Overview of potential human pathogens in the environment

Chief Scientist's Group report

October 2024

Project: SC220030/R

We are the Environment Agency. We protect and improve the environment.

We help people and wildlife adapt to climate change and reduce its impacts, including flooding, drought, sea level rise and coastal erosion.

We improve the quality of our water, land and air by tackling pollution. We work with businesses to help them comply with environmental regulations. A healthy and diverse environment enhances people's lives and contributes to economic growth.

We can't do this alone. We work as part of the Defra group (Department for Environment, Food & Rural Affairs), with the rest of government, local councils, businesses, civil society groups and local communities to create a better place for people and wildlife.

Published by:

Environment Agency
Horizon House, Deanery Road,
Bristol BS1 5AH

www.gov.uk/environment-agency

Further copies of this report are available from our publications catalogue: www.gov.uk/government/publications or our National Customer Contact Centre: 03708 506 506

Email: research@environment-agency.gov.uk

Author(s):
Lisa M Avery, Amy Cooper, Orla Shortall, Eulyn Pagaling, Mads Troldborg and Rupert L Hough.

Keywords:
vector, climate change, soil, water, organic amendments, aerosol, viruses, bacteria, protozoa, fungi

Research contractor:
The James Hutton Institute, Craigiebuckler, Aberdeen AB15 8QH

Environment Agency's Project Manager: Dr China Hanson

Project number: SC220030

Citation:
Environment Agency (2024) Overview of potential human pathogens in the environment. Environment Agency, Bristol.

Research at the Environment Agency

Scientific research and analysis underpins everything the Environment Agency does. It helps us to understand and manage the environment effectively. Our own experts work with leading scientific organisations, universities and other parts of the Defra group to bring the best knowledge to bear on the environmental problems that we face now and in the future. Our scientific work is published as summaries and reports, freely available to all.

This report is the result of research commissioned by the Environment Agency's Chief Scientist's Group.

You can find out more about our current science programmes at https://www.gov.uk/government/organisations/environment-agency/about/research

If you have any comments or questions about this report or the Environment Agency's other scientific work, please contact research@environment-agency.gov.uk.

Dr Robert Bradburne
Chief Scientist

Contents

Executive summary

Addressing microbial pollution in the environment can be important for the protection of human health. To do this, an understanding is needed of which human pathogens are present in the UK environment. Through literature review and elicitation of expert opinion, four pathogens associated with the outdoor environment in the UK were identified as being of serious concern and a further nineteen that were identified as of significant concern.

Diseases caused by viruses, bacteria, fungi, and protists are increasing across Europe and there is evidence that climate change is increasing the severity and likelihood of over half of known pathogenic diseases globally. In addition, people in the UK may be increasing their exposure to environmental pathogens with changes in behaviour such as an increase in outdoor recreational activities.

This study addressed the need to understand the pathogens present in the UK environment, their impact on the environment, and the risks they pose to people now and, in the future, particularly under climate and land use change. The overarching aim was to conduct a broad scoping review of the evidence on human pathogens that people could be exposed to via the outdoor environment (surface waters and open land and air) in England and evaluate the relative level of concern of those pathogens.

Risk drivers for organisms of serious concern include prevalence and survival in animal (*Campylobacter*) or human (norovirus) faecal material, seasonal drivers, in particular heavy rainfall (*Campylobacter*, STEC *E. coli*) including flooding and combined sewer overflows (Norovirus).

A review of pathogen monitoring policies in other countries was undertaken. This was restricted to countries with a similar climate to the UK or those with a climate which could be representative of the UK in the future. Pathogen monitoring information was found for a range of different environmental matrices for the USA, Canada, Australia, New Zealand and the European Union and showed that pathogen monitoring policies were broadly similar to those in England.

In evaluating the relative level of concern about pathogens in the UK environment, the exposure routes considered comprised exposure *via* surface waters (ingestion, inhalation), outdoor air (inhalation), vectors (contact with vector), faecal material and organic amendments (direct contact – ingestion). A three-pronged approach was applied comprising a literature review, a questionnaire survey eliciting expert opinion and an expert workshop to consolidate findings. The Approved List of Biological Agents (ADCP) list was used as a starting list of pathogens and after screening out out-of-scope pathogens (e.g., human pathogens that could only be spread via human-to-human contact etc.), 138 remained and were reviewed recording information including:

- Environmental sources for the pathogen
- Matrices in which the pathogen is commonly detected
- Pathways of transfer through the environment, human exposure routes

- Typical concentration of the pathogen in environmental samples
- The prevalence of the pathogen within the UK or EU
- Likelihood of infection of immunocompetent adults
- Severity of disease caused by the pathogen in immunocompetent adults
- Impacts of land management activity
- Potential impact of future change (e.g. climate, land use)

A RAG (Red, Amber, Green) hazard assessment was developed, scoring pathogens according to their prevalence in the UK, likelihood of infection of an immunocompetent adult exposed to the pathogen, disease severity (for an immunocompetent adult). This assessment split pathogens into three hazard categories in relation to the public health concern; serious concern (red), significant concern (amber) and limited concern (green).

A questionnaire solicited information from experts about which pathogens they felt were of concern and around the same topics as were recorded from the review as well as information pertaining to their background and areas of expertise. Questionnaire-derived information was combined with findings from the review and presented at a workshop attended by experts and the project team and sought consensus for the RAG hazard category for each organism. Following integration of expert opinion at the workshop and some subsequent additional review, a final RAG hazard rating was completed.

Pathogens identified as of serious concern (red; scoring 9 out of a possible 12) were: *Campylobacter jejuni*; other *Campylobacter spp.* (including *C. coli and C. lari*); *Escherichia coli,* STEC strains (e.g. O157:H7 or O103); *Cladophialophora bantiana*; norovirus.

Pathogens identified as of significant concern (amber; scoring 8 out of a possible 12) were: *Aliarcobacter butzleri*; *Anaplasma phagocytophilum*; *Bacillus anthracis*; *Borrelia burgdorferi*; *Escherichia coli* (pathogenic strains); *Legionella pneumophila*; *Salmonella typhi*; *Shigella flexneri; Shigella sonnei*; *Cryptococcus neoformans var neoformans*; *Lomentospora prolificans*; *Rhizomucor pusillus*; *Scedosporium apiospermum*; *Cryptosporidium parvum*; *Giardia lamblia (Giardia intestinalis/duodenalis)*; *Naegleria fowleri*; *Toxoplasma gondii*; Sapovirus; tick-borne encephalitis virus.

Some pathogens not currently in the UK would be classed by this hazard assessment as of serious concern if they were to enter the UK. These were: *Francisella tularensis* (Type B); Crimean/Congo haemorrhagic fever virus; Dobrava-Belgrade orthohantavirus; Puumala orthohantavirus and Thogoto virus.

This research work provides a starting point to improve our risk identification of human pathogens. It showcased that current UK policy guidelines were broadly similar to other nations; however, these might need to be updated with time and anticipated climate and land use changes.

1. Introduction

1.1 Aims of the Project

The aims of this project were to 1) review which pathogens are monitored in other developed countries and 2) to conduct a broad scoping review of the evidence on human pathogens that people could be exposed to via the outdoor environment (surface waters and open land and air) in England now and in the future. Furthermore, the aim was to evaluate the relative level of concern of those pathogens.

1.2 Background

We lack an understanding of what human pathogens are, or could be, present in the UK environment, and how much risk these pose to people now and in the future, especially under climate and land use change. The incidence and risk of emerging human pathogenic diseases in the environment, which are not routinely monitored, are increasing across Europe (e.g., Semenza and Paz, 2021). These include viruses, bacteria, fungi, and protists, such as amoeba. In bathing waters, regulatory monitoring, such as the Environment Agency's bathing water monitoring programme (Environment Agency, 2022) provides an indication of potential health risks posed by microbial pollution. This is monitored by detecting contamination of the water with faecal indicator bacteria (FIOs). *Escherichia coli* (*E. coli*) and intestinal enterococci are monitored as indicators of faecal pollution and some strains within these indicator groups may be pathogenic. In the United Kingdom (UK), bathing water monitoring is carried out primarily in marine coastal locations, which are the dominant UK locations for designated bathing waters. Less monitoring of FIOs is undertaken on freshwaters despite non-designated water bodies being utilised for recreational use, including activities likely to involve full immersion, such as swimming (Environmental Audit Committee, 2022). Further, bathing water monitoring was designed to detect FIOs primarily entering from faecal sources, such as human wastewater effluent or livestock faeces, and may not be indicative of non-faecal pathogens or those entering via other routes, e.g., the growth of amoebae, which will potentially be encouraged by climate warming and fertiliser run-off (Tiwari et al, 2021).

Changes are not restricted to water-associated pathogens. For example, climate and land use change may already be promoting the proliferation of insect vectors (e.g., ticks, mosquitoes) for various diseases in the UK (Baylis, 2017). The geographic range of the Aedes mosquito has expanded in Europe, increasing the risk of mosquito-borne diseases including Chikungunya, Zika, and Dengue viruses (ECDC, 2023).

Known pathogenic diseases can increase in severity and/or likelihood because of climate change (Mora et al., 2022), suggesting there are many pathogens that will begin to emerge for the first time in the UK in the coming decades. At the same time, changing climate and other factors may also affect behaviours and usage of the natural environment (e.g., wild swimming - McDougall et al., 2022) which would mean potential changes to exposure to

pathogens in the environment. We have even less information on health risk for pathogens that may be present or increasing in outdoor air and on land in England.

However, it is not clear which of the wide range of pathogens and the underlying environmental exposure routes the Environment Agency should be most concerned about. In order to begin to prepare for an increasing risk of pathogens in the environment, a better understanding of a) what pathogens are, or could be, present in the UK environment, and b) how much risk these pose to people now and, in the future, especially under climate and land use change is needed.

1.3 Scope and Definitions

A pathogen is defined as a biological agent that causes disease. Organisms covered within this report include human pathogenic viruses, bacteria, fungi, protists, helminths and prions that are known to be disease-causing in humans. These are henceforth referred to throughout as 'pathogens'. Some of these organisms can also cause disease in non-human animals or be carried by a non-human intermediate host or 'vector' (often insects or rodents), which were considered as part of the 'exposure route' of the pathogen. The latter are known as 'vector-borne' pathogens/disease.

Exposure routes considered comprised exposure *via* surface waters (ingestion, inhalation), outdoor air (inhalation), vectors (transmission of pathogen via a (host) species/ organism), faecal material and organic amendments (direct contact – ingestion). These matrices are often interconnected and figure 1 provides a schematic overview.

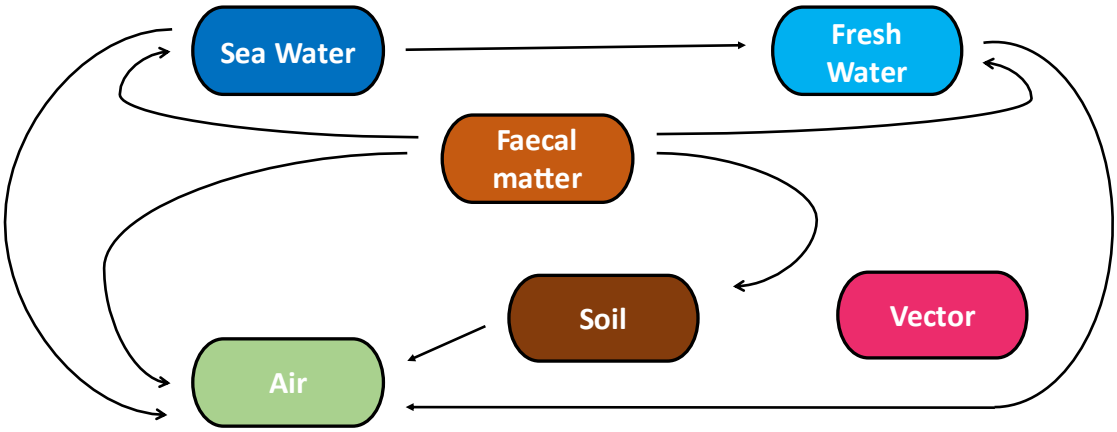


Figure 1: Movement of pathogens between sources and environmental matrices. The "air" route includes both airborne pathogens and pathogens that can be transmitted *via* aerosolised water. Faeces includes wild (and domestic) animal faeces in addition to

livestock manure and human sewage. Fresh water refers to rivers, lakes and ponds, and private drinking water sources. Vector refers to pathogens transmitted among others via flies, ticks, mites and mosquitoes.

1.4 Approach

The source-pathway-receptor principle was applied to frame this work. Using an example of faecally derived pathogens, sources included routes of entry into the environment, such as human or animal faecal material (sewage, livestock, wildlife or domestic animal defecation, organic amendments, run-off). They also included environmental matrices (e.g., soil, water, dust) which have an indigenous microflora that may include pathogens. For a vector-borne pathogen, the source could be considered to be the vector itself (e.g. tick) or the main host of the vector (e.g. deer). Pathways considered the routes through the environment (e.g., overland flow, percolation, vectors, plants/crops, water bodies) by which the receptor (humans) may become exposed through direct contact with the environment. Human behaviours that lead to exposure were also considered.

We undertook a literature/ policy search to identify regulatory monitoring relating to pathogens present in the environment to understand the monitoring framework across developed countries with climates comparable to the UK. This was then followed by a quick scoping review on pathogens in the environment, hazard assessment and expert elicitation through a questionnaire survey and workshop.

2. International regulation and monitoring of pathogens in the environment

2.1 Methodology

The focus of the review was environmental monitoring policy in developed countries with a similar climate to the UK or a climate similar to one the UK may experience in 50 to 100 years. Therefore, searches were limited to six areas: the European Union, the United States, Canada, Japan, Australia and New Zealand. As this required broad search conditions, a basic Google search was conducted. Initially, the more general search terms “monitoring of environmental pathogens” + geographic region and “pathogen environmental monitoring policy” + geographic region were used.

Following this, a more specific search was conducted which utilised the search terms above but included environmental matrices (i.e. matrix + “monitoring of environmental pathogens” + geographic region.) Matrix refers to the environmental material being monitored. The matrices searched were: “aerosol”, “anaerobic digestate”, “biosolids”, “compost”, “environment”, “faeces”, “manure”, “sewage”, “shellfish”, “soil”, “bathing water”, “drinking water”, “greywater”, “groundwater”, “recreational water”, “surface water”, “wastewater” and “water”. As these searches regularly produced several hundred thousand results only the first page of results (most relevant) was considered for the identification of which organisms are routinely monitored. The regulatory limits for those organisms by country and environmental matrix were reviewed and noted. Where these were not readily accessible, research manuscripts with figures directly related to specific monitoring policies were reviewed.

Several international government websites were also searched directly by inputting matrices + “pathogen monitoring” or matrices + “environmental pathogens” into search tools provided on each site. Websites included the European Environment Agency (https://www.eea.europa.eu/en), United States Environmental Protection Agency (www.epa.gov), United States Geological Survey (https://www.usgs.gov/), Ministry of the Environment – Government of Japan (https://www.env.go.jp/en/), Department of Climate Change, Energy, the Environment and Water – Australian Government (https://www.eea.europa.eu/en), Ministry for the Environment – Manatū Mō Te Taiao (https://environment.govt.nz/). All literature was accessed in English.

2.2 Review Findings

In terms of environmental matrices assessed, pathogens monitored and regulatory or guidance limits for those pathogens, all developed countries considered were similar. In several cases regulatory documents directly referenced the regulations of other countries. Table 1 contains the most common (and often the most stringent) parameters for testing. Therefore, to understand the full complexity of environmental testing for each country or

area the full regulatory documents should be consulted directly. Regulatory information was retrieved for all twelve environmental matrices searched across four countries (USA, Canada, Australia and New Zealand) and one political entity (European Union). As a developed country with some similar climate to the UK, Japan was also initially included in this review. However, finding and accessing the relevant Japanese policy documentation in English proved beyond the scope of this project.

Whilst conducting the literature search, potential future recommendations were noted for several matrices. For example, the European Compost Network made recommendations to remove limit values for *E. coli* and/or Enterococci in organic fertilisers, organic soil improvers and growing media because they can re-grow naturally in the final product (Siebert and Lystad, 2018). They recommended retaining the requirement to determine that no *Salmonella* was present. In contrast, a report prepared for Water New Zealand argued that there was no justification for reducing the number of microbial indicators required for verification testing of biosolids sold to, or handled by, the public after treatment. They recommended that in these products, pathogen re-growth testing be conducted annually (Horswell and Hewitt, 2015). We found no evidence of a requirement for routine monitoring of pathogens or indicator organisms in animal manure in any of the countries reviewed. It can be applied to land without processing and with no limits on microbial content. The main routes by which pathogens in manure are transmitted to humans are through direct contact with animal faeces or indirectly through contaminated food, water, surfaces. It is here instead that pathogens are routinely monitored. Pathogens in animal manure that are of risk to humans are like those found in human sewage sludge (Horswell and Hewitt, 2014). Therefore, it is suggested that manure should meet the same criteria as other biosolids (i.e. sewage sludge) to safeguard public health (Horswell and Hewitt, 2015).

Similarly, no monitoring for pathogen content of bioaerosols in or around biosolid treatment facilities is mentioned in the current European, American, Canadian or New Zealand regulations for dealing with biosolids (EUR-Lex Council Directive, 1986; New Zealand Water and Wastes Association, 2003; Code of Federal Regulations, 2018; British Columbia Regulations, 2022). In Australia it is recognised within regulatory material that it is possible for pathogens, such as *Legionella longbeachae, Apergillus fumigatus, Mycobacterium tuberculosis* and *Hantavirus* to be transmitted as an aerosol from compost and organics-processing facilities to facility workers and potentially nearby members of the public. However, available guidelines do not offer performance requirements or parameters for bioaerosols as standardised sampling methodology is lacking. Instead, mitigation measures are employed such as not allowing organic matter to lose too much moisture, avoiding uncontrolled emissions of biogas, and ensuring batches are subject to pathogen stabilisation conditions during processing (New South Wales Department of Environment and Conservation, 2003).

