Recreational exposure to pathogenic microorganisms from resuspended fine aquatic sediments: Literature review

May 2025

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CLIENT REPORT No: FW25014

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ACKNOWLEDGEMENTS

The authors would like to thank the Ministry of Health Manatū Hauora for funding this current review. We would also like to acknowledge the funders of previous literature reviews completed by ESR, since generic information on microbial hazards has been sourced from these reviews. These previous funders include Ministry of Health Manatū Hauora, New Zealand Food Safety (Ministry for Primary Industries), the New Zealand Food Safety Science and Research Centre and United Fresh.

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ABBREVIATIONS

CFU	Colony forming units
FIB	Faecal indicator bacteria
HAV	Hepatitis A virus
MST	Microbial source tracking
NZ	Aotearoa New Zealand
PCR	Polymerase chain reaction
PFU	Plaque forming units
QMRA	Quantitative microbial risk assessment
RCP	Representative concentration pathways
STEC	Shiga toxin-producing *E. coli*
T_{90}	The time required to reduce a microbiological population by 90% (1 log), usually expressed as hours or days
UK	United Kingdom
USA	United States of America
WHO	World Health Organization

SUMMARY

In Aotearoa New Zealand (NZ), water quality monitoring is carried out at freshwater lakes, rivers, estuaries and coastal beaches to minimise human illness through recreational water contact and shellfish gathering. Monitoring focuses on detecting indicators of faecal contamination in water samples. Those taking the water samples are encouraged to minimise sediment disturbance. The microbial quality of aquatic sediments is not currently monitored. The objective of this review is to identify if fine aquatic sediments (fine sand, silt and clay) could be a source of pathogenic microorganisms (bacteria, viruses and protozoan parasites) and pose a health risk to people as they swim, play and wade in low energy aquatic environments (lakes, rivers, estuaries, lagoons, etc.). Understanding the potential health risks from resuspended sediments will assist public health officials and regional council water quality managers to manage recreational water quality.

Pathogenic microorganisms may be present in aquatic sediments, including faecal-associated microorganisms and natural inhabitants which are opportunistic human pathogens. Microorganisms attach to sediment particles and these initial attachments can become stronger as biofilms develop. Sediment environments are more favourable for microbial survival compared to the overlying water, since the sediments protect microorganisms from sunlight, provide surfaces to support biofilms inhabited by microorganisms, trap organic matter and offer protection from protozoan grazing. A range of physical, chemical and biological factors collectively affect the survival of microorganisms in sediments. While natural microbial inhabitants are well adapted to aquatic environments, faecal-associated microorganisms tend to progress towards non-viability once they enter these environments, although at different rates. Laboratory studies suggest that the concentrations of faecal indicator bacteria (FIB) decrease at a similar rate to bacterial pathogens in sediment, but this is not supported by field studies except those completed near known human faecal point-sources, which will be affected by continuous deposition.

Studies of paired water and sediment samples almost consistently find that the concentration of faecal indicator bacteria (FIB) is higher in sediments compared to overlying water. There are fewer studies of faecal-associated pathogenic bacteria, viruses and protozoan parasites and the results from these do not show the same consistent trend. Sediment concentrations of naturally occurring *Vibrio* spp. tend to be higher than the overlying water. The presence and concentration of microorganisms measured in the water may not reflect sediment-associated health risks. Studies have demonstrated that sediment disturbance and resuspension cause FIB and pathogenic microorganism concentrations to increase in the water, where they could become a health hazard for swimmers.

The calmer waters of lakes, river eddies, estuaries and low energy harbours are attractive areas for people seeking safer swimming areas, particularly for younger children. These areas often feature fine sediments that are easily disturbed and slow to resettle. As people swim in these areas, they are likely to disturb the sediment and any associated microorganisms. Studies have shown correlations (some weak) between the concentration of FIB in water, the presence/concentration of bathers and measures of water clarity that indicate the presence of suspended sediments. However, epidemiological evidence to support resuspended aquatic sediment as a source of human illness is lacking.

Aquatic sediments and the microbes within these are likely to be variably impacted by climate change-induced increases in temperature, changes to rainfall/run-off and erosion

patterns, increased coastal sea levels and changes in the frequency of severe weather events. These changes will not necessarily negatively affect the survival of FIB and pathogenic microorganisms. An increased frequency of severe weather events will create more opportunities for sediment deposition from external sources and in-stream resuspension.

This review has identified several important data gaps regarding the presence and survival of pathogenic microorganisms in aquatic sediments. A quantitative microbial risk assessment (QMRA) framework would help to quantify the risk to recreational swimmers under different scenarios, potentially focusing on representative microbial pathogens as informed by NZ infectious disease data. The scoping of this QMRA would identify priority data gaps. Additionally, NZ studies involving the collection of paired water and sediment samples in low energy aquatic environments popular for recreation, and testing these for FIB, selected pathogens and microbial source tracking markers, would help to generate data towards assessing human health risk.

1. INTRODUCTION

Aotearoa New Zealand (NZ) regional and unitary councils monitor coastal and estuarine water quality at over 350 sites, most located along the East coast (Fraser *et al.*, 2021). Water quality monitoring is also carried out at more than one thousand freshwater lake and river sites, although not all quality indicators are measured at each site (Stats NZ Tatauranga Aotearoa, 2022; Whitehead *et al.*, 2022). The *Microbiological water quality guidelines for marine and freshwater recreational areas* provide a standardised approach for water managers to monitor, report and communicate the public health risks associated with the water in recreational aquatic environments (Ministry for the Environment, 2003). The guidelines consider swimming and other recreational activities carried out in the water of marine and freshwater beaches, and recreational shellfish gathering in marine waters. Water sampling and testing underpins decisions about initial recreational site grading (the Suitability for Recreation Grade) and subsequent actions, including when the public needs to be warned that a beach is unsuitable for swimming or shellfish gathering.

Water quality monitoring is carried out at recreational beaches during the period of the year when bathing is more frequent, generally being the months November to March. Instructions for marine water sample collection specify that the sample is taken at approximately 15 cm below the water surface at a point where the depth of water is 0.5 metres (Ministry for the Environment, 2003). For freshwater samples, collection should be approximately 30 cm below the water surface at a point where the depth of water is 1 metre. The guidelines do not provide instructions to the sampler to minimise sediment disturbance while taking the water sample, but the standard procedure for water quality sampling is to collect the samples without disturbing the sediments. On low energy beaches this means taking a sample without entering the water or waiting until any disturbed sediments have resettled before taking the sample.

Pathogenic microorganisms may be present in aquatic sediments. These pathogens can be introduced from a range of sources including overland flows from land-based activities, human or animal waste deposited in beach environments or released from nearby septic tanks, boat sewage or bilge water, and stormwater or wastewater discharges (including wastewater from industrial activities). Potentially pathogenic *Vibrio* and *Aeromonas* bacteria are examples of natural inhabitants of aquatic environments that can also be found in sediment. The concentration and survival of pathogenic microorganisms in aquatic sediments depends on many factors including the characteristics of the microorganism, beneficial or detrimental interactions with other organisms, nutrient availability, temperature, salinity, sediment characteristics and wave energy. Pathogenic microorganisms present in aquatic sediments can be mobilised into the overlying water and become a health hazard for swimmers.

The calmer waters of lakes, river eddies, estuaries and low energy harbours are attractive areas for people seeking safer swimming areas, particularly for younger children. Fine sand, silt and/or clay particles often dominate the sediments in these areas. These fine sediments are easily disturbed and slow to resettle. As people disturb the water in these areas, they are likely to disturb the sediment and any associated microorganisms. Subsequent exposure is more likely for younger children, who tend to actively splash, dig and immerse themselves in shallow waters. A survey of gastrointestinal disease cases notified in NZ during 2016 showed that recreational water contact was a risk factor reported by 33% of giardiasis cases and 26% of cryptosporidiosis cases, noting this includes swimming pools (Gilpin *et al.*, 2018). A more recent survey of freshwater found that the concentrations of these protozoa were low (Leonard *et al.*, 2021a). Resuspension of protozoan pathogens from aquatic sediments may be an important exposure route.

The World Health Organization (WHO) *Guidelines for recreational water quality* recommend that the microbiological risks from beach sand be incorporated into a recreational water safety plan (WHO, 2021). The potential risk from microbiological pathogens in beach sands has been reviewed in the NZ context (King and Leonard, 2023). That work focused on identifying which microbial hazards could pose a public health risk to NZ recreational beach users, considering exposure to these hazards via direct skin contact with sand or ingestion of sand (e.g. through sand play). The focus was on sandy beaches (fine, mud-like sediments were excluded) and exposure to pathogens in the dry and intertidal zones (ingestion of suspended sediment during swimming was a minor consideration). Submerged aquatic sediment is also not considered in the WHO guidelines, other than as part of managing harmful algal blooms and noting any potential risks associated with sediment resuspension during sanitary surveys.

National freshwater, coastal and estuarine monitoring programmes include monitoring of faecal indicator bacteria and suspended solids in water, and for estuaries, the percentage of mud in sediments and sedimentation rates. The microbial quality of aquatic sediments is not routinely monitored in NZ although there are *ad hoc* studies. Aquatic sediments can provide a record of cumulative contamination whereas water column monitoring only provides a snapshot of the potential health risk at a single instant in time.

The objective of this review is to identify if fine aquatic sediments (fine sand, silt and clay) could be a source of pathogenic microorganisms and pose a health risk to people as they swim, play and wade in aquatic environments. Understanding the potential health risks from resuspended sediments will assist public health officials and regional council water quality managers to manage recreational water quality. The information provided through this review may also assist those assessing the safety of fine aquatic sediments intended for relocation to recreational areas.

Within the scope of this review (Section 2 and Appendix A), the scientific literature was reviewed to provide information towards answering the following questions:

1. What biophysical factors affect the concentration of faecal indicator bacteria and pathogenic microorganisms in sediments? (e.g. temperature, salinity, sediment type)
2. Are the concentrations of pathogenic microorganisms in sediments positively correlated with the sediment concentrations of faecal indicator bacteria and/or other faecal markers?
3. Are there studies to show an increase of pathogenic microorganisms or faecal indicators in water column once sediments have been disturbed?
4. How might climate change impact the risk?

Appendix A details the literature review scope and method. The primary literature search was carried out during the period January–March 2025 and reflects information available at that time. Relevant information from the beach sand review by King and Leonard (2023) has been incorporated into this current document.

2. AQUATIC SEDIMENT ENVIRONMENTS

Summary

Within the scope of this review are low energy coastal or tidal lagoons, estuaries, harbours, and swimmable areas of freshwater streams, rivers and lakes. Preference is given to studies considering sediments dominated by mud (silt and clay particles sized <0.063 mm) and/or fine and very fine sands (0.063–<0.25 mm).

Natural aquatic sediment environments are variable, being influenced by the characteristics of the catchment and the living organisms in the ecosystem. Sediments contain organic material and may also contain fragments of shells, bones and synthetics (e.g., microplastics). Oxygen gradients can be present in the water column and underlying sediments.

Biofilms are formed by microorganisms living in the sediment, which bind and stabilise fine sediment beds. In the water, living and non-living biological materials and mineral particles can form aggregates (flocs) that can also settle to the sediment. Low energy aquatic environments favour both biofilm formation and floc settlement.

The forces stabilising the sediment surface and holding sediment together to prevent erosion (shear strength) are overcome as water energy increases, e.g., during storms or flood tides. This leads to sediment resuspension. Disturbance by people and animals can also resuspend fine sediments.

This review focuses on low energy aquatic environments with fine sediments where people wade and swim at depths that would cause sediments to be disturbed and resuspended, and potentially ingested. The sediments could also be resuspended through increased water movement from the weather (e.g. wind action, increased inflows from stormwater) or other human activities such as using powered watercraft or dredging.

These environments can be classified and characterised in different ways. This section provides some general information about the aquatic environments and sediments of interest for this review.

