in the presence and absence of antimicrobial agents.

From left to right a sample tested in the absence of antimicrobial agents; same sample tested in the presence of ciprofloxacin (4µg/ml); same sample tested in the presence of cefotaxime (2µg/ml). The yellow colour indicates growth of Coliform bacteria and the proportion of coliform bacteria resistant to each antimicrobial agent can be determined.

This project describes the first reported detection of ESBL-producing *E. coli* in the outflow of a wastewater-treatment facility. It also describes the detection of a novel genetic determinant of transferable resistance to fluoroquinolone antimicrobial agents, QnrB21.

Data generated by this project indicated that antimicrobial-resistant *E. coli* are prevalent in the environment, with varying levels of these bacteria detected in most locations examined, including some relatively remote rural areas. Hospital effluent is a significant source of antimicrobial-resistant bacteria, with all samples tested containing higher proportions of antimicrobial-resistant bacteria compared with other sample locations. The discharge of hospital effluent also appears to have an impact on the bacterial populations in municipal sewage. The total number of *E. coli* per 100ml of effluent and the percentage of *E. coli* resistant to a number of antimicrobial agents were examined upstream and downstream of the inflow of hospital effluent. In comparison to samples taken upstream of the hospital outflow, samples taken downstream showed a lower total number of *E. coli* but with a trend towards a higher proportion of antimicrobial-resistant bacteria.

With respect to those antimicrobial agents that have been in widespread use for decades to treat human and veterinary infections (such as ampicillin, sulphonamides, tetracycline and streptomycin), *E. coli* resistant to these agents were observed in almost all locations, including rural areas. Bacteria resistant to more recently introduced antimicrobial agents such as ciprofloxacin, cefoxitin and cefotaxime were observed predominantly in samples taken in urban areas. This may reflect the longer time period during which the selective effect of the older agents has operated, the more widespread use of the older agents (possibly including use as growth promoters prior to the introduction of greater regulatory control in the EU) and the continuing more general prescription of many older agents in human and animal health care because of their lower cost.

As expected, the secondary wastewater treatment resulted in a very marked reduction in the absolute number of *E. coli* in the effluent discharged. However, antimicrobial-resistant bacteria were detected in the outflow, indicating that the process does not completely remove antimicrobial-resistant bacteria; in particular, those *E. coli* with the ESBL antibiotic resistance pattern were detected frequently in the outflow of the wastewater-treatment plant. As noted above, these types of *E. coli* are resistant to treatment with many widely used antibiotics, including antibiotics that are currently largely limited to hospital use. These ESBL *E. coli* were characterised in detail and were shown to carry the same family of mobile genetic elements (CTX-M beta-lactamase genes) that predominate in human ESBL infection in this region and throughout Europe. Globally, this is the first report of ESBL *E. coli* detection in the outflow of a wastewater-treatment plant. Further studies are under way to try to assess the extent to which it is possible to quantify the risk of human exposure to antimicrobial-resistant bacteria discharged from a wastewater-treatment plant.

Antimicrobial-resistant *E. coli* are widespread in the environment, reflecting the impact of decades of overuse of antimicrobial agents. *E. coli* (ESBL-producers and fluoroquinolone-resistant), and Enterococci (vancomycin-resistant) with more recently emerged antimicrobial-resistant patterns appear to be particularly associated with hospital effluent. At a European level it is appropriate to consider if specific regulatory control of hospital effluent is required.

With respect to farming practices (dairy, pig, sheep, organic beef and tillage), with the exception of pig slurry samples, no antimicrobial-resistant bacteria were detected in slurry and/or soil samples. On the other hand, they were detected in river samples taken upstream and downstream of all farm types. No significant difference in the proportion of resistant *E. coli* upstream versus downstream of specific farm locations was observed. Moreover, the levels of antimicrobial-resistant bacteria present in the river samples taken in close proximity to the tillage farm were high both upstream and downstream.

It is reasonable to suppose that animal husbandry in proximity to rivers might contribute to antibiotic-resistant bacteria in rivers: however, this project did not find evidence of such a link. Antibiotic-resistant *E. coli* were not detected in animal slurry and antibiotic-resistant *E. coli* were not more numerous downstream of livestock farms and indeed were more numerous in the vicinity (upstream and downstream) of tillage farms. It is important however to interpret this result with caution. The number of samples and sites tested was necessarily limited, and the approach to categorization of land-use pattern subjective. Furthermore, the inflow and outflow of water and of *E. coli* in rivers is dynamic and there are many influences other than agriculture on the *E. coli* content of rivers. For all these reasons, a simple relationship between the immediate agricultural environment and the occurrence of antimicrobial-resistant bacteria in the samples taken would not be anticipated. A comprehensive description of sources of contamination in the catchment of these rivers was beyond the scope of this project.