Greywater is the household wastewater from kitchen sinks, showers, bathtubs, washing machines, laundries, and hand basins (Khajvand et al, 2022). It is increasingly re-cycled for non-potable uses to mitigate against increasing pressure on water resources due to drought and increasing population densities. Furthermore, although there are data detailing pathogens found in greywater (Winward et al, 2009; Khajvand et al, 2022), there is nothing

yet written into policy concerning the monitoring of such pathogens in the European Union or New Zealand. In the USA, some states allow the re-use of greywater while others lack greywater regulations and some states do not prohibit its reuse. Although it is widely acknowledged that greywater contains human pathogens, (such as enteric viruses, parasitic protozoa, helminths, and enteric bacteria (Winward et al, 2009; Khajvand et al, 2022) and therefore carries a risk, no pathogen monitoring regulations seem to be in place yet. Research is currently being carried out by the US Environmental Protection Agency regarding pathogen modelling, monitoring, and treatment of greywater for reuse and pathogen log-reduction targets were proposed in 2017 (Sharvelle et al., 2017). This is being carried out with increasing water scarcity pressures in mind (Environmental Protection Agency, 2023). In Canada there is no monitoring policy in place for pathogens found in greywater. Regulations and guidelines are instead in place to limit the use of greywater and therefore limit human exposure (Canadian Ministry of Health, 2017). Similarly, to the USA, Australia allows the re-use of greywater in certain circumstances and acknowledges that pathogens in greywater require mitigation and eventually monitoring. A monitoring programme is not, however, written into strategy yet and requires further research and discussion (Water Quality Australia, 2006).

Table 1: Pathogens monitored in several developed areas (European Union, Canada, United States, Australia and New Zealand) with parameters and testing frequency (where available) across different matrices (compost, manure, sewage sludge, aerosols from decorative fountains, aerosols from organic soil amendments (OSA) drinking water (private and mains supply), bathing/recreational waters (inland and coastal), surface water, shellfish water, ground water and greywater). MPN = most probable number of viable cells, MPCN = most probable cytopathic number (MPN based on observation of damage to host cells), CFU = colony forming units, PFU = plaque forming units (an approximation of virus or bacteriophage counts based on the formation of plaques on a host cell).

	Substrate	Area	Pathogen Monitored	Parameter limits	Frequency	Source
ORGANIC SOIL AMENDMENTS (OSA)	Compost	Europe	*E. coli*	1000 bacteria in CFU/g or 1mL	at least annually*	[1]
			Enterococcaceae	1000 CFU of bacteria in 1g or 1mL	at least annually	[2]
			Salmonella spp.	absent in 25g or 25mL	at least annually	[1]
	Compost	USA	Faecal coliforms	1000 MPN/g dry compost	annually/every 1000 t	[3]
			Salmonella spp.	< 3 MPN/4g dry compost	annually/every 1000 t	
	Compost	Canada	Faecal coliforms	1000 MPN/g dry compost	annually/every 1000 t	[4,5]

	Substrate	Area	Pathogen Monitored	Parameter limits	Frequency	Source
			Salmonella spp.	< 3 MPN/4g dry compost	annually/every 1000 t	
	Compost	New Zealand	*Campylobacter*	< 1/25g	<u>Applicable to all pathogens listed here:</u> <u>Product verification</u> ≥ 15 evenly dispersed grab samples per month for a 3 month period with ≤ 3 failures. If > 3 failures then the 15 following consecutive grab samples must comply. <u>Routine sampling</u> ≥ 1 grab sample per week	[6]
			E. coli	< 100 MPN/g		
			Enteric viruses	< 1 PFU/4g		
			Helminth ova	< 1/4g		
			Salmonella spp.	< 1/25g		
	Compost	Australia	*E. coli*	< 100 MPN/g (dry weight)	<u>Applicable to all pathogens listed here:</u> 5 grab samples (combined into 1 composite sample) for	[7]
			Faecal coliforms	1000 MPN/g (dry weight)		

	Substrate	Area	Pathogen Monitored	Parameter limits	Frequency	Source
			Enteric viruses	<1 PFU/4g (dry solids)	every 300 dry solid tonnes. Standards must also be met when the product is used, sold, given away or disposed of.	
			Helminth ova (*Ascaris spp*. and *Taenia spp*.)	< 1/4g (dry solids)		
			Salmonella spp.	absent in 50g (dry weight)		
	Manure		no limits			
	Sewage Sludge	EU/Austria	*Enterococci*	< 10^3 CFU/g dry matter		[8]
			E. coli	100 CFU/g dry matter		
			Helminth ova	absent in in 1kg dry matter		
			Salmonella spp.	absent in 1g		
		EU/Bulgaria	*Clostridium perfringens*	300 MPN/g wet weight		
			E. coli	100 MPN/g wet weight		

Substrate	Area	Pathogen Monitored	Parameter limits	Frequency	Source
		Helminth ova	1 egg/kg dry matter		
		Salmonella spp.	absent in 20g wet weight		
	EU/Czech Republic	*Enterococci*	< 10^3 CFU/g dry matter		
		Thermotolerant coliforms	< 10^3 CFU/g dry matter		
		Salmonella spp.	absent in 1g		
	EU/Denmark	Faecal *Streptococci*	< 100/g		
		Salmonella spp.	No occurrence		
	EU/Finland	*E. coli*	1000 CFU/g		
		Salmonella spp.	absent in 25g		
	EU/France	*Enterovirus*	3 MPCN/10g dry matter		

Substrate	Area	Pathogen Monitored	Parameter limits	Frequency	Source
		Helminth ova	3 eggs/10g dry matter		
		Salmonella spp.	8 MPN/10g dry matter		
	EU/Italy	*Salmonella spp.*	1000 MPN/g dry matter		
	EU/Lithuania	*Clostridium perfringens*	100,000 CFU/g		
		E. coli	1000 CFU/g		
		Enterobacteria	0 CFU/g		
		Helminth ova	0 CFU/g		
	EU/Luxembourg	*Enterobacteria*	<100g		
		Helminth ova	No eggs of worm likely to be contagious		
	EU/Malta	*Salmonella spp.*	absent in 50g wet weight		

Substrate	Area	Pathogen Monitored	Parameter limits	Frequency	Source
	EU/Poland	*Helminth ova*	absent in 1 kg dry matter		
		Salmonella spp.	absent in 100g dry matter		
	EU/Portugal	*E. coli*	1000 CFU/g		
		Salmonella spp.	absent in 50g dry matter		
	EU/Slovakia	*Faecal streptococci*	$2x10^6$ CFU/g dry matter		
		Thermotolerant coliforms	$2x10^6$ CFU/g dry matter		
Sewage Sludge	USA	Faecal coliforms	1000 MPN/g dry compost	annually/every 1000 t	[3]
		Salmonella spp.	< 3 MPN/4g dry compost	annually/every 1000 t	

	Substrate	Area	Pathogen Monitored	Parameter limits	Frequency	Source
	Sewage Sludge	Canada	Faecal coliforms	1000 MPN/g dry compost	annually/every 1000 t	[9]
	Sewage Sludge	New Zealand	*Campylobacter*	< 1/25g	<u>Applicable to all pathogens listed here:</u> <u>Product verification</u> ≥ 15 evenly dispersed grab samples per month for a 3 month period with ≤ 3 failures. If > 3 failures then the 15 following consecutive grab samples must comply. <u>Routine sampling</u> ≥ 1 grab sample per week	[10]
			E. coli	< 100 MPN/g		
			Enteric viruses	< 1 PFU/4g		
			Helminth ova	< 1/4g		
			Salmonella spp.	< 1/25g		
	Sewage Sludge	Australia	*E. coli*	< 100 MPN/g (dry weight)	5 grab samples (combined into 1 composite sample) for every 300 dry solid tonnes.	[7]
			Faecal coliforms	1000 MPN/g (dry weight)		

	Substrate	Area	Pathogen Monitored	Parameter limits	Frequency	Source
			Enteric viruses	<1 PFU/4g (dry solids)		
			Helminth ova (*Ascaris spp*. and *Taenia spp*.)	< 1/4g (dry solids)	Standards must also be met when the product is used, sold, given away or disposed of.	
			Salmonella spp.	absent in 50g (dry weight)		
BIOAEROSOLS	Decorative Fountains	Europe	*Legionella*	1000 CFU/mL	Dependent on conditions and management plans	[11,12]
	Decorative Fountains	USA	*Legionella*	n/a	Dependent on conditions and management plans	[13]
	Decorative Fountains	Canada	*Legionella*	n/a	Dependent on conditions and management plans	[14]
	Decorative Fountains	New Zealand	*Legionella*	1000 CFU/mL	Depends. In some cases, monthly	[15]
	Decorative Fountains	Australia	*Legionella*	1000 CFU/mL	Depends. In some cases, monthly	[16]

	Substrate	Area	Pathogen Monitored	Parameter limits	Frequency	Source
DRINKING WATER	Private supply	Europe	Total coliforms	<1 MPN/100mL	prior to exploitation of water source	[17]
			Faecal coliforms	<1 MPN/100mL	prior to exploitation of water source	
			Faecal streptococci	<1 MPN/100mL	prior to exploitation of water source	
			Sulphite-reducing Clostridia	≤1 MPN/20mL	prior to exploitation of water source	
	Private supply	USA	Faecal coliforms	0 in 100mL (recommended)	Annually (recommended)	[18]
	Private supply	Canada	*Cryptosporidium*		Depends on system	[19]
			E. coli	0 in 100mL (recommended)	6 months (recommended)	
			Enterococci		Depends on system	
			Enterovirus		Depends on system	

	Substrate	Area	Pathogen Monitored	Parameter limits	Frequency	Source
			Giardia Lamblia		Depends on system	
			Total coliforms		6 months (recommended)	
	Private supply	Australia			Depends on system	[20]
	Mains	Europe	*Enterococci*	0/100mL (0/250mL for bottled)	At time of distribution	[21]
			E. coli	0/100mL (0/250mL for bottled)	At time of distribution	
			Clostridium perfringens	0/100mL	If risk assessment deems necessary (water originating from/influenced by surface water)	
			Pseudomonas aeruginosa	0/100mL	If water is offered for sale in bottles	
	Mains	USA	*Cryptosporidium*	0; 99% removal during treatment	At time of distribution	[22]

	Substrate	Area	Pathogen Monitored	Parameter limits	Frequency	Source
			Enteroviruses	0; 99% removal during treatment	At time of distribution	
			Giardia Lamblia	0; 99% removal during treatment	At time of distribution	
			Legionella	no limit but public health goal is 0	At time of distribution	
			Total coliforms	0 in 100 mL (no more than 5.0 percent or 1 in 40 samples if < 40 samples/month collected total coliform-positive in a month). Positives analysed for *E. coli.* >2 consecutive total coliforms positive with 1 or more *E. coli* positive results in acute violation	At time of distribution	
			Heterotrophic plate counts	n/a		

	Substrate	Area	Pathogen Monitored	Parameter limits	Frequency	Source
	Mains	Canada	*Cryptosporidium*	Min 3 log removal and/or inactivation of cysts and oocysts	At time of distribution	[23]
			E. coli	0/100mL	At time of distribution	
			Enteroviruses	Min 4 log reduction	At time of distribution	
			Giardia Lamblia	Min 3 log removal and/or inactivation of cysts and oocysts	At time of distribution	
			Total coliforms	0/100mL	At time of distribution	
	Mains	New Zealand	*E. coli*	0/100mL	Daily – weekly	[24]
			Total pathogenic protozoa	0/100mL	Dependent on treatment process	
	Mains	Australia				[25]
OTHER	Bathing/recreational (inland)	Europe	*E. coli*	500 - 1000 CFU/100mL	Dependent on each bathing water, after the	

Substrate	Area	Pathogen Monitored	Parameter limits	Frequency	Source
				end of each bathing season	
		Intestinal *Enterococci*	200 - 300 CFU/100mL	Dependent on water quality data for that season and the 3 seasons preceding it (~fortnightly)	[26,27]
		Enteroviruses	0 PFU/10L	if suspected	
		Faecal *Streptococci*	100 MPN/100mL	if suspected	
		Salmonella spp.	0 MPN/L	if suspected	
Bathing/recreational (inland)	USA	*E. coli*	≤ 126 CFU / 100mL	~weekly	
		Enterococci	≤ 35 CFU / 100mL	~weekly	[28]
Bathing/recreational (inland)	Canada	*E. coli*	≤ 200 / 100mL	~weekly	
		Enterococci	≤ 35 / 100mL	~weekly	[29]
Bathing/recreational (inland)	New Zealand	*E. coli*	≤ 130 - 550 / 100mL	~weekly	

Substrate	Area	Pathogen Monitored	Parameter limits	Frequency	Source
Bathing/recreational (inland)	Australia	*Enterococci*	≤ 40 - 500	~weekly	[30]
Bathing/ recreational (coastal)	Europe	*E. coli*	250 - 500 CFU/100mL	see inland frequency	[31]
		Intestinal *Enterococci*	100 - 200 CFU/100mL		[26,27]
Bathing/ recreational (coastal)	USA	*Enterococci*	≤ 35 / 100mL	~weekly	
Bathing/ recreational (coastal)	Canada	*Enterococci*	≤ 35 / 100mL	~weekly	[28]
		E. coli	≤ 200 / 100mL	~weekly	[29]
Bathing/ recreational (coastal)	New Zealand	*Enterococci*	140 - 280 / 100mL	~weekly	
Bathing/ recreational (coastal)	Australia	*Enterococci*	≤ 40 - 500	~weekly	[32]
Surface	Europe	Total coliforms	5 - 500 MPN/100mL	4-12 times a year	[31]

	Substrate	Area	Pathogen Monitored	Parameter limits	Frequency	Source
			Faecal coliforms	2 - 200 MPN/100mL	4-12 times a year	[33]
			Faecal *Streptococci*	2 - 200 MPN/100mL	4-12 times a year	
			Salmonella spp.	1/5000mL	4-12 times a year	
	Surface	USA	*Cryptosporidium*	0 mg/L or 0 ppm	~monthly	
			E. coli	0 mg/L or 0 ppm	~monthly	[34,35]
			Enteroviruses	0 mg/L or 0 ppm	~monthly	
			Giardia Lamblia	0 mg/L or 0 ppm	~monthly	
	Surface	Canada	*Cryptosporidium*		Frequent	
			E. coli		Frequent	[36]
			Enterococci		Frequent	
			Enteroviruses		Frequent	
			Giardia lamblia		Frequent	

Substrate	Area	Pathogen Monitored	Parameter limits	Frequency	Source
		Total coliforms		Frequent	
Surface	New Zealand	n/a	n/a	n/a	
Surface	Australia	n/a	n/a	n/a	
Shellfish	Europe	Faecal coliforms	≤ 300 MPN/100mL (non-mandatory)	Quarterly (minimum)	
Shellfish	USA	Faecal coliforms	28 - 49 MPN/100mL	Five times a year (minimum)	[37]
		Total coliforms	70 - 330 MPN/100mL	Five times a year (minimum)	[38]
Shellfish	Canada	Faecal coliforms	< 14 MPN/100mL	Throughout the year, under different environmental conditions	
Shellfish	New Zealand	Faecal coliforms	< 14 MPN/100mL	Throughout the year, under different environmental conditions	[39]

Substrate	Area	Pathogen Monitored	Parameter limits	Frequency	Source
Shellfish	Australia	Faecal coliforms	< 14 MPN/100mL	Throughout the year, under different environmental conditions	[40]
Groundwater	Europe	n/a	n/a	n/a	[41]
Groundwater	USA	Coliphage	0 in 100mL	Depends on groundwater system	
		E. coli	0 in 100mL	Depends on groundwater system	[18,42]
		Enterococci	0 in 100mL	Depends on groundwater system	
Groundwater	Canada	*Cryptosporidium*		Depends on groundwater system	
		E. coli		Depends on groundwater system	[36]
		Enterococci		Depends on groundwater system	

	Substrate	Area	Pathogen Monitored	Parameter limits	Frequency	Source
			Enteroviruses		Depends on groundwater system	
			Giardia lamblia		Depends on groundwater system	
			Total coliforms		Depends on groundwater system	
	Groundwater	New Zealand	*E. coli*		Depends on groundwater system	
	Groundwater	Australia	n/a	n/a	n/a	[43]
	Greywater	Europe	n/a	n/a	n/a	
	Greywater	USA	n/a	n/a	n/a	
	Greywater	Canada	n/a	n/a	n/a	
	Greywater	New Zealand	n/a	n/a	n/a	
	Greywater	Australia	n/a	n/a	n/a	

References as follows: [1] González-Sierra, 2019, [2] EU, 2019, [3] Code of Federal Regulations, 2018, [4] Bureau de Normalisation du Quebec, 2016, [5] CCME, 2005, [6] New Zealand Water and Wastes Association, 2003, [7] Environment Protection Authority, 2020, [8] Collivignarelli et al., 2019, [9] British Columbia Regulations, 2022, [10] New Zealand Water and Wastes Association, 2003, [11] European Centre for Disease Prevention and Control, 2017, [12] European Society of Clinical Microbiology and Infectious Diseases, 2017, [13] American National Standards Institute, 2015, [14] British Columbia Centre for Disease Control, 2021, [15] The New Zealand Ministry of Health, 2012, [16] New South Wales Ministry of Health, 2018, [17] EUR-Lex Council Directive, 1980, [18] Environmental Protection Agency 2006a, [19] Health Canada, 2021, [20] New South Wales Ministry of Health, 2016, [21] EUR-Lex Council Directive, 2020, [22] Environmental Protection Agency, 2019, [23] Health Canada, 2019, [24] Ministry of Health, 2018, [25] National Health and Medical Research Council, 2011, [26] EUR-Lex Council Directive, 2006a, [27] EUR-Lex Council Directive, 1975, [28] Environmental Protection Agency, 2012, [29] Health Canada, 2012, [30] Institute of Environmental Science and Research, 2021, [31] National Health and Medical Research Council, 2008, [32] National Institute of Water & Atmospheric Research, 2019, [33] EUR-Lex Council Directive, 1979, [34] Environmental Protection Agency, 2006b, [35] Environmental Protection Agency, 2020, [36] Health Canada, 2019, [37] EUR-Lex Council Directive, 2006b, [38] Food and Drug Administration, 2019, [39] Environment and Climate Change Canada, 2020, [40] Ministry for the Environment and Ministry of Health, 2003, [41] Australian Shellfish Quality Assurance Advisory Committee, 2022, [42] Environmental Protection Agency, 2006c, [43] Land Air Water Aotearoa, 2020.