2.1 SCOPE: AQUATIC ENVIRONMENTS

In coastal areas, wave dominated beaches are out of scope. Examples of coastal environments that are within scope are (NIWA, 2016a):

- Coastal lagoons: Shallow lagoons barred from the sea by a barrier beach with no outlet, or an outlet that is narrow, changeable or intermittent. Limited ingress from the sea, so mostly freshwater, for most of the time. Highly susceptible to sedimentation and muddiness.
- Tidal lagoons (may also be called estuaries): Shallow lagoons barred from the sea but with a permanent outlet to the sea (or one that is only intermittently closed). River input is small compared to tidal inflow, so the water is closer in salinity to that of the sea and most of the water leaves the estuary on the outgoing tide. The sediments are often mixed and resuspended at high tide through wind-generated water movement.

- Harbours (shallow, drowned valleys; may also be called estuaries): Tidally dominated, always open to the sea, deeper than tidal lagoons. Usually confined at the ocean end by hard headlands and largely infilled with sediment. Large harbours tend to be sandy at the mouth and in the central basin areas, and muddy in the tidal arms and headwaters. The sediments are often mixed and resuspended by wind-generated water movement. Tidal movement occurs but areas of the harbour are subtidal.
- Tidal river mouths (may also be called estuaries): Permanent connection to the sea, with the water salinity driven by the freshwater flow. While usually well flushed, in deeper systems the water can become stratified, where a wedge of seawater can extend upstream underneath the outflowing freshwater. This stratification protects the sediments from wind-generated mixing and wave-driven resuspension, so they tend to become muddy.

Beach streams are shallow freshwater streams flowing over a beach face to the sea (NIWA, 2016a). While these are within the scope of this review, they are less relevant because the dominant substrate is sand or mixed sand and gravel, although fine sediments can be present. The shallow depth limits recreational contact to paddling, usually by children.

Inland, low energy areas of streams, rivers and lakes can attract swimmers. Fine sand or muddy sediments may be present where the water velocity is low (e.g. river eddies), depending on other factors such as the characteristics of the catchment (e.g. land use, geology, erosion rate), local conditions (e.g. vegetation, water quality, human activities) and recent weather events. These low energy freshwater environments are within the scope of this review.

While the above describes the different kinds of low energy aquatic systems where people might swim, these environments and their sediments are spatially variable and temporally dynamic.

2.2 SCOPE: FINE SEDIMENTS

Silt and clay sediments are readily resuspended in water and take longer to resettle compared to larger particles. These are collectively called ‘mud’, a term that encompasses sediment particles less than 63 µm (<0.063 mm) in diameter. Particles in the range 3.9–62.9 µm in diameter are characterised as silt, with clay particles measuring <3.9 µm in diameter (Hunt and Jones, 2019; LAWA, 2022).

Sand could be temporarily resuspended in the within-scope aquatic environments of interest for this review. There are five sand size classes (NIWA, 2016b):

- 0.063–<0.125 mm, very fine sand
- 0.125–<0.25 mm, fine sand
- 0.25–<0.5 mm, medium sand
- 0.5–<1 mm, coarse sand
- 1–<2 mm, very coarse sand

For this review, preference is given to information about fine and very fine sands, noting that information on sand grain size is not always available in the studies of interest.

As introduced in Section 1, estuary monitoring is undertaken by most NZ councils as part of their State of the Environment programmes. This includes measuring the percentage of the sediment that is made up from mud (% mud), since a higher proportion of mud is ecologically detrimental.[1] A 2019 study has demonstrated that the results of this monitoring are difficult to compare between regions and over time due to the different analytical methods used to measure sediment particle sizes (Hunt and Jones, 2019).

For the period 2010–2023 there were 2947 results reported for % mud, from 415 estuarine sites around NZ.[2] Some estuaries are monitored at more than one site, and the number of % mud results for each site ranges from one to fourteen. Noting these caveats, and the caution over analytical methods expressed by Hunt & Jones (2019), these data show that the average % mud value for each site ranged 0–97%, i.e. some sites had no measurable mud and the sediment samples from some of the other sites were composed almost entirely of mud. The median % mud value was 25%.

The stream bed coverage by fine sediment (<2 mm diameter) has also been repeatedly measured in 215 hard-bottomed, wadable streams and rivers at locations dominated by pastoral, forest or urban land coverage (Stats NZ Tatauranga Aotearoa, 2020). Fine sediment covering 20% or more of the area surveyed is considered detrimental to streambed life in these ecosystems. The 20% threshold was exceeded in 50% of the urban sites (n=10), 14% of pastoral sites (n=144), 6% of sites located in native forests (n=51) and none of the sites in exotic forests. From a summary report that considered 336 sites, including those measured only once, the median deposited fine sediment cover was 4.5% (Clapcott *et al.*, 2020). A few sites exceeded 90% fine sediment coverage. All sites in these surveys were where the flowing water was shallow enough for wading but smooth flowing, i.e., running between pools and riffles. Sedimentation may be higher in deeper pools where people are more likely to swim. According to Clapcott *et al.* (2020), some NZ councils have also measured sediment depth (in a run habitat) and the potential for sediment resuspension, but the compiled data were not located.[3]

2.3 CHARACTERISTICS OF FINE SEDIMENTS

Natural aquatic sediments come from the erosion or disruption (e.g., by humans or animals) of soil and rocks in the wider catchment and from the bed and banks of the aquatic environment being scoured by water (liquid or ice). Aside from particle size, there are a range of characteristics that may create favourable conditions for microbes to inhabit this inorganic material. This includes the extent of porosity or cavitation (which provide protective environments), the concentrations and bioavailability of elements such as iron, the surface charge, and the acidity (pH) of the inorganic material that forms the sediment.

Sediments also contain organic material that has been transported into the aquatic environment or generated within it, and may also contain harder particles remaining from deceased aquatic animals such as shell or bone fragments. Sediments can also contain mobile particles generated through human activities, e.g., tyre and road wear particles or microplastics (Baensch-Baltruschat *et al.*, 2020; De Bhowmick *et al.*, 2021). Similarly to natural sediment particles, these synthetic particles can be redistributed with water

[1] For further information see https://www.lawa.org.nz/learn/factsheets/estuaries/mud-content-in-estuaries.
[2] Data provided by Land And Water Aotearoa (LAWA) on behalf of the authorities responsible for monitoring and reporting (https://www.lawa.org.nz/download-data). Data accessed 10 February 2025.
[3] Resuspension is measured by inserting a core into the sediment, vigorous stirring within the core, then measuring the suspended sediments in the resulting slurry, or by making a qualitative assessment of the size and duration of the sediment plume after someone vigorously moves their feet on the stream bed for five seconds (Clapcott *et al.*, 2020).

movement and accumulate in sediments over time. Within the sediments lives a vast community of living organisms including microbes, plants and animals.

A large portion of the biological community associated with aquatic sediments exists in biofilms. A biofilm is an aggregation of microorganisms that interact to form a community (Flemming and Wuertz, 2019). These microbial aggregates are diverse but share some common features, with an important one being the production of a stabilising matrix formed by extracellular polymeric substances (EPS). The EPS matrix, containing proteins and sugars, houses the microbial cells and has a role in their aggregation and adhesion to surfaces (Flemming and Wuertz, 2019; Liang *et al.*, 2016). Biofilms develop on sediment particles as microorganisms attach, aggregate and produce EPS, which anchors bacterial cells to the sediment and to each other (Gerbersdorf *et al.*, 2020). Biofilms can also form on stones and plants in the aquatic environment.[4] The hydrodynamics of low energy aquatic environments favour biofilm formation in sediments because they have long sediment retention times, providing greater opportunities for microorganisms to form initial sediment attachments and develop into biofilms.

Biofilms can also bind fine sediments together. Where this occurs extensively, the biofilm can stabilise the sediment, change the surface morphology and alter the flow of nutrients at the sediment/water interface (Gerbersdorf *et al.*, 2020). In a study of sediments from estuaries in Scotland, the EPS concentration was significantly higher in muddy and mixed mud sediments compared to mixed sand or sand (Wyness *et al.*, 2019a). The concentrations of coliforms and *E. coli* were also more abundant in the muddy and mixed mud sediments.

Aquatic biofilms are very diverse since they are influenced by the physical characteristics of the sediment and the wider aquatic environment, available nutrients, the types of microorganisms (bacteria, microalgae) and their level of cell-cell communication (Gerbersdorf *et al.*, 2020). The relative growth rates of the individuals in the biofilm community can be impacted by environmental stressors such as sunlight penetration and temperature.

While suspended in the water, living and non-living biological materials and mineral particles can form aggregates through a process called flocculation. Flocs are delicate, with their aggregate form being supported by EPS exuded by bacteria (Malham *et al.*, 2014). These flocs differ in size, shape, density and porosity compared to the primary particles from which they are made, plus they attract and concentrate dissolved nutrients from the water column (Koiter *et al.*, 2013; Malham *et al.*, 2014). When conditions are suitable, flocs can settle into the sediments. In estuarine and coastal environments where freshwater and saltwater meet, the salt modifies the charges of fine-grained mineral particles and this increases flocculation (Forrest *et al.*, 2024; Koiter *et al.*, 2013). This salinity driven flocculation can increase fine sediments in these areas.

The biological community in the sediments of low energy aquatic environments is also affected by the oxygen gradient. Water stratification can occur in tidal river estuaries when low or stable river flows allow a saltwater wedge to push upstream underneath the outflowing freshwater (Forrest *et al.*, 2024). Oxygen diffusion from the freshwater layer is prevented while benthic (sediment-dwelling) bacteria consume remaining oxygen as they

[4] The general term ‘biofilm’ is used in this document. Gerbersdorf *et al.* (2020) explain that biofilms might be named according to the substrate or environment they are associated with. These names are: Epipelic (growing on mud), epipsammic (growing on sand), epilithic (growing on stone), epiphythic (growing on a plant), periphyton (the biofilm community on any submerged surface in the aquatic habitat), and microphytobenthos (growing in shallow coastal waters or intertidal flats).

decompose organic matter. Prolonged stratification leads to oxygen depletion in the bottom saline layer. These conditions affect nutrient cycling and impact benthic biota survival.

Oxygen can also be depleted in aquatic sediments when there are high concentrations of organic matter in the aquatic environment, or influxes of nitrogen from agricultural land use (eutrophic state). These nutrients stimulate prolific growth of phytoplankton and algae, which depletes sediment oxygen (Forrest *et al.*, 2024; Plew *et al.*, 2020). The oxygenation of sediments is measured by its redox status. Visually, sediment colour and odour can indicate eutrophication, since eutrophic sediments can have a “rotten egg” odour (from sulphur oxidising bacteria) and an intense black colour throughout the entire profile (Forrest *et al.*, 2024). A sediment core might also show the brown, oxygenated surface sediment layer transitioning to deeper grey or black sediments. The oxygenated layer is reduced under high organic loading.

The above paragraphs explain how the characteristics of fine sediments are highly variable, and this affects the survival of pathogenic microorganisms in these environments.

2.4 SEDIMENT RESUSPENSION

There are studies focussing on identifying the conditions that resuspend sediment, which are usually conducted to support aquatic system models that predict sediment budgets. These studies focus on natural resuspension processes so are only partly informative for this current review, since they do not consider sediment resuspension from people in the water.

The stability of sediments is usually characterised by measuring shear strength and surface stability (Wyness *et al.*, 2019b). Wyness *et al.* (2019) describe shear strength as the measure of ‘internal stability’ and the resistance of the sediment to mass erosion, e.g., shear strength increases with increased sediment packing (bulk density) and reduced water content. Surface stability is described as the resistance to surface shear stress, e.g., from tidal action, and is affected by particle size and the amount of biofilm or bioturbation by fauna moving through the sediment.