Bacteria can acquire resistance to antimicrobial agents through the acquisition of genetic material from other organisms or potentially from DNA in their general environment. In addition to being used for detecting antibiotic-resistant bacteria, molecular methods were applied to identify the genetic elements responsible for the resistance in these bacteria. This allowed the identification of specific mobile genetic elements and antimicrobial resistance determinants in many bacteria isolated from all areas. The genetic mechanisms found in these environmental isolates are similar to those associated with resistance in clinical isolates of *E. coli* in this region previously studied by this research group. In the course of this work a new variant of the QnrB family of proteins (named QnrB21) associated

with transferable resistance to fluoroquinolones was detected, thus adding to the growing body of knowledge in this field.

In addition, a biological assay was used to screen samples for the presence of antimicrobial agents. Antimicrobial activity was present at biologically significant levels only in hospital effluent samples and in municipal sewage downstream of the hospital effluent discharge point. Of particular note was the detection of quinolone-like activity in all hospital effluent samples tested. Other studies have previously reported detection of the specific fluoroquinolone, ciprofloxacin, in effluent samples using chemical methods. Based on these reports and the fact that ciprofloxacin is the predominant fluoroquinolone used in the hospital studied, the project team anticipated that ciprofloxacin was the specific chemical agent most likely to account for the antimicrobial activity observed: however, ciprofloxacin was not detected by chemical analysis. At present, therefore, the specific chemical that accounts for this antimicrobial activity in hospital effluent is undefined and this is the subject of a further project.

Overall, the work in this area highlights the extent to which antimicrobial-resistant *E. coli* and related bacteria are now widely disseminated in the Irish environment. Antimicrobial-resistant bacteria appear to persist through secondary treatment systems at least as effectively as antimicrobial-susceptible bacteria. The findings indicate that in some respects effluent from major hospitals differs in composition to general urban effluent. This highlights a need to consider if such effluent requires specific monitoring and control. This question is the subject of an EPA-funded collaborative risk assessment project between researchers at NUI Galway and University College Dublin.

3 Summary of Overall Project

3.1 Project Output

The output of this project includes new information, new methods, and increased awareness. It has built a capacity for and developed new partnerships focused on research in environment and health.

3.2 New Information

The output of this research project is immediately relevant to understanding the impact of existing methods of sanitation, water pollution and water treatment on population health in Ireland and in developing policies to improve human health.

- 1 The potential for very rapid changes in microbiological parameters (*E. coli* levels) in groundwater in response to heavy rainfall has important implications for ensuring safe drinking-water supplies.
- 2 At the time of the study some rural populations were exposed to piped water that was substantially contaminated with faeces all of the time and with the added factor of exposure to *E. coli* with an array of acquired antimicrobial resistance mechanisms. It is encouraging in this regard that overall improvement in drinking water quality was reported in the recent EPA report *The Provision and Quality of Drinking Water in Ireland a Report for the Year 2010*.
- 3 The importance of source protection and the vulnerability of conventional treatment systems to operational failures were identified using a mathematical model to examine the risk of human waterborne infection with *Cryptosporidium*.
- 4 The extent to which acquired antimicrobial resistance in *E. coli* and Enterococci have become disseminated in the aqueous environment in Ireland have been described and the potential role of intensive health care settings as particular foci for pharmaceutical and bacterial contaminants has been highlighted.

3.3 New Methods

- 1 A matrix for classification of the vulnerability of groundwater sources to faecal contamination was developed.
- 2 A mathematical model for the prediction of flow rates and *E. coli* levels in a river catchment was developed. The model predicts water flow rates satisfactorily but further refinement is required to improve *E. coli* predictions.
- 3 A process for the adaptation of complex databases relating to physical and social factors from multiple sources in Ireland into a format suitable for application in a GIS was demonstrated and applied to the study of sporadic *Cryptosporidium* infection. This system is available for application to the study of other infections.
- 4 Novel molecular markers for use in identifying the animal species responsible for faecal contamination of water were developed and their application piloted. This work has been published but the methods require further validation before routine application.
- 5 Molecular assays for the detection of specific pathogens (Verocytotoxigenic *E. coli* and Norovirus) were developed and piloted. The methods require further validation before routine application.
- 6 A novel approach to the enumeration of antimicrobial-resistant *E. coli* and Enterococci was validated and published (Galvin *et al.*, 2010).