3. Quick Scoping Review: pathogens in the UK environment

A quick scoping review (QSR) is an evidence synthesis designed to be transparent and minimise bias and can be conducted within a short timeframe (Collins et al., 2015). This approach was chosen to facilitate a broad overview of the literature on human pathogens in the environment by systematically searching, selecting and summarising information. A quick scoping review protocol was developed to provide as much reproducibility and transparency of the review methodology as possible.

3.1 Methodology

3.1.1 Eligibility Criteria and Searching

A systematic Web of Science search was performed to identify manuscripts in English published between January 2018 and March 2023, or January 2013 and March 2023, or all years, depending on the number of studies the search returned. To be included, studies had to describe a specific pathogen within a range of environmental matrices and the search focused on review literature (Figure 2). However, case studies and research literature were accepted where insufficient reviews were available. Specific pathogens reviewed included all those on the Advisory Committee on Dangerous Pathogens (ACDP) Approved List of Biological Agents (https://www.hse.gov.uk/pubns/misc208.pdf) that could cause disease in humans as a result of them experiencing the countryside recreationally. This list was also supplemented by a panel of experts during a workshop (section 3.3) and a separate search was conducted using the non-specific term “pathogen”, alongside environmental matrices, to ascertain whether any other relevant pathogens had been missed. Human pathogens that could only be spread via human-to-human contact (e.g., influenza), via close or prolonged contact with animals (e.g., rabies), pathogens considered solely an occupational hazard (e.g., orf virus) or pathogens considered solely foodborne (e.g., *Taenia saginata*) were excluded from the study. Further exclusion criteria included literature only pertaining to developing countries or countries with environmental conditions very different to that of the UK. For environmental matrices the search terms were as follows: “aerosol”, “biosolids”, “compost”, “environment”, “faeces”, “manure”, “sewage”, “soil” and “water”. For cases in which no relevant studies could be identified using these Web of Science searches, the specific pathogen was searched for using a basic Google search. This applied primarily to rarer or more unusual organisms (e.g., *Brachyspira* spp.), and pathogens transmitted by a vector (e.g., *Borrelia burgdorferi*).

The information extracted from documents included:

- Any alternative names for the studied pathogen
- Environmental sources for the pathogen

- Matrices in which the studied pathogen is commonly detected
- Pathways of transfer through the environment, human exposure routes
- Typical concentration of the pathogen in environmental samples
- The prevalence of the pathogen within the UK or EU
- Likelihood of infection of immunocompetent adults
- Severity of disease caused by the pathogen in immunocompetent adults
- Land management activity impacts
- Potential impact of future changes (e.g., climate, land use).

When this information could not be identified within the chosen studies, a Google search was conducted using the specific pathogen name and the specific information sought (e.g., “organism name + prevalence”). This information was collated in an Excel spreadsheet (‘list of pathogen’).

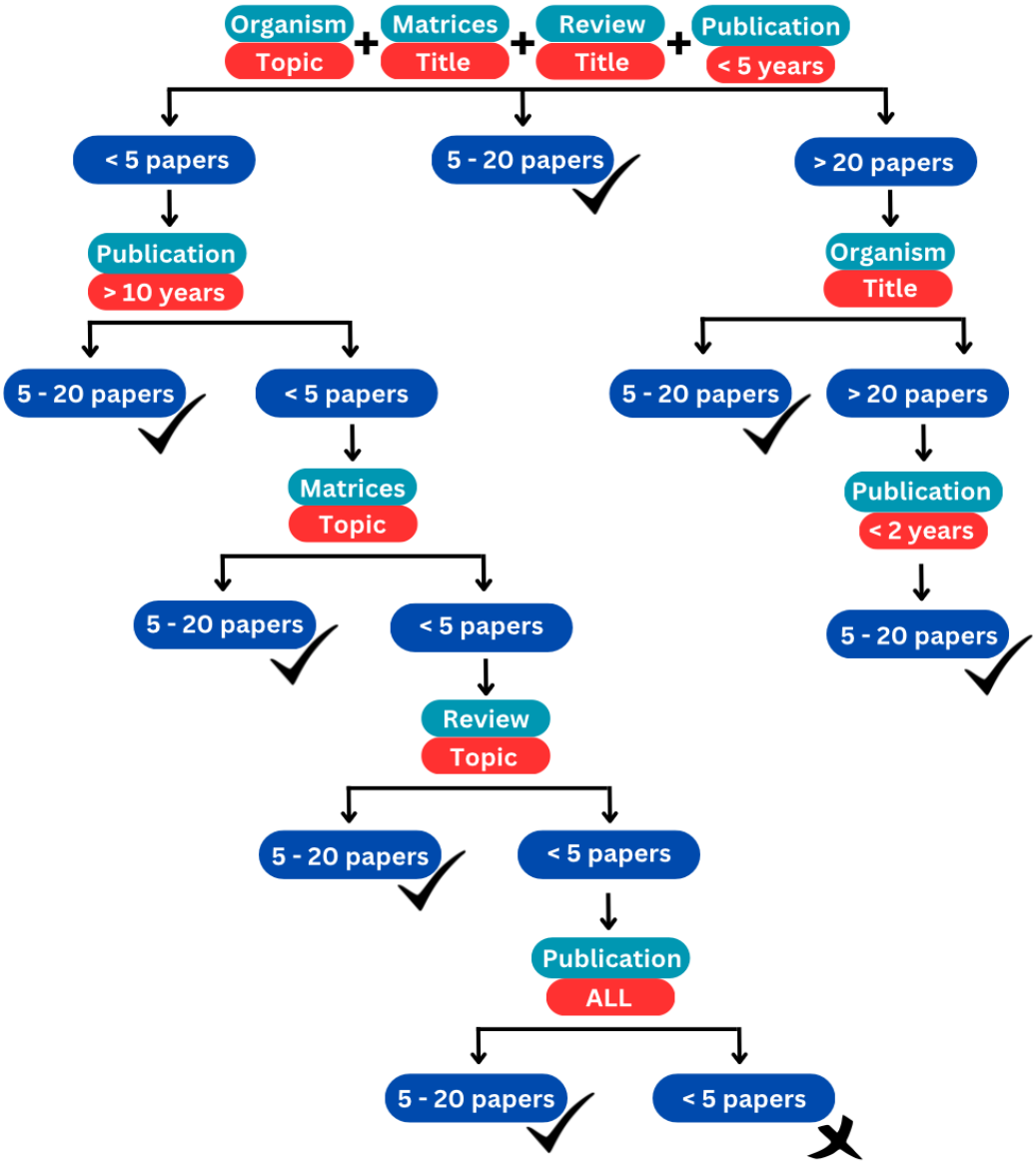


Figure 2: Decision tree for Web of Science searches. Searches were carried out with the specific "organism" name for each pathogen, plus all environmental "matrices" of interest (air, compost, faeces, manure, soil, water etc.) plus the term "review" plus year parameters for "publication" date. Searches returned with 5 – 20 papers were considered acceptable. Searches that yielded under five papers were resubmitted with increasingly relaxed search parameters (a change from "title" to "topic" or an increase in range for publication date). Searches that generated over 20 papers were made more stringent (by a change from "topic" to "title" or a decrease in range for publication date).

3.1.2 QSR Summary

519 pathogens from the ACDP Approved List of Biological Pathogens were screened, covering bacteria, fungi, viruses, protozoa, helminths and prions. After the initial screening to disregard any pathogens that were out of scope, e.g., tropical, only spread from human

to human, foodborne etc., 138 pathogens including bacteria, fungi, helminths, protozoa and viruses were fully reviewed. No prions were within scope for further review. Two fungal pathogens not on the ACDP list were added during the literature search and six pathogens (bacteria, fungi, helminths and viruses) were also added as a result of expert elicitation in the questionnaire and workshop. Throughout the process of the literature review new, former and alternative names were recorded for various pathogens. Although these names were not specifically searched for, when they were found they were all included into the pro-forma spreadsheet.

Over 150 papers were used as the evidence base for the QSR. These included reviews, as per the QSR protocol, but also included research literature and case studies when reviews were not available or did not include the required information. If literature was difficult to source using Web of Science searches, government and medical websites were used for review instead. These include the CDC (Centers for Disease Control and Prevention (CDC) (www.cdc.gov), the ECDC (European Centre for Disease Prevention and Control (ECDC) (https://www.ecdc.europa.eu/en), the NHS (National Health Service (NHS) (www.nhs.uk), the UK government (https://www.gov.uk/topic/health-protection/infectious-diseases) and occasionally WHO (World Health Organisation (WHO) (www.who.int).

The QSR was focused on how immunocompetent adults experience contact with environmental pathogens as this is the largest group using the environment recreationally (Natural England, 2022). Therefore, this review lacks nuanced information that is pertinent to children, the elderly, immunocompromised individuals and those with chronic conditions such as cystic fibrosis or diabetes.

3.1.3 Pathogen Hazard Rating

A RAG (Red, Amber, Green) hazard assessment was designed to split pathogens into three hazard categories in relation to the public health concern: serious concern (red), significant concern (amber) and limited concern (green). This assessment considered the prevalence of the pathogen within the UK, the likelihood of infection (for an immunocompetent adult) and disease severity (for an immunocompetent adult).

Prevalence of each pathogen in the UK was given a score between two and four:

2 = Pathogen is not currently in the UK,
3 = Pathogen is rare/ uncommon in the UK,
3 = Pathogen is common in the UK, and
4 = Pathogen is ubiquitous in the UK.

It should be noted that although terms such as “ubiquitous” are often used to describe pathogens within published literature, this is rarely backed up with quantitative data.

The likelihood of infection if an immunocompetent adult comes into contact with the pathogen was given a score between one and three:

1 = infection is unlikely,

2 = infection is moderately likely, and
3 = infection is likely.

Likelihood of infection was based on the minimum infectious dose where available but also descriptions within research papers detailing pathogenicity or frequency of infection.

Severity of disease was scored between one and five as follows:

In healthy, immunocompetent adults,

1 = the disease is commonly asymptomatic,
2 = disease is self-limiting,
3 = treatment is usually required outside of a hospital setting,
4 = hospital treatment is required, and
5 = death or chronic health issues following infection are common.

Where a pathogen had a broad disease outcome across immunocompetent adults, the most common outcome was chosen for this assessment. For example, the condition aspergillosis is caused by the fungus *Aspergillus* spp. (NHS, 2021). As *Aspergillus* spp. is ubiquitous in the environment, immunocompetent individuals regularly encounter small amounts of it (around an estimated several hundred *Aspergillus* spp. spores per day) with no adverse effects (Latgé, 1999; CDC, 2021). Individuals that are exposed to a large dose of *Aspergillus* spp. or are exposed regularly and repeatedly can experience an allergic reaction in the lungs or sinuses which is most commonly self-limiting but can, in some cases, require medical treatment (Latgé, 1999; Barnes and Marr, 2006). In some cases, aspergillosis can develop into a more severe lung or sinus condition which would require long-term medical treatment or surgical intervention (Barnes and Marr, 2006; CDC, 2021; NHS, 2021). In addition to inhalation, *Aspergillus* spp.can also occur by entering the body through a wound causing cutaneous (skin) aspergillosis (CDC, 2021). Therefore, in the case of *Aspergillus* spp., a disease severity of “2 = disease is self-limiting” was chosen as this was judged as the most likely and common outcome for an immunocompetent adult.

Scores for each category were combined by adding them together. Both addition and multiplication of scores was explored. Adding of scores together gave a better spread of pathogens across the three hazard categories (green, amber and red) and pathogens with a widely recognised level of concern, such as *Campylobacter* spp., were sorted into appropriate categories using this additive model. Those falling between three and five were considered of limited concern (green), those between six and eight were considered significant concern (amber) and those between nine and twelve were of serious concern (red).

It is appreciated that although this method aimed to be as systematic as possible it does omit important considerations such as paediatric and geriatric infection and infection in immunocompromised individuals. It also misses nuanced details such as heterogenous pathogen prevalence across the UK and unusual disease outcomes. Taking these limitations into account a questionnaire was sent out to a wide range of experts (section 3.2)

who were also invited to an online workshop (section 3.3). Information submitted and discussed by this panel of experts were used to adjust several hazard categories.

3.2 Questionnaire Survey

3.2.1 Methodology

A questionnaire (appendix B) was developed using Qualtrics software (Qualtrics, Provo, UT), reviewed by the project team and steering group and trialled by the project team and selected external contacts with a knowledge of the field. It was then administered using Qualtrics to 61 recipients deemed to have either general expertise in the field of pathogens in the environment or with specific expertise on one or more individual pathogens or groups of pathogens of interest. Recipients of the questionnaire were identified through the project team and steering group's existing expert contacts and/or other experts identified online and through the QSR. Responses were collated within Qualtrics and exported to spreadsheets for further analysis.

Questions focussed on understanding which current or emerging pathogens the respondent felt were of particular concern, their sources of entry to the environment, environmental matrices in which they are found and how their prevalence might be impacted by behaviours, management activities and future changes such as land use or climate change.

3.2.2 Summary

There were 23 survey responses equating to a 38 % response rate. Academics were most strongly represented with coverage of food and water industry, public and animal health and government/policy institutions. The "other" category represented a non-governmental organisation (NGO), a retired academic/consultant and an academic who is also a livestock farmer (appendix C, table 1). Respondents were in a variety of roles, dominated by senior positions (appendix C, figure 1). Expertise covered included microbial ecology, environmental/water microbiology, environmental engineering/engineering, environmental/soil/water science, design and technology/materials science, water quality, epidemiology, molecular biology, environmental microbiology, microbiology, livestock agriculture, parasitology, clinical microbiology, bacteriology, one health, biogeochemistry & toxicology, public health, chemistry, materials science, and veterinary science. They operated primarily in the UK, across England, Scotland and Wales but there were also representatives from the US, Europe and Africa (appendix C, figure 2).

Responding to which pathogens were of concern, a wide range of genera were mentioned across different taxonomic groups (appendix C, table 2). Bacterial genera were the most mentioned (109 mentions) with *Escherichia*, *Salmonella*, *Campylobacter*, *Vibrio*, *Leptospira, Legionella and Borrelia* each receiving between 5 and 18 mentions. Where more detailed taxonomic information was given, different pathogenic strains of *E. coli* were mentioned, and named species of other top-ranking bacteria included: *Leptospira interrogans, Borrelia burgdorferi sensu lato complex, Borrelia miyamotoi.* In total, 25 individual genera were

mentioned. There were 40 mentions of viruses by different respondents, with norovirus and hepatitis viruses (A and E) receiving the most mentions within the virus group (5 and 6 respectively). Fifteen fungal genera/groups received mentions, but all were only mentioned once except for *Aspergillus fumigatus* which received two mentions. There were 33 mentions of protozoa, however this covered only 8 genera. The most mentioned protozoa were *Cryptosporidium* (*parvum, andersoni, meleagridis, cuniculus* – 11 mentions), *Toxoplasma gondii* and *Giarda duodenalis* (8 mentions each). Three other organisms mentioned (only once each) and not in the above groupings were: *Echinococcus* (a helminth) Avian Schistomes (fluke) and algae.

Where there were high numbers of mentions, this was taken as indicative of a broad level of concern around a specific organism. However, because expertise across different taxonomic groups was not necessarily even among respondents, organisms with only one hit could not be ruled out as being of concern and were thus also discussed during the subsequent workshop.

3.2.2.1 Sources

The main sources identified by multiple respondents included human sewage (treated and untreated, including septic tanks and combined sewer overflows (CSOs, OSAs such as livestock manures, compost, digestate, and biosolids, animal faeces, run off (urban and agricultural) and insect vectors (appendix C, table 3). It was noted that some pathogens are indigenous to soils and therefore soils were also included as a source. Examples include *Clostridia* which are naturally present in soils (Voidaru et al., 2011) and *E. coli* and Mycobacteria which can naturalise and/or persist in soils for years (Brennan et al., 2010; Elliott et al., 2015).

3.2.2.2 Environmental matrices

Environmental matrices in which pathogens are found were identified by respondents as sediments (including intertidal), sand, soil, water (fresh and marine), sewage, animal faeces, aerosols/air/dust, surfaces, and plants (appendix C, table 4). Some respondents mentioned live animals, humans, birds and ticks, but these are not generally referred to as environmental matrices.