Sediments begin to act cohesively, and become more resistant to erosion, if they contain ≥10% mud (particle sizes <63 μm) (Wyness *et al.*, 2019b). However, sediments dominated by a mud fraction are not necessarily the most resistant to erosion. For example, at sites along two estuaries in Scotland, sediments described as being composed of mixed mud and sand had significantly higher shear strengths and greater stability than sediments comprised of either sand or mud (Wyness *et al.*, 2019b). The mud sediments were least resistant to erosion during winter and autumn compared to summer and spring. However, in this study, the mud samples with low erosion resistance were located in the upper reaches of the estuaries where they were vulnerable to resuspension and redistribution downstream.

The forces stabilising the sediment surface and holding sediment together to prevent erosion are overcome as water energy increases, e.g., during storms. In tidal areas, resuspension and deposition can be cyclical as flood tides prevent particle settling and could cause sediment resuspension, while ebb tides may be less turbulent and allow settling (or at least minimise resuspension) (Malham *et al.*, 2014). Over longer periods, tidal cycles can result in a net increase or decrease of sediment.

Further information on sediment resuspension is included in Section 5.2, which details studies of the impact on microbial indicators in the overlying water. This includes studies of sediment being disturbed by humans or animals.

3. FAECAL INDICATORS AND PATHOGENIC MICROORGANISMS

Summary

The presence of faecal indicator bacteria (FIB) indicates faecal contamination and the potential for pathogenic microorganisms to be present. *E. coli*, faecal coliforms and enterococci are commonly measured FIB. There are some issues associated with FIB, e.g. they do not provide information on the source of faecal contamination, die-off rates differ from viral and protozoan pathogens, some species or strains can become naturalised in the environment (although this can indicate non-recent faecal contamination and continued risk from environmentally persistent pathogens), and they do not indicate the potential presence of pathogenic microorganisms from non-faecal sources. However, testing for FIB is a practical method to detect recent faecal contamination.

Molecular techniques can be used to complement FIB monitoring. Metagenomic methods analyse the entire genetic material extracted from a sample and reveal the diversity of microorganisms present, including potential pathogens from faecal and non-faecal sources. Molecular microbial source tracking (MST) markers target specific host-associated genetic material to identify sources of faecal contamination (e.g., sewage, dog, birds, ruminants). Combining MST and FIB testing provides a more comprehensive result for informing risk.

The pathogenic microorganisms of interest for this review are pathogenic bacteria, viruses and protozoan parasites that are known to be present in NZ environmental waters and could settle into aquatic sediments at concentrations sufficient to cause illness upon resuspension and subsequent human exposure through ingestion or other water contact. Reported illnesses linked to recreational water contact and studies of environmental water microbiology indicate which pathogens are important. These are *Cryptosporidium* spp., *Giardia* spp. and *Campylobacter* spp. Others that could be important when sediments have a high faecal loading are *Salmonella* spp. and Shiga toxin-producing *E. coli*, and when that contamination arises from human wastewater/sewage, enteric viruses such as norovirus, adenovirus and rotavirus. Of the opportunistic pathogens naturally present in aquatic environments, *Vibrio* spp. are of most interest because they are known to cause adverse health effects through recreational water contact (via ingestion or skin contact).

This section provides an overview of faecal indicators, and the pathogenic microorganisms selected as being relevant to this current work. Most of the material in this section has been adapted from King and Leonard (2023).

3.1 FAECAL INDICATOR BACTERIA (FIB)

FIB are used to indicate a potential risk to human health from faecal contamination. Routine monitoring for the presence of pathogenic microorganisms is impractical because a wide range of pathogen species could be present. Compared to FIB test methods, tests for pathogens can be complex, have low recovery rates and are expensive. *E. coli* and enterococci are commonly used FIB because they are consistently present in high concentrations in the faeces of warm-blooded animals and there are standard methods available for testing different types of environmental samples. Other FIBs include total coliforms (TC) and faecal coliforms (FC). Coliform is a collective term used for a large group of gram-negative, non-sporeforming, rod-shaped bacteria that all belong to the Enterobacteriaceae family. While the coliform group includes normal intestinal bacteria, it also includes environmental bacteria (Paruch and Mæhlum, 2012). FCs are a thermotolerant sub-group of TCs.

In NZ, FIB testing is used routinely to monitor the safety of drinking and recreational waters.[5] Currently, there are two microbiological measures used to monitor coastal water quality, these being enterococci and faecal coliforms. The abundance of these bacteria indicates recent faecal contamination and the potential presence of pathogenic microorganisms. The enterococci measure indicates the suitability of the water for recreational contact and the faecal coliform measure indicates whether shellfish are safe to gather (Dudley and Jones-Todd, 2018). Freshwater bodies (rivers, lakes) are monitored for faecal contamination using *E. coli* (Ministry for the Environment, 2003). Estuarine and brackish waters may be monitored through tests for both enterococci and *E. coli*.

When using FIB as indicators of faecal contamination, there are some important considerations:

1. The presence of FIB does not confirm the presence of enteric (faecal) pathogens, only that these might be present. FIB are common inhabitants of the gastrointestinal tracts of mammals and birds, but their detection does not indicate the source of faecal matter nor confirms that pathogenic microorganisms are present (Korajkic *et al.*, 2018). Pathogenic microorganisms might only be present intermittently in faeces from individuals or groups of warm-blooded animals. Human enteric pathogens will be present in sewage if illness is circulating in the community.
2. FIB are indicators of faecal contamination but not indicators for opportunistic pathogenic microorganisms that are natural environmental inhabitants. Examples include skin and mucous-borne pathogens such as *Staphylococcus aureus*, natural inhabitants of the marine environment such as *Vibrio* spp., and environmentally widespread fungi that are opportunistic human pathogens. Spore-forming clostridia, which can also cause foodborne illness, are naturally found both in faeces and the environment (Palmer *et al.*, 2019).
3. FIB survival in environmental samples can be different to pathogenic microorganisms. For this reason, FIB may be poor indicators for pathogenic microorganisms that survive longer in environmental samples. For example, parasites that are excreted with faeces but have environmentally resistant life stages, such as *Toxoplasma gondii, Giardia* spp. and *Cryptosporidium* spp., have longer survival times than FIB. This means that low concentrations of FIB do not necessarily imply a low risk to human health.
4. In some conditions, FIB can persist and replicate in the environment. This could trigger 'false positive' results.

Regarding point 4, the presence of naturalised (persistent) FIB populations in the environment has been reviewed from the perspective of recreational water quality monitoring (Devane *et al.*, 2020). The authors established that naturalised *Escherichia* and *Enterococcus* species have been identified in environmental matrices including soil, sediment and aquatic vegetation and standard tests are unlikely to differentiate these 'non-

[5] For further information on faecal indicators and water quality monitoring, see this LAWA factsheet https://www.lawa.org.nz/learn/factsheets/faecal-indicators/

enteric' strains from enteric (faecal) FIB.[6] The naturalised strains may be considered as two groups: Those that are defecated into the environment and are able to persist under favourable conditions by adapting to a non-host lifestyle (i.e. indicators of past faecal contamination), and those that are truly environmental (separate lineages that lack the genes important for survival in the gut of animals). Laboratory methods are needed to distinguish between FIB from fresh faeces, aged faeces (i.e. faecal contamination in the past) and naturalised populations. Devane *et al.* (2020) proposed that additional methods were needed to determine whether there is a health risk from environmental samples with elevated numbers of *E. coli* but no obvious source of faecal contamination.

A second NZ study has investigated the above issue further (Cookson *et al.*, 2024). Through examining water collected from catchment sites dominated by native forest or different types of agricultural farms, the researchers showed that as the concentration of *E. coli* increased (as measured by standard laboratory tests), the diversity of the *E. coli* strains present in the samples also increased. *Escherichia* species other than *E. coli* were present in these samples, albeit at a low relative concentration (22/426 *Escherichia* amplicon sequence variants). The increased diversity of *E. coli* subtypes was attributed to both increased faecal contamination from nearby agriculture and increased diversity of faecal source inputs. Further examination of 168 environmental samples (water, biofilms, faeces, sediment and soils) showed the presence of both *E. coli* and non-*coli Escherichia* species. An important finding was that the presence of non-*coli Escherichia* species was not confounding the water quality monitoring and causing false positives. Samples with elevated *E. coli* were from areas impacted by faecal contamination.

3.2 GENETIC INDICATORS FOR FAECAL CONTAMINATION

Analytical techniques have been developed by molecular biologists that target genetic material from microorganisms. When these methods are designed to analyse all the genetic material in a sample, to determine which organisms are present, this is called metagenomics. Metagenomic next generation sequencing is an example of a high-throughput method that amplifies and sequences short pieces of extracted DNA or RNA in a sample. The sequences are compared with a library of genetic data to identify the microorganisms present and the relative abundance of different microorganisms can be calculated. Next generation sequencing can be used for different metagenomic approaches. One approach, called amplicon metagenomics, targets a selected portion of a gene (or genes) in the genetic material that relate to taxonomy or virulence factors. For example, targeting the 16S rRNA gene provides information on the range of bacterial species present in a sample. Shotgun metagenomics is an untargeted approach where the entire genomic content of a sample is subjected to sequencing, which reveals the microbial diversity.

Metagenomic methods address some of the FIB weaknesses noted in Section 3.1, since the methods can detect multiple microorganisms in one test and indicate the likely sources of contamination. Some weaknesses are:

- These molecular techniques only detect gene fragments and so do not indicate whether this genetic material came from viable microorganisms.
- It is difficult to quantify the different microorganisms in a sample (calculating relative abundance is achievable).

[6] *E. coli* and non-*coli Escherichia* species are phenotypically indistinct and grow in the same media, e.g., that used in Colilert tests.

- Without further investigations, the results may not provide high enough resolution of the microbial species present in a sample to determine potential health risk (e.g., analysis might reveal the presence of *Listeria* spp. but may not identify the important human pathogenic species *L. monocytogenes*).

Microbial Source Tracking (MST) uses qPCR (quantitative Polymerase Chain Reaction) to target specific host-associated genetic material from the gut of animals and humans. The concentration of these markers can be calculated. MST is used to identify the sources of faecal contamination by targeting and quantifying genetic markers of species-specific microorganisms or host-bacteria interactions. This allows the source of faecal contamination to be identified, e.g., human sewage, faeces from birds or dogs. Some markers can additionally indicate aged faecal contamination. For example, the human marker crAssphage has a slower decay rate than both FIB and bacterial MST markers, and its continued presence when there are very low concentrations of other human MST markers is considered indicative of aged or treated sewage (Boehm *et al.*, 2018; Leonard *et al.*, 2021b). Examples of other faecal markers include GenBac3 and ruminant BacR (Leonard, 2022). GenBac3 indicates the presence of bacteria in the Order *Bacteroidales*, which are abundant in the intestines of warm-blooded animals and humans and are not able to grow in the environment (Shanks *et al.*, 2010). Ruminant BacR is a *Bacteroidetes* marker present in cattle, deer, chamois, sheep and goat faeces (Reischer *et al.*, 2006).

Pairing of MST with FIB testing provides a more comprehensive result for informing risk.

3.3 PATHOGENIC MICROORGANISMS

The pathogenic microorganisms of interest for this review can be natural inhabitants of aquatic environments or introduced from faecal contamination. Of relevance for this review are pathogenic bacteria, viruses and protozoan parasites that are known to be present in NZ environmental waters and could settle into aquatic sediments at concentrations sufficient to cause illness upon resuspension and ingestion by swimmers. Because sediment studies have focused on FIB (Section 4.3) there are fewer data to indicate which pathogenic microorganisms are most important for human health in this context (Section 4.3). These studies do not link pathogen presence with human infection via sediment exposure.

However, reported illnesses linked to recreational water contact and studies of environmental water microbiology both provide guidance. As mentioned in Section 1, recreational water contact is an important risk factor for giardiasis and cryptosporidiosis in NZ (Gilpin *et al.*, 2018). A study of NZ notifiable disease data for 2023 additionally identified campylobacteriosis as a disease arising from recreational water contact (Hipgrave, 2024). All three of the microorganisms responsible for causing these diseases are excreted in faeces from animals or infected humans.