3.4 Awareness

Throughout the project extensive outreach activities have increased awareness of the issue of the central role of water quality in protecting human health across a broad spectrum of agencies and the wider public.

3.5 Capacity Building

The project has provided post- graduate and post-doctoral research and project-management training and experience to nine individual scientists and engineers building the capacity for environmental research and environmental protection in Ireland. The project provided an important impetus for the establishment of The Centre for Health from Environment at the Ryan Institute NUI Galway to promote awareness of the relationship between health and environment.

3.6 Partnerships for Environmental Research

A positive relationship has been developed between key stakeholders in the region, which offers considerable potential for future environmental research. The engagement and commitment of local authorities and health care providers in the region provides critical infrastructure for future research.

4 Conclusions from Research and Future Research Needs

This project was one of the largest projects to date in Ireland linking the environment with health. The commitment to fund this project and its successful delivery reflect the growing awareness that the protection of the environment is much more than the protection of the birds and the fish. We too live in and depend upon the environment and our health and well-being and the health and well-being of future generations are inseparable from the health of the ecosystem that we are part of.

Environmental action for health will lead to better health in the population and can address inequities in health – the impact of environmental degradation on health is greatest on the poor and the uneducated who may lack effective access to relevant information and lack the capacity and resources to protect themselves against specific hazards. Environmental action to improve health is a highly cost-effective approach to maximising population health and health equity and is therefore especially important in these times of economic difficulty and constraint of public financing. Prevention is better than cure; it costs less than cure; it is more sustainable than cure; and is more equitable than cure. Many of the work-packages have improved

understanding of the relationship between microbial contamination of water and human infection and provided tools to help manage this threat. In addition, this project has examined one aspect (antimicrobial resistance) of the impact of contemporary health care delivery on the environment. There is a general need for more rigorous evaluation of the environmental impact of the health care delivery system relative to the health gains achieved.

Methods developed in this project for identifying the sources of faecal contamination, detection of specific pathogens and antimicrobial-resistant organisms, mapping disease incidence in relation to physical and social environment, assessing vulnerability of water sources to contamination and models for predicting impacts on water sources may be of direct relevance to local authorities. The translation of these technologies into practical application is one of the challenges that universities are increasingly engaged in.

Environment and Health will be a major theme of policy and research in the medium term. This project has built the capacity and relationships necessary to provide a platform for further research on the relationships between the Environment and Health.

5 Recommendations for Implementation and Uptake of Research Findings

- 1 There is a need to increase the awareness of the public and policy makers of the health impact of environmental degradation and of the pivotal role of the environment in achieving sustainable health and health equity.
- 2 The project emphasises the need for urgent action at all levels to ensure access to safe drinking water for all sectors of our society, including rural populations.
- 3 Further development of geographical information systems for real-time application in managing environmental threats to public health should be supported.
- 4 There is a need for further study of the potential environmental and human health impact of major health care delivery centres in Ireland and Europe.
- 5 Mathematical modelling systems should be developed as routine tools for evaluation and management of risks associated with water supply systems.
- 6 Further development of the molecular technologies piloted in this study (microbial source tracking, specific pathogen detection) and the effective transfer of this technology into a service delivery enterprise should be prioritized to provide a service not currently available to water authorities and companies in Ireland and more widely in Europe.

Table 5.1 Recommendations for Implementation and Uptake of Research Findings

Issue	Recommendation	Target	Time Frame
Awareness of the link between the environment and health	Environmental awareness tends to focus on humans as an agent of environmental change, loss of amenity and biodiversity and needs to focus more on our dependence on the environment for health and well-being. The establishment of the Centre for Health from Environment at the Ryan Institute, National University of Ireland (NUI) Galway represents a step toward realising this objective.	Educators EPA	Long term
Microbial contamination of rural water supplies	Programme of action to ensure that people are more aware of the quality of water supplied to their home and to upgrade services to ensure consistent access to potable water for all citizens.	DECLG Local authorities DoH	Short term and medium term
Identification of sources of faecal contamination of water sources and detection of specific pathogens	A national service to develop and deliver new laboratory technologies for microbial source tracking to assist in detecting, managing and tracking water contamination. This could be delivered as a component of an integrated national public health reference laboratory system or as a commercial service.	DECLG HSE DoH	Medium term
Environmental impact of health care delivery	Further assessment of the environmental and human health impact of effluent discharged from major health care centres and of potential measures to minimise impact should be considered at the EU level.	EPA DECLG HSE European Commission/ WHO	Short term

