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Public Health Impact of Exposure to Antibiotic Resistance in Recreational Waters (PIER)

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Rialtas na hÉireann
Government of Ireland

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4. Office of Radiation Protection and Environmental Monitoring
5. Office of Communications and Corporate Services

The EPA is assisted by advisory committees who meet regularly to discuss issues of concern and provide advice to the Board.

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Lead organisation: University of Galway

Identifying pressures

Antimicrobial resistance (AMR) is recognised globally as one of the greatest challenges to human and animal health. It has major implications for our agriculture and food production systems, environment and economy. In 2021, Ireland's second National Action Plan on AMR strengthened Ireland's commitment to tackling the challenge of AMR using the One Health approach, which recognises the link between human, animal and environmental health.

There are socio-economic, health and wellbeing benefits associated with access to clean water and blue spaces. Findings from the Public Health Impact of Exposure to Antibiotic Resistance in Recreational Waters (PIER) project help to bridge knowledge gaps on the public health implications of environmental exposure to antimicrobial-resistant organisms and how this impacts on use of blue/green spaces, wellbeing and quality of life.

Informing policy

The second National Action Plan acknowledges that there remains a growing need to enhance our understanding of the environmental dimension of AMR. This is necessary for the development and implementation of public health-related risk assessment and risk management strategies. The PIER project provides key evidence and recommendations to support the second National Action Plan and informs several different national and international policies[1].

Developing solutions

The PIER project adopted a One Health approach and brought together experts in microbiology, public health, epidemiology and social marketing. The PIER project has: (1) generated data on the relative risk of colonisation with antimicrobial-resistant bacteria following exposure to recreational waters, (2) revealed the persistence of carriage of antimicrobial-resistant bacteria by healthy individuals and (3) created a recreational water environment dynamic stakeholder map to enable analysis of the most feasible and impactful options to maximise use of our blue spaces.

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1 1 Water Framework Directive (2000/60/EC); Bathing Water Directive (2006/7/EC); Groundwater Directive (2006/118/EC); Drinking Water Directive (80/778/EEC) as amended by Directive (98/83/EC); Environmental Impact Assessment Directive (85/337/EEC); Sewage Sludge Directive (86/278/EEC); Urban Waste-water Treatment Directive (91/271/EEC); Habitats Directive (92/43/EEC); Integrated Pollution Prevention Control Directive (96/61/EC); Floods Directive (2007/56/EC); Marine Strategy Framework Directive (2008/56/EC); EC (Water Policy) Regulations, 2003 (S.I. No. 722 of 2003); EC (Drinking Water) Regulations 2014 (S.I. 122 of 2014); EC Environmental Objectives (Surface Waters) Regulations, 2009 (S.I. No. 272 of 2009); EC Environmental Objectives (Groundwater) Regulations, 2010 (S.I. No. 9 of 2010); EC (Good Agricultural Practice for Protection of Waters) Regulations, 2010 (S.I. No. 610 of 2010); and EC (Technical Specifications for the Chemical Analysis and Monitoring of Water Status) Regulations, 2011 (S.I. No. 489 of 2011).

EPA RESEARCH PROGRAMME 2014–2020

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EPA Research Report

Prepared for the Environmental Protection Agency

by

University of Galway

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Executive Summary

Antimicrobial resistance (AMR) is recognised worldwide as one of the greatest threats to human health. Often referred to as "the silent pandemic", the spread of AMR not only impacts human health, but has major implications for animals, food production systems, the environment and the economy. The "One Health" concept recognises that the health of humans, animals, plants and our environment are interlinked. Adopting a One Health approach is key to effectively tackling the global problem of AMR. The World Health Organization's *Global Action Plan on Antimicrobial Resistance* sets out five key ways to tackle the challenge of AMR. The Irish government has also adopted a One Health approach and, in 2017, published Ireland's first National Action Plan on AMR. The publication of Ireland's second National Action Plan on AMR in 2021 strengthened Ireland's commitment to taking a One Health approach to address the challenge of AMR. The second National Action Plan acknowledged a growing need to enhance our understanding of the environmental dimension of AMR and this need was further highlighted by the research gap analysis commissioned by the Environmental Protection Agency in 2021, which detailed key gaps in our understanding of the environmental dimension of AMR in Ireland. The findings of the Public health Impact of Exposure to antibiotic Resistance in recreational waters (PIER) project, as detailed in this report, add to our knowledge in this area.

The emergence and dissemination of AMR are related to the use of antimicrobial agents. Significant quantities of the antimicrobial agents administered to humans and animals are excreted in urine or faeces in a form that remains biologically active. Furthermore, a high proportion of humans and animals may have antimicrobial-resistant bacteria (ARB) resident in their gut, significant numbers of which can ultimately enter the environment through the waste of the human or animal. In Ireland, as in most European countries, the majority of human waste water is treated in waste water treatment plants before being discharged to the environment. Our waters represent an important potential transmission route for ARB to humans, as surface waters are often both discharge points for waste water or run-off from agricultural land and sources for drinking water supplies and/or waters used for food production or recreational purposes.

As part of the PIER project, a scoping literature review was conducted to assess the occurrence of waterborne organisms of public health concern, such as ARB, pathogenic bacteria or viruses, in identified natural bathing waters across the European Union (EU). This review critically evaluated the potential risk of human exposure and examined the suitability of the current EU Bathing Water Directive for the protection of public health. Understanding the role of exposure to natural recreational waters in the acquisition and transmission of AMR is necessary in order to assess whether or not current bathing water regulations adequately protect public health.

A point prevalence survey, conducted over a 1-year period as part of the PIER project, evaluated the relative risk of gut colonisation with ARB following exposure to natural recreational waters and examined whether or not recreational water users were more at risk than control participants of gut colonisation with ARB. A total of 411 healthy participants were recruited from across the island of Ireland (199 frequent open water users and a control group of 212 non-/infrequent open water users). The PIER project's findings revealed that recreational water users were not at greater risk of gut colonisation with ARB than those in the control group, and assessment of risk factors suggests that exposure to waters classified as "excellent" may protect against colonisation with ARB. Findings also revealed that ARB colonisation was more frequently detected in water users outside the designated bathing water season (1 June to 15 September each year).

Carriage of ARB may have no consequences for the colonised individual. However, those colonised with ARB are at risk of illness, owing to bacteria migrating from their gut and causing infection elsewhere in the body, such as the urinary tract or bloodstream, as are their elderly or immunocompromised close contacts, to whom the bacteria may be transferred. As part of the PIER project, persistent gut carriage of ARB by healthy participants was assessed. This involved assessing the carriage of ARB by 45 individuals over a 1-year period. Participants were invited to submit faecal samples every 2 months, with findings indicating carriage durations of between 4 and 23 months.

Systems thinking acknowledges that one person or organisation alone cannot address challenges such as improving and protecting our recreational water quality. By understanding a system, and the dynamics within it, strategies can be developed to mobilise multilevel systemic behaviour change. A review of current literature, completed as part of the PIER project, revealed a lack of guidance on both the role of stakeholders in the water quality system and methods for engaging with them from a holistic systems perspective. The system map co-created as part of the PIER project can assist stakeholders across the system to prioritise change strategies and investment in both the short and long term.

Overall, the PIER project has (1) generated data on the relative risk of colonisation with ARB following exposure to recreational waters, (2) revealed the persistence of carriage of ARB by healthy individuals and (3) created a recreational water quality system map that enables analysis of the most feasible and impactful options for maximising blue space usage.

1 Introduction

1.1 Background

Antimicrobial resistance (AMR) is recognised globally as one of the greatest threats to human health. The emergence and spread of AMR, as a result of both appropriate and inappropriate antimicrobial use, as well as inadequate infection prevention and control measures, has become a huge burden on both health services and economies worldwide. In 2019, it was estimated that AMR resulted in extra healthcare costs of approximately €1.1 billion per annum in the EU/European Economic Area (OECD and ECDC, 2019). A recent study estimated that 4.95 million deaths related to AMR, including 1.27 million deaths directly attributable to AMR, occurred across 204 countries in 2019 alone (Murray *et al*., 2022).

Bacteria can be intrinsically resistant to antimicrobial agents or may acquire resistance as a consequence of genetic change. There are a number of different types of antimicrobial-resistant bacteria (ARB), some of which are resistant to last-resort antibiotics, e.g. carbapenemase-producing Enterobacterales (CPE). In many cases of infection with CPE, there are very few available options for treatment, including colistin, tigecycline and fosfomycin. CPE were declared a public health emergency in Ireland in 2017, and are categorised as “critically important” in the World Health Organization’s (WHO’s) list of priority pathogens for which new antimicrobials are needed (Tacconelli *et al*., 2018).

The emergence and dissemination of AMR is related to the use of antimicrobial agents. Antimicrobial agents have been used for decades in humans and animals and for other applications. The role of the environment in the emergence and spread of AMR and the potential impact on human and animal health is increasingly recognised as an area requiring more focus (Department of Health, 2021; European Commission, 2017; WHO, 2015). The need to better understand the role of the environment in the emergence, dissemination, persistence and transmission of AMR is crucial to informing future strategies and policy developments, as highlighted in both the European and Irish Action Plans on AMR (Department of Health, 2021; European Commission, 2017).

Globally, the major sources of antimicrobials, ARB and antimicrobial-resistant genes (ARGs) in the environment include human and animal waste, inappropriately disposed of unused antimicrobial agents and effluent from facilities that manufacture antimicrobial agents. On any given day, about one in three patients in any major hospital in Ireland is taking antibiotics. In many cases, a patient may be on several different antibiotics simultaneously. The situation is similar in long-term care facilities. A significant quantity of the antimicrobials administered to humans and animals is excreted in urine or faeces in a form that is still biologically active. Furthermore, a high proportion of humans and animals may have ARB resident in their guts, significant numbers of which can ultimately enter the environment through the waste of the human or animal. In Ireland, as in most European countries, the majority of human waste water is treated in waste water treatment plants before being discharged to the environment. Under the EU’s Urban Waste Water Treatment Directive (91/271/EEC) and Water Framework Directive (2000/60/EC), the Environmental Protection Agency (EPA) monitors and reports annually on waste water discharges. The most recent data, from 2022, reveal that 15 out of 173 large urban areas did not meet national and EU requirements for secondary waste water treatment, and that untreated waste water was routinely discharged into rivers, estuaries and coastal waters at 26 locations around Ireland (EPA, 2023). This represents a very significant risk of the transmission of AMR to the aquatic environment. The recently completed EPA/Health Service Executive-funded Antimicrobial Resistance and the Environment – Sources, Persistence, Transmission and Risk Management (AREST) project highlights the widespread contamination of Ireland’s waters, including recreational waters, with ARB of clinical concern (Morris *et al*., 2024).

Where contaminated waters are used for drinking or recreational purposes there is a risk of transmission of AMR to humans. A recent EPA-funded study (Curtis and Hynes, 2017) found that water quality greatly impacts the public’s water-based recreational activities. Higher water quality locations were more likely to attract recreational visits from boaters, anglers, walkers, cyclists and water sports enthusiasts. High water quality locations were also associated with visits of longer duration. There are therefore potential health implications for a significant proportion of the Irish population as a result of exposure to ARB and ARGs in recreational waters.

A number of reports have highlighted the great potential for ingestion of antimicrobial-resistant organisms (AROs) and ARGs during activity in recreational waters (Leonard *et al.*, 2015, 2018a). A UK-wide prospective study found that frequent surfers of coastal waters were four times more likely to be colonised by antimicrobial-resistant *Escherichia coli* than matched control participants (Leonard *et al.*, 2018b). A recent systematic review and meta-analysis by Leonard *et al.* (2018a) also identified an increased risk of experiencing gastrointestinal ailments, symptoms of ear infection and symptoms of any ailment in bathers exposed to coastal waters compared with non-bathers. As outlined in this report, further work needs to be carried out to elucidate the health implications and clinical relevance of exposure to AROs in recreational waters in order to fully understand the risk to public health and inform regulatory agencies and policy. Exposure may or may not lead to colonisation, and colonisation may not lead to infection.

It is evident that there are socio-economic, health and wellbeing benefits associated with access to clean water and blue spaces (Völker and Kistemann, 2011; Wheeler *et al.*, 2012). There is also strong evidence that higher levels of recreational demand occur at sites with better water quality (Curtis and Hynes, 2017). It is recognised in the government's *Healthy Ireland: A Framework for Improved Health and Wellbeing 2013–2025* report that the environment and human health are inextricably linked (Department of Health, 2013).

As detailed in this report, the Public health Impact of Exposure to antibiotic Resistance in recreational waters (PIER) project has generated data on the carriage of ARB by healthy individuals in Ireland and assessed the risk of infection posed by exposure to recreational waters. This report also highlights the barriers to, and enablers of, interaction with our blue spaces, including examination of the role of ARB contamination. The data generated support Ireland's National Action Plan on AMR (Department of Health, 2021).