The causative organism of giardiasis is *Giardia duodenalis*, which infects humans and other mammals (Feng and Xiao, 2011; Winkworth, 2010). Human cryptosporidiosis is usually caused by the zoonotic species *Cryptosporidium parvum*, and the human-associated species *Cryptosporidium hominis* (Vanathy *et al.*, 2017). *Giardia* spp. and *Cryptosporidium* spp. are protozoan parasites that require a host to complete their life-cycle but also have environmentally-resistant life stages (cysts and oocysts, respectively). These (oo)cysts are released into the environment with host faeces and have been detected in faeces from livestock and wild birds in NZ (Abeywardena *et al.*, 2012; Moriarty *et al.*, 2011b; Moriarty *et al.*, 2011c; Moriarty *et al.*, 2008). They have also been detected in NZ surface waters

(Devane *et al.*, 2019; Leonard *et al.*, 2020; Leonard *et al.*, 2021b; Phiri *et al.*, 2021; Till *et al.*, 2008).

Campylobacter spp. are commonly found in animal faeces, particularly that of ruminants and poultry. *Campylobacter jejuni* is most frequently isolated from campylobacteriosis cases in NZ. *C. coli* also causes disease in NZ. Emerging species in humans are *C. concisus*, *C. upsaliensis*, *C. ureolyticus*, *C. hyointestinalis* and *C. sputorum* (Facciolà *et al.*, 2017). *Campylobacter* spp. have been detected in the faeces of wild birds, livestock and pets in NZ (Anderson *et al.*, 2012; Irshad *et al.*, 2015; Mohan, 2015; Moriarty *et al.*, 2015; Moriarty *et al.*, 2011a; Moriarty *et al.*, 2011c; Pattis *et al.*, 2017). These bacteria have also been detected in NZ rivers and other surface waters (Leonard *et al.*, 2020; Leonard *et al.*, 2021b; Phiri *et al.*, 2021; Shrestha *et al.*, 2019).

In NZ, faecal matter entering aquatic environments from sewage, wild animals or domesticated animals can contain a wide range of other pathogenic microorganisms including *Salmonella* spp., pathogenic *E. coli* (e.g., Shiga toxin-forming *E. coli* – STEC), *Yersinia* spp. and *Shigella* spp.[7,8,9,10] Human enteric viruses such as norovirus, hepatitis A virus and rotavirus can also be found in sewage if infection is circulating in the human population.[11]

Water bodies provide habitats for aquatic birds and in NZ, faeces from ducks, gulls, swans and geese have been found to contain *Campylobacter* spp., *Cryptosporidium* spp., *B. cereus* and *Clostridium perfringens* (Moriarty *et al.*, 2011a; Murphy *et al.*, 2005).

In NZ, *Campylobacter* spp., *Salmonella* spp., STEC and rotavirus have been detected in freshwater from rivers, lakes and streams, and human adenovirus and norovirus additionally in estuarine water (Hewitt *et al.*, 2013; Leonard *et al.*, 2020; Leonard *et al.*, 2021b; Till *et al.*, 2008; Williamson *et al.*, 2011).

Some natural microbial inhabitants of aquatic systems can also cause opportunistic infections in humans. These can manifest as gastroenteritis, soft tissue infections, ear infections or other conditions. Relevant examples include *Vibrio* spp., *Pseudomonas aeruginosa*, *Clostridium* spp., *Legionella* spp. and *Aeromonas* spp. Of these, *Vibrio* spp. are of most interest for this current review. As natural inhabitants of freshwater and coastal marine environments, *Vibrio* spp. are important hazards for seafood consumers and swimmers. The three main species important for human health are *Vibrio parahaemolyticus* (primarily causes foodborne disease via seafood consumption), *Vibrio vulnificus* (a cause of foodborne disease and serious wound infections) and *Vibrio cholerae* (in NZ, where cholera is not endemic, serotypes other than O1 and O139 have caused disease in non-travellers, suggesting domestic exposure is occurring) (Baker-Austin *et al.*, 2018; Powell *et al.*, 2019).

[7] The typhoidal serotypes of *Salmonella enterica* spp. *enterica*, Typhi and Paratyphi, only infect humans and are excreted in the faeces of infected people. *S*. Typhi and *S*. Paratyphi are not endemic in NZ but have caused infections in people returning from countries where the disease is endemic, meaning there is a low risk of these being introduced into the New Zealand environment with human faeces.

[8] Some *E. coli* strains are known to be opportunistic human pathogens, causing enteric or extraintestinal disease. STEC are one group of pathogenic *E. coli* which carry one or more genes that enable them to produce a Shiga-like toxin. *E. coli* serotype O157:H7 is an example of an STEC.

[9] *Yersinia pestis*, the causative organism of plague, is not of relevance to this review.

[10] Approximately 60% of NZ shigellosis cases are caused by exposures in other countries (ESR, 2025). Humans are the primary reservoir for *Shigella* spp.

[11] A rotavirus vaccine was introduced into the New Zealand child immunisation during 2014, decreasing population infection rates (https://www.tewhatuora.govt.nz/for-health-professionals/clinical-guidance/immunisation-handbook/20-rotavirus, accessed 24 April 2025).

However, a range of other *Vibrio* spp. have also caused adverse health effects in people exposed within NZ.[12] *Vibrio* spp. can be free living (planktonic) but are more likely to colonise fish and marine organisms or attach to biotic or abiotic surfaces including plankton and sediments (Baker-Austin *et al.*, 2018).

P. aeruginosa are better known for causing infections in healthcare environments and skin/ear infections via puncture wounds or contact with swimming pools/hot tubs (Silby *et al.*, 2011; Wilson and Pandey, 2022). *Clostridium* spp. are spore-forming bacteria found in the gastrointestinal tracts of animals and as spore-formers are environmentally stable, so are sometimes used as faecal indicators (Heaney *et al.*, 2012; Shah *et al.*, 2011; Vierheilig *et al.*, 2013). Only some clostridia are pathogenic; those more commonly causing human illness are *Clostridium botulinum*, *Clostridium difficile* and *Clostridium perfringens* (Guo *et al.*, 2020).[13] Foodborne and nosocomial transmission are established transmission routes. Community-acquired *C. difficile* infections are being increasingly reported but the transmission routes are not known (Johnston *et al.*, 2022). *Legionella* spp. are found in freshwater but legionellosis cases in NZ are associated with exposure to compost, potting mix or soil, or to water from hot water systems, spas/pools, air conditioning, etc. (ESR, 2021). Aeromonads have caused wound infections in people swimming in outdoor environments and have caused illness in immunocompromised people via drinking water, but recreational exposure to *Aeromonas* spp. in environmental water is not a risk factor for illness (Katz *et al.*, 2015; Pessoa *et al.*, 2022).

[12] King *et al.* (2025). Manuscript in preparation (ESR).

[13] *C. difficile* has been classified as *Clostridioides difficile* due to this species being more distantly related to the other clostridia (Lawson *et al.*, 2016), but the old name is still used in some literature.

4. MICROORGANISMS IN AQUATIC SEDIMENTS

Summary

Microorganisms are abundant in the sediments of aquatic environments where they may be attached to the sediment and become part of biofilms, or may be suspended in the interstitial pore water, attached to (or ingested by) other living organisms or associated with decomposing organic matter. Those microorganisms which are natural inhabitants of these environments, but opportunistic human pathogens, are well adapted.

In general, once faecal-associated microorganisms enter aquatic environments with wastewater, direct faecal deposits or diffuse sources, they progress towards non-viability, although some may survive for long periods (enabling them to persist long enough to infect another host) and others may adapt and multiply. These microorganisms readily attach to organic and inorganic particles, which increases their settling rate into the sediment. Further particle attachment and biofilm development within the sediment helps to retain microorganisms. Studies have shown that the concentrations of FIB are higher in the upper layers of the sediment compared to deeper layers.

Sediment environments are more favourable for microbial survival compared to the overlying water, since the sediments protect microorganisms from sunlight, provide surfaces to support biofilms, trap organic matter and offer protection from predators. A range of physical, chemical and biological factors collectively affect the survival of FIB and pathogenic microorganisms in sediments. Examples of extrinsic factors are temperature, turbidity, salinity, oxygen concentration, pH and nutrient availability (organic matter). Predation and competition both contribute to microbial population decline. Some important intrinsic factors for microorganisms include the ability to form biofilms and/or having an environmentally resistant life stage (e.g. spores, cysts/oocysts). While FIB survival tends to be longer in sediments containing higher proportions of silt/clay particles and organic matter, it is difficult to predict which physicochemical factors are important for the survival of different microorganisms in varied aquatic environments.

Most sediment studies focus on FIB. From the few studies seeking to detect pathogenic microorganisms in sediment, most of interest for this review have been detected at least once, however data on their prevalence, concentration and viability are scarce.

Laboratory studies using inoculated microcosms suggest that the concentration of FIB decreases at a similar rate to bacterial pathogens in sediment. However, field studies do not provide consistent evidence that FIB or faecal markers can be used to indicate the presence of bacterial, viral or protozoan pathogens in sediments, except near known point sources of human faecal pollution.

Aquatic sediments are inhabited by numerous microorganisms such as protozoans (single-celled eukaryotes), small algae, bacteria and viruses. Bactericidal viruses called bacteriophages are considered to be an important component of aquatic microbial communities because they infect and lyse bacteria and release organic matter into the water (Duhamel and Jacquet, 2006). Protozoans also graze on bacteria and are a major contributor to bacterial mortality in aquatic systems (Korajkic *et al.*, 2019). A study of a freshwater lake in Switzerland found that the concentration of benthic viruses was almost 200 times higher in the sediments than the overlying pelagic waters, and the concentration of bacteria was up to 2200 times higher in the sediments compared to the water (Duhamel and Jacquet, 2006). This study counted all bacteria and viruses that could be detected using flow cytometry and epifluorescence microscopy.

This section considers the origin and survival of FIB and human pathogenic microorganisms of relevance to this study. However, it is important to recognise that their survival is influenced by this wider microbial community and the physicochemical conditions in the environment. In general, faecal-associated microorganisms progress towards non-viability once they enter aquatic environments, although some may survive for long periods (enabling them to persist long enough to infect another host) and others may adapt and multiply (Korajkic *et al.*, 2019).

4.1 MICROORGANISM SETTLEMENT INTO THE SEDIMENT

Faecal-associated microorganisms are typically introduced into aquatic environments with wastewater (point-source), agricultural runoff (diffuse source) and direct faecal deposits from animals (e.g., aquatic birds) (Hassard *et al.*, 2016). These microorganisms may be free entities or attached to organic or inorganic particles (Weaver and Sinton, 2009). If water turbulence and flow rates are low enough, these microorganisms can settle into the sediment. Other microorganisms may be natural aquatic inhabitants (e.g., *Vibrio* spp.).

Faecal-associated microorganisms entering the water column as free entities may attach to suspended sediments. This attachment increases the likelihood of them settling out of the water column by increasing their settling rate (Weaver and Sinton, 2009). Bacteria, viruses and protozoan parasites readily attach to suspended sediments. A study of a river estuary in North Carolina (USA) reported that 30% of enterococci and 52% of *Vibrio* spp. in the water were attached to particles (Fries *et al.*, 2008). During periods of runoff into this aquatic environment, 14% of *E. coli* were attached to suspended particles, but this increased to 68% during periods of sediment resuspension.

In another study, water samples collected from Galveston Bay (Texas, USA) were filtered to remove suspended solids and the water and suspended sediment fractions were separately tested for viruses (Rao *et al.*, 1986a). Enterovirus and rotavirus were detected in 14% and 16% of the filtered water samples, respectively. These prevalence values were higher for the extracted suspended solid fractions, being 72% positive for enterovirus and 50% positive for rotavirus. In this study, the concentration of viruses detected in the suspended sediment fractions were higher than concentrations in the bed sediments.