to be continued overleaf

Table 5.1 Recommendations for Implementation and Uptake of Research Findings (*continued*)

Issue	Recommendation	Target	Time Frame
Use of GIS technology in health services for surveillance, planning	Develop training in the use of GIS within the health service to support health protection and health education. Link academic institutions and local authorities involved in using GIS for planning and sharing information	HSE DECLG Local authorities	Short to medium term
Managing water sources and water-treatment systems	Computer-based models of water catchments and water-treatment systems have potential applications in understanding hazards and in predicting changes in water supply and water quality and should be translated from research tools to become routine management tools.	EPA DECLG Local authorities	Long term
Data for development of matrix is incomplete and limited to public supply catchments	Data to support the application of the matrix for assessment of supply vulnerability (described in this report) to private/group water schemes should be generated. Factors such as slope, soil type and land use should be dealt with in an expanded matrix to aid in the protection of groundwater sources and public health.	EPA GSI	Medium term
Transient contamination of vulnerable supplies	The conditions that may lead to surges of transient faecal contamination of vulnerable supplies (e.g. heavy rainfall) need to be better understood so that water-treatment infrastructure and operational systems are designed with the capacity to control risks to human health from surges in contamination.	EPA DECLG	Short term

DECLG = Department of Environment, Community and Local Government; DoH = Department of Health; EPA = Environmental Protection Agency; GSI = Geological Survey of Ireland; HSE = Health Service Executive; WHO = World Health Organisation.

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Acronyms and Annotations

ED	Electoral division
ESBL	Extended-spectrum beta-lactamase
GIS	Geographical information system
GSI	Geological Survey of Ireland
MST	Microbial source tracking
MPN	Most probable number
NUI	National University of Ireland
SWAT	Soil and Water Assessment Tool
VRE	Vancomycin-resistant enterococcus
WFD	Water Framework Directive

Appendix 1 Names of those Involved Directly in Project

Permanent Staff Supporting Project

Name	Category	Period
Prof. Martin Cormican	Academic staff	Feb. 06 – Sept. 09
Prof. Emer Colleran	Academic staff	Feb. 06 – June 2007
Dr Vincent O'Flaherty	Academic staff	Feb. 06 – Sept. 09
Dr Diarmuid O'Donovan	HSE & Academic staff	Feb. 06 – Sept. 09
Dr Enda Cummins	Academic staff	Feb. 06 – Sept. 09
Dr Martina Prendergast	Administrative staff	Feb. 06 – Sept. 09
Dr Dearbhaile Morris	Academic staff	Feb. 06 – Sept. 09
Dr Heidi Pelly	HSE	Feb. 06 – Sept. 09
Mr Juan Carlos Castenada	Technical	Feb. 06 – Jan. 07
Mr Stephen Kelly	Technical	Feb. 06 – Feb. 07
Dr Sharon McHugh	Postdoctoral fellow	Feb. 06 – June 06
Akke Vellinga	Research staff	Feb. 06 – July 06
Dr Karl Richards	Collaborator	Feb. 06 – Feb. 09
Dr Donal Daly	Collaborator	Feb. 06 – Feb. 09
Dr Monica Lee	Collaborator	Feb. 06 – Feb. 09

Research and Administrative Staff Funded Directly by Project (Salaried)

Name	Category	Period
Dr Donna Kilmartin	Administrative (Project Manager)	Mar. 06 – Aug. 08
Dr Oonagh Dwane	Administrative (Project Manager)	Aug. 08 – Mar. 09
Siobhan Dorai-Raj	Research assistant	Mar. 06 – Mar. 08
Sandra Galvin	PhD student	Feb. 06 – Feb. 09
Katie McNamara	PhD student	Feb. 06 – summer 06
Rory Coffey	PhD student	Apr. 06 – Sept. 09
Mary Callaghan	Research assistant	Sept. 06 – Sept. 09
Richard Kennedy	M. Eng student	Sept. 06 – Dec. 07
Niamh Bhreathnach	Postdoctoral fellow	Feb. 07 – Jan. 09
Fiona Boyle	Research assistant	Jan. 07 – Dec. 07
Hazel Meredith	M. Eng. student	Feb. 08 – Feb. 09