1.2 The PIER Project's Aims

The overall aims of the PIER project were to:

- complete a scoping literature review of the public health implications (colonisation and infection) associated with exposure to ARB in recreational waters;
- assess the carriage rate and persistence of carriage of ARB by individuals who engage in recreational water activities, as well as a control group of non-/infrequent water users (WUs) who do not engage in water activities;
- conduct a review examining AMR transmission in recreational waters and the associated risks to public health, quality of life and use of blue spaces;
- build a recreational water environment dynamic stakeholder map to enable analysis of the most feasible and impactful options for overcoming barriers and maximising enablers.

1.3 Report Structure

This report provides an overview of the research conducted as part of the PIER project and outlines its key findings and recommendations. The research was carried out through four integrated work packages. Each chapter of this report provides an overview of the studies carried out in each work package and includes references to publications arising from this work.

The report is structured as follows:

- Chapter 2: Scoping Literature Review of Potential for Exposure to Organisms of Public Health Concern in Naturally Occurring Bathing Waters.
- Chapter 3: Assessing the Impact of Recreational Water Use on Carriage of Antimicrobial-resistant Organisms.
- Chapter 4: The Persistence Study – Assessing the Duration of Antimicrobial-resistant Enterobacterales Gut Carriage in Healthy Participants and the Impact of Recreational Water Use.
- Chapter 5: Stakeholder Dynamic Mapping and Modelling.
- Chapter 6: Recommendations.

In line with Ireland's National Action Plan on AMR (Department of Health, 2021), we use the term AMR throughout this report. In general, AMR refers to resistance to antibacterials (antibiotics), antivirals, antifungals and antiparasitics. However, for the purposes of the PIER project and this report, where AMR is referred to, we are referring to resistance to antibacterials (antibiotics) only.

2 Scoping Literature Review of Potential for Exposure to Organisms of Public Health Concern in Naturally Occurring Bathing Waters

2.1 Key Highlights

- A critical lack of surveillance of pathogenic organisms in bathing waters is evident.
- There is a need to incorporate more inclusive parameters into current monitoring methods.
- Further study of health risks from organisms undetected by current regulatory methods is needed.
- Greater understanding of the health risks associated with bathing waters is needed.

2.2 Overview

Water-based bathing pastimes are important for both mental and physical health. However, exposure to waterborne organisms could present a substantial public health issue. Bathing waters are shown to contribute to the transmission of illness and disease, and represent a reservoir and pathway for the dissemination of AROs. Current bathing water quality regulations focus on the enumeration of faecal indicator organisms and are not designed to detect specific waterborne organisms of public health concern (WOPHC), such as ARB, pathogenic bacteria or viruses. This is the first review to assess the occurrence of WOPHC, including bacteria, viruses and protozoa, in identified natural bathing waters across the EU. It aims to critically evaluate the potential risk of human exposure and to assess the suitability of the current EU Bathing Water Directive (BWD) (2006/7/EC) for the protection of public health. Further details of the work outlined in this chapter, including the methods used and the findings and knowledge gaps identified, have been published elsewhere (Farrell *et al.*, 2021).

2.3 Methods and Materials

To direct and focus the scoping review, the following research question was used: "What is the prevalence of WOPHC in EU bathing waters and is there a risk to human health beyond what is detected under the current BWD" (Farrell *et al.*, 2021).

The researchers identified, collated and analysed literature pertaining to a selection of bacterial (*Campylobacter* spp., *E. coli, Salmonella* spp., *Shigella* spp., *Vibrio* spp., *Pseudomonas* spp. and ARB), viral (hepatitis spp., enteroviruses, rotavirus, adenovirus and norovirus) and protozoan (*Giardia* spp. and *Cryptosporidium* spp.) contaminants in EU bathing waters. Following a literature search, the screening of all articles retrieved and the elimination of articles based on predefined inclusion and exclusion criteria, 60 articles remained (see Farrell *et al.*, 2021, for further details).

2.4 Key Findings and Discussion

The 60 articles included spanned 18 European countries and were published over a time span of 35 years, with 30% being published between 2011 and 2015. A variety of water bodies were included, with 27 investigations focused solely on coastal bathing waters, 16 focused solely on freshwater sites and 17 analysing two or more water types. Overall, the majority of investigations were performed in Italy ($n=15$), followed by Spain ($n=12$) and the UK ($n=10$). Waterborne organisms were classified into the three categories of bacteria, viruses and protozoa and were present in 58%, 36% and 17% of the total investigations, respectively.

2.4.1 WOPHC detection with respect to bathing season and bathing water quality classification

Of the 60 investigations, 53 (88%) took place either exclusively during the bathing season or both during the season and outside the season. Three investigations took place exclusively outside the bathing season and four failed to include the time of sampling. One-third of the investigations involved bathing waters classified as "sufficient" or higher quality, according to BWD parameters. Just over half

(55%) of the total investigations failed to clearly outline bathing water quality, 5% investigated water bodies that had a classification of "poor" and 7% investigated waters that were classified across more than one water quality level. Bacteria, viruses and protozoa were detected in "excellent" and "sufficient" waters and bacteria and viruses were detected in "good" and "poor" waters.

2.4.2 Detection rate of waterborne organisms

The total number of samples across all investigations was 8118, with detection of one or more organisms in 2449 (30%) of these. Viruses was the most common category detected (in 1281 samples), followed by bacteria (865 samples) and protozoa (303 samples). Within the virus category, adenovirus was the most frequently detected, found in 761 (68%) of the 1124 samples tested for it. Reovirus had the second largest number of detections, with 107 out of 253 samples testing positive (42%), and norovirus was detected in only 155 (10%) of the 1576 samples investigated. In the bacteria category, *Salmonella* spp. was detected in the largest number of investigations ($n = 990$); however, *Vibrio* spp. had the highest detection rate, found in 392 (84%) of the 466 samples analysed. ARB had the third highest detection rate, found in 208 (47%) of the 442 samples analysed. Finally, in the protozoa category, *Cryptosporidium* spp. had the most positive investigations ($n = 894$), but *Giardia* spp. had the highest detection rate, at 17% ($n = 854$).

2.4.3 Organisms of public health concern in bathing waters

The review highlighted the detection of several bacterial pathogens capable of causing gastrointestinal illness in bathing waters that met or exceeded the BWD standards for microbial quality, including *Vibrio* spp., *Salmonella* spp. and *Campylobacter jejuni*. The review highlighted not only the presence of such pathogens in bathing waters, but also the detection of virulence factors and AMR within these pathogens (see Farrell *et al.*, 2021, for further details). The high detection rate of ARB (47%) found in the review highlights the potential for bathing waters to be a source of ARB and ARGs, as well as a pathway for infection and colonisation of humans and other animals that use the waters as habitat. Viral and protozoan pathogens were also detected, neither of which are currently regulated by the BWD.

2.4.4 Recommendations for research policy and practice

- An increased temporal sampling regime, rather than a one-off sampling methodology.
- A universal, homogeneous methodology with harmonised sample volumes, allowing for comparisons between study outcomes.
- Increased research into AMR in bathing waters (regulated and unregulated), and its potential inclusion as a parameter in the BWD.
- Standardised methodologies, such as those recommended by the WHO global Tricycle programme for surveillance of extended-spectrum beta-lactamase-producing *E. coli* (ESBL-EC), should be established to provide a cohesive multidisciplinary surveillance of AMR in bathing waters.
- Further research to define suitable indicators that represent each of the three categories of pathogen, alongside risk-based identification of locally important WOPHC for monitoring.

2.4.5 Limitations and key knowledge gaps

Farrell *et al.* (2021) outline the limitations of, and critical knowledge gaps in, the current research identified in this review in further detail. However, their key observations included gaps in the information provided by investigations, which led to their exclusion from the review. The most common of these was a failure to report sample volume. There was a lack of standardisation among environmental sampling and processing methodologies across the studies reviewed. The review was limited to European waters, as it focused on bathing waters under the remit of the EU's BWD.

2.5 Conclusions

In conclusion, the findings of this review highlight the extent and significance of contamination in European bathing waters owing to a variety of potentially harmful organisms that are currently beyond the scope of the revised BWD, and support the inclusion of a wider spectrum of parameters in the BWD.

3 Assessing the Impact of Recreational Water Use on Carriage of Antimicrobial-resistant Organisms

3.1 Key Highlights

- The rate of carriage of antimicrobial-resistant Enterobacterales by recreational WUs and control participants was compared.
- A carriage rate of 7.1% for extended-spectrum beta-lactamase-producing Enterobacterales (ESBL-PE) in healthy individuals was observed.
- WUs were less likely than control participants to carry ESBL-PE (relative risk = 0.34, $p = 0.007$).

3.2 Overview

Understanding the role of exposure to natural recreational waters in the acquisition and transmission of AMR is an area of increasing interest. This chapter provides an overview of a point prevalence study that was carried out on frequent natural recreational WUs and matched control participants across Ireland, to determine the prevalence of colonisation with two medically important types of ARB that frequently cause difficult-to-treat infections in humans. These organisms are ESBL-PE and carbapenem-resistant Enterobacterales (CRE), which are commonly found in the intestinal flora of patients in healthcare facilities. Key findings are presented and discussed in this chapter; further details on the methodology and findings can be found in Farrell *et al.* (2023a).

3.3 Methods and Materials

3.3.1 Study population and design

Between March 2020 and October 2021, a cross-sectional point prevalence study was conducted on adult volunteers living in Ireland. Participants were separated into two categories based on their self-reported exposure to natural recreational waters, including rivers, lakes and coastal waters. For the purposes of this study, recreational WUs were defined as those who used natural waters at least three times per month for recreational activities that involve immersion of the participant's head in the water. The control group were defined as those who did not frequently engage in recreational water activities (once per month or less). See Farrell *et al.* (2023a) for full details on the inclusion and exclusion criteria. One of the study's secondary objectives was to examine whether or not there was an increase in the prevalence of colonisation with ESBL-PE or CPE in study participants during the bathing season (1 June to 15 September), when more frequent exposure would be expected. To investigate this, a subset of participants who had already submitted samples during the non-bathing period (16 September 2021 to 31 May 2022) were invited to submit a second sample during the bathing period (1 June to 15 September 2022).

3.3.2 Participant recruitment, sample and data collection

As a result of the implementation of COVID-19 restrictions in April 2020, the recruitment strategy was changed from in-person engagement to traditional and social media campaigns, which were launched in August 2020 and continued until October 2021. Those interested in participating in the study initially registered their interest via an online form, with eligibility checks and informed consent forms subsequently completed by phone call. Participants were sent study kits, which included an information sheet, a consent form, faecal sample collection instructions, a sample collection pot, a pre-paid addressed envelope for return and a survey, and were asked to return a self-collected faecal sample, a signed consent form and a completed study survey. The survey gathered demographic data alongside reported exposures to recreational waters, participants' potential risk factors for gut colonisation with ARB (e.g. diet and occupational exposure) and the locations of beaches the participants frequently used.

3.3.3 Faecal sample processing and antimicrobial-resistant bacteria characterisation

Faecal samples were processed in the laboratory to identify and characterise ESBL-PE and CPE. The ARB of interest were isolated through culture-based methods and their susceptibility to a panel of antimicrobials used in clinical medicine was assessed. ESBL-PE and CPE were confirmed by polymerase chain reaction (PCR) and characterised using whole-genome sequencing and bioinformatics. Differences in the rate of carriage between groups was assessed using statistical analysis. The full methodology used is detailed in Farrell *et al.* (2023a).

3.4 Key Findings and Discussion

3.4.1 Study population

A total of 411 participants from 28 of the 32 counties of Ireland were included in analyses. The study population comprised 199 WUs and 212 control participants. Most participants identified their ethnicity as white Irish (91%) and were female (60.3%). Almost half ($n=200$, 48.7%) were in the age range 35–54 years.