3.2.2.3 Pathways

When respondents were asked about the pathways by which pathogens move through the environment, the main responses related to water and wastewater routes (sewage/septic effluents, resuspension from sediment, rain-driven run-off, irrigation), animals (deposition of faeces, movement, land application of organic amendments & subsequent leaching) and vector pathways (insect, invertebrate, protozoal, movement via particulates including microplastics) (appendix C, table 4).

However, there were also responses that did not relate to a specific pathway but referred to the scale of movement processes at work – from micro to catchment scale, particularly with respect to water-borne movement. It was also noted that pathways are “pathogen

dependent". This was interpreted to reflect the differences in pathogen life cycle and biology. There was notable overlap between responses about sources (appendix C, table 3), responses about the matrices in which pathogens are commonly found in the environment and responses about pathways (appendix C, table 4). Consistent with the literature there is a lack of clarity within the source and pathway terms because parts of the pathways can become or act as sinks (Byappanahalli et al., 2012) which become sources for subsequent movement. Examples include transfer from livestock faeces (source) to soils (pathway, but also an environmental sink which can act as a source) or e.g., from agricultural run-off (pathway) to stream bed sediment (pathway, but also environmental store which can act as a pathway (e.g., Schang et al., 2018). The key here is the ability to identify where exposure is likely to occur and where interruption of the flow by applying an intervention or mitigation option is practical and has greatest impact in reducing human exposure to pathogens. Responses also mentioned the food chain, which is undoubtedly a route by which humans are exposed to pathogens originating in the environment, but this was outside the scope of the study and therefore was not included in appendix C, table 4.

3.2.2.4 Human Exposure

Responses to how human exposure takes place could be summarised by a modification of a comment from one respondent:

"Eating, touching, breathing, swimming, walking through ecological niches, vectors".

The main responses indicated that the main routes of exposure arose through outdoor recreational activities, particularly those involving water (especially where there was full immersion) or touching soil or vegetation. Different pathways are relevant for separate groups of pathogens, for example pathways involving intentional or unintentional ingestion of water – drinking contaminated water, water sports – are pertinent to pathogens transmitted via faeco-oral route, such as *Cryptosporidium*, enteric bacteria, and viruses. Pathways involving immersion in water are relevant to pathogens likely to cause skin or ear infections. Vector-borne disease exposure will be determined by the vector life cycle – for example tick borne disease are much more likely to be associated with contact with vegetation, whereas mosquito-borne disease would be associated with geographic prevalence of specific mosquito species and warm, damp weather patterns.

3.2.2.5 Management Activities

In terms of activities or management practices that could change the likelihood of pathogens of concern being found in the environment, practices associated with wastewater and wastewater treatment featured commonly in responses, as did responses related to management of livestock faeces and run-off (appendix C, table 5). Most responses did not highlight specific pathogens, but it was noted in one response that answers would be very dependent on the pathogen. One response noted that farm animal and faecal management would reduce environmental contamination, referring specifically to *Cryptosporidium*, *Giardia* and *Toxoplasma*. Another respondent indicated that they were specifically considering parasites when commenting that poor farm waste management, poor animal health, poor biosecurity and housing conditions could all lead to greater likelihood of these pathogens being present in the environment. Another respondent was specific about

Babesia, noting that tick control measures would reduce prevalence of this parasite. Other comments of interest included that the risk of accidental contact was generally low and therefore it was suggested that identification and monitoring of high-risk areas would be important. With reference to emerging pathogenic amoebae, a respondent noted that it would not be desirable to try to reduce their prevalence in the environment as they are important for soil fertility. Eating was mentioned by one respondent and although food-chain exposure was outside the scope of this study, it was considered pertinent because outdoor eating (e.g., picnics) was identified as a potential route of exposure were washing of hands and poorer food hygiene (e.g., food falling onto soil or vegetation and being picked up and eaten) come into play.

3.2.2.6 Reducing human contact with pathogens in the environment

Suggested practices (appendix C, table 6) to reduce environmental exposure to pathogens included use of signage, warnings and awareness raising, practical measures such as fencing off of animals to reduce direct deposition of faeces into streams, very specific health and safety advice (such as not to swim in open water wearing contact lenses) and then much broader suggestions such as better global management of waste. Practices mentioned which were likely to increase human exposure ranged from how people use the environment (recreational use of waters and walking in overgrown areas) to agricultural practices and sewage management. Other suggestions related to personal hygiene practices such as hand washing.

While most of the responses were general, some were given for specific pathogens. A respondent noted that for *Cryptosporidium, Giardia* and *Toxoplasma,* farm visits and outdoor recreational use of water would increase the risk of exposure to humans and that exposure to *Babesia* would be increased by walking in areas where ticks are present. They highlighted specific behaviours that would reduce tick transmitted disease: Checking for ticks, prompt removal of ticks, wearing clothing impregnated with acaricides, wearing clothing that covers skin and minimises tick access to skin (trousers tucked into socks), use of insect repellents.

3.2.2.7 Impacts of Future Changes on Pathogens in the Environment

While it was noted that impacts of future changes would be pathogen-specific, a range of responses were given (table 7). Many of these fell under the category of climate change – all related to increased rainfall or drought – which were likely to have direct effects on pathogens entering the environment through increased sewage overflows and increased overland flow or indirect effects such as changing wildlife behaviours or changes in the concentration of pathogens in surface waters due to increased or decreased rainfall and associated water volumes. Increased rainfall is widely considered to increase the prevalence of diarrhoeal diseases (Levy et al, 2016, Semenza et al., 2020). Drought can impact the microbial quality of private water supplies and increases the concentration of pathogens in water bodies in general (Yusa et al., 2015)). Climate change was also noted to lead to changes in distribution and migration of wildlife, and it was highlighted that warmer, wetter weather would also lead to an increase in pathogen vectors, such as ticks, and therefore an increase in the diseases that they transmit. This is consistent with the literature

(e.g., Bouchard et al, 2019) which indicates climate mediated increases in survival, activity period of ticks, range of tick hosts and a longer season during which people are likely to be exposed to ticks (appendix C, table 7).

Other changes that were considered related to land use change, changes in human population density and behaviour and infrastructural changes which may mitigate some of the aforementioned changes (appendix C, table 7).

3.3 Workshop

3.3.1 Methodology

In addition to collaborators from the James Hutton Institute, Department for Environment, Food and Rural Affairs and the Environment Agency, the workshop was attended by academic, regulatory, and independent experts.

All experts who attended the workshop were tasked with reviewing three lists of pathogens; pathogens with prior consensus, pathogens without prior consensus and pathogens listed by one expert only in the questionnaire. The list of pathogens with prior consensus were those with a hazard rating 8 – 12, amber/red **and** had multiple experts flag them as important in the questionnaire. The list of pathogens without prior consensus were pathogens which were either considered of serious concern in the RAG assessment (hazard rating 8 – 12, amber/red) **or** had more than one expert record them in the questionnaire Finally, the list of pathogens with only one vote in the questionnaire was compiled from all pathogens that were only listed once by a single expert. Of these, two were also considered of serious concern in the RAG assessment (hazard rating 8 – 12). Those who attended the workshop were asked to work through each list as a group and sort them into four categories; serious concern (red), significant concern (amber), limited concern (green) and unknown/don't know (blue). This final category was added in the event of a lack of expertise in a particular area or a particularly rare or unusual pathogen that required further research.

Additionally, after the workshop was completed, further advice was sought via email from experts who could not attend. Supplementary literature review on specific pathogens was conducted where necessary and this information was combined with the expert conclusions. Finally, the quick scoping review was updated with these outcomes.

3.3.2 Summary

During the workshop 93 pathogens were discussed by experts and sorted into four categories. Overall, 37% of all pathogens discussed were moved into a different category following discussion. Of these, 47% were downgraded to a category of lower concern and the remainder (53%) were upgraded to a category of higher concern.

A further 24% of the pathogens reviewed were designated further category which signified that the experts did not feel they knew enough to assess them. An additional 36 % had been

discarded at the initial screening for the QSR as out of scope (i.e. hospital-acquired, occupational, solely food-borne, or tropical) or were not on the ADCP list.

There was some overlap between these pathogens that were not reviewed and those that experts could categorised in the workshop due to a lack of knowledge of these particular pathogens. They were also commonly those highlighted only by one questionnaire respondent. The RAG hazard assessment was designed to be objective and not heavily influenced by personal opinion, whereas the expert opinion elicitation allowed for a more nuanced discussion of hazard thus maintaining a balance between an objective assessment and a nuanced opinion.

4. Pathogens of Serious Concern

The final hazard rating derived from the combined QSR, questionnaire and workshop data (appendix A) was used to identify the pathogens of serious concern. This list comprises all pathogens which, in the hazard rating, scored 9 or more and were assigned to the “red” category – pathogens of serious concern.

Bacteria

- *Campylobacter jejuni*
- *Campylobacter spp.* (inc *C. coli* and *C. lari*)
- *Escherichia coli*, STEC strains (e.g., O157:H7 or O103)

Fungi

- *Cladophialophora bantiana* (formerly *Xylohypha bantiana, Cladosporium bantianum*)

Viruses

- Norovirus

5. Pathogens of Significant Concern

This list comprises all pathogens which, in the hazard rating, scored 8 – the maximum score in the “amber” category – designated pathogens of serious concern.

Bacteria

- *Aliarcobacter butzleri* (formerly *Arcobacter butzleri*, formerly *Campylobacter butzleri*)
- *Anaplasma phagocytophilum* (formerly *Ehrlichia phagocytophilum*)
- *Bacillus anthracis*
- *Borrelia burgdorferi*
- *Escherichia coli* (with the exception of non-pathogenic strains)
- *Legionella pneumophila*

- *Salmonella typhi*
- *Shigella flexneri*
- *Shigella sonnei*

Fungi

- *Cryptococcus neoformans var neoformans* (*Filobasidiella neoformans var neoformans*)
- *Lomentospora prolificans* (formerly *Scedosporium prolificans*)
- *Rhizomucor pusillus*
- *Scedosporium apiospermum (Pseudallescheria boydii,* formerly *Monosporium apiospermum)*

Protozoa

- *Cryptosporidium parvum*
- *Giardia lamblia (Giardia intestinalis/duodenalis)*
- *Naegleria fowleri*
- *Toxoplasma gondii*

Viruses

- Sapovirus
- tick-borne encephalitis virus (in the UK central European tick-borne encephalitis virus)

5.1 Pathogens of concern by environmental matrix

Table 2: The pathogens of most concern to immunocompetent adults in the environment, listed by matrix (soil, freshwater, seawater, faeces, airborne). The final hazard rating in addition to the risks driving the pathogens importance to human health are additionally listed.

Matrix	Organism Type	Organism	Hazard Rating	Comment
Soil	Bacteria	*Campylobacter spp.*	9	Ubiquitous and found in many matrices.
		Bacillus anthracis	8	Common in the environment and causes serious disease.
		Legionella pneumophila	8	Common, moderate likelihood of disease if inhaled and often requires medical attention.
	Fungi	*Cladophialophora bantiana* (formerly *Xylohypha bantiana, Cladosporium bantianum*)	9	Death likely if infected.
		Cryptococcus neoformans var. neoformans (Filobasidiella neoformans va.r neoformans)	8	Ubiquitous in terrestrial environment.
		Lomentospora prolificans (formerly *Scedosporium prolificans*)	8	Likely to cause serious disease if infected.

Matrix	Organism Type	Organism	Hazard Rating	Comment
		Rhizomucor pusillus	8	Death likely if infected.
		Scedosporium apiospermum (*Pseudallescheria boydii*, formerly *Monosporium apiospermum*)	8	Likely to cause serious disease if infected.
	Protozoa	*Naegleria fowleri*	8	Death likely if infected.
		Toxoplasma gondii	8	Common in the environment with a high likelihood of infection.
Freshwater	Bacteria	*Campylobacter jejuni*; *Campylobacter coli*; *Campylobacter lari*	9	Ubiquitous and found in many matrices.
		Escherichia coli, verocytotoxigenic strains (e.g., O157:H7 or O103)	9	Common in the environment, likely to cause disease (low infectious dose) and medical treatment required if infected.
		Aliarcobacter butzleri (formerly *Arcobacter butzleri* or *Campylobacter butzleri*)	8	Ubiquitous in the environment.
		Bacillus anthracis	8	Common in the environment

Matrix	Organism Type	Organism	Hazard Rating	Comment
				and causes serious disease.
		Escherichia coli (other pathogenic strains)	8	Ubiquitous in the environment.
		Legionella pneumophila	8	Common, moderate likelihood of disease if inhaled and often requires medical attention.
		Shigella flexneri; *Shigella sonnei*	8	Low infective dose.
	Fungi	*Lomentospora prolificans* (formerly *Scedosporium prolificans*)	8	Likely to cause serious disease if infected.
		Rhizomucor pusillus	8	Death likely if infected.
		Scedosporium apiospermum (*Pseudallescheria boydii,* formerly *Monosporium apiospermum*)	8	Likely to cause serious disease if infected.
	Protozoa	*Cryptosporidium parvum*	8	Common, moderate likelihood of disease and often requires

Matrix	Organism Type	Organism	Hazard Rating	Comment
				medical attention.
		Giardia lamblia (*Giardia intestinalis/duodenalis*)	8	Low infective dose.
		Naegleria fowleri	8	Death likely if infected.
		Toxoplasma gondii	8	Common in the environment with a high likelihood of infection.
	Viruses	Norovirus	9	Ubiquitous and infectious.
		Sapovirus	8	Common and highly infectious.
Sea water	Bacteria	*Aliarcobacter butzleri* (formerly *Arcobacter butzleri*, formerly *Campylobacter butzleri*)	8	Ubiquitous in the environment.
	Protozoa	*Toxoplasma gondii*	8	Common in the environment with a high likelihood of infection.
	Viruses	Norovirus	9	Ubiquitous and infectious.
		Sapovirus	8	Common and highly infectious.

Matrix	Organism Type	Organism	Hazard Rating	Comment
Vector	Bacteria	*Anaplasma phagocytophilum* (formerly *Ehrlichia phagocytophilum*)	8	Common, moderate likelihood of disease and often requires medical attention.
		Borrelia burgdorferi; *Borrelia duttonii* (Tick-borne)	8	Common, moderate likelihood of disease and often requires medical attention.
	Viruses	tick-borne encephalitis virus (in the UK central European tick-borne encephalitis virus) (Tick-borne)	8	Likely to cause serious disease if infected.
Faeces	Bacteria	*Campylobacter jejuni; Campylobacter coli* and *C. lari*	9	Ubiquitous and found in many matrices.
		Escherichia coli, verocytotoxigenic strains (e.g., O157:H7 or O103)	9	Common in the environment, likely to cause disease and medical treatment required if infected.
		Aliarcobacter butzleri (formerly *Arcobacter butzleri*, formerly *Campylobacter butzleri*)	8	Ubiquitous in the environment.

Matrix	Organism Type	Organism	Hazard Rating	Comment
		Escherichia coli (with the exception of non-pathogenic strains)	8	Ubiquitous in the environment.
		Salmonella typhi	8	Infectious and disease likely to require medical treatment.
		Shigella flexneri; *Shigella sonnei*	8	Low infective dose.
	Protozoa	*Cryptosporidium parvum*	8	Common, moderate likelihood of disease and often requires medical attention.
		Giardia lamblia (*Giardia intestinalis/duodenalis*)	8	Low infective dose.
		Toxoplasma gondii	8	Common in the environment with a high likelihood of infection.
	Viruses	Norovirus	9	Ubiquitous and infectious.
		Sapovirus	8	Common and highly infectious.
Airborne	Bacteria	*Legionella pneumophila*	8	Common, moderate likelihood of

Matrix	Organism Type	Organism	Hazard Rating	Comment
				disease if inhaled and often requires medical attention.
	Fungi	*Cladophialophora bantiana* (formerly *Xylohypha bantiana, Cladosporium bantianum*)	9	Death likely if infected.
		Cryptococcus neoformans var neoformans (*Filobasidiella neoformans var neoformans*)	8	Ubiquitous in terrestrial environment.
		Rhizomucor pusillus	8	Death likely if infected.
		Scedosporium apiospermum (*Pseudallescheria boydii*, formerly *Monosporium apiospermum*)	8	Likely to cause serious disease if infected.
	Protozoa	*Naegleria fowleri*	8	Death likely if infected.

5.2 Pathogens likely to enter the UK

A number of pathogens that scored highly for severity and, in some cases, were noted as a potentially severe threat through the expert elicitation exercises did not score as such because they are not currently present in the UK. Therefore, for the purpose of horizon-scanning for disease threat, it is important to consider the likelihood of these pathogens entering the UK. If the pathogens listed below entered the UK and it is assumed that at the point of entry, they would be 'rare/uncommon' several pathogens would then score a level 8 (significant concern - amber). If they then became 'common' within the environment these pathogens would score a level 9 (severe concern – red).