The (oo)cysts of protozoan parasites also readily attach to organic and inorganic particles (Malham *et al.*, 2014). In a study of settlement kinetics using wastewater effluent, approximately 35% of the *G. lamblia* cysts or *C. parvum* oocysts attached to suspended particles within five minutes, with the proportion attached increasing to approximately 70% after 24 hours (Medema *et al.*, 1998). In another study, *C. parvum* oocysts readily attached to suspended river sediments (≤45 µm size) in natural water and this increased the number of oocysts settling out of the liquid (Searcy *et al.*, 2005). In the absence of suspended sediments, approximately 40% of the oocysts remained in the supernatant after a 20 hour settling period, compared to approximately 26% in the presence of river sediments.

Thus, microorganisms may arrive in the sediment already attached to particles or subsequently adsorb to sediment particles. This adsorption has been reviewed (Hassard *et al.*, 2016). In summary:

- Initial sediment attachment is governed by the physiochemical properties of particle surfaces and the microorganisms, and the differences in their surface charges. These are influenced by a wide range of factors such as the metabolic state of the microorganism, the genes the microorganism expresses (e.g., those associated with adhesion, or for viruses, those directing the capsid properties), the organic and mineral content of the particle, and the particle size and roughness.
- Faecal-derived bacteria are more frequently associated with finer sediments and particles compared to being free in the water.
- Faecal-derived viruses readily absorb to sediments, but higher absorption efficiencies have been reported for estuarine and marine sediments compared to freshwater sediments. Salinity, pH, organic matter and temperature influence absorption and desorption.

Contrary to the first point above, a laboratory study of *E. coli* sediment adhesion found that strain differences were more important for determining cell-particle adhesion than salinity, the type of sediment and the bacterial surface charge (zeta potential) (Wyness *et al.*, 2018). In another study, *E. coli* strains isolated from the sediment of a freshwater stream were significantly more hydrophobic and contained higher concentrations of the biofilm substance EPS in their cell surfaces compared to *E. coli* strains from the same stream's water (Liang *et al.*, 2016). The researchers had initially screened the *E. coli* isolates from both environments to ensure that all isolates taken forward for their hydrophobicity and EPS tests were genomically distinct. Rather than attributing differences to strains and genomic variation, they proposed that it was the habitat that regulated expression of the genes that enhance sediment survival. These studies hint at the complexity of the microbe-sediment bond.

In aquatic systems with a consistent source of faecal contamination and fairly stable water flows, there are likely to be areas of sediment where faecal associated microorganisms accumulate due to higher organic matter and consistent repopulation. This was exemplified in a survey of *Campylobacter* spp. in estuarine bank sediments in Australia, which suggested that the concentrations of *Campylobacter* spp. were affected more by the proximity of the sample sites to nearby *Campylobacter* sources than by sediment size and associated moisture content (Schang *et al.*, 2016).

Resuspended sediment is another source of microorganisms for downstream environments like estuaries and lakes. Water turbulence increases shear stress at the sediment surface (Section 2.4), resulting in sediments (and their associated microflora) being lifted back into the water flow (Section 5.2).

4.2 SURVIVING IN THE SEDIMENT

Aquatic sediments offer a variety of habitats for microorganisms. They may be attached to the sediment, where they often become part of biofilms, they might be suspended in the interstitial pore water, they might be attached to (or ingested by) living organisms such as plankton, algae, coral and shellfish, or they may be associated with decomposing organic matter such as branches and dead macroalgae. Microorganisms may actively or passively move between different aquatic habitats.

For the purposes of this review, pathogenic microorganisms in the surface layers are of most interest because these would be disturbed by swimmers. Generally, studies have shown that the concentrations of FIB are higher in surface layers compared to deeper sediment layers, with the highest FIB concentration being in the upper 2 cm of sediment (Hassard *et al.*, 2016). While these findings would not be unexpected in low energy waters receiving faecal inputs, a study in NZ suggests that this stratification can be prolonged in the absence of further faecal inputs (Drummond *et al.*, 2014). In this study, researchers measured the distribution and retention of both *E. coli* and fluorescing fine particles injected into a stream with a sediment bed composed of both clay/silt and fine/medium sand intermixed with seasonal emergent vegetation. While background *E. coli* concentrations in the stream did create measurement difficulties, an estimated 69% of the injected *E. coli* settled within 200 m, with the highest concentrations being found in the upper 3 cm of the sediment. These bacteria were retained in the sediments for the duration of the five-month trial, despite there being three high flow events. The *E. coli* strain used had originally been isolated from the same stream, so was well adapted to this environment. Using sediment cores extracted two months after injection, 39% of the *E. coli* population was found in the interstitial water, 12% in the organic debris and 49% in the sediment fraction. Furthermore, the researchers reported a positive correlation between the concentration of *E. coli* and that of organic matter in the sediments, indicating that the roots of submerged macrophytes and organic debris at the sediment-water interface were important bacterial reservoirs.

For non-native microorganisms, such as those associated with faeces, the sediments provide an environment that extends their survival compared to the water column. In addition to the advantages of being part of a biofilm (Section 2.3), sediments are likely to offer more nutrients, protection from the damaging effects of ultraviolet (UV) radiation and protection from protozoan grazing (Wyness *et al.*, 2018). While enteric viruses do not multiply outside the host, these can also attach to bacteria and EPS in the sediments and gain protection from UV (Malham *et al.*, 2014).

A range of factors collectively affect the survival of FIB and pathogenic microorganisms in sediments (and for bacteria, their ability to multiply). Once in the sediment of an aquatic environment, their survival (and growth potential) depends on the combination of physical, chemical and biological factors in their environment, and the characteristics of the microorganisms themselves. Extrinsic factors include temperature, turbidity, salinity, oxygen concentrations, pH, nutrient availability (organic matter), water depth (including tides), sediment type/texture and deposition rates, and predation, viral lysis or competition (Hassard *et al.*, 2016; Korajkic *et al.*, 2019; Wyness *et al.*, 2019a; Yoneda *et al.*, 2024). Some of these physical factors are affected by season. The environment may also contain chemical contaminants introduced through wastewater or runoff, or by other means. Some important intrinsic factors include the ability to form biofilms and/or having an environmentally resistant life stage (e.g. spores, (oo)cysts). Figure 1 provides an overview of these extrinsic and intrinsic factors, along with considering processes that shift microorganisms between sediments and overlying water.

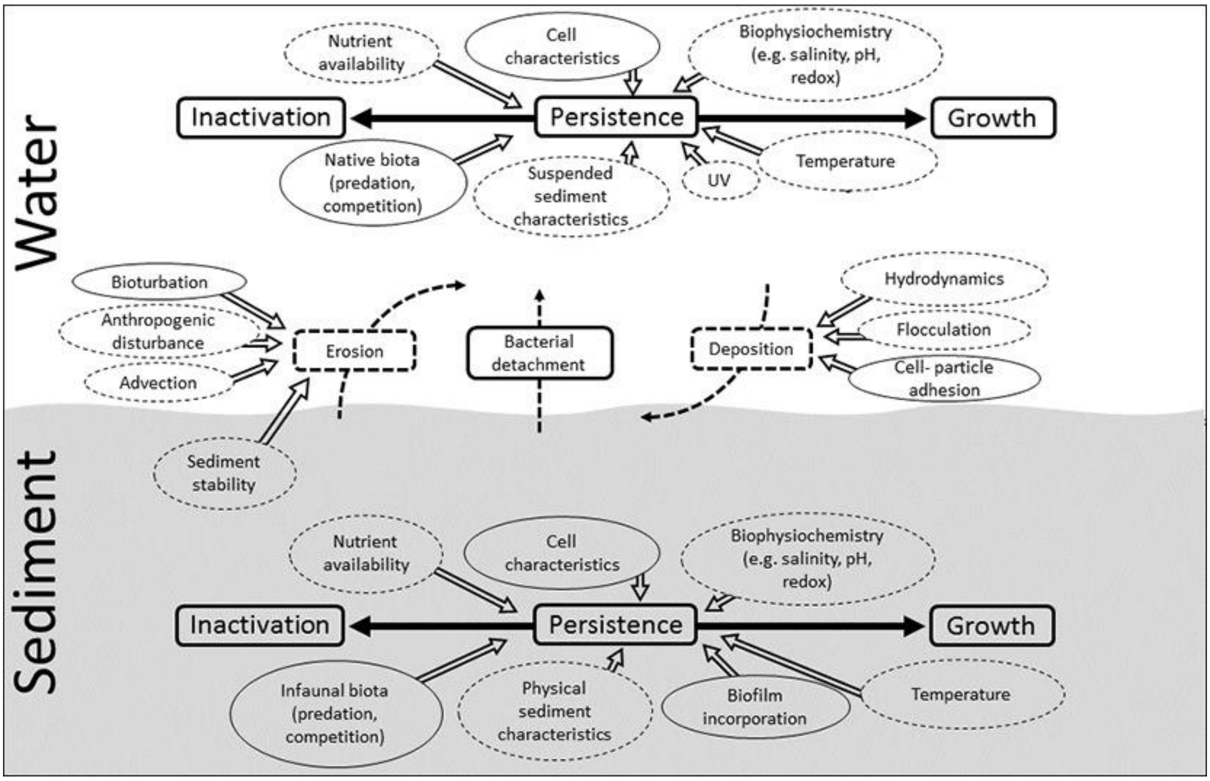

Figure 1. Factors affecting the survival of microorganisms in aquatic systems

Image reproduced with permission from A. Wyness (Wyness *et al.*, 2019a). Image was designed for FIB (and *E. coli* in particular) but is applicable to other microorganisms.

A 2011 review of *E. coli* survival in sediments concluded that (Pachepsky and Shelton, 2011):

- Survival tends to be longer in sediments containing higher proportions of silt and clay particles, or in lower saline environments.
- Temperature influences survival but is not a dominant factor.
- Studies investigating correlations between *E. coli* concentrations in sediment and the amount of organic matter do not show consistent results. One reason is that additional organic matter may not necessarily favour *E. coli* since it can be outcompeted by other microorganisms also utilising the nutrients.

A review published in 2016 considered the results from six studies examining the survival of faecal-associated bacteria in aquatic sediments (Hassard *et al.*, 2016). The original researchers measured concentrations of *E. coli*, faecal coliforms, faecal streptococci, *C. perfringens* (total and spore fraction) and/or enterococci over time. The calculated decay rates showed these bacteria were unlikely to grow, even in faecal-contaminated sediments, but could survive for longer than one month. *C. perfringens*, in particular, survives extended periods as spores rather than vegetative cells (Davies *et al.*, 1995). An exception was a study that observed growth of *E. coli* in a riverbank soil from a tidally influenced tributary, with the authors noting that influxes from this periodically wet soil reservoir were likely contributing to higher *E. coli* concentrations in the water during high tides (Solo-Gabriele Helena *et al.*, 2000). Inactivation rates tend to be slower in sediments compared to paired water samples (Pachepsky and Shelton, 2011). Enteroviruses and rotaviruses have also been shown to survive longer in the presence of sediment, when their survival was measured in microcosms containing seawater and sediments, or seawater alone (Rao *et al.*, 1984). Survival for longer than 18 days was reported.

A more recent review has considered studies of faecal-associated microorganisms or genetic faecal indicators in natural or simulated aquatic habitats, where these studies have included submerged sediment and aquatic vegetation, have examined different treatments and have calculated decay rates (Korajkic *et al.*, 2019). While this review focused on microbial survival in the water fraction of aquatic environments, some attention was given to the sediment fraction. FIB survival was better in sediments with smaller grain sizes and elevated nutrient content, although the results underpinning this finding were all from studies of sediment samples with varied grain sizes (including sand-dominated samples) taken from freshwater systems. Fine sediments were also more supportive for the survival of *S.* Typhimurium and *Shigella dysenteriae*, and prolonged the time during which MST markers could be detected.