3.4.2 Identification of antimicrobial-resistant bacteria in water users and control participants

A total of 80 Enterobacterales were isolated from 27 WUs ($n=30$ isolates) and 46 control participants ($n=50$ isolates). Over half were classified as multi-drug resistant, showing resistance to one or more antimicrobial agents from three or more different antimicrobial classes. Species identified included *E. coli* ($n=62$, 77.5%), *Citrobacter freundii* complex ($n=8$, 10%), *Enterobacter cloacae* complex ($n=3$), *Klebsiella* spp. ($n=3$), *Hafnia alvei* ($n=2$), *Serratia fonticola* ($n=1$) and *Raoultella ornitholytica* ($n=1$). Of the 411 participants, 7.1% ($n=29$) had ESBL-PE isolates and 2.2% ($n=9$) had CRE isolates. ESBL-PE prevalence was highest in participants aged between 55 and 64 years (8%) and was slightly higher in women (8% (20/249), compared with 6% (9/161) for men). The colonisation rate of 7.1% across the whole study population for ESBL-EC is comparable to those in similar studies conducted elsewhere in Western Europe, in which ESBL-EC carriage was observed at 9%, 8.6% and 11.3% in London, Amsterdam and Birmingham, respectively (Otter *et al*., 2019; Reuland *et al.*, 2016; Wickramasinghe *et al.*, 2012). Findings indicated that more control participants were colonised with ARB than WUs. The prevalence of carriage in WUs and control participants for ESBL-PE was 3.5% ($n=7$) and 10.4% ($n=22$), respectively, and for CRE it was 2% ($n=4$) and 2.4% ($n=5$), respectively. WUs were about one-third as likely to be colonised by ESBL-PE as control participants (risk ratio = 0.34, 95% confidence interval (CI) 0.148 to 0.776, $\chi^2=7.37$, $p=0.007$). When WUs were compared with control participants who reported no exposure to recreational waters in the past year ($n=120$), the colonisation risk for WUs was even lower, about one-quarter as likely as control participants (risk ratio = 0.24, CI 0.106 to 0.581, $\chi^2=12.2$, $p=0.0005$). There were no risk factors (e.g. occupational) identified that were associated with an increased risk of colonisation in either group. All WUs who were colonised with ESBL-PE used bathing waters with an annual classification of “excellent” according to the BWD. These results contrast with a recent UK study, which found that frequent surfers were three times more likely than non-bathers to be colonised with third-generation cephalosporin-resistant *E. coli* (Leonard, *et al*., 2018b). These differences may be attributable to the different study populations, variation in the water qualities to which participants may have been exposed and different analytical methods used to detect ESBL-PE. Leonard *et al.* (2018b) recruited frequent surfers, who ingest more water during surf sessions than other WU groups (Leonard *et al*., 2015; Stone *et al*., 2008). In the present study, various types of WUs (primarily sea swimmers) were recruited, who may experience fewer unexpected head immersions and therefore ingest smaller volumes of water per session than surfers (Leonard *et al*., 2018a). A higher proportion of people engaging in water sports involving boards (e.g. surfing) in our study harboured ESBL-PE than those who engaged in other popular water activities, such as swimming (Table 3.1). This may be because of the greater frequency of water ingestion reported by these participants; however, the sample size meant that statistical significance could not be established. Bathing water quality also differed between the UK study and the present study, with 76% of Irish waters classified as “excellent” during the study period,

Table 3.1. Characteristics of antimicrobial-resistant bacterial isolates

Isolate ID	Participant category	Species	ST	Beta-lactamase genes	Plasmid replicons detected
MEH633	Control	*Enterobacter hormaechei*	Novel ST	$bla_{\text{ACT-14}}^{*}$	ND
MCF1305	WU	*Citrobacter braakii*	Novel ST	$bla_{\text{CMY-74}}^{*}$	ND
MEC813	Control	*E. coli*	Novel ST	$bla_{\text{CTX-M-15}}$	Col156, IncFIB, IncFIC
MSF1196A	Control	*S. fonticola*	Novel ST	$bla_{\text{FONA-6}}^{*}$	Col1, IncFIB, IncFIC
MEC2701	Control	*E. coli*	Novel ST	$bla_{\text{CTX-M-15}}$	ColRNAI
MEC724A	WU	*E. coli*	10	$bla_{\text{CTX-M-14}}$, $bla_{\text{TEM-1B}}$	Col(MG828), ColRNAI, IncB/O/K/Z, IncFIA, IncFIB, IncFIC
MEC2902	Control	*E. coli*	10	$bla_{\text{CTX-M-55}}$, $bla_{\text{TEM-1B}}$	IncFIB, IncFIC, IncI1
MEC1047	WU	*E. coli*	10	$bla_{\text{SHV-12}}^{*}$	ColRNAI, IncFIC
MEC2637	Control	*E. coli*	10	$bla_{\text{CTX-M-14}}$, $bla_{\text{TEM-1B}}$	Col(MG828), ColRNAI, IncB/O/K/Z, IncFIA, IncFIB, IncFIC
MEC2479	Control	*E. coli*	14	$bla_{\text{TEM-1B}}^{*}$ $bla_{\text{SHV-12}}$	Col156, ColRNAI, IncFIA, IncFIB, IncFIC, IncFII
MEC2831	Control	*E. coli*	14	$bla_{\text{TEM-1B}}^{*}$ $bla_{\text{SHV-12}}$	Col156, ColRNAI, IncFIA, IncFIB, IncFIC, IncFII
MEC1940	WU	*E. coli*	14	$bla_{\text{TEM-1B}}^{*}$, $bla_{\text{SHV-12}}^{*}$	Col156, ColRNAI, IncFIA, IncFIB, IncFIC, IncFII
MEC6749	Control	*E. coli*	38	$bla_{\text{CTX-M-15}}^{*}$, $bla_{\text{TEM-1B}}$	Col156, IncFIB, IncFIC
MEC2595A	Control	*E. coli*	38	$bla_{\text{CTX-M-15}}^{*}$	Col156, IncFIB, p0111
MCF2589	Control	*C. freundii*	62	$bla_{\text{CMY-150}}^{*}$	IncFIA
MEC1043	WU	*E. coli*	69	$bla_{\text{CTX-M-15}}$, $bla_{\text{TEM-1B}}$	Col(MG828), Col156, Col8282, ColRNAI, IncB/O/K/Z, IncFIA, IncFIB, IncFIC
MEC1862	WU	*E. coli*	69	$bla_{\text{DHA-1}}$, $bla_{\text{TEM-1B}}$	Col156, Col8282 ColRNAI, IncFIA, IncFIB, IncFIC, IncX1, IncY
MEC2233	Control	*E. coli*	69	$bla_{\text{CMY-138}}$, $bla_{\text{TEM-1B}}$	Col156, Col8282, IncB/O/K/Z, IncFIB, IncFII, IncX1
MEC2078	Control	*E. coli*	69	$bla_{\text{CTX-M-1}}$, $bla_{\text{TEM-1B}}$	IncFIB, IncFII
MEC2674	Control	*E. coli*	69	$bla_{\text{CTX-M-15}}$	Col156, Col8282, IncFIA, IncFIB, IncFII, IncX1
MEC760	Control	*E. coli*	101	$bla_{\text{CTX-M-55}}$, $bla_{\text{TEM-141}}$	Col(MG828), IncFIB, IncFIC, IncFII, IncFII,IncI1
MEC2840A	Control	*E. coli*	127	$bla_{\text{CTX-M-15}}^{*}$	Col156, IncB/O/K/Z, IncFIB, IncFII
MEC1502A	Control	*E. coli*	131	$bla_{\text{CTX-M-15}}$, $bla_{\text{OXA-1}}$	Col(BS512), IncFIA, IncFIB, IncFIC
MEC1601	Control	*E. coli*	131	$bla_{\text{CTX-M-15}}^{*}$, $bla_{\text{TEM-1B}}$	Col156, ColRNAI, IncFIB, IncFII
MEC2088	Control	*E. coli*	131	$bla_{\text{CTX-M-15}}$	Col156, IncFIA, IncFII
MEC681	WU	*E. coli*	131	$bla_{\text{CTX-M-27}}$	Col(MG828), Col156, IncFIA, IncFIB, IncFII
MEC2269	WU	*E. coli*	131	$bla_{\text{CTX-M-14}}^{*}$, $bla_{\text{TEM-1B}}$	Col1, IncFIB, IncFII
MEC1107	Control	*E. coli*	131	$bla_{\text{CTX-M-27}}^{*}$, $bla_{\text{TEM-1B}}$	Col1, IncFIB, IncFII
MEC883	Control	*E. coli*	141	$bla_{\text{CTX-M-1}}$, $bla_{\text{TEM-210}}$	IncFIB, IncFIC, IncI1
MEC2196	Control	*E. coli*	212	$bla_{\text{CTX-M-15}}$	Col440I, IncFIB, IncI1
MCF2205	Control	*Citrobacter youngae*	243	$bla_{\text{CMY-53}}^{*}$	Col440II, ColRNAI, RepA
MEC1622	Control	*E. coli*	357	$bla_{\text{DHA-1}}$	Col1, Col1, ColRNAI, IncFII
MCF2874	WU	*Citrobacter murliniae*	496	$bla_{\text{CMY-104}}^{*}$	RepA
MCF2197	Control	*Citrobacter portucalensis*	728	$bla_{\text{CMY-39}}^{*}$	Col440I
MEC2488	Control	*E. coli*	2852	$bla_{\text{CTX-M-15}}$, $bla_{\text{TEM-1B}}$	IncY
MEC2457	Control	*E. coli*	6438	$bla_{\text{CTX-M-15}}^{*}$	Col440I, Col12, ColRNAI, ColpVC, IncB/O/K/Z, IncFIB, IncFIC, IncI1
MEC2539	WU	*E. coli*	11226	$bla_{\text{CTX-M-15}}$, $bla_{\text{TEM-1B}}$	ColpVC, IncFIB (2)

***Chromosomally located genes determined by Platon and ResFinder.**

ND, not detected; ST, sequence type.

compared with just 59.6% of UK waters during the UK study. It is plausible that swimming and other recreational activities in good-quality water, with a low probability of ESBL-PE exposure, may be protective, owing to positive impacts on microbiome diversity. Evidence is emerging to support the relationship between microbiome diversity and a reduction in invasion or colonisation probability by enteric pathogens (Khan *et al.*, 2021; Panwar *et al.*, 2021). Furthermore, there is potential that a water quality-dependent dose–response relationship exists, with natural recreational waters of high quality having a protective effect that reverses to an increased colonisation risk in lower-quality water for individuals with high exposure risk (Leonard *et al.*, 2018a)

3.4.3 Variation in the carriage of antimicrobial-resistant bacteria detection across sampling periods

To investigate variation in the carriage of ESBL-PE across the sampling periods, 140 individuals (72 WUs, 68 controls) submitted samples during both the non-bathing season and the bathing season. Five participants carried ESBL-PE in both sampling periods (one WU, four controls). There was evidence that the same antimicrobial-resistant strain was persistent in the four control participants during both the bathing and non-bathing seasons. During the non-bathing season, two individuals from each group carried ESBL-PE, which was not detected in their samples during the bathing season. There were six new detections of ESBL-PE in the bathing season (four WUs, two controls). Overall, there were more detections of ARB in the non-bathing period.

3.4.4 Genomic characterisation of the antimicrobial-resistant bacteria colonising participants

Overall, 230 genes for AMR were detected in the 36 bacterial isolates collected from participants. The most common ($n = 56$) were for resistance to beta-lactam antimicrobials, including the genes encoding ESBL enzymes that break down clinically important antimicrobials. The median number of resistance genes carried by isolates was six, and isolates were usually multi-drug resistant, i.e. resistant to at least one agent from three or more different classes of antimicrobials. Several high-risk virulent and antimicrobial-resistant clones of *E. coli* were detected in the participants, which are known to cause difficult-to-treat infections in hospital patients in many countries. These included the sequence types (STs) ST131, ST69, ST10 and ST38, all of which carried ESBL genes. These clones have virulence genes that account for their ability to cause infections. Their detection in healthy members of the community is concerning for the spread of antimicrobial-resistant pathogens (Figure 3.1).

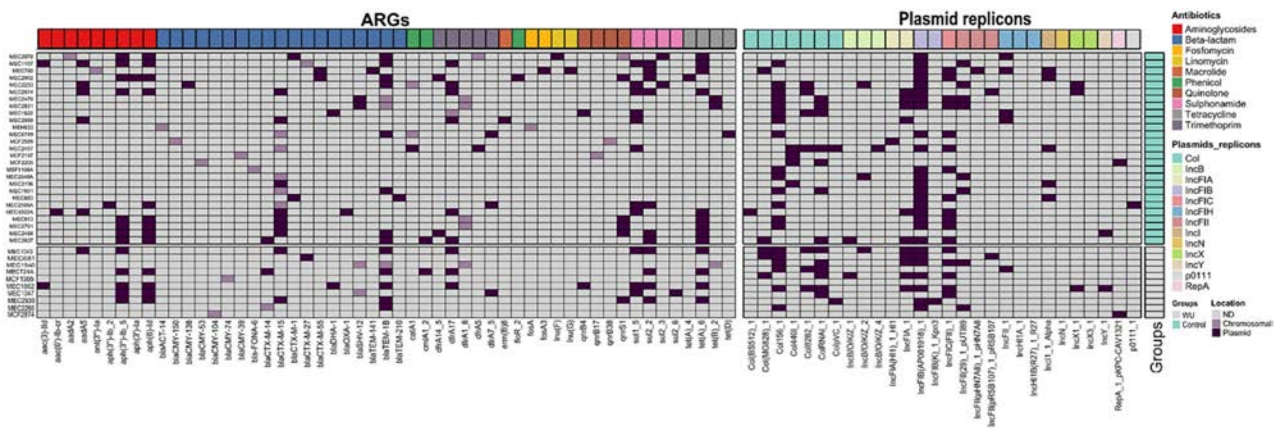

Figure 3.1. Heatmap depicting ARGs detected by ResFinder (left); and plasmid replicons detected and their probable locations within the genome (right). The coloured bars at the top of the ARG section (left) indicate the antimicrobial class the gene confers resistance to, whereas the coloured bars at the top of the plasmid replicon section (right) indicate the replicon class. The genomic location of resistance genes is identified as a plasmid (dark purple), a chromosome (violet) or absent/not detected (ND, grey). The heatmap was created in RStudio using ComplexHeatmap (Gu *et al.*, 2016).