- *Francisella tularensis* (Type B)

- Crimean/Congo haemorrhagic fever virus
- Dobrava-Belgrade orthohantavirus
- Puumala orthohantavirus
- Thogoto virus

5.3 Drivers of pathogens of serious concern

The bacterial pathogens highlighted as of serious concern in the UK – *Campylobacter* species and verocytotoxigenic *E. coli* - are enteric pathogens, transmitted faeco-orally. *Campylobacter* is one of the most common causes of diarrhoeal disease globally and the high rate of infection is in part driven by its widespread prevalence in animal faeces (e.g. Nag et al., 2021). Sources of environment-associated exposure include contaminated water and direct contact with animals and or animal faeces. Its classification in this study as a pathogen of concern arises through a combination of its prevalence, typical disease outcome (diarrhoeal disease), and complications such as Guillane-Barre syndrome in some cases. It can survive in slurry and manure in high numbers, providing a clear entry route to the outdoor environment (Hutchinson, et al., 2004) via direct deposition of animal faeces or application of organic soil amendments (OSA). While frequently reduced during anaerobic digestion treatment, it may not be fully removed and can remain unchanged (Avery et al., 2014). Human cases of Campylobacteriosis in the UK show seasonal patterns, with peaks in May/June and September to December. This may be linked to temperature, UV exposure, desiccation, changes in incidence in animal reservoirs, seasonality in human behaviours or prevalence of flies transferring the organisms from faeces. The primary driver has yet to be identified (Djennad et al., 2019; Nag et al., 2021), however *Campylobacter* species are climate sensitive and likely to be impacted by changes in weather patterns as well as land use changes or management approaches that increase or reduce inputs of faecally-derived contaminated organic amendments to land. *Campylobacter* species are also commonly found in wastewater-contaminated freshwaters. Rechenberg and Kistemann (2008) noted that highest *Campylobacter* spp. loads and high risk of infection occurred after heavy rainfall during the summertime, which should be a focus for mitigation approaches.

Pathogenic strains of *E. coli* (known as STEC, previously VTEC, *E. coli*), such as *E. coli* O157:H7, capable of producing Shiga toxin (stx), cause diarhhoeal disease, including bloody diarrhoea and complications such as hemolytic uremic syndrome which can lead to kidney failure and thrombocytopaenic purpura (a low platelet condition). Non-O157 STEC also cause disease as severe as the more widely recognised O157 strains. While food-borne infections are most common, infections associated with environmental exposure are also responsible for several infections and outbreaks (Butt et al, 2022). Indeed, Adams et al (2016) identified changes in the source of infections, including increases in cases associated with petting farms. The Republic of Ireland and parts of Scotland appear to have a high incidence of human STEC infection and one of the drivers is thought to be reliance on private water supplies which are not regulated in the same way as public supplies (Health Protection Scotland, 2018; Andrade et al., 2022). Health Protection Scotland noted in 2018 that the evidence bases for risks associated with outdoor pursuits and events that could lead to exposure remain poorly defined and require further research.

Similarly to *Campylobacter*, environment-associated risks are likely to be driven by taking part in activities that involve contact with STEC-contaminated environments (i.e. waters, vegetation, outdoor surfaces such as gates and soils which are contaminated by animals or faeces) (Kintz et al., 2023), intensification of agriculture, and cattle which shed high concentrations of STEC in their faeces (known as super-shedders) (Griffin and Karmali, 2017). Shedding itself is influenced by diet, health and climatic factors (Williams et al, 2015). STEC infections peak during the summer months – sheep and cattle, the main reservoir for STEC, are grazed outdoors from spring to autumn, increasing potential for human contact with faeces or faecally-contaminated environments (although this could be confounded by greater likelihood of eating contaminated food e.g., barbeques). Kintz et al (2023) noted that other STEC strains showed different seasonal patterns. Interestingly, their study also identified a lower risk of STEC infection associated with contact with soil and dogs. This may reflect increased immunity due to frequent exposure as has been observed in farmers (Quilliam et al, 2012). Increased ambient temperature may lead to higher rates of STEC infection (Phillipsborn et al., 2016). Rainfall is widely understood to increase run off from agricultural land, which may be faecal contaminated from livestock grazing or by organic soil amendment. Further, untreated wastewater inputs increase during heavy rainfall. However, patterns are not straightforward and complicated by the nature of the catchment, sources, discharge rates, preceding weather conditions and bed-sediment stores (e.g., Cho 2020).

Approaches to reduce risk would include liaising with agencies who undertake surveillance and research on emerging strains of STEC to understand how prevalence and emergence of strains is changing over time, communications and public education strategies, and improved policies and interventions to mitigate risks, including those related to the contamination of produce and the environment, using a “One Health” approach. (Griffin and Karmali, 2017).

Exposure routes are likely to be similar among faeco-orally transmitted pathogens and therefore general guidance such as ‘Avoiding bugs and germs outdoors’ - Avoiding bugs and germs outdoors | NHS inform is relevant (NHS inform, 2023). This also provides information on being tick aware. Livestock biosecurity regulations are also pertinent and adherence to these will be helpful in good husbandry practices that minimise the spread of pathogens (Health Protection Scotland, 2018). Liaising with agencies that already undertake surveillance of emerging STEC and *Campylobacter* strains, will also help to understand changes to risk drivers and geographic prevalence of these organisms (Griffin and Karmali, 2017), especially as it has been noted that there may be distinct reservoirs for different STEC strains (Kintz et al., 2023).

Norovirus, also known as the winter vomiting bug, is thought to be responsible for over 3 million infections per year in the UK, (Hassard et al., 2017), with recent increases in case numbers reported (Hassard et al., 2017, UK Health Security Agency, 2023). While most cases of norovirus are spread person to person or via contaminated food, contaminated water is also associated with infections. Genotype GII.4 is responsible for most outbreaks and is more often associated with person-to-person transmission. Other genotypes (such as GI.3, GI.6, GI.7, GII.3, GII.6 and GII.12) are more frequently associated with foodborne transmission and GI strains are more often associated with waterborne transmission and

have been shown to survive for longer periods of time in water (de Graff et al., 2016; Villabruna et al., 2022). As a human virus shed in faeces at concentrations up to 10^{12} genome copies per gram (Atmar et al., 2008), norovirus enters the environment primarily through release of sewage into water bodies, although there have also been cases where water users have directly contaminated water bodies, leading to outbreaks. Treatment of biosolids prior to land application has minimised inputs from this source. Wastewater treatment does not necessarily remove norovirus and therefore sources include both untreated and treated wastewater (Hassard et al., 2017). Risk of infection is therefore through contamination of drinking water supplies and recreational use of water. The assignment as a pathogen of serious concern arises from its prevalence in wastewater and high infectivity. It is also likely to spread further once infection is acquired by an individual and an increase in recreational water use could lead to higher rates of infection.

Population is likely to be a driver of risk as sewage discharges tend to be greatest in areas of denser population (Hassard et al., 2017) and the greatest risk appears to be from large WWTPs which discharge continuously (DEFRA, 2015), particularly in urban dominated catchments. High viral loads occur at the point of WWTP discharge and reduce with distance from WWTP inputs. They can, however, be detected several km away from point sources. Coastal waters tend to have lower numbers of norovirus than inland receiving waters (Hassard et al., 2017). Norovirus is reported to survive for up to 30 days in the environment (Pommepuy, 2004).

Norovirus prevalence in waters in the northern hemisphere are greatest between April and October and this seasonality is reflected in infection rates. Elevated temperature and solar UV radiation tend to decrease viral loads in water (Hassard et al., 2017). Impacts of future change are therefore unclear, as warming/increased solar radiation may decrease viral loads in waters but flood events are likely to increase untreated discharges from CSOs, increasing viral loads entering the waters.

Mitigation measures might include enhanced wastewater treatment, such as use of membrane bioreactors, reducing or applying UV-treatment to CSO flows (these measures may not always be practical or cost-effective) and/ or increasing awareness of microbial water quality for recreational users of water (Hassard et al., 2017).

Cladophialophora bantiana (formerly *Xylohypha bantiana, Cladosporium bantianum)* is a saprophytic black mould that can cause infections of the central nervous system. Although incidence of infection is rare, classification in this study as a pathogen of serious concern was driven by the severity of infection (mortality rate of 71%; Ozgun et al., 2019), the fact that high mortality occurs in otherwise healthy individuals, treatment may be highly invasive (brain surgery), and fatality occurs rapidly (Kantarcioglu, 2016). The fungus is likely to be of environmental origin, thought to be a soil fungus (Badali et al., 2008) although it has only been isolated infrequently from environmental matrices (soil, tree bark, hot tub water) (Rantala et al., 2015). *Cladosporium* species are airborne and opportunistic infections occur via skin/wounds and inhalation (Tasic and Miladinovic-Tasic, 2007).

More cases have been associated with warmer climates, which may have implications for changes in prevalence under future climate change. One study highlighted occupational

associations with infection – including gardening and agriculture (Kantarcioglu, 2016) – contact with decaying organic matter and compost may be a risk factor but this is an emerging pathogen with limited information on risk drivers or mitigations.

Vulnerable Groups

It must be noted that the hazard rating of pathogens in this review was focussed specifically on immunocompetent adult individuals and related to the most common disease outcomes. Vulnerable groups will be more susceptible to infection and therefore may be affected more severely than immunocompetent individuals. Vulnerable groups include children and adults in need of special care, support, or protection because of age, disability, risk of abuse or neglect, and can be influenced by socioeconomic factors (Office for Health Improvement and Disparities, 2022). For example, it is widely accepted that children and the elderly tend to be impacted more significantly by infectious disease as they have less effective immune systems which are either developing or ageing, although the association with age and vulnerability varies (as in the example of SARS-CoV-2 where children were relatively unaffected, but the elderly were at higher risk of mortality). Those with compromised immune-systems (e.g., undergoing chemotherapy or taking immuno-suppressants) are also more likely to develop more serious infections from any infectious disease (McGrath et al., 2020) including those to which they are exposed in the outdoor environment. For example, immunocompromised patients with nocardiosis experience more severe disease symptoms and higher mortality than non-immunocompromised individuals (Steinbrink et al., 2018). Specific conditions also render individuals more susceptible to infection and serious outcomes, as in the case of cystic fibrosis (CF). Historically, most CF patients were thought to acquire infections from the environment, although person-person transmission is now much more widely recognised (Schaffer, 2015). Environmental pathogens such as Mycobacteria, *Pseudomonas aeruginosa* and *Burkholderia* are likely to infect CF patients more readily than those without the condition.

6. Limitations

The use of a QSR and a simple RAG scoring framework minimised bias associated with individuals' expertise and organisms of interest While some adjustment was made based on the questionnaires and workshop and follow-up research and consultations, the scoring framework constrained manipulation of scores which limited the capture of more nuanced narrower categories. Further, the scoring parameters focussed on the most common outcome of disease and approaching this differently (e.g., worst-case scenarios or impacts on vulnerable populations) may change the hazard rating.

Dependence primarily on review papers was necessary to screen over 500 pathogens and undertake a hazard assessment for 138 pathogens within the short timeframe of the study. More nuanced information may be gleaned from undertaking a more detailed systematic review of individual organisms.

It is also important to note that risks are dependent upon compliance. For example, diffuse pollution inputs to waters from agriculture should minimally impact norovirus numbers in waters, because the high risk OSAs (human-derived biosolids) are substantially treated prior to application. However, if compliance is not adhered to, and untreated wastes (e.g., septic tank contents) are applied to land, there is an increased risk of norovirus inputs to waters. Similarly for the bacterial pathogens – Campylobacter and STEC, application of manures and slurries during weather conditions that generate increased run off poses a greater risk than if guidance is followed.

7. References

American National Standards Institute. (2015). 'ANSI/ASHRAE Standard 188-2015. Legionellosis: Risk Management for Building Water Systems'. *ASHRAE Standards Committee*. Pp1-22

Andrade, L., Boudou, M., Hynds, P., Chique, C., Weatherill, J., and O'Dwyer, J. (2022). Spatiotemporal dynamics of Escherichia coli presence and magnitude across a national groundwater monitoring network, Republic of Ireland, 2011–2020. Science of The Total Environment 840,156311, https://doi.org/10.1016/j.scitotenv.2022.156311

Atmar, R.L.; Opekun, A.R.; Gilger, M.A.; Estes, M.K.; Crawford, S.E.; Neill, F.H.; Graham, D.Y. Norwalk virus shedding after experimental human infection. Emerg. Infect. Dis. 2008, 14, 1553–1557.

Australian Shellfish Quality Assurance Advisory Committee. (2022). Australian Shellfish Quality Assurance Programme: Operations Manual. Volume 6. Retrieved from https://www.fish.wa.gov.au/Documents/Aquaculture/ASQAP%20Manual_(V6)_2022.pdf

Avery, L.M., Yongabi Anchang, K., Tumwesige, V., Strachan, N. and Goude,P.(2014). Potential for Pathogen reduction in anaerobic digestion and biogas generation in Sub-Saharan Africa. Biomass and Bioenergy 70, 112-124, https://doi.org/10.1016/j.biombioe.2014.01.053

Badali H, Gueidan C, Najafzadeh MJ, Bonifaz A, van den Ende AH, de Hoog GS. Biodiversity of the genus Cladophialophora. Stud Mycol 2008; 61: 175-191

Barnes, P. D., and Marr, K. A. (2006). 'Aspergillosis: Spectrum of Disease, Diagnosis, and Treatment'. *Infectious Disease Clinics of North America*. 20(3). Pp 545 – 561. https://doi.org/10.1016/j.idc.2006.06.001

Baylis, M. Potential impact of climate change on emerging vector-borne and other infections in the UK. Environ Health 16 (Suppl 1), 112 (2017). https://doi.org/10.1186/s12940-017-0326-1

Bouchard, C., Dibernardo, A., Koffi, J., Wood, H., Leighton, P. A., and Lindsay, L. R. N. (2019). 'Increased risk of tick-borne diseases with climate and environmental changes'. *Can Commun Dis Rep*. 45(4). Pp83-89. https://doi.org/10.14745/ccdr.v45i04a02

Brennan, F. P., O'Flaherty, V., Kramers, G., Grant, J., and Richards, K. G. (2009). 'Long-Term Persistence and Leaching of Escherichia coli in Temperate Maritime Soils.' *Applied and Environmental Microbiology*. 76(5). https://doi.org/10.1128/AEM.02335-09

British Columbia Regulations. (2022). 'Environmental Management Act and Public Health Act – Organic Matter Recycling Regulation'. *B.C. Reg*. 18/2002. Retrieved from https://www.bclaws.gov.bc.ca/civix/document/id/complete/statreg/18_2002 Accessed on 25/1/23

Bureau de Normalisation du Quebec. (2016). *CAN/BNQ 0413-200 Organic Soil Conditioners – Composts*. Retrieved from https://www.bnq.qc.ca/en/standardization/environment/composts.html#:~:text=Standard%20CAN%2FBNQ%200413-200%20Organic%20Soil%20Conditioners%20%E2%80%94%20Composts,is%20safe%20for%20human%20health%20and%20the%20environment

Butt S, Jenkins C, Godbole G, et al. The epidemiology of Shiga toxin-producing Escherichia coli serogroup O157 in England, 2009–2019. Epidemiol Infect. 2022;150:150.

Byappanahalli, M. N., Nevers, M. B., Korajkic, A., Staley, Z. R., and Harwood, V. J. (2012). 'Enterococci in the Environment'. *Microbiology and Molecular Biology Reviews*. 76(4). https://doi.org/10.1128/mmbr.00023-12

Canadian Ministry of Health. (2017). 'Health Information Greywater Re-Use'. 57aters57ed from https://www2.gov.bc.ca/assets/gov/environment/waste-management/sewage/onsite-sewerage-systems/what_is_grey_water.pdf Accessed 02/02/23

Carrington, E.G. (2002). 'Evaluation of Sludge Treatments for Pathogen Reduction – Final Report'. *The European Commission Directorate*. Pp1-52.

CCME (Canadian Council of Ministers of the Environment). (2005). 'Guidelines for Compost Quality'. *Canadian Council of Ministers of the Environment*. Pp1 – 26.

CDC. (2021). 'Aspergillosis'. Retrieved from https://www.cdc.gov/fungal/diseases/aspergillosis/index.html

Code of Federal Regulations (2012). 'Part 141 – National Primary Drinking Water Regulations'. Retrieved from https://www.govinfo.gov/content/pkg/CFR-2019-title40-vol25/pdf/CFR-2019-title40-vol25-part141.pdf

Code of Federal Regulations. (2018). 'Part 503 – Standards for the use or disposal of sewage sludge'. Vol 32. Retrieved from https://www.govinfo.gov/content/pkg/CFR-2018-title40-vol32/xml/CFR-2018-title40-vol32-part503.xml

Collins, A. M., Coughlin, D., Miller, J., and Kirk, S. (2015). 'The Production of Quick Scoping Reviews and Rapid Evidence Assessments: A How to Guide'. Joint Water Evidence Group. Pp1-78.

Collivignarelli, M., Abbà, A., Frattarola, A., Carnevale Miino, M., Padovani, S., Katsoyiannis, I., & Torretta, V. (2019). Legislation for the Reuse of Biosolids on

Agricultural Land in Europe: Overview. *Sustainability, 11*(21). https://doi.org/10.3390/su11216015

DEFRA. (2015). FSA Project FS246004/Deffra Project WT1529—Enhancing knowledge of norovirus behaviour in the marine environment to enable better risk management in molluscan shellfisheries. Department for Environment, Food and Rural Affairs, from http://randd.defra.gov.uk/Document.aspx?Document=13029_WT1529Riskfactorsfornorovirusinoysters.pdf

de Graaf, M., van Beek, J. & Koopmans, M. Human norovirus transmission and evolution in a changing world. Nat Rev Microbiol 14, 421–433 (2016). https://doi.org/10.1038/nrmicro.2016.48

Djennad, A., Lo Iacono, G., Sarran, C. et al. Seasonality and the effects of weather on Campylobacter infections. BMC Infect Dis 19, 255 (2019). https://doi.org/10.1186/s12879-019-3840-7

Elliott, G. N., Hough, R. L., Avery, L. M., Maltin, C. A., and Campbell, C. D. (2015). 'Environmental risk factors in the incidence of Johne's disease'. *Critical Reviews in Microbiology*. 41(4): 488-507, https://doi.org/10.3109/1040841X.2013.867830

Environment Agency. (2022). 'Bathing Water Sampling'. Retrieved from https://environmentagency.blog.gov.uk/2022/12/02/bathing-water-sampling/

Environment and Climate Change Canada (2020) Canadian Environmental Sustainability Indicators: Shellfish harvest area quality. Retrieved from https://www.canada.ca/en/environment-climate-change/services/environmental-indicators/shellfishharvest-area-quality.htm

Environmental Audit Committee (2022). Water Quality In Rivers. Fourth Report of Session 2021-22. 13th January, 2022. Water quality in rivers - Environmental Audit Committee (parliament.uk).