Appendix 2 Selected Outputs of Project

Research Outputs

Publications

Callaghan M, Cormican M, Prendergast M, Pelly H, Cloughley R, Hanahoe B, O'Donovan D. 2009. Temporal and spatial distribution of human cryptosporidiosis in the west of Ireland 2004–2007. *International Journal of Health Geographics*, 8: 64.

Coffey R, Cummins E. 2009. Microbial contamination of water sources. *Encyclopaedia of Agricultural, Food, and Biological Engineering (EAFE)* 1, 1: 1–5.

Coffey R, Cummins E, Bhreathnach N, O'Flaherty V and Cormican M. 2010. Pathogen source characterisation and scenario analysis using the Soil and Water Assessment Tool (SWAT). *Human and Ecological Risk Assessment*, 16, 4: 913–33.

Coffey R, Cummins E, Flaherty VO and Cormican M. 2010. Analysis of the Soil and Water Assessment Tool (SWAT) to model *Cryptosporidium* in surface water sources. *Biosystems Engineering*, 106, 3: 303–14.

Coffey, R, Cummins, E, Bhreathnach, N, O'Flaherty, V, Cormican, M. 2010. Development of a pathogen transport model for Irish catchments using ArcSWAT. *Agricultural Water Management*, 97:101–11.

Coffey R, Cummins E, Cormican M, O'Flaherty V, Kelly S. 2007. Microbial exposure assessment of waterborne pathogens. *Human and Ecological Risk Assessment*, 13(6): 1313–51.

Cummins E, Kennedy R, Cormican M. 2009. Quantitative risk assessment of *Cryptosporidium* in tap water in Ireland. *Science of the Total Environment*, 408: 740–53.

Dorai-Raj S, O'Grady J, Colleran E. 2009. Specificity and sensitivity evaluation of novel and existing *Bacteroidales* and *Bifidobacteria*-specific PCR assays on feces and sewage samples and their application for microbial source tracking in Ireland. *Water Research*, 43: 4980–8

Dwane, O and Cormican M. 2009. A thirst for knowledge. *Environmental Health Officers' Association Yearbook*, pp. 50–1.

Galvin S, Boyle F, Hickey P, Vellinga A, Morris D, Cormican M. 2010. Enumeration and characterization of antimicrobial-resistant *E. coli* in effluent from municipal, hospital and secondary treated sources. *Applied and Environmental Microbiology*, 76, 14: 4772–9.

Conference Presentations (International Meetings)

Oral Presentations

Event	Contributors	Title
European Conference of Clinical Microbiology and Infectious Disease, Munich. 31 March 2007.	S. Galvin, D. Morris, M. Cormican	Occurrence of ESBL-producing <i>E. coli</i> in outflow from a wastewater-treatment plant.
AgEng 2008, Agricultural and Biosystems Engineering for a Sustainable World; Hersonissos, Crete, Greece. 23–25 June, 2008.	R. Coffey, E. Cummins, M. Cormican, V. O'Flaherty, N. Bhreathnach, S. Dorai-Raj	Prediction of microbial contamination in Irish catchments.
ESRI European User Conference, Stockholm. 26–28 September 2008.	M. Callaghan, M. Cormican, D. O'Donovan, H. Pelly.	The development of a geographic information system (GIS) to investigate factors influencing the occurrence of cryptosporidiosis in the west of Ireland.
SWAP 2007 –The European Symposium on Waterborne Pathogens in Surface and Drinking Waters, Luxembourg. 19–20 April, 2007.	N.C. Bhreathnach, K. Richards, V. O'Flaherty	Groundwater in Ireland: Coliforms, coliforms everywhere, so not a drop to drink?
19th ECCMID – European congress of clinical microbiology and infectious disease, Munich. 31 March–3 April, 2009.	S. Galvin, D. Morris, F. Boyle, P. Hickey, M. Cormican	The occurrence of ESBL-producing <i>E. coli</i> in the outflow of a wastewater-treatment plant.
II International Giardia and Cryptosporidium Conference, Morelia,. 14–18 May, 2008.	M. Callaghan, M. Cormican, M. H. Pelly, D. O'Donovan	The development of a geographic information system (GIS) to investigate factors influencing the occurrence of cryptosporidiosis in the west of Ireland.
19th ECCMID European Congress of clinical microbiology and infectious disease, Munich, Germany. 31 March–3 April, 2009.	S. Galvin, F. Boyle, D. Morris, M. Cormican	Novel plasmid mediated quinolone resistance determinant (Qnr-B21) identified in <i>E. coli</i> isolated from hospital effluent.
European Water Research Day (Zaragoza Expo), organised by the European Commission. Gobierno de Aragon, Zaragoza. 8 September, 2008.	M. Prendergast	Water-related research at the Environmental Change Institute