3.5 Conclusions

These results suggest show that frequent WUs were less likely to carry ESBL-PE than control participants. Furthermore, this research provides an estimate of the carriage rate of ESBL-PE in healthy individuals in Ireland. The presence of high-risk clones and resistance genes in healthy individuals without recent antimicrobial exposure is a cause for concern. It highlights the extent to which the AMR phenomenon, which was infrequently detected, even in the healthcare setting, in the late 20th century, is now endemic in the community, as well as the potential for this pattern to be repeated with CPE. This study makes important contributions to the evidence base exploring human interactions with natural environments and their impacts on health. Further research is needed to elucidate the environmental AMR risks and microbiological mechanisms underpinning gut colonisation by ARB to understand the risk of AMR transmission in natural environments and develop effective mitigation strategies to protect public health.

4 The Persistence Study – Assessing the Duration of Antimicrobial-resistant Enterobacterales Gut Carriage in Healthy Participants and the Impact of Recreational Water Use

4.1 Key Highlights

- The study compared the carriage of antimicrobial-resistant Enterobacterales in healthy participants over 1 year.
- ESBL-EC persisted in the gut for a median duration of 10.3 months (range 4–23 months).
- Eleven (24.4%) participants had ESBL-EC detected in their samples at least once.
- ESBL-EC levels were higher in WUs during the non-bathing season than during the bathing season (relative risk = 1.99).

4.2 Overview

This study aimed to assess the prevalence and persistence of gut colonisation with the medically important ARB ESBL-PE and CPE among healthy Irish people. Longitudinal surveillance facilitated identification of resistant strains in individuals in whom they were not previously detected. As a secondary objective, participants who were frequently in contact with recreational waters (WUs) were compared with those who did not utilise recreational waters (control participants) to investigate if this exposure influenced the 1-year incidence and persistence (duration of gut colonisation) of antimicrobial-resistant Enterobacterales in the community. Key findings are presented and discussed in this chapter, and further details on the methodology and findings can be found in Farrell *et al.* (2023b).

4.3 Methods and Materials

4.3.1 Recruitment of participants and study design

A subset of participants carrying antimicrobial-resistant Enterobacterales ($n = 40$) were recruited from the point prevalence study (see Chapter 3) to participate in a “persistence study” to investigate the duration of antimicrobial-resistant Enterobacterales’ gut carriage. An additional 10 participants who did not have antimicrobial-resistant Enterobacterales detected in the point prevalence study and did not report any of the previously defined domestic or occupational risks for antimicrobial-resistant Enterobacterales were invited as control participants (Farrell *et al.*, 2023a). Participants were invited to submit a faecal sample and complete a risk factor checklist once every 2 months over a 12-month period (November 2021 to October 2022). Checklists included questions regarding antimicrobial use, hospitalisation and travel, with participants asked to state if they partook in recreational water activities. WUs and control participants were defined based on their self-reported exposure to natural recreational waters, as in the point prevalence study.

4.3.2 Microbial analysis of participants’ samples

All faecal samples were screened for the presence of CPE and ESBL-PE using phenotypic (i.e. culture-based and antimicrobial susceptibility testing) and genotypic methods (i.e. real-time PCR or whole-genome sequencing). All bacterial genome sequences were analysed using bioinformatics to characterise their STs, ARGs, virulence genes and plasmids. To confirm the persistence of identical ESBL-PE isolates in samples from the same participant, the average nucleotide identities (ANIs) of isolates were compared using the EZBioCloud ANI Calculator. An ANI score of > 99.9% for the chromosomal contigs was assumed to be confirmation of persistence of the same isolate. Full details of the methods used are described in Farrell *et al.* (2023b).

4.3.3 Analysis of water use patterns and their association with colonisation status

Recreational water use, defined as recreational activities involving immersion in natural waters, was recorded for all participants for each sampling period and compared with the detection of ESBL-PE and/or CPE. Publicly available data on bathing water quality (as per BWD) from website beaches.ie was collated for bathing locations that participants had previously indicated they used most frequently on their point prevalence study surveys (Farrell *et al.*, 2023a). The impact of recreational water quality on ESBL-PE colonisation in the gut was assessed. To investigate the impact of seasonality on colonisation, detection rates in samples collected from WUs during the bathing period (May to September) were compared with detection rates for samples collected during the non-bathing period (October to April). The overall rate of ESBL-PE/CPE detection in WUs and control participants was compared. The statistical analyses used are detailed in Farrell *et al.* (2023b).

4.4 Key Findings and Discussion

Forty-five participants returned three or more faecal samples over the study period and were included in the analysis. A total of 255 faecal samples and risk factor checklists were received over the 12 months. From these samples, 55 resistant Enterobacterales were isolated. Of these, 48 were ESBL-EC, belonging to five STs: ST38 (*n* = 19, 40%), ST69 (*n* = 17, 35%), ST131 (*n* = 7, 15%), ST127 (*n* = 4, 8%) and ST398 (*n* = 1). One CPE was detected, an *Enterobacter asburiae,* which was isolated from a WU sample in the final sampling period and carried the class A serine carbapenemase gene $bla_{\text{IMI-2}}$ on a plasmid. In total, 12 of the 45 (27%) participants had an ESBL-PE or CPE detected at some point during the persistence study. No significant associations were established between detection of ESBL-PE/CPE and descriptive characteristics or risk factors. The detection pattern of ESBL-PE and CPE in participants over time is represented in Figure 4.1.

4.4.1 Extended-spectrum beta-lactamase and carbapenemase genes detected

The most frequent $bla_{\text{CTX-M}}$ gene detected among the 48 ESBL-EC was $bla_{\text{CTX-M-15}}$ (*n* = 28, 58.3%), followed by $bla_{\text{CTX-M-122}}$ (*n* = 9, 18.8%), $bla_{\text{CTX-M-14}}$(*n* = 8, 16.7%), $bla_{\text{CTX-M-1}}$ (*n* = 2, 4.2%) and $bla_{\text{CTX-M-32}}$ (*n* = 1, 2.1%). In addition, the majority of ESBL-EC (*n* = 31, 65.9%) had genes conferring resistance to other antimicrobial classes, including aminoglycosides (*n* = 26, 54.2%), sulphonamides (*n* = 26, 54.2%), trimethoprim (*n* = 26, 54.2%), tetracyclines (*n* = 15, 31.3%) and quinolones (*n* = 7, 14.6%). Among the plasmid-carrying ESBL-EC isolates (*n* = 47), plasmid replicons included the commonly ESBL-associated IncFII (*n* = 34), and IncI1 (*n* = 2). Seventeen ESBL-EC, isolated from four individuals (one WU, three controls), were predicted to carry plasmid-borne $bla_{\text{CTX-M}}$ genes, namely $bla_{\text{CTX-M-15}}$ (*n* = 16) and $bla_{\text{CTX-M-1}}$ (*n* = 1). The IncFII replicon was detected in all predicted plasmid-borne ESBL-EC. The remaining 31 ESBL-EC, isolated from six individuals (four WUs, three controls), were predicted by Platon analysis to have chromosomally encoded $bla_{\text{CTX-M}}$ genes (Figure 4.1).

The CPE isolate harboured the chromosomally encoded multi-drug efflux pumps OqxA and OqxB, alongside the fosfomycin resistance genes *fosA* and $bla_{\text{ACT-1}}$. The CPE isolate was phenotypically resistant to the beta-lactam (cefpodoxime, cefoxitin) and carbapenem (meropenem, ertapenem) antimicrobials. The $bla_{\text{IMI-2}}$ gene was associated with the lysR-like transcriptional regulator imiR, which has previously been reported in several species of $bla_{\text{IMI-2}}$-bearing CPE (Börjesson *et al.*, 2022; Hopkins *et al.*, 2017) (Figure 4.2).

4.4.2 Duration of carriage and patterns of detection

ESBL-PE were detected in the preceding point prevalence study in all but 1 of the 12 participants who were positive in the persistence study; however, 6 out of the 11 previously colonised participants acquired a new type of ESBL-PE or CPE during the persistence study. Of the 21 participants (9 WUs, 12 controls) who had ESBL-EC detected in samples provided during the preceding point prevalence study (Farrell *et al.*, 2023a), 12 had no ESBL-PE detected in this study. Interestingly, however, CPE was detected in one such participant in the final sample they provided (participant O). Of the 10 participants with ESBL-EC detected in both studies, six had isolates with the same gene and ST detected at four or more sampling points, with five of the six still positive for this ESBL-EC in the final sampling round, indicating carriage of over 1 year (Figure 4.1). One of the 10 control participants (participant H), who previously had no resistant Enterobacterales detected, had ESBL-EC detected in their second, third and

Figure 4.1. Timeline of ESBL-EC and CPE detection in participant samples at six sample collection points during the study. Within each, the last six capsules represent the faecal carriage of one individual over the six sampling points of the study period, with participant identification (ID) on the left. Each capsule represents a single sampling period, with the left half indicating the ST detected and the right half indicating an ESBL gene or CPE. A light grey fill in the capsule indicates no detection, while dark grey indicates that the sample was not submitted. Blue fill in the right half of the capsule indicates a plasmid-located gene, while an orange fill indicates the presence of a chromosomally located gene, according to Platon analysis. The point prevalence study was conducted from October 2020 to September 2021. In the participant ID column, carrier status is indicated by green (incidental carrier, one or two detections), yellow (frequent carrier, three or four detections) and red boxes (persistent carrier, five or more detections).

fourth persistence study samples and was therefore re-categorised as a frequent carrier. Five participants had isolates with differing STs or genes detected than those identified in bacteria isolated from their samples in the point prevalence study (participants C, D, I, J and M), while five other participants had the same ST and gene detected as before. The CTX-M gene carried by the most participants was $bla_{CTX\text{-}M\text{-}15}$ (n = 6), followed by $bla_{CTX\text{-}M\text{-}14}$ (n = 3) and $bla_{CTX\text{-}M\text{-}122}$ (n = 2), with $bla_{CTX\text{-}M\text{-}1}$ and $bla_{CTX\text{-}M\text{-}32}$ each detected in one

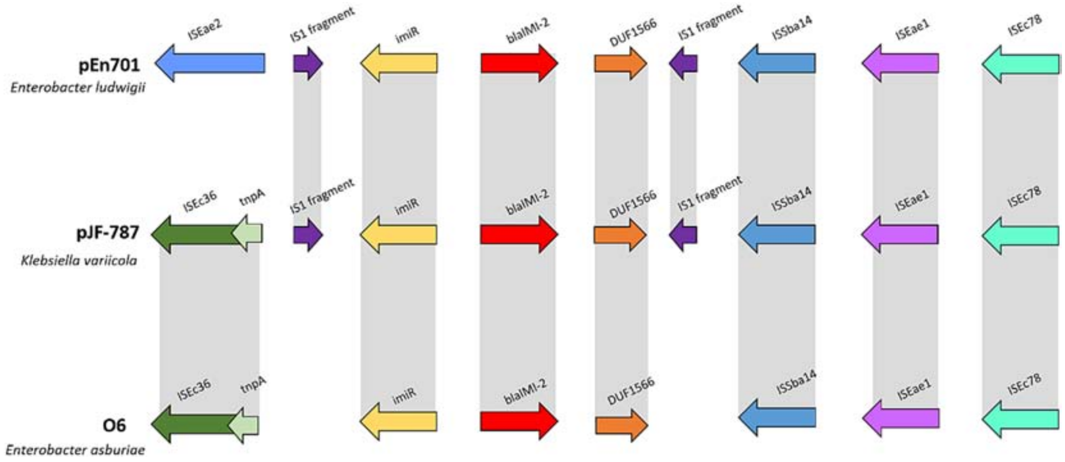

Figure 4.2. The alignment of two *bla*$_{IMI-2}$ genes, pJF-787 (Hopkins *et al.*, 2017) and pEn701 (Börjesson *et al.*, 2022), and adjacent insertion elements to the *E. asburiae* genome generated in this study (O6). The aligned segments connected with grey shading show >95% sequence identity.

participant. Four participants had isolates identified as ST69, with three of these carrying *bla*$_{CTX-M-15}$ (participants B, E and I) and one carrying *bla*$_{CTX-M-1}$ (participant A).