Environmental Protection Agency (2006a). Occurrence and Monitoring Document for the Final Ground Water Rule. Retrieved from https://nepis.epa.gov/Exe/ZyPDF.cgi?Dockey=P1002XR7.txt

Environmental Protection Agency (2006b). Source Water Monitoring Guidance Manual for Public Water Systems for the Final Long Term 2 Enhanced Surface Water Treatment Rule. EPA 815-R06-005 Retrieved from https://nepis.epa.gov/Exe/ZyPDF.cgi?Dockey=2000CZCJ.txt

Environmental Protection Agency (2006c). National Primary Drinking Water Regulations: Ground Water Rule; Final Rule. 40 CFR Parts 9, 141, and 142. 71 (216). Retrieved from https://www.govinfo.gov/content/pkg/FR-2006-11-08/html/06-8763.htm

Environmental Protection Agency (2012). Recreational Water Quality Criteria. Retrieved from https://www.epa.gov/sites/default/files/2015-10/documents/rwqc2012.pdf

Environmental Protection Agency (2019). The Safe Drinking Water Act. As Amended Through P.L. 116–92. Retrieved from https://www.epa.gov/sites/default/files/2020-05/documents/safe_drinking_water_act-title_xiv_of_public_health_service_act.pdf

Environmental Protection Agency (2020). Surface Water Treatment Rules. What do they mean to you? Retrieved from https://www.epa.gov/sites/default/files/2020-06/documents/swtr_plain_english_guide_final_508_0.pdf

Environmental Protection Agency (2023). Onsite Non-Potable Water Reuse Research. Retrieved from https://www.epa.gov/water-research/onsite-non-potable-water-reuse-research#monitor

Environmental Protection Agency. (2006a). 'Occurrence and Monitoring Document for the Final Ground Water Rule'. Retrieved from https://nepis.epa.gov/Exe/ZyPDF.cgi?Dockey=P1002XR7.txt

Environmental Protection Agency. (2006b). 'Source Water Monitoring Guidance Manual for Public Water Systems for the Final Long Term 2. Enhanced Surface Water Treatment Rule. EPA 815-R06-005'. Retrieved from https://nepis.epa.gov/Exe/ZyPDF.cgi?Dockey=2000CZCJ.txt

Environmental Protection Agency. (2006c). 'National Primary Drinking Water Regulations: Ground Water Rule; Final Rule. 40 CFR Parts 9, 141, and 142'. 71 (216). Retrieved from https://www.govinfo.gov/content/pkg/FR-2006-11-08/html/06-8763.htm

Environmental Protection Agency. (2012). 'Recreational Water Quality Criteria'. Retrieved from https://www.epa.gov/sites/default/files/2015-10/documents/rwqc2012.pdf

Environmental Protection Agency. (2019). 'The Safe Drinking Water Act. As Amended Through P.L. 116–92'. Retrieved from https://www.epa.gov/sites/default/files/2020-05/documents/safe_drinking_water_act-title_xiv_of_public_health_service_act.pdf

Environmental Protection Agency. (2020). 'Surface Water Treatment Rules. What do they mean to you?' Retrieved from https://www.epa.gov/sites/default/files/2020-06/documents/swtr_plain_english_guide_final_508_0.pdf

Environmental Protection Agency. (2023). 'Onsite Non-Potable Water Reuse Research'. Retrieved from https://www.epa.gov/water-research/onsite-non-potable-water-reuse-research#monitor

EU. (2019). *REGULATION (EU) 2019/1009 OF THE EUROPEAN PARLIAMENT AND OF THE COUNCIL*.

EUR-Lex Council Directive (1975). 76/160/EEC of 08 December 1975 concerning the quality of bathing water. *Official Journal of the European Communities, 319*, 1-7.

EUR-Lex Council Directive (1979). 79/869/EEC of 15 July 1980 relating to the quality of water intended for human consumption. *Official Journal of the European Communities, 229*, 1-11.

EUR-Lex Council Directive (1980). 80/778/EEC of 09 October 1979 concerning the methods of measurement and frequencies of sampling and analysis of surface water intended for the abstraction of drinking water in the Member States. *Official Journal of the European Union, 271*, 1-10.

EUR-Lex Council Directive (1986). 86/278/EEC of 12 June 1986 on the Protection of the Environment, and in Particular of the Soil, when Sewage Sludge is Used in Agriculture. *Official Journal of the European Union, 181*, pp6-12.

EUR-Lex Council Directive (2006)a. 2006/7/EC of 15 February 2006 concerning the management of bathing water quality and repealing Directive 76/160/EEC. *Official Journal of the European Union*, 64, p37

EUR-Lex Council Directive (2006)b. 2006/113/EC of 12 December 2006 of the quality required of shellfish waters. *Official Journal of the European Union*, 376, pp1-7

EUR-Lex Council Directive (2006b). '2006/113/EC of 12 December 2006 of the quality required of shellfish waters'. *Official Journal of the European Union*. 376. pp1-7

EUR-Lex Council Directive. (1975). '76/160/EEC of 08 December 1975 concerning the quality of bathing water'. *Official Journal of the European Communities. 319*, pp1-7

EUR-Lex Council Directive. (1980). '80/778/EEC of 09 October 1979 concerning the methods of measurement and frequencies of sampling and analysis of surface water intended for the abstraction of drinking water in the Member States'. *Official Journal of the European Union. 271*. pp1-10.

EUR-Lex Council Directive. (1986). '86/278/EEC of 12 June 1986 on the Protection of the Environment, and in Particular of the Soil, when Sewage Sludge is Used in Agriculture'. *Official Journal of the European Union. 181*. pp6-12.

European Centre for Disease Prevention and Control. (2017). 'European Legionnaires' Disease Surveillance Network (ELDSNet) – Operating procedures for the surveillance of travel-associated Legionnaires' disease in the EU/EEA'. *ECDC*. pp1-25

European Centre for Disease Prevention and Control (2023). Website: Increasing risk of mosquito-borne diseases in EU/EEA following spread of Aedes species (europa.eu)

European Parliament and the Council of the European Union. (2019). 'Regulation (EU) 2019/1009 of the European Parliament and of the Council'. Retrieved from https://www.legislation.gov.uk/eur/2019/1009#:~:text=Regulation%20%28EU%29%202019%2F1009%20of%20the%20European%20Parliament%20and,Regulation%2

0%28EC%29%20No%202003%2F2003%20%28Text%20with%20EEA%20relevance%29

European Society of Clinical Microbiology and Infectious Diseases. (2017). 'European Technical Guidelines for the Prevention, Control and Investigation, of Infections Caused by Legionella species'. *ESGLI*. pp1-126

Food and Drug Administration (2019). National Shellfish Sanitation Programme (NSSP). Guide for the Control of Molluscan Shellfish 2019 Revision. Retrieved from https://www.fda.gov/media/143238/download

González-Sierra, R. P., Arizmendiarrieta, j. s., Sánchez, B.P., Iriarte, I.I., & Duarte, G. N. (2019). *Community Composting: A Practical Guide for Local Management of Biowaste. Zero Waste Europe Guides/01*.

Hassard, F., Sharp, J.H., Taft, H. *et al.* Critical Review on the Public Health Impact of Norovirus Contamination in Shellfish and the Environment: A UK Perspective. *Food Environ Virol* **9**, 123–141 (2017). https://doi.org/10.1007/s12560-017-9279-3

Health Canada (2012). Guidelines for Canadian Recreational Water Quality, Third Edition. Water, Air and Climate Change Bureau, Healthy Environments and Consumer Safety Branch, Health Canada, Ottawa, Ontario. (Catalogue No H129-15/2012E). Retrived from https://www.canada.ca/content/dam/canada/health-canada/migration/healthy-canadians/publications/healthy-living-vie-saine/water-recreational-recreative-eau/alt/pdf/water-recreational-recreative-eau-eng.pdf

Health Canada (2019). Guidance on the Use of Quantitative Microbial Risk Assessment in Drinking Water. Water and Air Quality Bureau, Healthy Environments and Consumer Safety Branch, Health Canada, Ottawa, Ontario. (Catalogue No. H144-59/2019E-PDF) Retrived from https://www.canada.ca/content/dam/hc-sc/documents/services/environmental-workplace-health/reports-publications/water-quality/guidance-qmra-drinking-water/QMRA-Final-ENG-July-8-2019.pdf

Health Protection Scotland (2018). Delivering the VTEC/E. coli O157 Action Plan for Scotland - Final Report. The VTEC Action Plan Implementation Group, the Scottish Health Protection Network. December 2018.

Horswell, J., & Hewitt, K. (2014). Organic Materials Guidelines Pathogens Review. *The Centre for Integrated Biowaste Research*.

Hutchison, M.L., Walters, L.D., Avery, S.M., Synge, B.A. and Moore, A. (2004). Levels of zoonotic agents in British livestock manures. Lett. Appl. Microbiol., 39 (2) (2004), pp. 207-214

Institute of Environmental Science and Research (2021) Recreational Water Quality Guidelines Update. Retrieved from https://www.esr.cri.nz/assets/WATER-CONTENT/files/Recreational-Water-Quality-Guidelines-Update-September-2021.pdf

Jahne, M. A., Schoen, M. E., Kaufmann, A., Pecson, B. M., Olivieri, A., Sharvelle, S., Anderson, A., Ashbolt, N. J., and Garland, J. L. (2023). 'Enteric pathogen reduction targets for onsite non-potable water systems: A critical evaluation'. *Water Research*. 233. https://doi.org/10.1016/j.watres.2023.119742

Khajvand, M., Mostafazadeh, A. K., Drogui, P., et al. (2022). 'Greywater characteristics, impacts, treatment, and reclamation using adsorption processes towards the circular economy'. *Environ Sci Pollut Res*. 29. Pp10966–11003. https://doi.org/10.1007/s11356-021-16480-z

Land Air Water Aotearoa (2020) Factsheet: Monitoring groundwater in New Zealand. Retrived from https://www.lawa.org.nz/learn/factsheets/groundwater/monitoring-groundwater-in-new-zealand/

Land Air Water Aotearoa. (2020). 'Factsheet: Monitoring groundwater in New Zealand'. Retrieved from https://www.lawa.org.nz/learn/factsheets/groundwater/monitoring-groundwater-in-new-zealand/

Levy, K., Woster, A. P., Goldstein, R. S. and Carlton, E. J. (2016). 'Untangling the Impacts of Climate Change on Waterborne Diseases: a Systematic Review of Relationships between Diarrheal Diseases and Temperature, Rainfall, Flooding, and Drought'. *Environmental Science & Technology*. 50(10). Pp4905-4922. https://doi.org/10.1021/acs.est.5b06186

McDougall, C.W.; Foley, R.; Hanley, N.; Quilliam, R.S.; Oliver, D.M. Freshwater Wild Swimming, Health and Well-Being: Understanding the Importance of Place and Risk. Sustainability 2022, 14, 6364. https://doi.org/10.3390/su14106364

McGrath, B., Broadhurst, M. and Roman, C. Infectious disease considerations in immunocompromised patients. JAAPA 33(9):p 16-25, September 2020. | DOI: 10.1097/01.JAA.0000694948.01963.f4Ministry for the Environment and Ministry of Health. (2003). 'Microbiological Water Quality Guidelines for Marine and Freshwater Recreational Areas'. Retrieved from https://www.moh.govt.nz/NoteBook/nbbooks.nsf/0/6276CB27E5C6AC34CC2580DA006EF81A/$file/microbiological-quality-jun03.pdf

Ministry for the Environment and Ministry of Health (2003) Microbiological Water Quality Guidelines for Marine and Freshwater Recreational Areas. Retrieved from https://www.moh.govt.nz/NoteBook/nbbooks.nsf/0/6276CB27E5C6AC34CC2580DA006EF81A/$file/microbiological-quality-jun03.pdf

Ministry of Health (2018). Drinking-water Standards for New Zealand 2005 Revised 2018. Retrieved from https://support.esdat.net/Environmental%20Standards/NZ/dwsnz-2005-revised-mar2019.pdf

Mora, C., McKenzie, T., Gaw, I.M. et al. Over half of known human pathogenic diseases can be aggravated by climate change. Nat. Clim. Chang. 12, 869–875 (2022). https://doi.org/10.1038/s41558-022-01426-1

National Health and Medical Research Council (2008). Guidelines for Managing Risks in Recreational Water. Australian government. ISBN Print: 1864962666

Nag, R., Markey, B.K., Whyte, P., O'Flaherty, V., Bolton, D., Fenton, O., Richards, K.G. and Cummins, E. (2021).A Bayesian inference approach to quantify average pathogen loads in farmyard manure and slurry using open-source Irish datasets. Science of The Total Environment 786,147474 https://doi.org/10.1016/j.scitotenv.2021.147474

National Health and Medical Research Council (2008). Guidelines for Managing Risks in Recreational Water. Australian government. ISBN Print: 1864962666

National Institute of Water & Atmospheric Research (2019). National Microbiological Water Quality Guidelines for Marine Recreational Areas. Retrieved from https://envirolink.govt.nz/assets/R12-2-National-Microbiological-Water-Quality-Guidelines-for-Marine-Recreational-Areas-Implications-from-a-Review-of-Recent-Research-v2.pdf

Natural England. (2022). 'The People and Nature Survey for England: Monthly indicators for December 2021 (Official Statistics)'. *Official Statistics*. Retrieved from https://www.gov.uk/government/statistics/the-people-and-nature-survey-for-england-monthly-indicators-for-december-2021-official-statistics/the-people-and-nature-survey-for-england-monthly-indicators-for-december-2021-official-statistics

New South Wales Department of Environment and Conservation. (2003). 'Composting and Related Organics Processing Facilities'. *Environment Protection Authority*. pp1-83

New South Wales Ministry of Health. (2018). Legionella Control in Cooling Water Systems. 1-64

New Zealand Water & Wastes Association (NZWWA). (2003). 'Guidelines for the safe application of biosolids to land in New Zealand'. *New Zealand Water & Wastes Association (NZWWA).* pp1-183

NHS. (2021). 'Aspergillosis'. Retrieved from https://www.nhs.uk/conditions/aspergillosis/

NHS inform. (2023). 'Avoiding bugs and germs outdoors'. Retrieved from https://www.nhsinform.scot/bugs-and-germs

Latgé, J-P. (1999). *Aspergillus fumigatus* and Aspergillosis. Clin Microbiol Rev, 12(2), 310 – 350, https://doi.org/10.1128/cmr.12.2.310

Office for Health Improvement and Disparities. (2022). 'Vulnerabilities: applying All Our Health'. *Health and Social Care*. Retrieved from https://www.gov.uk/government/publications/vulnerabilities-applying-all-our-health/vulnerabilities-applying-all-our-health#:~:text=Being%20vulnerable%20is%20defined%20as,risk%20of%20abuse%20or%20neglect

Ozgun, H.D., Jacobs, D.L., Toms, S.A. (2019). *Cladophialophora bantiana* . In: Turgut, M., Challa, S., Akhaddar, A. (eds) Fungal Infections of the Central Nervous System. Springer, Cham. https://doi.org/10.1007/978-3-030-06088-6_14

Patricia M. Griffin , Mohamed A. Karmali, Emerging Public Health Challenges of Shiga Toxin–Producing Escherichia coli Related to Changes in the Pathogen, the Population, and the Environment, Clinical Infectious Diseases, Volume 64, Issue 3, 1 February 2017, Pages 371–376, https://doi.org/10.1093/cid/ciw708

Pommepuy, M., Dumas, F., Caprais, M. P., Camus, P., Mennec, Le, et al. (2004). Sewage impact on shellfish microbial contamination. Water Science Technology, 50, 117–124.

Quilliam, R.S., Chalmers, R.M., Williams, A.P., Chart, H., Willshaw, G.A., Kench, S.M., Edwards-Jones, G., Evans, J., Thomas, D.R., Salmon, R.L. and Jones, D.L. (2012), Seroprevalence and Risk Factors Associated with Escherichia coli O157 in a Farming Population. Zoonoses and Public Health, 59: 83-88. https://doi.org/10.1111/j.1863-2378.2011.01430.x

Rantala, M., Attia, Koukila-Kähkölä, S., de Hoog, P., Anttila, M. and Katila, T. (2015). Cladophialophora bantiana as an Emerging Pathogen in Animals: Case Report of Equine Endometritis and Review of the Literature. Journal of Clinical Microbiology 53; 9 Cladophialophora bantiana as an Emerging Pathogen in Animals: Case Report of Equine Endometritis and Review of the Literature (asm.org)

Rebecca Philipsborn and others, Climatic Drivers of Diarrheagenic Escherichia coli Incidence: A Systematic Review and Meta-analysis, The Journal of Infectious Diseases, Volume 214, Issue 1, 1 July 2016, Pages 6–15, https://doi.org/10.1093/infdis/jiw081

Rechenburg, A. and Kistemann, T. (2009) Sewage effluent as a source of Campylobacter sp. in a surface water catchment, International Journal of Environmental Health Research, 19:4, 239-249, https://doi.org/10.1080/09603120802460376

S. Cho, C.R. Jackson, J.G. Frye, The prevalence and antimicrobial resistance phenotypes of Salmonella, Escherichia coli and Enterococcus sp. in surface water, Letters in Applied Microbiology, Volume 71, Issue 1, 1 July 2020, Pages 3–25, https://doi.org/10.1111/lam.13301

Schaffer, K. (2015). 'Epidemiology of infection and current guidelines for infection prevention in cystic fibrosis patients'. *Journal of Hospital Infection*. 89(4) Pp309-313. https://doi.org/10.1016/j.jhin.2015.02.005

Schang, C., Lintern, A., Cook, P. L. M., Rooney, G., Coleman, R., Murphy, H. M., Deletic, A., and McCarthy, D. (2018). '*Escherichia coli* survival and transfer in estuarine bed sediments'. *River Research and Applications*. 34(6). Pp606-614. https://doi.org/10.1002/rra.3281

Semenza, J. C. (2020). 'Cascading risks of waterborne diseases from climate change'. *Nat Immunol*. 21. Pp484–487. https://doi.org/10.1038/s41590-020-0631-7

Semenza, J.C. and Paz, S (2021). Climate change and infectious disease in Europe: Impact, projection and adaptation. The Lancet Regional Health Eutope 9, 100230.