In fact, upon reviewing studies of the survival of faecal-associated microorganisms in natural or simulated aquatic habitats (freshwater, estuarine and marine), the authors of this 2019 report stated "*In a rare consensus, all the studies comparing decay in sediments versus the overlying water column found extended persistence in sediments*" (Korajkic *et al.*, 2019). The authors further reported that this finding applied to culturable FIB and FIB quantified by qPCR (Entero1a and *uidA*), MST markers (for ruminant, dog, human and poultry faeces), and bacterial pathogens quantified by both culture and qPCR (*C. coli*, *E. coli* O157:H7, *Salmonella* spp. and *V. parahaemolyticus*).

As indicated by Figure 1, sediment characteristics like grain size and nutrient availability (% organic matter) are just two of many factors that affect the survival of FIB or pathogenic microorganisms in aquatic systems. **Table 1** provides examples of studies that have utilised microcosms, field studies and mathematical models to identify important physical and chemical factors that affect survival. As can be seen from these examples, it is difficult to predict which physicochemical factors may be most important for survival of different microorganisms in different aquatic environments.

There is, however, one recurrent finding, discussed separately here. Several studies of aquatic systems have compared the decay rates of FIB, MST markers or human pathogens in the presence (controls) or absence (treatments) of naturally present microbiological predators, bacteriophages and/or competitors. It has almost consistently been reported that the decay rates were faster in the presence of these indigenous microbiota (Korajkic *et al.*, 2019). Where studies preferentially excluded either microbial predators or bacterial competitors, both conditions were found to affect FIB decay rates, but predation was the dominant process. However, there are few studies of the impact of predation and/or competition in the sediment fraction of aquatic systems:

- Using outdoor microcosms constructed using water and sediment from a freshwater river (Florida, USA), *E. coli* O157 or *Salmonella* Typhimurium were inoculated either with or without the protozoan predator *Tetrahymena pyriformis* (Wanjugi and Harwood, 2014). *S.* Typhimurium concentrations increased in the sediments, but the rate of population increase was slower in the presence of *T. pyriformis* and overall, the combined population in the water and sediments decreased with predation. Survival of *E. coli* O157 was extended without predation. In contrast to this, another study by the same authors showed that survival of *E. coli* O157:H7 in the sediment was not affected by the removal of all indigenous microbiota nor by the addition of *T. pyriformis* (Wanjugi and Harwood, 2013).

- *E. coli*, *S.* Paratyphi and *V. parahaemolyticus* survived longer in sterilised sediments taken from a freshwater lagoon in India compared to non-sterilised sediments (Chandran *et al.*, 2011). The T_{90} values calculated from the sterilised sediment experiments were approximately three times higher than those calculated for the non-sterilised sediments.[14]
- Removal of competition and predators by autoclaving sediments from freshwater lakes in Japan positively affected *E. coli* survival during storage at 10, 20 or 30°C (Yoneda *et al.*, 2024).
- Microcosm studies using wastewater-affected marine sediments showed that predation by protozoa contributed to the concentration of faecal coliforms reducing over time (Davies *et al.*, 1995).

Data on the effect of the indigenous microbiota on the decay rates of genetic MST markers and viral or protozoan pathogens in sediments are needed (Korajkic *et al.*, 2019). One study suggested that ingestion by zooplankton may protect suspended viruses from sunlight inactivation (Wang *et al.*, 2025). Similarly, viruses and bacteria ingested by protozoa such as amoebae or larger zooplankton may survive digestion, receive interim protection from environmental stressors, and be expelled back into the environment (Atanasova *et al.*, 2018; Di Cesare *et al.*, 2022; Rayamajhee *et al.*, 2021).

While the presence of indigenous microbiota negatively affects FIB survival, the presence of aquatic vegetation could provide an environment that supports FIB survival, but research is needed (Badgley *et al.*, 2010; Korajkic *et al.*, 2019).

Table 1. Examples of studies that investigated the effects of physicochemical factors on the survival of FIB or pathogenic microorganisms

Field studies	Conclusion and references
A spatial study of the Conwy Estuary (Wales) found significantly positive correlations between fine sediments (grain size <4 μm, higher proportions of silt and/or clay) and the concentrations of *E. coli*, *enterococci*, *Vibrio* spp. and total coliforms. Significant negative correlations were observed between these bacterial groups and the sediment being formed from fine or medium sand. It was also reported that sediments dominated by clay and silt contained the highest concentrations of organic material. No relationships between the bacterial sediment concentrations and temperature or salinity were found.	(Perkins et al., 2014) • Higher bacterial concentrations in finer sediments (mud/clay) compared to sandier sediments • No relationships with temperature or salinity
A survey of 18 bathing beaches around the Iberian Peninsula (Spain) found a positive correlation between the concentration of faecal coliforms in sediments and organic matter, although the presence of wastewater discharges contributed organic matter to some of these sites. Similarly, a study of the Hudson River Estuary (New York, USA) found a correlation between sediment organic carbon concentrations and the concentrations of enterococci and *E. coli* concentrations, but these results were impacted by the presence of sewage discharges.	(Garrido-Pérez *et al.*, 2008; O'Mullan *et al.*, 2019) • FIB and organic matter concentrations positively correlate, but the higher organic matter can be due to the close proximity of wastewater discharges

[14] T_{90} is the time required to reduce a microbiological population by 90% (1 log).

A study of sediments from different parts of two estuaries in the UK, collected four times during a one-year period, found there was no single physicochemical factor that could explain the presence and concentration of FIB or pathogenic bacteria and viruses. In water samples, temperature, salinity, turbidity and pH were identified as significant factors affecting bacterial abundance, but these were not found to be statistically important for sediment bacterial abundance. Instead, and depending on the season, factors such as mean grain size, % clay, % porosity and concentration of various elements (e.g. zinc, potassium) were found to be important. However, none of these was singularly responsible for more than 25% of the variance in bacterial abundance in sediment.	(Hassard *et al.*, 2017) • No one factor was significantly associated with bacterial abundance • Sediment size and porosity, and the concentration of specific elements, were important
A model developed from sediments sampled from two estuaries in Scotland found that a range of factors affected *E. coli* abundance. The salinity of the interstitial pore water was the most important single variable, with the abundance of *E. coli* decreasing as salinity increased. However, this effect was likely to be the result of higher salt conditions reducing the concentration of culturable *E. coli* (VBNC *E. coli* may have been present) and dilution by seawater containing a lower concentration of *E. coli* compared to the estuary's freshwater. Despite the strong salinity effect, the model was further improved when season, organic content, bulk density and maximum air temperature were included. *E. coli* concentrations increased with increasing organic content, during summer and autumn, with decreasing bulk density (total mass of sediment) and decreasing maximum air temperature.	(Wyness *et al.*, 2019a) • A range of factors affected *E. coli* abundance • Interstitial pore water salinity, organic content and seasonal effects were important
The presence of organic matter was significantly correlated with the concentration of faecal coliforms and faecal streptococci in sediment samples taken at different distances from a wastewater overflow outlet in the tidal regions of the Georges River (Sydney, Australia). However, concentrations of these bacteria were higher in sediments after rainfall events, when sewage overflows were more likely.	(Ferguson *et al.*, 1996) • Faecal-associated bacteria positively correlated with organic matter but this was influenced by sewage overflows
Laboratory studies	**Conclusion and references**
The concentration of inoculated *E. coli* decreased in microcosms made from intact sediment columns collected from three sites around Adelaide (Australia), which had been standardised using the same estuarine water. *E. coli* survival was affected by the combination of temperature, grain size and the concentration of organic carbon. In general, the *E. coli* decay rate in sediment was faster when cores were held at higher temperatures, although the results were not consistent. For example, the T_{90} value for the 98% sand substrate taken from a beach was 3.1 days at both 10 and 20 °C, but reduced to 0.9 days at 30 °C. For the finer sediment (10% clay, 4% silt) taken from a port, the T_{90} values were 7.1 days at 10 °C and 2.0 days at 20 °C. Overall, *E. coli* inactivation rates were fastest in the beach sand (largest particle sizes, lowest concentration of organic carbon).	(Craig *et al.*, 2004) • *E. coli* survival is improved at low temperatures, in finer sediments and in the presence of higher concentrations of organic carbon.

Bed sediment cores from the Yarra River estuary (Australia) were maintained for up to 27 days in conditions mimicking the sample site (submerged in aerated water from the same site, kept at 10–13 °C) and examined at selected time points for the concentrations of *E. coli* and *Campylobacter* spp. The *E. coli* concentrations fluctuated over time in layers up to 90 mm deep, but the overall result was a very slow decrease (the fastest mean inactivation rate was 0.04 log MPN/day). The inactivation rates were approximately ten times slower than that calculated from separate trials with water samples. *E. coli* were not detected at any time point in the bottom sediment layer (90–100 mm). The die-off rates for *Campylobacter* spp. could not be calculated but these bacteria were detected in the top 20 mm of bed sediment after 27 days, demonstrating their ability to survive for approximately one month in the absence of other environmental stressors such as irradiation. During the experiment, oxygen depletion was measured in the upper 5–7 cm of the sediment core and anoxic conditions developed at deeper layers, however both *E. coli* and *Campylobacter* spp. were detected below 7 cm so oxygen depletion was not a strong driver of survival in this study (noting *Campylobacter* spp. are microaerophilic).	(Schang *et al.*, 2016) • *E. coli* inactivation can be very slow, and much slower in the sediment compared to in the water • *E. coli* and *Campylobacter* spp. can survive for at least one month in the top 20 mm of bed sediment in controlled conditions • *E. coli* and *Campylobacter* spp. can survive the development of anoxic conditions in sediments
Sediments collected from the bank of the Yarra River estuary (Australia) were stored outdoors in transparent bags under a transparent roof to mimic temperature and irradiation field conditions. The concentration of *E. coli* decreased in most of the samples during the 24-day study and remained at a similar level in others. The inactivation rates were affected by the level of moisture in the sample (faster inactivation in lower moisture samples) and, possibly, by the presence of strains adapted to longer desiccation periods (samples taken further from the waterline during low tide). *Campylobacter* spp. were also monitored in these sediments and were detected 27 days after initial sediment storage, indicating survival for approximately one month.	(Schang *et al.*, 2016) • Without overlying water, the numbers of sediment *E. coli* decrease but the rate slows with residual moisture and/or the presence of desiccation-tolerant *E. coli* • *Campylobacter* spp. can survive for at least one month in sediments exposed to outdoor conditions without overlying water
By modifying the temperature, pH, water-extractable Total Dissolved Solids (TDS) and the presence/absence of coexisting microbes in sieved sediment samples from three freshwater lakes in the Yamagata Prefecture (Japan), it was found that some environmental factors can strongly affect *E. coli* survival, but survival is ultimately driven by the combination of factors. Overall, *E. coli* growth was observed at warmer temperatures (20 or 30 °C), at pH 6 and when microbiological predators and competitors were removed through autoclaving. Increasing the acidity to pH 4 was most detrimental to survival (decreasing the acidity to pH 8, which may occur in eutrophic lakes, did not strongly affect survival). Both independently and interactively, pH and the presence of co-existing microorganisms strongly affected *E. coli* survival. The work also highlighted that *E. coli* were affected by the interaction between co-existing microorganisms and either TDS or temperature.	(Yoneda *et al.*, 2024) • *E. coli* survival and growth were affected by pH, the presence of co-existing microorganisms, the concentration of total dissolved solids and temperature