Four participants had ESBL-EC detected in all samples submitted and were therefore classified as persistent carriers (van Duijkeren *et al.*, 2018). Furthermore, four participants were defined as frequent carriers and three participants were classified as incidental carriers, with ESBL-EC detected in two samples or fewer. For two frequent carrier participants (participants E and K), the pattern of detection was variable, in that they provided two or more consecutive negative samples among five positive samples (including their point prevalence samples) (Figure 4.1). The median duration of carriage of ESBL-EC was 10.3 months overall (95% CI 6.445–14.155). A previous study in the Netherlands on healthy individuals found a shorter duration of carriage of 8 months (van Duijkeren *et al.*, 2018). However, another study on long-term care facility residents found a longer median duration of carriage of 13 months (Overdevest *et al.*, 2016). The varying durations of ESBL-EC persistence in different studies may be attributed to several factors, including patient populations, geographical locations and antibiotic usage. Kaplan–Meier survival analysis showed that colonisation persisted longer in the controls than in WUs ($p = 0.94$, $\chi^2 = 0.0061$). The longest period of colonisation detected was 23 months, in participant F, in whom an *E. coli* ST38 carrying *bla*$_{CTX-M-15}$ was detected in every sample provided across both studies (Figure 4.1). Overall, eight participants (15.6%) were classified as having a prolonged duration of carriage (i.e. as frequent and persistent carriers).

Although the longest duration of carriage was identified as 23 months, this participant, along with six others ($n = 7/45$, 15.6%), was still colonised with ESBL-EC at the end of the sampling period. In accordance with Jørgensen *et al.* (2017), who recommended defining decolonisation or clearance as two consecutive negative samples, after providing two consecutive negative samples, participant E (Figure 4.1) was deemed to no longer be colonised with ESBL-EC. However, in the final sampling period, an identical ESBL-EC was isolated. Therefore, it is likely that this was the result of variance in detection by the culture-based methods used. As noted by Jørgensen *et al.* (2017), a lack of detection does not confirm the absence of colonisation, but a reduction in faecal shedding can lower the risk of dissemination. Interestingly, participant E had reported undergoing antimicrobial treatment before the last sample was taken, which could have increased the selection pressure within the gut microbiome, resulting in a reduced population of normal flora and an increase in resistant isolates (Becattini *et al.*, 2016). Similarly, participant K had identical ST127 isolates detected with an intervening period of non-detection of 8 months (July 2021 to March 2022), although, unlike participant E, no reported risk factors could account for this. However, it is also possible that, in both cases, recolonisation with the same isolate from either a household or a community contact could have occurred (Doi *et al.*, 2007; Tandé *et al.*, 2010).

4.4.3 Persistent carriage of high-risk clones

Prolonged ESBL-EC carriage was associated with ST38 and ST69, although ST131 was also detected among participants with prolonged duration of carriage. The prolonged carriage of ST38 and ST69 has been previously documented (Jørgensen *et al*., 2017; van Duijkeren *et al.*, 2018), with ST69 being the most frequent ST to be identified in college students attending a northern California university during 1999–2017 (Reina *et al.*, 2018). While *E. coli* ST38 is commonly found as a commensal bacterium, it has also been implicated as a causative agent in infections such as urinary tract infections and sepsis (Fonseca *et al.*, 2022). As demonstrated in the present study, the persistence of ST38 in the gut may contribute to the development of antimicrobial-resistant strains. This was seen in participant C, in whose samples two different ESBL-EC isolates were initially identified ($bla_{\text{CTX-M-122}}$ positive ST38 and $bla_{\text{CTX-M-14}}$ positive ST131). However, by the final sampling round both $bla_{\text{CTX-M-122}}$ and $bla_{\text{CTX-M-14}}$ genes were detected in discrete ST38 isolates from that participant. The frequent identification of ST38 has previously been described in environmental and sewage samples in Ireland, providing further evidence for its importance as a community carriage-associated AMR reservoir (Hooban *et al*., 2022). *E. coli* ST131 is a high-risk clone frequently associated with community-acquired colonisation (Doi *et al.*, 2007). Throughout the study, *E. coli* ST131 was detected in three participants, each with differing $bla_{\text{CTX-M}}$ genes. *E. coli* ST131 is important in the epidemiology of fluoroquinolone- and third-generation cephalosporin-resistant *E. coli* infections worldwide and has been designated a globally multi-drug resistant clone (Nicolas-Chanoine *et al.*, 2014).

4.4.4 Association of colonisation with recreational water quality and season

All WUs, including those with ESBL-EC detected in their samples, used monitored bathing waters with annual classifications of “excellent”. Therefore, no associations could be made between water quality and colonisation status. Colonisation was higher among WUs in the non-bathing season ($n = 10$ detections from 60 samples (16.7%), November 2021 to April 2022), than among WUs in the bathing season ($n = 5$ detections from 57 samples (8.8%), May to September 2022) with a relative risk calculation of 1.9 (95% CI 0.69–5.22, $\chi^2 = 1.63$, $p = 0.202$). However, this association had wide confidence intervals and was not statistically significant.

Given the potential for the rapid spread of CPE in human populations, surveillance of environmental and community carriage reservoirs could enable early detection of emerging clones in the community. A critical knowledge gap remains regarding the potential for colonisation by AROs from exposure to recreational waters. This persistence study found ESBL-EC in at least one sample from five participants who used recreational waters classified as excellent. The samples in which ESBL-EC were detected were mostly collected during the non-bathing season, which indicates that there may be potential for an increased risk of colonisation during the non-bathing season, especially the winter months. This may be due to heavier contamination rates, linked to increased rainfall (Williams *et al.*, 2022).

4.5 Conclusions

This research describes the persistence of ESBL-EC in healthy individuals, which has significant implications for the transmission and spread of AMR. These findings highlight the ability of several ESBL-EC clones to colonise and persist in the human gut, with a median duration of 10.3 months. Consequently, healthy community carriers of ESBL-EC may represent a persistent and underestimated source of AMR. Given the growing concern about the prevalence of ESBL-EC, there is an urgent need for more effective measures to address its impact on the gut microbiome and its spread within the community. The carriage and onward dissemination of ESBL-EC contributes further to its prevalence in the community and could facilitate transfer of resistance genes to commensal bacteria in the gut through horizontal gene transfer. This study highlights how faecal colonisation monitoring of AMR in healthy individuals can facilitate a better understanding of the dynamics of resistance development and may contribute to the design of appropriate control strategies to preserve the effectiveness of antimicrobial therapies.

5 Stakeholder Dynamic Mapping and Modelling

5.1 Key Highlights

- A review of the current literature revealed a lack of guidance on the role of stakeholders and how to engage with them from a holistic systems perspective.
- System dynamics modelling is an effective methodology for understanding the complexity of the recreational water quality system and the interrelationships between different factors within the system.
- A co-created system map can assist stakeholders across the system in prioritising change strategies and investment in the short and long terms.

5.2 Overview

A holistic systems-based approach is urgently required to address the highly complex environmental crisis facing our society. A report published by the European Environment Agency, which reviewed the state and outlook of the European environment, suggested that systemic change is required to "transform the key societal systems pressures that drive environmental pressures and health impacts" (European Environment Agency, 2020a). In addition, the United Nations Sustainable Development Goals (2024), the Organisation for Economic Co-operation and Development (OECD, 2019) and the European Green Deal (European Environment Agency, 2020b) all propose "systems thinking" as key to addressing major societal challenges. Systems thinking promotes inclusion of and collective action by all stakeholders across all levels within a system (micro – the individual; meso – community engagement; macro – policy reform) and between the sectors present within that system. Systems and ecosystems comprise people, institutions and resources and their interactions.

This chapter adopts a systems social marketing framework and applies a qualitative system dynamics modelling methodology to visually map the relationships and interrelationships between barriers to and enablers of improving recreational water quality.

5.3 Role of Stakeholders in Systems Thinking

Systems thinking acknowledges that one person or organisation alone cannot address challenges such as improving and protecting our recreational water quality. By understanding the system and the dynamics within, strategies can be developed to mobilise multilevel systemic behaviour change (Brychkov *et al.*, 2021). The One Health concept provides an overarching framework for applying interdisciplinary thinking to complex problems. However, the role of social sciences has been under-represented in One Health research (Lapinski *et al.*, 2015). The PIER project uses social marketing as a complementary framework that has also been successful in developing behavioural and social strategies to overcome complex issues by adopting a systems thinking approach (Domegan, 2021). Social marketing seeks to "develop and integrate marketing concepts with other approaches to influence behaviours that benefit individuals and communities for the greater social good … It seeks to integrate research, best practice, theory, audience and partnership insight, to inform the delivery of competition sensitive and segmented social change programmes that are effective, efficient, equitable and sustainable" (International Social Marketing Association *et al.*, 2013).

Systems thinking recognises the power and role of transdisciplinary strategies in engaging multiple cross-sectoral stakeholders. However, before change strategies can be applied, it is important to understand the roles and functions of the various cross-sectoral stakeholders and how they interact with each other in the recreational water system.

A scoping review was undertaken to understand the role and function of stakeholders in the recreational water context. For the purpose of the scoping review, Freeman's highly cited definition of a stakeholder was adopted: "any group or individual who can affect or is affected by the achievement of the organization objectives" (Freeman, 1984, p. 47). This broad definition embraces the direct and indirect effects stakeholders can have within a system. For example, swimmers, anglers, researchers and policymakers can all be part of the same recreational water system, yet they may all see recreational water issues from different perspectives and even have complementary or competing roles and values within the same system. Stakeholders can therefore have common interests that span boundaries, from geographical location to resources (McHugh *et al.*, 2018). Understanding the relationships and interactions within the stakeholder network, and how these can evolve over time, becomes extremely important for long-term engagement as we move from stakeholder management approaches to collaborative problem solving.

To direct and focus the critical review, the following research question was defined: "What is the role and function of stakeholders in the recreational water system?".

Following the literature search, the screening of all articles retrieved and the elimination of articles based on predefined inclusion and exclusion criteria, 25 articles remained.

Overall, the themes discussed within the studies included were broader than stakeholder engagement; however, four papers did discuss some dimension of stakeholder relationships as part of their primary aims. Maguire *et al.* (2011) sought to understand stakeholder engagement, while McNicholas and Cotton (2019) attempted to understand the diverse views of stakeholders on the issue of marine pollution. Two other papers discussed stakeholder involvement in specific environmental initiatives from the stakeholder perspective (Wyles *et al.*, 2019; Zettler *et al.*, 2017).

Only two papers defined the term stakeholder specifically; its meaning remained implicit in the remaining papers. Landre and Knuth's (1993) definition acknowledges that entities with different interests come together to participate in change activities. Stakeholders in this context have an active role in the relationship (Landre and Knuth, 1993). The definition given by Maguire *et al.* (2011) mirrors Freeman's by including both passive and active participation affected by an activity. These definitions are in keeping with broader systems thinking perspectives (Maguire *et al.*, 2011).

Across all papers, the actual stakeholders involved were often described using umbrella terms such as "community group", which offer little guidance on who the stakeholders actually are and how they became engaged in the specific pieces of research. These terms often reflected the sector they represented, rather than specific information related to the organisations or individuals' identities. The implicit nature of the terms' usage may represent an acceptance of the role of stakeholder engagement in change activities and the context-driven nature of these relationships.

To deepen our analysis of the role and function of stakeholders three classification systems were applied: (1) classification across the levels in the social system – micro (the individual), meso (community) and macro (policy level); (2) the classification of McHugh *et al*. (2018) into incumbents, challengers and regulators; and (3) the classification of power and interest, which helps to evaluate stakeholder enagement strategies (Clausen *et al*., 2020). This classification was used to assess the degree of stakeholder multilevel engagement taking place and the range of stakeholders who are participating in water quality initiatives and/or policy development.

Of the 22 articles selected, nine discussed stakeholders from across the three levels of the social system (macro, meso and micro). Studies that reported multilevel engagement acknowledged the necessity of a system-wide response. For example, McNicholas and Cotton (2019) acknowledge that impactful change can only occur once a better understanding of the goals of multiple perspectives is achieved. By adopting a dynamic systems approach and understanding water quality issues from multiple perspectives, strategies can be built that try to engage with and satisfy the needs of all stakeholders. This is significant, as it corresponds to the adoption of a holistic approach to addressing water quality activities. It also reflects the non-linearity in system-level responses.

Key findings show that ambiguity about the role and implementation of stakeholder approaches remains. Collaboration between stakeholders can lead to impacts beyond what a single organisation could achieve on its own (Zettler *et al*., 2017). However, coordination remains difficult (McNicholas and Cotton, 2019), as uses and values are dependent on the situation (Rogers *et al*., 2013) and the nurturing of co-responsibility (McNicholas and Cotton, 2019). In relation to holistic systemic approaches, transdisciplinary perspectives are required (Moore *et al.*, 2013), with collaborative engagement resulting in shared research agendas and enhanced research impacts (Zettler *et al.*, 2017). Guidelines may be useful for organisations; however, they must be flexible and address the needs of all stakeholders.