Siebert, S., and Lystad, H. (2018). 'ECN recommendations on exclusion of bio-waste from CMC2, on alternative time-temperature profiles for composting and deleting the PFC criteria on *E.coli* and Enterococcaceae.' *European Compost Network*. REF. ECN_EC_FR_01/2018. pp1-5

Steinbrink, J., Leavens, J., Kauffman, C. A., and Miceli, M. H. (2018). 'Manifestations and outcomes of nocardia infections: Comparison of immunocompromised and non-immunocompromised adult patients'. *Medicine (Baltimore)*. 97(40):e12436. doi: 10.1097/MD.0000000000012436

Tasic, S. and Miladinovic-Tasic, N. (2007). Cladosporium spp. - cause of opportunistic mycoses. Acta Fac Med Naiss 24, 15-19

The New Zealand Ministry of Health. (2012). 'The Prevention of Legionellosis in New Zealand: Guidelines for the Control of Legionella Bacteria'. *Wellington: Ministry of Health*. Pp1 - 116

Tiwari, A., Oliver, D. M., Bivins, A., Sherchan., S. P., Pitkänen, T. (2021). 'Bathing Water Quality Monitoring Practices in Europe and the United States'. *Int. J. Environ. Res. Public Health. 18*, 5513. https://doi.org/10.3390/ijerph18115513

UK Health Security Agency (2023). News Story 9th March 2023. Accessed 6th June 2023. Norovirus cases increase significantly in England - GOV.UK (www.gov.uk)

Villabruna, N., Izquierdo-Lara, R.W., Schapendonk, C.M.E. et al. Profiling of humoral immune responses to norovirus in children across Europe. Sci Rep 12, 14275 (2022). https://doi.org/10.1038/s41598-022-18383-6

Voidarou, C., Bezirtzoglou, E., Alexopoulos, A., Plessas, S., Stefanis, C., Papadopoulos, I., Vavias, S., Stavropoulou, E., Fotou, K., Tzora, A., and Skoufos, I. (2011). 'Occurrence of *Clostridium perfringens* from different cultivated soils'. *Anaerobe*. 17(6). Pp320-324. https://doi.org/10.1016/j.anaerobe.2011.05.004

Water Quality Australia. (2006). 'Australian Guidelines for Water Recycling: Managing Health and Environmental Risks (Phase 1)'. Retrieved from https://www.waterquality.gov.au/sites/default/files/documents/water-recycling-guidelines-full-21.pdf

WILLIAMS, K., WARD, M., DHUNGYEL, O., & HALL, E. (2015). Risk factors for Escherichia coli O157 shedding and super-shedding by dairy heifers at pasture. Epidemiology & Infection, 143(5), 1004-1015. doi: 10.1017/S0950268814001630

Winward, G. P., Avery, L, M., Stephenson, T., Jeffrey, P., Le Corre, K. S., Fewtrell, L., and Jefferson, B. (2009). 'Pathogens in urban wastewaters suitable for reuse'. *Urban Water Journal*. 6(4). Pp291-301. https://doi.org/10.1080/15730620802673087

Yusa, A., Berry, P. J., Cheng, J., Ogden, N., Bonsal, B., Stewart, R., and Waldick, R. (2015). 'Climate Change, Drought and Human Health in Canada'. *International Journal of Environmental Research and Public Health*. 12(7). Pp8359-8412. https://doi.org/10.3390/ijerph120708359

List of abbreviations

ADCP – Advisory Committee on Dangerous Pathogens

RAG – Red-Amber-Green

QSR – Quick Scoping Review

STEC – Shiga-toxin producing *E. coli*

FIOs – Faecal Indicator Organisms

EU – European Union

CFU – Colony Forming Units

MPN – Most Probable Number

MPCN - Most Probable Cytopathic Number

PFU – Plaque Forming Units

OSA – Organic Soil Amendments

CSO – Combined Sewer Overflows

spp. – Species (plural)

WWTP – Wastewater Treatment Plant

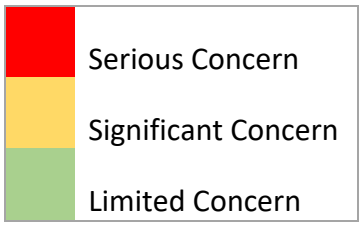
UKWIR – UK Water Industry Research

UKHSA – UK Health Security Agency

Appendix A

RAG (red, amber, green) pathogen risk assessment. Hazard scores (3 – 12) and associated colouring for all pathogens (bacteria, fungi, helminths, protozoa and viruses). Red colouration indicates pathogens which are a serious concern, amber signifies those that are a significant concern and green shows pathogens that are of limited concern.

Organism	Environmental Hazard Category
Name	(based on UK prevalence + likelihood on infection + disease severity)
Bacteria	
Acinetobacter calcoaceticus	5
Alcaligenes spp	6
Aliarcobacter butzleri (formerly Arcobacter butzleri, formerly *Campylobacter butzleri)*	8
Anaplasma phagocytophilum (formerly Ehrlichia phagocytophilum)	8
Bacillus anthracis	8
Bacillus cereus	7
Bordetella spp	6
Borrelia burgdorferi	8
Borrelia duttonii	7
Borrelia spp *(specifically B. miyamotoi)*	6
Brachyspira spp *(formerly Serpulina spp)*	7
Brucella abortus	7
Brucella canis	6
Brucella melitensis	6



Organism	Environmental Hazard Category
Brucella suis	6
Burkholderia cepacia	5
Campylobacter fetus	6
Campylobacter jejuni	9
Campylobacter spp	9
Chlamydophila psittaci	5
Clostridium botulinum	7
Clostridium perfringens	7
Clostridium spp	7
Clostridium tetani	7
Cyanobacteria	6
Enterobacter spp	6
Enterococcus spp	6
Escherichia coli (with the exception of non-pathogenic strains)	8
Escherichia coli, verocytotoxigenic strains (eg O157:H7 or O103)	9
Francisella tularensis (Type B)	7
Legionella pneumophila	8
Legionella spp	6
Leptospira interrogans	6
Mycobacterium avium/intracellulare	7
Mycobacterium chelonae	7
Mycobacterium malmoense	6
Mycobacterium paratuberculosis	7
Mycobacterium marinum	7

Organism	Environmental Hazard Category
Mycobacterium simiae	6
Neoehrlichia mikurensis	6
Nocardia asteroides	7
Nocardia braziliensis	6
Nocardia farcinica	6
Nocardia nova	6
Nocardia otitidiscaviarum	6
Plesiomonas shigelloides	5
Porphyromonas spp	4
Proteus mirabilis	5
Proteus vulgaris	6
Rhodococcus equi	6
Rickettsia akari	6
Rickettsia conorii	5
Rickettsia typhi (Rickettsia mooseri)	6
Salmonella paratyphi A/C (choleraesuis)	7
Salmonella paratyphi B/java	9
Salmonella spp	7
Salmonella typhi	8
Shigella flexneri	8
Shigella sonnei	8
Vibrio cholerae (including El Tor)	6
Vibrio parahaemolyticus	4
Vibrio spp	4
Yersinia spp	7

Organism	Environmental Hazard Category
Fungi	
Alternaria spp.	6
Aspergillus fumigatus	6
Aspergillus spp	7
Cladophialophora bantiana (formerly Xylohypha bantiana, Cladosporium bantianum)	9
Cryptococcus neoformans var neoformans (Filobasidiella neoformans var neoformans)	8
Emmonsia crescens	5
Emmonsia parva	4
Fusarium spp	6
Histoplasma capsulatum var capsulatum (Ajellomyces capsulatus)	7
*Lichtheimia corymbifera (*synonym *Absidia corymbifera)*	6
*Lomentospora prolificans (*formerly *Scedosporium prolificans)*	8
Microsporum spp	6
Nannizia praecox (formerly *Microsporum praecox)*	6
Pseudallescheria boydii	7
Rhizomucor pusillus	8
Saksenaea vasiformis	7
Saprochaete capitata (formerly Geotrichum capitatum and Blastoschizomyces capitatus)	6
Scedosporium apiospermum (Pseudallescheria boydii, formerly *Monosporium apiospermum)*	8

Organism	Environmental Hazard Category
Scopulariopsis brevicaulis	7
Helminths	
Ancylostoma duodenale	4
Ascaris lumbricoides	7
Ascaris suum	7
Capillaria hepatica (synonym *Calodium hepaticum)*	6
Dicrocoelium dendriticum	4
Echinococcus granulosus	7
Echinococcus multilocularis	6
Fasciola hepatica	6
Hymenolepis diminuta	3
Hymenolepis nana	4
Taenia solium	4
Toxocara canis	7
Toxocara cati	7
Trichobilharzia regenti	5
Trichostrongylus spp	4
Protozoa	
Acanthamoeba spp	6
Babesia divergens	7
Babesia microti	7
Babesia spp	7
Balantidium coli (Balantoides coli)	5
Blastocystis hominis	7
Cryptosporidium hominis	7

Organism	Environmental Hazard Category
Cryptosporidium parvum	8
Cryptosporidium spp	5
Cytoisospora belli (Formerly *Isopora belli)*	6
Dientamoeba fragilis	7
Encephalitozoon cuniculi	6
Encephalitozoon hellem	6
Encephalitozoon intestinalis	6
Entamoeba histolytica	7
Enterocytozoon bieneusi	7
Giardia lamblia (Giardia intestinalis/duodenalis)	8
Leishmania donovani	6
Naegleria fowleri	8
Toxoplasma gondii	8
Viruses	
Adenovirusus	7
BK polyomavirus	5
Chikungunya virus	6
Coxsackieviruses (A and B) (synonym human enteroviruses A and B)	7
Crimean/Congo haemorrhagic fever virus	7
Dengue virus	5
Dobrava-Belgrade orthohantavirus	7
Echovirus (synonym human enterovirus B)	6
Hepatitis A virus (human enterovirus type 72)	7

Organism	Environmental Hazard Category
Hepatitis E	7
Human rotaviruses A, B and C	5
Influenza (Avian)	5
JC polyomavirus	5
Lymphocytic choriomeningitis virus LCMV (all strains other than Armstrong)	6
Mammalian orthoreoviruses 1 to 3	7
Newcastle disease virus (synonym avian paramyxovirus)	5
Norovirus	9
Orbiviruses	5
Parechoviruses	6
Poliovirus type 2 (vaccine derived poliovirus)	3
Polioviruses (synonym human enterovirus C)	3
Puumala orthohantavirus	7
Sandfly fever Naples virus	6
Sapovirus	8
Sindbis virus	5
Thogoto virus	7
tick-borne encephalitis virus (in the UK central European tick-borne encephalitis virus)	8
Torovirus (human torovirus subspecies, bovine torovirus subsepcies, equine torovirus subspecies, porcine torovirus)	6
West Nile virus	5

Appendix B – Questionnaire Survey

Environmental Exposures to Human Pathogens

Start of Block: Project Information

Q1.1 **PROJECT INFORMATION** This questionnaire is part of the “Environmental exposures to human pathogens” project funded through a DEFRA Framework agreement managed by the Centre for Ecology and Hydrology (January 2021 - April 2023). The project involves using literature and expert opinion to deliver information to the Environment Agency.

The aims of this project are to synthesise what is known about human pathogens in the environment relevant to England and to build a shared picture of pathogens of concern in the environment in England with policy recommendations. This includes:
i) A review of the human pathogens monitored in the environment in other countries, particularly the US, Australia, New Zealand and other European countries.
ii) A review and evaluation of what is currently known about human pathogens in surface waters, land and outdoor air and how their presence and behaviour could change in the future under climate and land-use change, and as a result of different management strategies.
iii) A qualitative evaluation of the relative level of concern posed by those pathogens and resulting recommendations that can be used by the Environment Agency and its partners to inform future research and management strategies.

The aim of this survey is to gather expert opinion on human pathogens in the environment relevant to England.

The survey takes approximately 15 minutes to complete. You can also carry out the survey over the phone. If you wish to ask us any questions before deciding whether to take part, or carry out the survey over the phone, please contact us _____. Your participation is voluntary and you may leave the study at any time. All data collected will be treated with full confidentiality and in line with UK data protection legislation.

End of Block: Project Information

Start of Block: Privacy Notice

Q2.1 **PRIVACY NOTICE** The James Hutton Institute (“Hutton”, “us” or “we”) will use your personal data for the purposes of the research undertaken in this project “Environmental exposures to human pathogens survey" (“The Project”) in accordance with our privacy notice at https://www.hutton.ac.uk/terms. Our lawful basis for processing your personal data is that this is necessary for publicly funded research we undertake as a task in the public interest. We are the data controller for the personal data collected for the purposes of above project.

Where questionnaires are conducted by voice rather than email, we may be engaging with third-party service providers, i.e. the Cisco WebEx video-conferencing platform and/or transcribers, who may be processing personal data on our behalf. In this case we will rely on appropriate data processing agreements with the service provider and adequate safeguards will be in place in order to ensure the security of your personal data. The Cisco WebEx privacy notice is available here: https://trustportal.cisco.com/c/dam/r/ctp/docs/privacydatasheet/collaboration/cisco-webex-meetings-privacy-data-sheet.pdf.

Personal data (names, contact details, job field/role) will be collected from the project team's existing address books and from web searches in order to make initial contact with participants. This information will be linked to consent forms and questionnaire responses through a unique identifier and all data will be stored in restricted access files on the James Hutton Institute server and/or secure cloud-based storage used by the James Hutton Institute. Responses will be anonymised through removal of names and directly identifying information and published only in summarised form. However, summaries and other research outputs may include information on respondent's background (e.g. academic, regulatory, policy-related, industry) and/or some original wording may be retained therein through which the individual may be indirectly identifiable.

We will share your personal data with the Environment Agency only if this is necessary for fulfilling the tasks and purposes of the Project. This will be carried out under a data sharing agreement between the James Hutton Institute and the Environment Agency. Where possible, we will anonymise data before sharing it with our collaborators. We will retain your personal data only for as long this is necessary (< 5 years) to fulfil the purposes and produce outputs for the Project and will delete/destroy it afterwards.

Our main privacy notice will explain what we do with personal data in more detail as well as your rights. Or, if you have any queries about your personal data you can contact our Data Protection Officer _____. For further information, including independent data protection advice and information in relation to your rights, you can contact the information Commissioner at: _____

End of Block: Privacy Notice

Start of Block: Research Consent Form

RESEARCH CONSENT FORM

Q1.1 What is your name?

_____

Q1.2

I confirm that I have read, or had read to me, and understand the above information about

this study. I have had the opportunity to ask questions and these have been answered fully and explicitly.

- Yes (1)
- No (2)

Q1.3
I understand that my participation is voluntary, and I am free to withdraw at any time, without providing any reason and without my legal rights being affected. Please note that once data from the project have been analysed or published in reports it will not be possible to remove contributions.

- Yes (1)
- No (2)

Q1.4
I understand the study is being conducted by researchers from The James Hutton Institute ("JHI") at the request of the Environment Agency under a DEFRA Framework agreement.

- Yes (1)
- No (2)

Q1.5
I understand that confidentiality will be maintained at all times and it will not be possible to be directly identifiable by name from any publications/outputs, however it is possible that these could include references to my organisation/affiliation and my role.

- Yes (1)
- No (2)

Q1.6
I agree to take part in the above study.

- Yes (1)
- No (2)

Q1.7
I agree to being contacted at a later date to request further information and for being provided with updates and information on the project.

- Yes (1)
- No (2)

Q1.8
I understand that the data which I provide may be shared by the research team with the Environment Agency in relation to this study.

- Yes (1)
- No (2)

Q1.9
We would like to be able to contact you at a later date to ask you to take part in a short online workshop. Please choose one of the following options:

- Yes, I’m happy to be contacted to take part in the workshop. (1)
- No, I don’t wish to be contacted to take part in the workshop. (2)

Q1.10
If I wish to carry out this questionnaire by phone, I agree for my responses to be recorded and transcribed.

- Yes (3)
- No (4)
- Not applicable - I do not wish to carry out the questionnaire by phone (5)

Q1.11
The Environment Agency would like to retain a list of experts who contributed to this

questionnaire with a view to contacting them to further discuss particular aspects of the study in the future. Please choose one of the following options:

- ○ Yes, I am happy for the Environment Agency to contact me to ask if I am willing to discuss aspects of this project in more depth. (1)
- ○ No, I am not happy for the Environment Agency to contact me to ask if I am willing to discuss aspects of this project in more depth. (2)

End of Block: Research Consent Form

Start of Block: Respondent information

RESPONDANT INFORMATION

Q2.1
At which type of institution are you employed?