To investigate the role of moisture, sediment from the Yarra River estuary (Australia) was sterilised, inoculated with *Salmonella* Typhimurium and *E. coli*, placed in outdoor microcosms with transparent covers, and subjected to periodic or continuous water inundation, or no inundation. Both test microorganisms survived for 21 days under all conditions, including when temperatures exceeded 40 °C, but their concentrations decreased over time. The inactivation rates were faster under dry or extended desiccation conditions. The inactivation rates for *S.* Typhimurium were slightly higher than for *E. coli*, although overall they showed similar patterns, e.g., 0.14 MPN/day for *E. coli* and 0.21 MPN/day for *S.* Typhimurium when periodically wetted (the continuously wet microcosms were affected by algal growth).	(Siddiqee *et al.*, 2018) • *Salmonella* spp. and *E. coli* concentrations decreased at similar rates and both species survived for 21 days in sterile sediments exposed to outdoor conditions without overlying water, or with water periodically covering the sediment
The salinity of the water, the concentration of suspended sediments and the origin of faecal contamination were all shown to be important to FIB survival in a microcosm study using samples from aquatic environments in North Wales. Mixtures of water and sediment from a brackish estuary or a freshwater river were each standardised to three concentrations of suspended particulate matter, and these microcosms incubated at 10 °C in the dark for five days. In microcosms not receiving further treatments, the average FIB concentration did not exceed 254 CFU coliforms/mL, 133 CFU *E. coli*/mL and 2 CFU enterococci/mL, and any increase or decrease in these bacterial concentrations over time was not reported. In other microcosms, ovine faeces or sewage were added before incubation to investigate the effect of organic matter source and particulate concentration on FIB survival. In the presence of these faecal contaminants, the concentrations of enterococci and coliforms decreased over time. The concentration of *E. coli* in sewage-inoculated microcosms also decreased but increased in microcosms receiving the ovine faeces inoculum. The suspended particulate matter concentration had a stronger effect on FIB survival in the estuarine microcosms.	(Perkins *et al.*, 2016) • Both the concentration of suspended particulate matter and the source of faecal contamination affect FIB survival in sediments

All the studies in **Table 1** have focussed on faecal-associated bacteria, with only one study also considering *Vibrio* spp. (Perkins *et al.*, 2014). Opportunistic pathogens naturally found in aquatic sediments are well adapted to these conditions although their populations will be higher in more favourable conditions, e.g., a study of three marine locations in Germany, Denmark and Finland found that *V. vulnificus* were almost always found in water samples of medium salinity (8.1–11.2 ppt) (Fernández-Juárez *et al.*, 2024). Another study has demonstrated that *Vibrio* spp. in the sediment were unaffected by an extreme weather event (Shaw *et al.*, 2014). Researchers found that the concentrations of *V. parahaemolyticus* and *V. vulnificus* in sediment samples collected before a hurricane event in the Chesapeake Bay estuary (Maryland, USA) were not significantly different to concentrations in samples collected after the hurricane. The sediments were dominated by silt (66.6%) and clay (13.0%) and were, at most, located 2.1 m below the water surface, so were likely to have been disturbed by the hurricane.

There are fewer studies of the factors that affect the infectivity of viruses in aquatic sediments. From laboratory studies with poliovirus and echovirus either maintained in conditions mimicking that of the field or exposed to a range of challenges, it was concluded that viral adsorption to the sediment was the most important factor that prolonged infectivity (LaBelle and Gerba, 1982; LaBelle and Gerba, 1980). The protective effect of sediment was observed in microcosm studies, where infectious enteroviruses were detected for longer in microcosms containing sediment compared to those without (Chung and Sobsey, 1993; Smith *et al.*, 1978). In another study, maintaining sediment microcosms in the dark extended the survival of adenovirus and murine norovirus (a surrogate for human norovirus) (Elmahdy *et al.*, 2018). Water salinity has not been shown to strongly affect viral survival, but UV is virucidal (Kevill *et al.*, 2025).

Despite their importance as waterborne pathogens, no studies were located investigating the factors that affect the infectivity of protozoan parasites in aquatic sediments. A study using microcosms constructed from wastewater and sediment collected from an artificial wastewater treatment wetland has found *G. muris* were inactivated faster in sediment compared to overlying water (Karim *et al.*, 2004). *Cryptosporidium* inactivation rates generated from studies in water and soils have been adopted for aquatic sediment models (Drummond *et al.*, 2018). The (oo)cysts of protozoan parasites are environmentally stable in water and soils, so are likely to survive well in aquatic sediments depending on the temperature, salinity, level of solar irradiation and presence of predators (Brookes *et al.*, 2004). While *Cryptosporidium* oocytes are sensitive to water salinity (Johnson *et al.*, 1997), studies have shown they can remain infectious for months in seawater (Fayer *et al.*, 1998; Tamburrini and Pozio, 1999). Experiments with *Giardia muris* cysts showed these were sensitive to both UV and the presence of salt in water, and were inactivated faster than *Cryptosporidium* oocysts (Johnson *et al.*, 1997). After exposure to marine water, the internal contents of *Giardia* cysts shrivelled up due to water moving out of the cyst.

FIB may be present in aquatic systems in a viable but non-culturable state (VBNC). This means that the bacterial cells are metabolically active, have the potential to become culturable when they encounter more favourable conditions, but will not necessarily be detected through standard laboratory culture methods used for their detection (Zhang *et al.*, 2021). Cells may enter a VBNC state under suboptimal conditions such as starvation or environmental stressors (pH, salinity, temperature). Quantifying VBNC in sediment is challenging due to interference from biofilm matrices and counts being affected by the presence of daughter cells produced by existing cells during resuscitation, although there are methods available that could be applied to sediment samples (Hassard *et al.*, 2017). However, ingestion of pathogenic bacteria in a VBNC state may not lead to infection and illness, so the public health implications of VBNC bacteria in sediments are not clear. It has also been noted that sediments receiving regular or continuous nutrient inputs are unlikely to stimulate bacteria to move to a VBNC state (Davies *et al.*, 1995).

4.3 PATHOGENIC SPECIES FOUND IN SEDIMENTS

Information to show that the pathogenic microorganisms discussed in Section 3.3 can be found in sediments relies on researchers specifically testing for these pathogens or their genetic material. The concentration of these microorganisms may not be determined, or these values may be affected by the extraction efficiency. For example, protozoa recovery from sediments can be low (<10%) (Devane *et al.*, 2014). **Table 2** summarises data collated during this review. There are far fewer studies of sediments that have included tests for pathogenic microorganisms compared to tests for FIB. From the information retrieved, all the pathogenic species of interest for this review have been detected at least once except for *Yersinia* spp.

Table 2. The presence of pathogenic microorganisms in aquatic sediments

Giardia spp.	Detected in sediment from the Avon River (Christchurch, NZ) during a period of raw municipal waste discharge, at concentrations up to 2,254 cysts/g (Devane *et al.*, 2019). Detected in resuspended sediments from Canterbury rivers (NZ) at concentrations up to 6.5 oocysts/g (Pattis *et al.*, 2023). Detected in estuarine sediments from the Cook Inlet (Alaska) at concentrations up to 8 cysts per 10 g (Norman *et al.*, 2013). An unpublished report indicates cysts were present in freshwater sediments from the Apies River (South Africa) (Mphephu and Momba, unpublished).
Cryptosporidium spp.	Detected in sediment from the Avon River (Christchurch, NZ) during a period of raw municipal waste discharge at concentrations up to 113 oocysts/g (Devane *et al.*, 2019). Detected in resuspended sediments from Canterbury rivers (NZ) at concentrations up to 2.1 oocysts/g (Pattis *et al.*, 2023). Detected in freshwater sediments from the Apies River (South Africa) (Mphephu *et al.*, 2021). Not detected in freshwater, estuarine and marine sediments from the Cook Inlet (Alaska) (Norman *et al.*, 2013).
Campylobacter spp.	Detected in sediments from the Avon River (Christchurch, NZ) during a period of raw municipal waste discharge at concentrations up to 11.1 MPN/g (Devane *et al.*, 2019). Detected in resuspended sediments from Canterbury rivers (NZ) at concentrations exceeding 110 MPN/100 mL (Pattis *et al.*, 2023). Detected in estuarine bank sediments from Melbourne (Australia), highest concentration 90 MPN/g dw (Schang *et al.*, 2016). Not detected in estuarine sediments from the Conwy Estuary (Wales) nor in sediments collected from two UK estuaries (Hassard *et al.*, 2017; Perkins *et al.*, 2014).
Salmonella spp.	Detected in sediments from a tidal river in Sydney (Australia), particularly during rainfall and sewage overflow events (Ferguson *et al.*, 1996). Presumptive *Salmonella* spp. detected in estuarine sediments from the Conwy Estuary (Wales), highest concentration 2.5 x 10^4 CFU/100 g ww (Perkins *et al.*, 2014). Not detected in freshwater, estuarine and marine sediments from the Cook Inlet (Alaska), estuarine sediments from the Tapi Estuary (India), nor in sediments collected from two UK estuaries (Borade *et al.*, 2014; Hassard *et al.*, 2017; Norman *et al.*, 2013).
Pathogenic *E. coli*	The genes associated with STEC virulence (*stx1*, *stx2* and *eae*) and STEC serotype (O157 *rfbE* and O26 *wzy*) were detected in sediment from rivers in Canterbury (NZ) (Davis *et al.*, 2021). The *stx2* gene was detected in sediments from an aquatic system in Georgia (USA) (Bradshaw *et al.*, 2016). The presence of these genes does not confirm the presence of viable STEC. At least one *stx* gene and or the *eae* gene were detected in sediment samples collected from three French coastal shellfish growing areas, and one sample contained viable STEC (no viable EPEC isolates were recovered from sediments) (Balière *et al.*, 2015).
Shigella spp.	Detected in freshwater sediments from faecal-contaminated sites along the Apies River (South Africa) (Abia *et al.*, 2016). Not detected in sediments collected from two UK estuaries (Hassard *et al.*, 2017).
Yersinia spp.	No relevant data located.

Human norovirus	Human norovirus GII RNA detected in one estuarine sediment sample from the Takagi River (Japan) at a concentration too low for quantification (Miura *et al.*, 2011). RNA from norovirus GI and GII were not detected in freshwater, estuarine and marine sediments from the Cook Inlet (Alaska), nor in sediments collected from two UK estuaries (Hassard *et al.*, 2017; Norman *et al.*, 2013).
Hepatitis A virus	HAV RNA detected in all but one estuarine sediment sample collected near a wastewater outfall in Auckland (NZ) during a one-year study (Green and Lewis, 1999). Also detected in sediments from La Baule Bay (France) (Le Guyader *et al.*, 1994). HAV RNA not detected in sediments collected from two UK estuaries, nor in sediments from a freshwater lagoon in southern Brazil and a river draining this lagoon (water samples were positive) (Elmahdy *et al.*, 2016; Hassard *et al.*, 2017).
Rotavirus	Infectious rotaviruses detected in loose surface sediments and compact sediments from Galveston Bay (USA) at a maximum concentration of 3.8 PFU/g (Rao *et al.*, 1986b; Rao *et al.*, 1984). Also detected in sediment from the Ria de Aveiro coastal lagoon (Portugal) at one site, at a concentration of 421 fluorescing particles per 10 kg sediment (Alcântara and Almeida, 1995). Rotavirus RNA detected in one estuarine sediment sample collected near a wastewater outfall in Auckland (NZ) during a one-year study (Green and Lewis, 1999). Also detected in sediment from a freshwater lagoon in southern Brazil and a river draining this lagoon (Elmahdy *et al.*, 2016).
Human adenovirus	Human adenovirus DNA was detected in sediments from springs, dams and streams in rural areas of Brazil (Staggemeier *et al.*, 2015), in sediments from Saginaw Bay in Michigan, USA (Oun *et al.*, 2017) and in sediments from the River Ruhr in Germany (Mackowiak *et al.*, 2018). DNA and infectious particles detected in sediments from a freshwater lagoon in southern Brazil and a river draining this lagoon (Elmahdy *et al.*, 2016).
Vibrio spp.	Detected in all estuarine sediment samples from the Conwy Estuary (Wales), at concentrations in the range 6.7×10^3–1.2×10^6 CFU/100 g ww (Perkins *et al.*, 2014). Speciation showed the presence of *V. splendidus* and *V. artabrorum*. Presumptive *Vibrio* spp. and *V. parahaemolyticus* detected in estuarine sediments from the Tapi Estuary (Gujarat, India) at maximum concentrations of 18,000 and 8,000 CFU/g respectively (Borade *et al.*, 2014). Detected in freshwater, estuarine and marine sediments from the Cook Inlet (Alaska), in which the identified species included *V. alginolyticus* and *V. fluvialis* (Norman *et al.*, 2013). Presumptive *Vibrio* spp. were detected in sediments collected from two UK estuaries at concentrations at times exceeding 7-log CFU/100 g (Hassard *et al.*, 2017).