This critical review provides insight into the state of stakeholder engagement and the characteristics of multi-stakeholder relationships, which may lead to successful implementation in the future. This review showed that there are some examples of adopting holistic system-level approaches to change strategies for complex recreational water quality issues, although, at this time, the practice is not widespread. However, more research needs to be undertaken to fully understand the role of stakeholders from a systems thinking perspective. Instead of defining stakeholders, it may be beneficial to evaluate the suitability of a stakeholder through common characteristics, an approach that Orr *et al.* (2007) adopted. The common characteristics identified within this review include effective communication, shared goals (implying a shared interest), co-responsibility and transparency, which must be established between stakeholder parties before they collaborate. Shared values, mutual goals and effective communication have been identified in other studies as important antecedents for developing longer term partnership strategies (Duane *et al.*, 2021; Duane and Domegan, 2019).

The remainder of this chapter will discuss the application of a system dynamics modelling approach within the PIER project.

5.4 Methods and Materials

Systems thinking and stakeholder engagement have pivotal roles to play in addressing societal challenges such as AMR in the environment. In general, a system can be defined as "a collection of parts that interact in a meaningful, inseparable way to function as a whole" (Ford, 2019, p. 377). Furthermore, a complex system is characterised by large networks of elements, decentralised control, complex collective behaviours and sophisticated information processing (Mitchell, 2009). System dynamics applies a highly participatory process of group model building (GMB), encompassing multiple stakeholders, to build and co-create a model of the system. Within the PIER project, system dynamics modelling was applied as a qualitative methodology to:

- deepen our understanding of dynamic societal problems such as recreational water quality;
- visualise or map the recreational water quality focal system;
- support the identification of tipping and leverage points for the design of strategies for change by stakeholders (Domegan, 2021).

This approach highlights the non-linearity of complex systems and helps to gain a greater understanding of how everything links together, encouraging a big-picture perspective. The stakeholders involved in this co-creation process explore and map the causal relationships between elements within the system (Brychkov *et al.*, 2021).

Recreational water quality – encapsulating our rivers, lakes and seas and the focal problem of this research – has been described as a "wicked problem" that affects and is affected by a complex array of stakeholders involved in water quality (EPA, 2022). It is a problem that has no one cause or solution and has many stakeholders involved, who in some cases can have competing or conflicting perspectives.

Figure 5.1 provides an overview of the GMB procedure that was implemented in the PIER project.

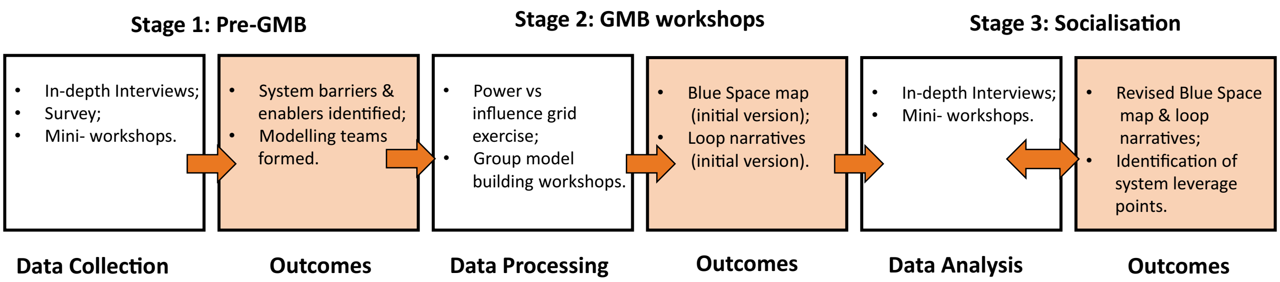

Figure 5.1. The GMB procedure.

5.4.1 Stage 1: Pre-group model building

Before the recreational water quality system could be mapped, the variables that affected the system needed to be identified – within this study, these variables are referred to as barriers and enablers. A barrier is something that is currently acting as a blockage within the system, whereas an enabler is something that is working well. First, 15 in-depth interviews were conducted with stakeholders across all levels within the system. The aim of these interviews was to recognise barriers and enablers and to identify stakeholders who might support the distribution of the survey. For the purpose of the survey and analysis, recreational waters were referred to as “blue spaces”. A national Blue Space survey was distributed across Ireland through email, a social media campaign and WhatsApp messaging. Any person residing in Ireland could take part in this survey. The key questions within the survey were as follows:

- What are the top three enablers for using blue spaces in Ireland?
- What are the top three barriers to using blue spaces in Ireland?

Participants were also asked to clarify their responses by providing the reasoning behind the barriers and enablers they included. The resulting barriers and enablers were categorised by theme in preparation for GMB workshops. The categorisation of barriers and enablers was validated by a wider team of experts in public health, microbiology and social marketing.

5.4.2 Stage 2: Group model building workshops

The primary goal of the GMB workshops was to understand the causal dynamics at play in the system involving recreational waters by constructing a system map based on a causal loop diagram (CLD). Two GMB workshops took place: workshop 1 focused on the barriers and workshop 2 on the enablers. For workshop 1, stakeholders from across the system were invited to take part and work with the modelling team to co-create the system map. The participants were pre-assigned to one of four tables, ensuring that participants from different backgrounds could discuss their views on the themes presented. At the beginning of the workshop, participants were introduced to the CLD process and provided with guidance on how to draw CLDs. A CLD consists of variables (in this case barriers and enablers) connected by arrows denoting the causal influences (links) between the variables. Each causal link is assigned a polarity, either positive (+) or negative (–). Once all themes had been discussed and added to diagrams, the participants began to draw in the interrelationships joining them.

Workshop 2 focused on the system enablers. Six participants took part in workshop 2, assisted by two facilitators. Four out of the six participants from workshop 2 had participated in workshop 1 to ensure the continuity of the process. The use of a smaller number of stakeholders during workshop 2 was dictated by the much smaller list of enabler themes, as multiple enablers operating in the system were the flipsides of corresponding (and already addressed) barriers. Workshop 2 generated its own CLD, which was later merged with the CLD from workshop 1.

5.4.3 Stage 3: Socialisation

To ensure that the final map represented the views of the stakeholders, a copy of the map was shared with the GMB participants and stakeholders who were not represented at the workshops. Minor amendments were suggested during the socialisation process.

5.5 Findings and Discussion

There were 1107 responses to the Blue Space survey. From the interviews and survey, 2715 barriers and 3324 enablers were identified. The barriers and enablers identified during the preliminary stage were screened for verbatim duplications and categorised into themes. The survey generated 86 barrier themes and 18 enabler themes. The categorisation of barriers and enablers was validated by a wider team of experts in public health, microbiology and social marketing.

Figure 5.2 presents the recreational water quality system map, which is made up of nearly 100 system variables and 38 feedback loops.

Blue space accessibility and use is a key multi-input multi-output (MIMO) variable. MIMO variables are “those which shape the system structure and significantly influence system behaviour” (Bureš, 2017, p. 15). Having access to and using blue space has multiple social benefits, such as community building and social networking, meeting companions, sharing

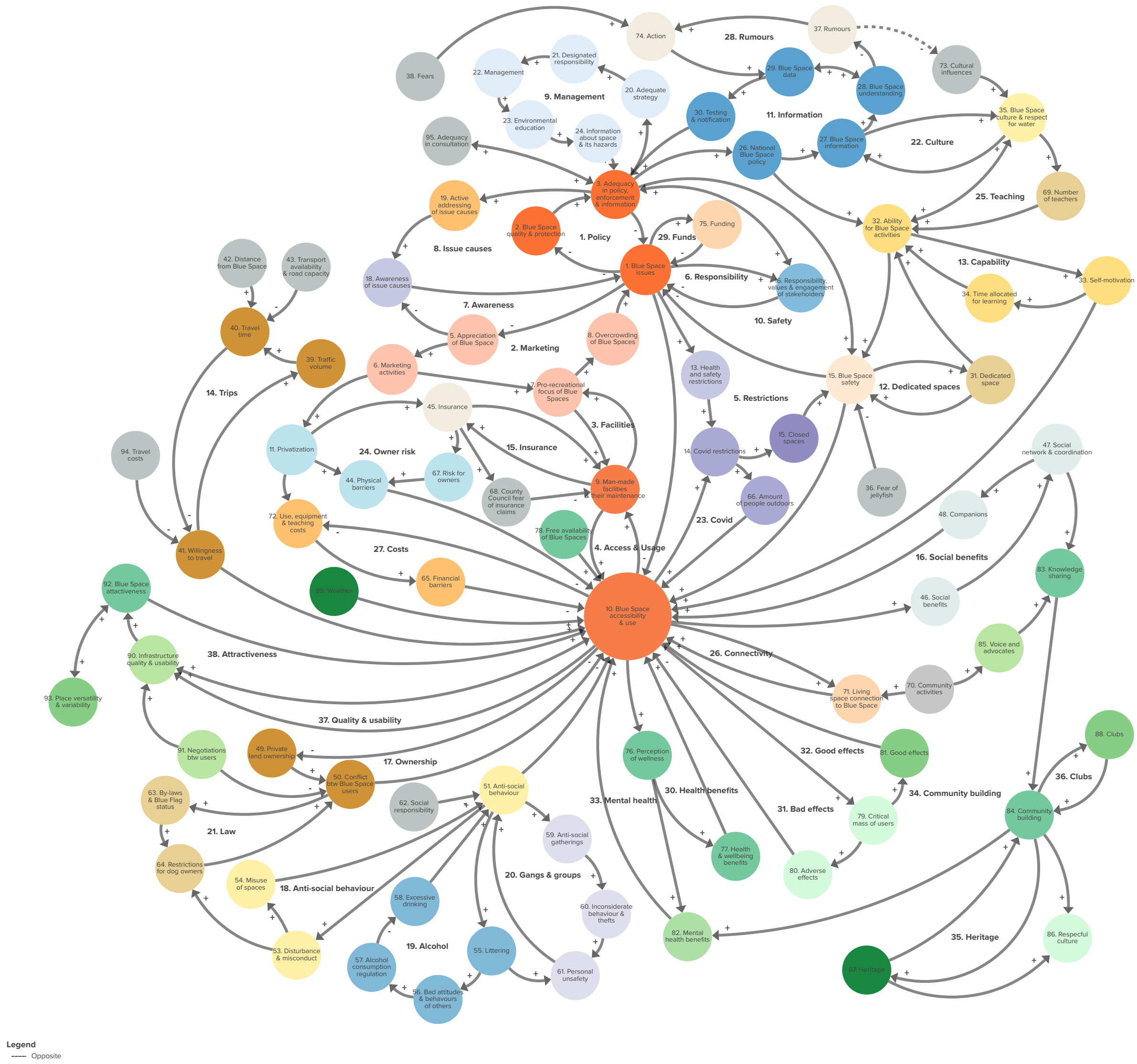

Figure 5.2. Recreational water quality system map.

knowledge, raising the voices of various stakeholders and improving advocacy, creating a favourable culture, cherishing heritage and increasing club activities. However, it is also clear that blue space use is also negatively affected by other factors, such as costs and conflicts between users, including ownership disputes and antisocial behaviour(s).

Blue space use also introduces the concept of "critical mass of users", which describes the quantity of users of/visitors to a specific blue space at a specific moment in time. If this critical mass is not exceeded, it may have beneficial (good) effects for the blue space, as the increased use may lead to improvements in its facilities and safety. Such improvements could further increase the place quality (described as "infrastructure quality and usability", which depends on "negotiations between blue space users") and "blue space attractiveness", which also hinges on "blue space versatility". However, exceeding the critical mass may have detrimental effects. At a certain point, this critical mass acts as a tipping point with the potential to overturn the health of the system, leading to detrimental (bad) effects, such as misuse, overuse, an increase in pollution and extreme noise.

Additional MIMO variables include "adequate policy, enforcement and information", "blue space issues" and "blue space safety". The map shows that these variables have multiple links. The interaction of these variables can improve the adequacy of blue space-related policy and its enforcement to address diverse elements of the focal system, such as maintaining water quality, improving facilities and improving people's access to blue spaces. A full discussion of the interconnections within the map can be found at www.universityofgalway.ie/pier.

Stage 3 of the process, socialisation, gave stakeholders the opportunity to consider leverage points within the map in the context of their own experiences. Some points are aspirational, whereas others have been adopted by communities already. Ten leverage points were described. For example, for community building, an important leverage point could be the engagement of local communities via local champions/leaders of change, who could assist in combating various issues and performing various interventions (including education). The role of personality is critical. This would help to build relevant social norms and stimulate meaningful local engagement.