Poster Presentations

Event	Authors	Title
11th International Symposium on Microbial Ecology, Vienna, Austria. 20–25 August, 2006.	S. Dorai-Raj, S. McHugh, E. Collieran	Culture independent analysis of Bacteroides-Prevotella species in human, cow and sheep faeces.
American Society for Microbiology, AGM, Toronto. May 2007.	S. Galvin, D. Morris, M. Cormican	Detection of antimicrobial residues in hospital effluent and rural piped water supplies
American Society for Microbiology, AGM, Toronto. May 2007.	S. Galvin, D. Morris, M. Cormican	Detection of antimicrobial resistant organisms in hospital effluent in Ireland.
SWAP 2007 – The European Symposium on Waterborne Pathogens in Surface and Drinking Waters, Luxembourg. 19–20 April, 2007.	S. Galvin, D. Morris, F. Boyle, M. Cormican	Observation of antimicrobial resistant <i>E. coli</i> (including ESBL producers) in outflow from a wastewater-treatment plant)
Interscience Conference for Antimicrobial Agents and Chemotherapy, Chicago. September 2007.	S. Galvin, F. Boyle, D. Morris, M. Cormican	Detection of antimicrobial resistant enterococci in hospital effluent in Ireland

Event	Authors	Title
European Symposium on Waterborne Pathogens in Surface and Drinking Waters, Luxembourg. 19– 20 April 2007.	S. Dorai-Raj, E. Collieran	The use of host-specific genetic markers in faecal bacteria for source identification of faecal pollution.
European Symposium on Waterborne Pathogens in Surface and Drinking Waters, Luxembourg, 19–20 April 2007.	M. Callaghan, M. Cormican, H. Pelly, D. O'Donovan	The development of a geographic information system (GIS) to investigate factors influencing the occurrence of cryptosporidiosis in the west of Ireland.
5 Nations Health Conference, Belfast. 22–23 May, 2007.	M. Callaghan, M. Cormican, H. Pelly, D. O'Donovan	The development of a geographic information system (GIS) to investigate factors influencing the occurrence of cryptosporidiosis in the west of Ireland.
European Symposium on Waterborne Pathogens in Surface and Drinking Waters, Luxembourg. 19–20 April 2007.	R. Coffey, E. Cummins, M. Cormican, V. O'Flaherty	Risk assessment of microbial pathogens in rural watersheds: a review of current modelling methodologies, capabilities and techniques.
Interscience Conference of Antimicrobial Agents and Chemotherapy (ICAAC), Chicago. 17–20 September, 2007.	S. Galvin, F. Boyle, D. Morris, M. Cormican	Detection of vancomycin resistant enterococci in hospital effluent in Ireland.
American Society for Microbiology 108th Annual General Meeting, Boston, 1–15 June, 2008.	S. Dorai-Raj, E. Collieran	Novel PCR assays based on bacteroidales 16S ribosomal RNA genes for faecal source identification in water.
12th International Symposium on Microbial Ecology ISME12, Cairnes, Australia. 17–22 August, 2008.	N.C. Bhreathnach, K. Richards, S. Wuertz, V. O'Flaherty	Identification of vulnerability factors and monitoring, detection and source tracking of microbial contamination in Irish groundwater systems.
18th ECCMID, Barcelona, Spain. April, 2008.	S. Galvin, B. Tolar, F. Boyle, D. Morris, M. Cormican	Prevalence of the TetA gene and class I and class II integrons in environmental isolates of <i>E. coli</i> .
American Society for Microbiology 108th Annual General Meeting, Boston, 1–5 June, 2008	F. Boyle, S. Galvin, D. Morris, M. Cormican	Detection of antimicrobial resistant <i>E. coli</i> in sand at a fresh water beach.
American Society for Microbiology 108th Annual General Meeting, Boston, 1–15 June, 2008.	F. Boyle, S. Galvin, D. Morris, M. Cormican	The impact of treated effluent and city run off water on the levels of antimicrobial resistant <i>E. coli</i> in sea water.
British Society for Antimicrobial Chemotherapy <i>E.coli</i> Conference, London. 5 June 2009.	S. Galvin, F. Brennan, F. Boyle, D. Morris, M. Cormican	Impact of agriculture on the prevalence of antimicrobial resistant <i>E. coli</i> in rivers in Ireland.
COST929 Symposium, Pisa, Italy: 'Current Developments in Food and Environmental Virology'. 9–11 October, 2008.	N.C. Bhreathnach, S. Wuertz, K. Richards, V. O'Flaherty	Virus detection in Irish groundwater sources: identification of vulnerability factors and molecular detection of seasonal occurrence of adenoviruses, enteroviruses and noroviruses.
Grassland and Water Framework Directive International Conference, Teagasc, Johnstown Castle, Wexford. 12–14 November, 2008.	N.C. Bhreathnach, S. Wuertz, K. Richards, V. O'Flaherty	Assessing the vulnerability of Irish aquifers to contamination by key pathogens.
Grassland and Water Framework Directive International Conference, Teagasc, Johnstown Castle, Wexford. 12–14 November, 2008.	M. Barrett, N.C. Bhreathnach, M. Khalil, K. Richards, V. O'Flaherty	Analysing the unexplored terrain of subsurface microbiology in Irish soils and groundwater systems.