- ○ Academic (1)
- ○ Environmental Regulator (2)
- ○ Food Regulator (3)
- ○ Government or Policy related (4)
- ○ Public Health (5)
- ○ Animal Health (6)
- ○ Water Industry (7)
- ○ Food Industry (8)
- ○ Farming (9)
- ○ Other, please state (10)

_____

Q2.2
What is your present role?

_____

Q2.3
What is your disciplinary background

_____

Q2.4
What country do you operate in?

- ○ UK - England (1)
- ○ UK - Scotland (2)
- ○ UK - Wales (3)
- ○ UK Northern-Ireland (4)
- ○ Other Country - please state (5)

_____

End of Block: Respondent information

Start of Block: Block 6

Q3.1 PATHOGENS IN THE ENVIRONMENT
In this study we are interested in pathogens in the environment that have potential to cause illness or harm to people. By "environment" we mean outdoor air, land, and water bodies, and the animals within them. We are interested in pathogens that people might be directly exposed to in the outdoor environment particularly in relation to land management or water management. For example, exposures during outdoor land and water-based recreational activities. However, we are not interested in pathogens that are only associated with occupational exposures.

Please list the pathogens you are aware of in the environment that people can be exposed to through recreational activities. Please answer for your own sector and/or more broadly, in line with your knowledge. Please include pathogens that are currently widely recognised as posing a risk to human health, and also additional 'emerging' pathogens that are not currently widely recognised as posing a risk, but you believe currently pose a risk and/or may pose an increasing risk in future.

_____

End of Block: Block 6

Q3.2 CHARACTERISING PATHOGENS IN THE ENVIRONMENT

In the next set of questions, we will ask you to think more about the pathogens you have listed above. If you have listed a large number of pathogens, in your answers below, please feel free to group them or to pick those that you feel are important to bring to our attention. You are welcome to write as much or as little as you wish.

Q3.2

In relation to both the currently recognised and emerging pathogens you listed, what are the sources from which they enter the environment (e.g. animal faeces, sewage etc.).

_____

Q3.3

In which environmental matrices (e.g. water, soil, air) are they commonly found, other than the sources you mention in the previous question?

_____

Q3.4

What are the main ways they move through the environment?

_____

Q3.5

How do humans come into contact with them?

_____

Q3.6

What activities or management practices do you think increase or reduce the likelihood of these pathogens being present in the environment?

_____

Q3.7

Are there any practices that would increase or reduce the likelihood of people coming into contact with these pathogens?

_____

Q3.8
How do you think prevalence, numbers, survival and ecology of these pathogens may change under future scenarios (e.g. climate and land use changes)?

_____

End of Block: Characterising Pathogens in the Environment

Start of Block: Sources of further information

Q4.1 **SOURCES OF FURTHER INFORMATION**
Please list any networks, project outputs and key publications you think we should be aware of relevant to the topic of this survey.

_____

Display This Question:

If Q2.4 What country do you operate in? = Other Country - please state

Q4.1 **NON-UK RESPONDENTS ONLY**
What pathogens are monitored in the environment in your country?

_____

Display This Question:

If Q2.4 What country do you operate in? = Other Country - please state

Q4.2
Who monitors them?

_____

End of Block: Sources of further information

Appendix C – Questionnaire Results and Analysis

Respondents

Table 1. Respondents by type of institution.

Type of Institution	Respondents
Academic	12
Food Industry	1
Water Industry	1
Animal Health	2
Public Health	3
Government or Policy related	1
Other	3
Total	23

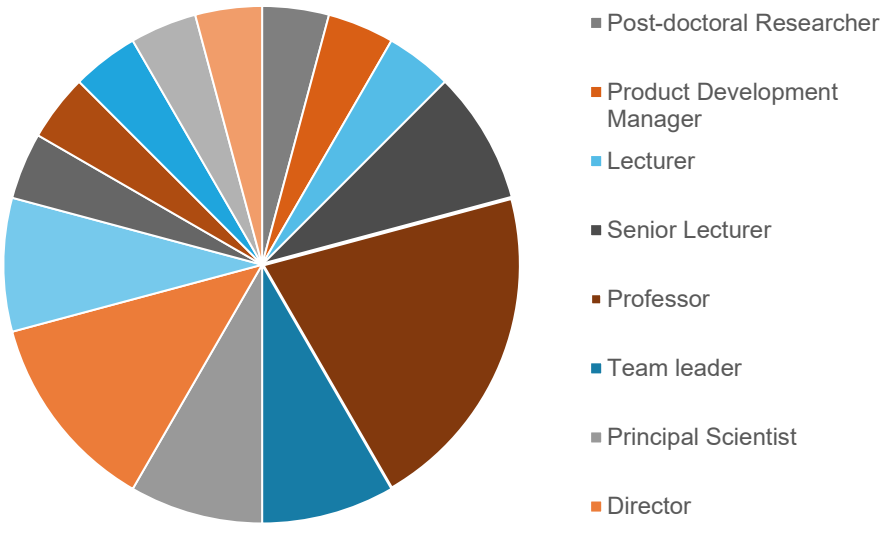


Figure 1. Present role distribution of respondents

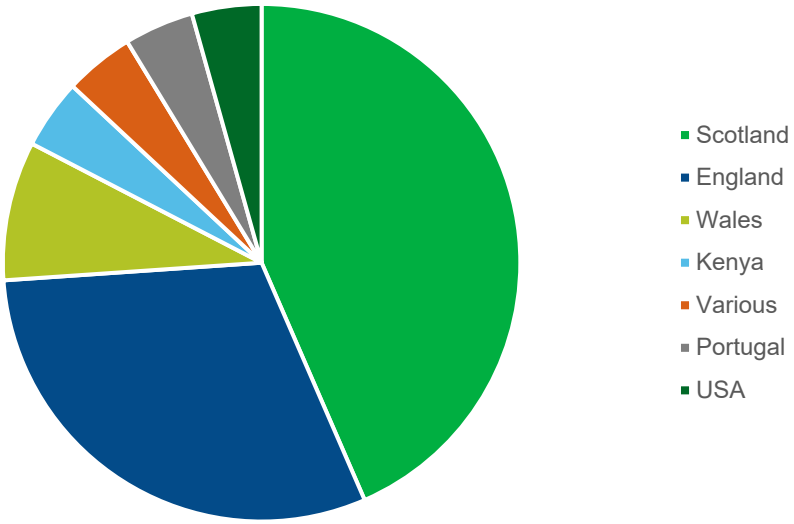


Figure 2. Respondents by country in which they operate professionally.

Pathogens of Concern

Respondents were asked to:

"list the pathogens you are aware of in the environment that people can be exposed to through recreational activities. Please answer for your own sector and/or more broadly, in line with your knowledge. Please include pathogens that are currently widely recognised as posing a risk to human health, and also additional 'emerging' pathogens that are not currently widely recognised as posing a risk, but you believe currently pose a risk and/or may pose an increasing risk in future."

Most respondents highlighted particular genera, species, strains or subtypes, while some listed more generic categories of pathogen or both. The generic categories mentioned were:

- AMR bacteria
- Apicomplexa
- Bacteria
- Enteric viruses
- Faecal coliforms
- Fungi
- Parasites
- Prions
- Viruses
- Worms/helminthes/nematodes

A wide range of specific genera were mentioned across different taxonomic groups (Table 2).

Table 2. Pathogens of concern highlighted in questionnaire survey, with number of mentions for each genus/grouping by different questionnaire respondents. Species, strains or subtypes that were mentioned are listed in column three, but not all mentions of a given genus had further taxonomic detail given in the response.

Genus	Mentions	Species, strains or subspecies mentioned
BACTERIA		
Escherichia	18	*coli*, STEC, EHEC, VTEC, pathogenic, O157, enteropathogenic AMR
Salmonella	13	
Campylobacter	13	
Vibrio	7	
Leptospira	7	*interrogans*
Legionella	5	
Borrelia	5	*burgdorferi sensu lato complex, miyamotoi*
AMR bacteria	4	
Listeria	3	*monocytogenes*
Myocbacterium	3	*avium* subsp. Paratuberculosis (MAP)
Rickettsia	4	
Shigella	3	
Clostridium	3	*tetani, botulinum, difficile,perfringens, septicum*
Coxiella	3	*burnetti*
Bacillus	3	*anthracis*
Enterococcus	2	
Faecal coliforms/bacteria	2	
Bartonella	1	
Treponema	1	*hyodysenteriae*
Erysipelothrix	1	*rhusiopathiae*
Acinetobacter	1	

Genus	Mentions	Species, strains or subspecies mentioned
Anaplasma	1	*phagocytophilum*
Neoehrlichia	1	*mikurensis*
Arcobacter	1	
Yersinia	1	*pestis*
Pseudomonas	1	
Toxocara	1	*canis*
Cyanobacteria	1	
VIRUSES		
Norovirus	6	
Hepatitis	5	A. E
Tick-borne encephalitis	3	
Rotavirus	3	
DEN (Dengue virus)	2	
influenza viruses	2	avian
Enteric viruses/enteroviruses	2	
CHIK	1	
Other arboviruses	1	
sapovirus	1	
Adenovirus	1	
West Nile virus	2	
Japanese Encephalitis virus	1	
Yellow fever	1	
Rabies	1	
hantavirus	2	
arenaviruses	1	

Genus	Mentions	Species, strains or subspecies mentioned
coronaviruses	1	
enterovirus	1	
CCHF virus	1	
Usutu virus	1	
Bornavirus	1	
FUNGI		
Aspergillus	2	*fumigatus*
Fusarium	1	
Dermatophytes	1	
Mucouraceaous molds	1	
Scedeosporium	1	
Lomentospora	1	*prolificans*
Paecilomyces	1	
Exophiala	1	
Purpureocillium	1	
Microascus	1	
Alternaria	1	
Stachybotrys	1	
Candida	1	*auris, glabrata* (now *Nakaseomyces glabrata*)
Cladophialophora	1	*bantiana*
PROTOZOA		
Cryptosporidium	11	*parvum, andersoni, meleagridis, cuniculus*
Toxoplasma	8	*gondii*
Giardia	8	*duodenalis*
Babesia	2	*divergens, venatorum*
Amoebae/*Naegleria*	1	fowleri

Genus	Mentions	Species, strains or subspecies mentioned
Trypansomiasis	1	
Cyclospora	1	
Leishmania	1	
OTHER		
Echinococcus (helminth)	1	
Avian Schistomes (fluke)	1	
Algae	1	

Source of pathogens entering the environment

Respondents were asked:

"In relation to both the currently recognised and emerging pathogens you listed, what are the sources from which they enter the environment (e.g. animal faeces, sewage etc.)".

Response phrases are collated in Table 3.

Table 3. Sources of pathogen entry into the environment.

Source Category	Source
Wastewater-related	Water industry
	Sewage/wastewater/CSOs (treated or untreated)
	Septic tanks (faulty or otherwise)
	Urban run off
Agriculture-related	Organic soil amendments/animal manures
	Animal Faeces (wild, farmed, domestic)
	Decaying animals
	Animal urine
	Agricultural Run off
	Cattle (livestock) access to rivers

Source Category	Source
Waste management-related	Anaerobic digestate
	Composting facilities
	Landfill
	Aerosols
	Pets/companion animals
Other	Ticks, Emerging insect vectors
	Some organisms indigenous to environment
	Contaminated soil
	Marine traffic

Environmental matrices in which pathogens are detected

Respondents were asked:

“In which environmental matrices (e.g. water, soil, air) are they commonly found, other than the sources you mention in the previous question?”.

Responses comprised: Sediments (including intertidal), sand, soil, water (fresh and marine), sewage, animal faeces, aerosols/air/dust, surfaces, live animals, humans, birds, plants and ticks.

Pathways of transfer through the environment

Respondents were asked:

“What are the main ways they move through the environment?” Specific responses were collated in Table 4.

Table 4. Pathways by which pathogens move through the outdoor environment.

Sewage	CSOs
	Septic tank effluent
Water	Resuspended into waters
	Overland flow/run-off
	Irrigation
	Rain-driven flows
Animals	Livestock accessing water directly
	Deposition of faeces
	Movement (natural and artificial)
Organic wastes/amendments	OSA to land
	Sludge to land
	Leaching from wastes
Vectors	Ticks
	Insects /flies
	Invertebrates
	Amoebc pathogens
	Biofilms
	Plastics
	Particles (organic/inorganic)
	Soil Macro fauna

Direct contact

Physical movement of humans

Exposure

Respondents were asked:

“How do humans come into contact with them [pathogens listed]?”

In addition to the following list, responses also referred to contaminated food and vegetables and home water supply as well as agricultural activities. Food chain elements and occupational activities were considered out of scope so not included. However, drinking untreated drinking water was left in because this could occur if an individual drinks from a natural water source while outdoors.

- Recreational activities involving water especially immersion - ingestion, aspiration (skin, ears, up nose)
- Direct contact with contaminated soil/vegetation; not washing hands
- Exposure of open wounds to soil, Thorn, splinter
- Untreated drinking water
- Outdoor pursuits
- Contamination during outdoor food prep
- Contact with animals
- Gardening
- Agricultural Activities
- Drinking, bathing, contact with animals, food
- Any movement through the environment
- Inhalation

These were summarised by a modification of a comment from one respondent as “Eating, touching, breathing, swimming, walking through ecological niches, vectors”.

Management Activities

Respondents were asked:

“What activities or management practices do you think increase or reduce the likelihood of these pathogens being present in the environment?”

The key themes are collated in Table 5.

Table 5. Management activities or practices which may influence prevalence of pathogens in the environment.

Management or Activity Category	Activity or Practice
Water-related	Water quality monitoring
	Buffer zones
	Managing livestock near streams
	Catchment management
Wastewater-related	Discharge Consents
	CSOs/ untreated wastewater release
	Maintenance of sewage infrastructure
	Effective sewage treatment
Agriculture-related	Agricultural practice
	Grazing
	Better animal husbandry/health/housing/biosecurity
	Management of farm effluent
	Agricultural monocultures
	Increasing animal-based food systems
	Faeces/waste management on farms
Waste Management-related	Composting increases prevalence in air around facilities,
	OSA/ waste treatment & application
	Human waste management
	Industrial waste management
Other	Tick control, including grass cutting where public access to reduce tick Habitat, tick vaccines/acaricides
	Personal sanitary practices
	Water-logged soils, soil types
	Monitoring and surveillance
	Checking food items for parasites/pathogens

Management or Activity Category	Activity or Practice
	Land Use Change
	Degradation of natural environments/wild habitats
	Education
	Cannot/should not reduce (important for soil fertility)
	Freshwater management
	Drivers of climate change
	Human travel
	Control at source, onsite disinfection
	Outdoor activities
	Eating

Reducing human contact with pathogens in the environment

Respondents were asked:

“Are there any practices that would increase or reduce the likelihood of people coming into contact with these pathogens?” Responses are collated in Table 6.

Some responses not included in the table related to drinking water supplies – for example use of boiled waters and warning notices to the public. This is pertinent particularly to the use of private supplies and there is a strong relationship between pathogens in the environment and in untreated drinking water.

Other comments included checking meat for parasites and cooking food instead of eating it raw. This were not included in the table because they were outside the remit of infections that are transmitted from the environment rather than food borne.

Table 6. Practices that could reduce human exposure to environmental pathogens.

Activities that may reduce human exposure
Bathing water advisory accounting for resuspension
Restricted contact /warning/signage
Increased investment in wastewater infrastructure
Fencing cattle from streams
Using sewage sludge as an energy source rather than applying to land
Tick prevention strategies
Use of gardening gloves
Raising awareness of specific risks
Dietary change away from animal-based foods.
Improved control of production
Improved control of global distribution of waste
Filter or boil unknown water sources
Not using contact lenses while swimming
Use of safety glasses and gloves for gardening
Activities that may increase human exposure
More bathing/recreational activities in polluted waters or waters surrounded by contaminated soils
Poor hygiene
Increase in popularity of open water swimming and other fresh and coastal water recreation
Intensification of agriculture
Untreated sewage discharge (especially with increased rainfall)
Treated sewage discharge
Greater land area used for livestock
Unsanitary environments
Farm visits

Walking in areas where ticks present
Specific management/ maintenance of sewage treatment
Specific farm management practices
Walking through overgrown areas
Drinking contaminated water
Poor hygiene, not washing hands

Impacts of Future Changes on Pathogens in the Environment

Respondents were asked:

“How do you think prevalence, numbers, survival and ecology of these pathogens may change under future scenarios (e.g., climate and land use changes)?”

Table 7. Impact of future changes on pathogens in the environment.

Type of Change	Future Change	Impact on Pathogens in the environment
Climate	Climate change	Effects on migration patterns and wildlife distributions
	Warmer wetter weather	enhanced survival, increased tick population
	Rainstorms	Soil Erosion, pathogen co-transport, overland flow
	Increased rainfall	sewage overflows. Flooding, more pathogens entering environment
	Drought, water scarcity	Increased concentration of pathogens in freshwater
Anthropogenic Change	Land Use Change	-
	Increased nutrients	Enhanced survival (?)
	Human induced ecological change	-
	Human behaviour changes e.g., wild swimming, diet type (vegan vs animal)	-
	Increasing human population/density	-
Infrastructure	Proposed investment in sewage infrastructure	Positive effect (fewer pathogens)
	New Emerging technology	May offset some other changes

Would you like to find out more about us or your environment?

Then call us on

03708 506 506 (Monday to Friday, 8am to 6pm)

Email: enquiries@environment-agency.gov.uk

Or visit our website

www.gov.uk/environment-agency

incident hotline

0800 807060 **(24 hours)**

floodline

0345 988 1188 **(24 hours)**

Find out about call charges (https://www.gov.uk/call-charges)

Environment first

Are you viewing this onscreen? Please consider the environment and only print if absolutely necessary. If you are reading a paper copy, please don’t forget to reuse and recycle.