5.6. Limitations

This research applied an exploratory qualitative system dynamics methodology. Further GMB workshops would assist in validating the model. Although stakeholders discussed solutions to some of the challenges identified within the system, it was beyond the scope of this research to explore these further.

5.7 Conclusions

Systems thinking is a proactive mindset; the map presented in Figure 5.2 moves stakeholders away from linear thinking towards considering the intended and/or unintended consequences of designing change activities. This modelling exercise presents a best practice approach to understanding a system in preparation for its transformation. Applying a holistic approach allows engaged stakeholders to make informed choices on both the current state of the recreational water system and how it could change in response to the cumulative effects of multiple activities across the whole system (Kadirov, 2018). This knowledge and understanding in turn will help to identify tipping points, leverage points and drivers of change within the system (Kotir, 2021).

6 Recommendations

Overall, the PIER project aimed to further our understanding of the public health implications of environmental exposure to AMR and how this impacts use of blue spaces, wellbeing and quality of life.

This project adopted a One Health approach and brought together experts in microbiology, public health, epidemiology and social marketing to achieve the project's aims and objectives.

The following key recommendations are based on the findings and conclusions of the research studies presented in Chapters 2–5.

- Further research into the dynamics of gut colonisation with ARB and the impacts of interaction with our environments is recommended.
- There is a need for increased frequency of bathing water quality monitoring, as bathing waters are accessed year round and not just in the designated bathing water season (1 June to 15 September).
- The limitations of the current guidelines and criteria relating to water quality assessment are evident. Both international and national guidelines on the assessment of water quality need to take AMR into account. The development of guidelines for the appropriate surveillance and reporting of AMR and antimicrobial presence in bathing waters is recommended.
- The system map created should be used by stakeholders to identify and prioritise opportunities for short- and long-term change strategies and to identify opportunities for stakeholder engagement and partnership development across the system as multilevel interventions are planned and implemented simultaneously.

References

Arcilla, M.S., *et al*. (2020). Prevalence and risk factors for carriage of ESBL-producing Enterobacteriaceae in a population of Dutch travellers: A cross-sectional study. *Travel Medicine and Infectious Disease* 33: 101547. https://doi.org/10.1016/J.TMAID.2019.101547

Becattini, S., *et al*. (2016). Antibiotic-induced changes in the intestinal microbiota and disease. *Trends in Molecular Medicine* 22(6): 458–478. https://doi.org/10.1016/J.MOLMED.2016.04.003

Börjesson, S., *et al*. (2022). Detection of an IMI-2 carbapenemase-producing *Enterobacter asburiae* at a Swedish feed mill. *Frontiers in Microbiology* 13. https://doi.org/10.3389/fmicb.2022.993454

Brychkov, D., *et al*. (2021). Coming and going in loops: Participatory modelling of a system with all its complexity. *Journal of Macromarketing* 42(1): 12–29. https://doi.org/10.1177/02761467211062504

Bureš, V. (2017). A method for simplification of complex group causal loop diagrams based on endogenisation, encapsulation and order-oriented reduction. *Systems* 5(3): 46.

Clausen, L.P.W., *et al*. (2020). Stakeholder analysis with regard to a recent European restriction proposal on microplastics. *PLoS One* 15(6): e0235062. https://doi.org/10.1371/journal.pone.0235062

Curtis, J., and Hynes, S. (2017). *Demand for Water-Based Leisure Activity: The Benefits of Good Water Quality*. Environmental Protection Agency, Johnstown Castle, Ireland.

Department of Health (2013). *Healthy Ireland: A Framework for Improved Health and Wellbeing 2013–2025.* Government of Ireland, Dublin, Ireland.

Department of Health (2021). *Ireland's One Health National Action Plan on Antimicrobial Resistance 2021–2025*. Government of Ireland, Dublin, Ireland.

Doi, Y., *et al*. (2007). Community-acquired extended-spectrum β-lactamase producers, United States. *Emerging Infectious Diseases* 13(7): 1121. https://link.gale.com/apps/doc/A166750065/AONE?u = anon~28b0ee22andsid = googleScholarandxid = 15ecd2f2 (accessed 13 August 2024).

Domegan, C. (2021). Social marketing and behavioural change in a systems setting. *Current Opinion in Environmental Science and Health* 23: 100275.

Duane, S., and Domegan, C. (2019). Social marketing partnerships: Evolution, scope and substance. *Marketing Theory* 19(2): 169–193.

Duane, S., *et al*. (2021). Partnering for UN SDG# 17: A social marketing partnership model to scale up and accelerate change. *Journal of Social Marketing* 12(1): 49–75.

EPA (Environmental Protection Agency) (2023). *Urban Waste Water Treatment in 2022*. EPA, Johnstown Castle, Ireland.

European Commission (2017). Communication from the Commission "A European One Health Action Plan against Antimicrobial Resistance (AMR)". COM(2017) 0339 final, 29.06.2017, Brussels.

European Environment Agency (2020a). *SOER 2020 – At a Glance*. Available online: https://www.eea.europa.eu/soer/2020/at-a-glance (accessed 27 August 2024).

European Environment Agency (2020b). *The European Environment – State and Outlook 2020: Knowledge for Transition to a Sustainable Europe*. EEA, Copenhagen.

Farrell, M.L., *et al*. (2021). Evaluating the potential for exposure to organisms of public health concern in naturally occurring bathing waters in Europe: A scoping review. *Water Research* 206: 117711. https://doi.org/10.1016/j.watres.2021.117711

Farrell, M.L., *et al*. (2023a). Assessing the impact of recreational water use on carriage of antimicrobial resistant organisms. *Science of The Total Environment* 888: 164201. https://doi.org/10.1016/j.scitotenv.2023.164201

Farrell, M.L., *et al*. (2023b). Longitudinal carriage of antimicrobial resistant Enterobacterales in healthy individuals in Ireland – Assessing the impact of recreational water use on duration of carriage. *Science of The Total Environmen*t 905: 167100. https://doi.org/10.1016/j.scitotenv.2023.167100

Fonseca, E.L., *et al*. (2022). Global genomic epidemiology of *Escherichia coli* (ExPEC) ST38 lineage revealed a virulome associated with human infections. *Microorganisms* 10(12): 2482. https://doi.org/10.3390/microorganisms10122482

Ford, D.N. (2019). A system dynamics glossary. *Systems Dynamics Review* 35: 369–379.

Freeman, R. (1984). *Strategic Management: A Stakeholder Approach*. Pitman, Boston.

Gu, Z., *et al*. (2016). Complex heatmaps reveal patterns and correlations in multidimensional genomic data. *Bioinformatics* 32(18): 2847–2849. https://doi.org/10.1093/BIOINFORMATICS/BTW313

Hooban, B., *et al*. (2022). A longitudinal survey of antibiotic-resistant Enterobacterales in the Irish environment, 2019–2020. *Science of The Total Environment* 828: 154488. https://doi.org/10.1016/J.SCITOTENV.2022.154488

Hopkins, K.L., *et al*. (2017). IMI-2 carbapenemase in a clinical *Klebsiella variicola* isolated in the UK. *Journal of Antimicrobial Chemotherapy* 72(7): 2129–2131. https://doi.org/10.1093/jac/dkx103

International Social Marketing Association, *et al*. (2013). *Consensus Definition of Social Marketing*. Available online: http://smana.org/wp-content/uploads/2017/04/iSMA-Consensus-definition-of-Social-Marketing-Oct-2013.pdf (accessed 13 August 2024).

Jørgensen, S.B., *et al*. (2017). Fecal carriage of extended spectrum β-lactamase producing *Escherichia coli* and *Klebsiella pneumoniae* after urinary tract infection – A three year prospective cohort study. *PLOS ONE* 12(3): e0173510. https://doi.org/10.1371/journal.pone.0173510

Kadirov, D. (2018). Towards a theory of marketing systems as the public good. *Journal of Macromarketing* 38(3): 278–297.

Khan, B.A., *et al*. (2021). Synthesis and characterization of polymeric responsive CMC/Pectin hydrogel films loaded with *Tamarix aphylla* extract as potential wound dressings. *Biocell* 45(5): 1273–1285. https://doi.org/10.32604/BIOCELL.2021.015323

Kotir, J.H. (2021). Managing and sustaining the coupled water-land-food systems in the context of global change: how qualitative system dynamic modelling can assist in understanding and designing high-leverage interventions. In Rhodes, E.R. and Naser, H. (eds) *Natural Resources Management and Biological Sciences*. IntechOpen.

Landre, B.K., and Knuth, B.A. (1993). The role of agency goals and local context in Great Lakes water resources public involvement programs*. Environmental Management* 17: 153–165.

Lapinski, M.K., *et al*. (2015). Recommendations for the role of social science research in One Health. *Social Science and Medicine* 129: 51–60.

Leonard, A.F.C., *et al*. (2015). Human recreational exposure to antibiotic resistant bacteria in coastal bathing waters. *Environment International* 82: 92–100. https://doi.org/10.1016/j.envint.2015.02.013

Leonard, A.F.C., *et al*. (2018a). Is it safe to go back into the water? A systematic review and meta-analysis of the risk of acquiring infections from recreational exposure to seawater. *International Journal of Epidemiology* 47(2): 572–586. https://doi.org/10.1093/ije/dyx281

Leonard, A.F.C., *et al*. (2018b). Exposure to and colonisation by antibiotic-resistant *E. coli* in UK coastal water users: Environmental surveillance, exposure assessment, and epidemiological study (Beach Bum Survey). *Environment International* 114: 326–333. https://doi.org/10.1016/j.envint.2017.11.003

Maguire, B., *et al*. (2011). Who, when, and how? Marine planning stakeholder involvement preferences – A case study of the Solent, United Kingdom. *Marine Pollution Bulletin* 62(11): 2288–2292.

McHugh, P., *et al*. (2018). Protocols for stakeholder participation in social marketing systems. *Social Marketing Quarterly* 24(3): 164–193.

McNicholas, G., and Cotton, M. (2019). Stakeholder perceptions of marine plastic waste management in the United Kingdom. *Ecological Economics* 163: 77–87.

Mitchell, M. (2009). *Complexity: A Guided Tour*. Oxford University Press, Oxford.

Moore, M.N., *et al*. (2013). Oceans and Human Health (OHH): A European perspective from the Marine Board of the European Science Foundation (Marine Board-ESF). *Microbial Ecology* 65: 889–900.

Morris, D., *et al*. (2024). *Antimicrobial Resistance and the Environment – Sources, Persistence, Transmission and Risk Management (AREST)*. Environmental Protection Agency. Available online: https://www.epa.ie/publications/research/environment--health/research-448-antimicrobial-resistance-and-the-environment--sources-persistence-transmission-and-risk-management-arest.php (accessed 13 August 2024).

Murray, C.J., *et al*. (2022). Global burden of bacterial antimicrobial resistance in 2019: A systematic analysis. *The Lancet* 399(10325): 629–655. https://doi.org/10.1016/S0140-6736(21)02724-0

Nicolas-Chanoine, M.H., *et al*. (2014). *Escherichia coli* ST131, an intriguing clonal group. *Clinical Microbiology Reviews* 27(3): 543–574. https://doi.org/10.1128/CMR.00125-13

OECD (Organisation for Economic Co-operation and Development) (2019). *The Heavy Burden of Obesity: The Economics of Prevention*. OECD, Paris.

OECD (Organisation for Economic Co-operation and Development) and ECDC (European Centre for Disease Prevention and Control) (2019). *Antimicrobial Resistance: Tackling the Burden in the European Union. Briefing Note for EU/EEA Countries.* Available online: https://health.ec.europa.eu/publications/antimicrobial-resistance-tackling-burden-european-union_en (accessed 13 August 2024).

Orr, P., *et al*. (2007). Involving stakeholders in integrated river basin planning in England and Wales. In Craswell, E., *et al*. (eds) *Integrated Assessment of Water Resources and Global Change: A North-South Analysis*, Springer, Dordrecht, Netherlands, pp. 331–349.

Otter, J.A., *et al*. (2019). Individual- and community-level risk factors for ESBL Enterobacteriaceae colonization identified by universal admission screening in London. *Clinical Microbiology and Infection* 25(10): 1259–1265. https://doi.org/10.1016/j.cmi.2019.02.026

Overdevest, I., *et al*. (2016). Prolonged colonisation with *Escherichia coli* O25:ST131 versus other extended-spectrum beta-lactamase-producing *E. coli* in a long-term care facility with high endemic level of rectal colonisation, the Netherlands, 2013 to 2014. *Eurosurveillance* 21(42): pii=30376. https://doi.org/10.2807/1560-7917.ES.2016.21.42.30376

Panwar, R.B., *et al*. (2021). Microbiota-mediated protection against antibiotic-resistant pathogens. *Genes and Immunity* 22: 255–267. https://doi.org/10.1038/s41435-021-00129-5

Reina, Y., *et al*. (2018). Persistent pandemic lineages of uropathogenic *Escherichia coli* in a college community from 1999 to 2017. *Journal of Clinical Microbiology* 56(4): 10.1128/jcm.01834-17. https://doi.org/10.1128/jcm.01834-17

Reuland, E.A., *et al*. (2016). Prevalence and risk factors for carriage of ESBL-producing Enterobacteriaceae in Amsterdam. *Journal of Antimicrobial Chemotherapy* 71(4): 1076–1082. https://doi.org/10.1093/jac/dkv441

Rogers, S.H., *et al*. (2013). Characterization of public and stakeholder objectives in environmental management: New Hampshire’s Lamprey River. *Journal of Water Resources Planning and Management* 139(2): 217–222.