Recognition/Acclaim for Research Work

28 Jan 2007	S. Dorai-Raj & E. Colleran. On the trail of water pollution – using bacteria to track the source of water pollution.	S. Dorai-Raj awarded Best Poster at Environ 2007, Carlow.
28 Jan 2007	R. McKeown & V. O’Flaherty. Low-temperature anaerobic biotreatment as a core technology for the remediation of groundwater.	R. McKeown awarded Best Oral Presentation at Environ 2007, Carlow.
3 May 2007	S. Galvin. Water, water everywhere, but is it safe to drink	Runner-up in National Science Speak Competition

Thesis Submissions

Degree	Author	Thesis Title	Date
PhD	Siobhan Dorai-Raj	Identification of the sources of faecal contamination by molecular methods.	March 2008.
PhD	Rory Coffey	Development of a pathogen transport model for Irish catchments.	April 2010.
PhD	Sandra Galvin	Antimicrobial-Resistant E. coli, Enterococci and antimicrobial drugs in the aquatic environment.	April 2010.
Masters	Richard Kennedy	Development of a quantitative risk assessment with particular reference to Cryptosporidium and water treatment for drinking water supplies in Ireland.	February 2009.
Masters	Hazel Meredith	Development of a quantitative risk assessment of E. coli in drinking water.	February 2009.

Outreach Programmes Delivered to Schools, General Public and Organisations

The project engaged in extensive outreach activities including school visits, a talk to the Galway Active retirement group and a workshop with local authorities in the region a public lecture on antimicrobial resistance: ‘Water Quality in the West of Ireland’—Convent of Mercy, Roscommon.

Media/Publicity

Newspapers – National and Regional

1. ‘NUI Galway scientists pay visit to Roscommon secondary schools’– January, 2007.
2. ‘Hospitals pollute our water’–Sunday Times, 15 April, 2007.
3. ‘Hospital effluent poses deadly water risk’–Irish Daily Mail, 16 April, 2007.
4. ‘Concerns over treatment of sewerage from hospitals’–Connacht Sentinel, 17 April, 2007.
5. ‘Student scoops national award with research on water quality’– Galway Advertiser, 10 May, 2007.
6. ‘Using ecstasy to keep little bundles apart’–Irish Times, 10 May, 2007.
7. ‘Speaking of Science’–Science Spin, July 2007.
8. ‘Safefood Newsletter’–Cryptosporidium Research Network–March 2007.

Television

Niamh Bhreathnach was interviewed for TG4 programme *Luach ár Linne*, 7 October, 2008. Interview given through the medium of Irish on Water Quality in Ireland. Aired in November 2008.