Stone, D.L., *et al*. (2008). Exposure assessment and risk of gastrointestinal illness among surfers. *Journal of Toxicology and Environmental Health, Part A* 71(24): 1603–1615. https://doi.org/10.1080/15287390802414406

Tacconelli, E., *et al*. (2018). Discovery, research, and development of new antibiotics: the WHO priority list of antibiotic-resistant bacteria and tuberculosis. *The Lancet Infectious Diseases* 18(3): 318–327. https://doi.org/10.1016/S1473-3099(17)30753-3

Tandé, D., *et al*. (2010). Intrafamilial transmission of extended-spectrum-β-lactamase-producing *Escherichia coli* and *Salmonella enterica* Babelsberg among the families of internationally adopted children. *Journal of Antimicrobial Chemotherapy* 65(5): 859–865. https://doi.org/10.1093/jac/dkq068

van Duijkeren, E., *et al*. (2018). Long-term carriage of extended-spectrum β-lactamase-producing *Escherichia coli* and *Klebsiella pneumoniae* in the general population in the Netherlands. *Clinical Infectious Diseases* 66(9): 1368–1376. https://doi.org/10.1093/cid/cix1015

Völker, S., and Kistemann, T. (2011). The impact of blue space on human health and well-being – Salutogenetic health effects of inland surface waters: A review. *International Journal of Hygiene and Environmental Health* 214(6): 449–460. https://doi.org/10.1016/J.IJHEH.2011.05.001

Wheeler, B.W., *et al*. (2012). Does living by the coast improve health and wellbeing? *Health and Place* 18(5): 1198–1201. https://doi.org/10.1016/J.HEALTHPLACE.2012.06.015

WHO (World Health Organization) (2015). *Global Action Plan on Antimicrobial Resistance.* WHO, Geneva, Switzerland.

WHO (World Health Organization) (2019). *One Health Challenge*. WHO, Geneva, Switzerland.

Wickramasinghe, N. H., *et al*. (2012). High community faecal carriage rates of CTX-M ESBL-producing *Escherichia coli* in a specific population group in Birmingham, UK. *Journal of Antimicrobial Chemotherapy* 67(5): 1108–1113. https://doi.org/10.1093/jac/dks018

Williams, N.L R., *et al*. (2022). Rainfall leads to elevated levels of antibiotic resistance genes within seawater at an Australian beach. *Environmental Pollution* 307: 119456. https://doi.org/10.1016/J.ENVPOL.2022.119456

Wyles, K.J., *et al*. (2019). An evaluation of the Fishing For Litter (FFL) scheme in the UK in terms of attitudes, behavior, barriers and opportunities. *Marine Pollution Bulletin* 144: 48–60.

Zettler, E.R., *et al*. (2017). Incorporating citizen science to study plastics in the environment. *Analytical Methods* 9(9): 1392–1403.

Abbreviations

AMR	Antimicrobial resistance
ARB	Antimicrobial-resistant bacteria
ARG	Antimicrobial-resistant gene
ARO	Antimicrobial-resistant organism
BWD	Bathing Water Directive
CI	Confidence interval
CLD	Causal loop diagram
CPE	Carbapenemase-producing Enterobacterales
CRE	Carbapenem-resistant Enterobacterales
EPA	Environmental Protection Agency
ESBL	Extended-spectrum beta-lactamase
ESBL-EC	Extended-spectrum beta-lactamase-producing *Escherichia coli*
ESBL-PE	Extended-spectrum beta-lactamase-producing Enterobacterales
EU	European Union
GMB	Group model building
MIMO	Multi-input multi-output
PCR	Polymerase chain reaction
PIER	Public health Impact of Exposure to antibiotic Resistance in recreational waters
ST	Sequence type
WHO	World Health Organization
WOPHC	Waterborne organisms of public health concern
WU	Water user

An Ghníomhaireacht Um Chaomhnú Comhshaoil

Tá an GCC freagrach as an gcomhshaol a chosaint agus a fheabhsú, mar shócmhainn luachmhar do mhuintir na hÉireann. Táimid tiomanta do dhaoine agus don chomhshaol a chosaint ar thionchar díobhálach na radaíochta agus an truaillithe.

Is féidir obair na Gníomhaireachta a roinnt ina trí phríomhréimse:

Rialáil: Rialáil agus córais chomhlíonta comhshaoil éifeachtacha a chur i bhfeidhm, chun dea-thorthaí comhshaoil a bhaint amach agus díriú orthu siúd nach mbíonn ag cloí leo.

Eolas: Sonraí, eolas agus measúnú ardchaighdeáin, spriocdhírithe agus tráthúil a chur ar fáil i leith an chomhshaoil chun bonn eolais a chur faoin gcinnteoireacht.

Abhcóideacht: Ag obair le daoine eile ar son timpeallachta glaine, táirgiúla agus dea-chosanta agus ar son cleachtas inbhuanaithe i dtaobh an chomhshaoil.

I measc ár gcuid freagrachtaí tá:

Ceadúnú

> Gníomhaíochtaí tionscail, dramhaíola agus stórála peitril ar scála mór;
> Sceitheadh fuíolluisce uirbigh;
> Úsáid shrianta agus scaoileadh rialaithe Orgánach Géinmhodhnaithe;
> Foinsí radaíochta ianúcháin;
> Astaíochtaí gás ceaptha teasa ó thionscal agus ón eitlíocht trí Scéim an AE um Thrádáil Astaíochtaí.

Forfheidhmiú Náisiúnta i leith Cúrsaí Comhshaoil

> Iniúchadh agus cigireacht ar shaoráidí a bhfuil ceadúnas acu ón GCC;
> Cur i bhfeidhm an dea-chleachtais a stiúradh i ngníomhaíochtaí agus i saoráidí rialáilte;
> Maoirseacht a dhéanamh ar fhreagrachtaí an údaráis áitiúil as cosaint an chomhshaoil;
> Caighdeán an uisce óil phoiblí a rialáil agus údaruithe um sceitheadh fuíolluisce uirbigh a fhorfheidhmiú
> Caighdeán an uisce óil phoiblí agus phríobháidigh a mheasúnú agus tuairisciú air;
> Comhordú a dhéanamh ar líonra d'eagraíochtaí seirbhíse poiblí chun tacú le gníomhú i gcoinne coireachta comhshaoil;
> An dlí a chur orthu siúd a bhriseann dlí an chomhshaoil agus a dhéanann dochar don chomhshaol.

Bainistíocht Dramhaíola agus Ceimiceáin sa Chomhshaol

> Rialacháin dramhaíola a chur i bhfeidhm agus a fhorfheidhmiú lena n-áirítear saincheisteanna forfheidhmithe náisiúnta;
> Staitisticí dramhaíola náisiúnta a ullmhú agus a fhoilsiú chomh maith leis an bPlean Náisiúnta um Bainistíocht Dramhaíola Guaisí;
> An Clár Náisiúnta um Chosc Dramhaíola a fhorbairt agus a chur i bhfeidhm;
> Reachtaíocht ar rialú ceimiceán sa timpeallacht a chur i bhfeidhm agus tuairisciú ar an reachtaíocht sin.

Bainistíocht Uisce

> Plé le struchtúir náisiúnta agus réigiúnacha rialachais agus oibriúcháin chun an Chreat-treoir Uisce a chur i bhfeidhm;
> Monatóireacht, measúnú agus tuairisciú a dhéanamh ar chaighdeán aibhneacha, lochanna, uiscí idirchreasa agus cósta, uiscí snámha agus screamhuisce chomh maith le tomhas ar leibhéil uisce agus sreabhadh abhann.

Eolaíocht Aeráide & Athrú Aeráide

> Fardail agus réamh-mheastacháin a fhoilsiú um astaíochtaí gás ceaptha teasa na hÉireann;
> Rúnaíocht a chur ar fáil don Chomhairle Chomhairleach ar Athrú Aeráide agus tacaíocht a thabhairt don Idirphlé Náisiúnta ar Ghníomhú ar son na hAeráide;
> Tacú le gníomhaíochtaí forbartha Náisiúnta, AE agus NA um Eolaíocht agus Beartas Aeráide.

Monatóireacht & Measúnú ar an gComhshaol

> Córais náisiúnta um monatóireacht an chomhshaoil a cheapadh agus a chur i bhfeidhm: teicneolaíocht, bainistíocht sonraí, anailís agus réamhaisnéisiú;
> Tuairiscí ar Staid Thimpeallacht na hÉireann agus ar Tháscairí a chur ar fáil;
> Monatóireacht a dhéanamh ar chaighdeán an aeir agus Treoir an AE i leith Aeir Ghlain don Eoraip a chur i bhfeidhm chomh maith leis an gCoinbhinsiún ar Aerthruailliú Fadraoin Trasteorann, agus an Treoir i leith na Teorann Náisiúnta Astaíochtaí;
> Maoirseacht a dhéanamh ar chur i bhfeidhm na Treorach i leith Torainn Timpeallachta;
> Measúnú a dhéanamh ar thionchar pleananna agus clár beartaithe ar chomhshaol na hÉireann.

Taighde agus Forbairt Comhshaoil

> Comhordú a dhéanamh ar ghníomhaíochtaí taighde comhshaoil agus iad a mhaoiniú chun brú a aithint, bonn eolais a chur faoin mbeartas agus réitigh a chur ar fáil;
> Comhoibriú le gníomhaíocht náisiúnta agus AE um thaighde comhshaoil.

Cosaint Raideolaíoch

> Monatóireacht a dhéanamh ar leibhéil radaíochta agus nochtadh an phobail do radaíocht ianúcháin agus do réimsí leictreamaighnéadacha a mheas;
> Cabhrú le pleananna náisiúnta a fhorbairt le haghaidh éigeandálaí ag eascairt as taismí núicléacha;
> Monatóireacht a dhéanamh ar fhorbairtí thar lear a bhaineann le saoráidí núicléacha agus leis an tsábháilteacht raideolaíochta;
> Sainseirbhísí um chosaint ar an radaíocht a sholáthar, nó maoirsiú a dhéanamh ar sholáthar na seirbhísí sin.

Treoir, Ardú Feasachta agus Faisnéis Inrochtana

> Tuairisciú, comhairle agus treoir neamhspleách, fianaise-bhunaithe a chur ar fáil don Rialtas, don tionscal agus don phobal ar ábhair maidir le cosaint comhshaoil agus raideolaíoch;
> An nasc idir sláinte agus folláine, an geilleagar agus timpeallacht ghlan a chur chun cinn;
> Feasacht comhshaoil a chur chun cinn lena n-áirítear tacú le hiompraíocht um éifeachtúlacht acmhainní agus aistriú aeráide;
> Tástáil radóin a chur chun cinn i dtithe agus in ionaid oibre agus feabhsúchán a mholadh áit is gá.

Comhpháirtíocht agus Líonrú

> Oibriú le gníomhaireachtaí idirnáisiúnta agus náisiúnta, údaráis réigiúnacha agus áitiúla, eagraíochtaí neamhrialtais, comhlachtaí ionadaíocha agus ranna rialtais chun cosaint chomhshaoil agus raideolaíoch a chur ar fáil, chomh maith le taighde, comhordú agus cinnteoireacht bunaithe ar an eolaíocht.

Bainistíocht agus struchtúr na Gníomhaireachta um Chaomhnú Comhshaoil

Tá an GCC á bainistiú ag Bord lánaimseartha, ar a bhfuil Ard-Stiúrthóir agus cúigear Stiúrthóir. Déantar an obair ar fud cúig cinn d'Oifigí:

1. An Oifig um Inbhunaitheacht i leith Cúrsaí Comhshaoil
2. An Oifig Forfheidhmithe i leith Cúrsaí Comhshaoil
3. An Oifig um Fhianaise agus Measúnú
4. An Oifig um Chosaint ar Radaíocht agus Monatóireacht Comhshaoil
5. An Oifig Cumarsáide agus Seirbhísí Corparáideacha

Tugann coistí comhairleacha cabhair don Ghníomhaireacht agus tagann siad le chéile go rialta le plé a dhéanamh ar ábhair imní agus le comhairle a chur ar an mBord.

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