4.4 CORRELATIONS BETWEEN FAECAL INDICATORS AND FAECAL PATHOGENS

Microcosm studies have been used to measure the survival of microorganisms in sediment samples over time. Two studies were located that compared the survival of FIB and pathogenic bacteria in the absence of added contaminants (e.g. added wastewater or animal waste).[15] Both were microcosm studies and together showed that the concentration of *E. coli* decreased at a similar rate to pathogenic bacteria (*P. aeruginosa*, *Klebsiella pneumoniae*, *Salmonella* spp. and *V. parahaemolyticus*).

The first microcosm study used fine sediments (≥76% clay and silt) collected from three freshwater lakes in the USA (Burton *et al.*, 1987). During the experiment these were kept flooded with a continuous flow of purified and aged water (salts and pH adjusted to replicate source water) at ambient temperatures (16–21 °C). *P. aeruginosa*, *E. coli*, *Klebsiella pneumoniae* and *S*. Newport were inoculated onto the sediment surface and their concentrations monitored for 14 days. The concentrations of all bacterial species decreased over time. The die off rates between the bacterial species were not statistically significant, but *P. aeruginosa* and *K. pneumoniae* consistently survived better than *E. coli* and *S*. Newport, and *E. coli* survived as well or better than *S*. Newport. When compared with another microcosm containing river sediments comprised of 98% sand, *E. coli* and *S*. Newport survived for longer in the lake sediments with the higher clay content.

The second microcosm study used intact water/sediment columns taken from a freshwater lagoon in India and inoculated the water fraction with *E. coli*, *S.* Paratyphi and *V. parahaemolyticus* (Chandran *et al.*, 2011). The microcosms were kept for 27 days at 25 °C. Again, the concentrations of all species decreased over time in the sediment fraction but there was little difference between the survival of each bacterial species; the calculated T_{90} inactivation rates were 6.1, 5.3 and 5.3 days for *E. coli*, *S.* Paratyphi and *V. parahaemolyticus*, respectively. This means it took 5–6 days for the concentration to reduce by 90% (1 log CFU/g). The particle size fractions making up the columns were not analysed, but grab samples taken from the same locations (see below) indicated that the surfaces of the sediment cores were dominated by sand.

As part of the same study (Chandran *et al.*, 2011), grab sampling at the same lagoon was used to collect three sediment types which differed in their particle size distribution and organic content. Within each sediment type, the concentration of all three bacterial species reduced at comparable rates. For example, in the small particle size/high organic content sediment the T_{90} values were 6.9, 8.4 and 7.5 day for *E. coli*, *S.* Paratyphi and *V. parahaemolyticus*, respectively (i.e., 7–8 days for the concentration to reduce by 90%). However, the sediment characteristics were not very different between sites, all being 75–90% sand (remainder mud) and 1.8–5.0% organic content.

Another study compared the survival of F+ coliphages, *B. fragilis* (*Bf*) phages, HAV, poliovirus and rotavirus in seawater-sediment mixtures collected from the Beaufort Inlet (North Carolina, USA) (Chung and Sobsey, 1993). The concentrations of these viruses were measured after “thorough mixing”, so both the water and sediment fractions were tested together. However, on three occasions the supernatant was collected before mixing and a comparison with seawater-only microcosms showed that viruses were increasingly associated with the sediment fraction. Overall, the viruses survived better when stored at 5 °C compared to 25 °C. However, the effect of temperature meant that there were few consistent correlations between phage and enteric virus survival. For example, the inactivation rates of both phages were not significantly different to that of poliovirus when stored at 25 °C, but at 5 °C storage F+ phage inactivation aligned best with rotavirus.

Field studies have also been conducted to find out if there are correlations between FIB, faecal markers and pathogenic microorganisms. In these studies, sediment samples were

[15] For example, microcosm studies have used sediments inoculated with poultry litter (Nayak *et al.*, 2015), or human and animal faeces (Kim and Wuertz, 2015).

typically tested for the target microorganisms or markers, then statistical methods and models used to determine if there were significant correlations. In general, these studies did not provide consistent evidence that FIB or faecal markers could be used to indicate the presence of bacterial, viral or protozoan pathogens, except near known point sources of human faecal pollution. Such results are not surprising, since faecal indicators are consistently present where there is faecal contamination, but the presence of pathogenic microorganisms depends on disease incidence or carriage rates in the faecal source populations (Weaver and Sinton, 2009). Examples follow.

Surface sediment samples were collected during the period 2011–2013 from three sites along the Avon River (Christchurch, NZ) during and after discharge of untreated human sewage resulting from the earthquakes (Devane *et al.*, 2019; Devane *et al.*, 2014). Samples were analysed for *E. coli*, *C. perfringens*, F-Specific RNA bacteriophage, *Campylobacter* spp., *Giardia* spp. and *Cryptosporidium* spp. While some correlations between *E. coli* and faecal source markers in water were reported, in the sediment there were few significant relationships between *E. coli* and the other microorganisms or the faecal source markers. There was a moderate correlation between *E. coli* and *Campylobacter* spp. in the sediment, and a weak correlation between *E. coli* and F-RNA phage. Accumulation of *C. perfringens* in the sediments was reported, suggesting this species is an unreliable indicator for fresh faecal contamination. Fluorescent whitening agents and faecal steroids were highlighted as potentially useful markers of historical human sewage contamination, but these did not correlate well with microbial indicators or pathogens in the sediment fraction so were not good indicators for human health risks from sediments. The study was likely affected by post-earthquake activities such as bankside construction, river dredging and undocumented sewage discharges after the major sewage discharge events had ceased.

A field study in the USA, intent on predicting the presence of pathogens based on FIB and MST markers, used test results from waters and sediments from 15 sites located beside a treated wastewater outfall, or in an area characterised by either agriculture or forestry (Bradshaw *et al.*, 2016). These samples were tested for FIB (*E. coli*, enterococci), *Campylobacter* spp., *Listeria* spp., *Salmonella* spp., the STEC virulence gene *stx2* and selected MST markers. The authors found inconsistent relationships between pathogens and FIB/MST markers and included other environmental variables into their models to try to identify useful correlations. In sediment, the presence of *stx2* was best predicted by including culturable FIB concentration, culturable *E. coli* concentration, water temperature and total suspended solids. The best model for predicting *Salmonella* spp. in sediments utilised water temperature, qPCR enterococci concentration and qPCR *E. coli* concentration.

A study in the Neuse River Estuary (North Carolina, USA) found a significant, positive correlation between the concentration of *E. coli* and *Vibrio* spp. in water samples, but only during periods of sediment resuspension (Fries *et al.*, 2008). In sediments, the concentrations of these two bacterial targets remained significantly correlated throughout the one-year study. However, *Vibrio* spp. are natural inhabitants of this environment, and the estuary was known for having declining water quality. Thus, the continued presence of both *E. coli* and *Vibrio* spp. is not unexpected in this particular aquatic environment.

The concentration of viruses and faecal coliforms were positively correlated in surface (upper 2 cm) sediment samples obtained from seven coastal canals and four oyster beds in the Galveston Bay area (Texas, USA), with a bias towards polluted sites (LaBelle *et al.*, 1980). This relationship was observed despite the method for measuring viral concentrations having a recovery efficiency of 50% and being restricted to viruses able to infect buffalo green monkey kidney cells (plaque assay). Subsequent viral culture confirmed the presence of enteroviruses (coxsackievirus, echovirus, poliovirus), which are associated with human faecal contamination. There was no significant correlation between the concentration of faecal coliforms in the water with viruses in the sediment, showing that water quality measures may not indicate sediment-associated health risks. The researchers also measured the concentrations of *Clostridium* spp. and *C. perfringens* but found no relationship between these and the concentrations of viruses. There appeared to be a positive correlation between the sediment concentration of clostridia and that of faecal coliforms, but the statistical significance was not reported. As reported elsewhere, *C. perfringens* may be a poor indicator for fresh faecal contamination (Devane *et al.*, 2014).

A study of sediments from freshwater, estuarine and marine sites in the Cook Inlet (Alaska) did not find any correlations between the presence or concentration of faecal coliforms or enterococci and that of *Salmonella* spp., *Cryptosporidium* spp., *Giardia* spp. or norovirus (Norman *et al.*, 2013).

5. MICROORGANISM DISTRIBUTION BETWEEN SEDIMENTS AND WATER

Summary

Studies of paired water and sediment samples almost consistently find that the concentration of FIB is higher in sediments compared to overlying water. There are fewer studies of faecal-associated pathogenic bacteria, viruses and protozoan parasites and the results from these do not show the same consistent trend, although studies have found higher concentrations of infectious viruses in the surface layers of sediments than the overlying water. *Vibrio* spp., as natural inhabitants of aquatic environments, also tend to be more abundant in sediments compared to overlying water. The presence and concentration of microorganisms measured in the water differ to that in sediment. This means that water quality measures may not indicate sediment-associated health risks.

When considered together, studies of water quality changes during natural events and artificial interventions that increase water turbulence show that sediment disturbance and resuspension cause FIB and pathogenic microorganism concentrations to increase in the water. Hydrodynamic models support these findings. Resuspended pathogenic microorganisms become health hazards for people in the water.

To inform actions that could improve bathing water quality in North West England, researchers developed a model to predict the spatial and temporal distributions of *E. coli* in riverine and coastal waters (Huang *et al.*, 2017). Of relevance to this current review, they found that the accuracy of the model's predictions was greater when they incorporated factors that described suspended sediment *E. coli* concentrations and the adsorption/desorption of *E. coli* from these sediments. These sediments were being washed into the estuarine and shallow coastal regions with river inflows. The model results highlighted the relationship between resuspension and/or transport of sediment-associated bacteria and downstream water quality. The researchers concluded that higher *E. coli* concentrations in water near bathing sites was linked to sediment resuspension and transportation by tidal currents in the offshore direction.

Studies of sediment resuspension tend to focus on natural events that increase water turbulence, such as rainfall events or storms, rather than sediment disturbance caused by people during swimming. However, all are informative for this review. The following sections collate information on the concentrations of microorganisms in water and sediments and interactions between these two matrices that cause resuspension of sediments and associated microbes. Chemical changes in the water may also cause microorganisms to detach from sediments and move into the water fraction, and a reduction in water salinity has been suggested as one trigger for this phenomenon (Hassard *et al.*, 2016; Weaver and Sinton, 2009). However, this is likely to be far less important for shifting microorganism from aquatic sediments into the water compared to physical resuspension (Weaver and Sinton, 2009).

5.1 MICROBIAL CONCENTRATIONS IN WATER AND SEDIMENTS

The information in this section shows that the presence and concentration of microorganisms measured in the water differ to that in sediment. This means that water quality measures may not indicate sediment-associated health risks.

The solid phase of sediment grains means that microorganisms will not be evenly distributed through this substrate. The microbial community in replicate sediment samples taken within 1 m of each other can be different (Akinwole *et al.*, 2021). In comparison, the overlying water tends to be more homogenous unless calm conditions induce stratification. The heterogenous nature of sediments can confound correlations between FIB and pathogens in sediment and water.

Faecal-associated microorganisms

There are numerous field surveys involving the collection of paired water and sediment samples. In most studies, the concentration of faecal-associated microorganisms (FIB and pathogens) is several times higher in sediments compared to water. **Error! Reference source not found.** highlights examples of studies focusing on faecal-associated microorganisms. When considering these results, it is important to note how these have been affected by methodology. Some important considerations are:

- The concentrations in sediment are usually expressed relative to mass (gram), which can be wet weight (ww) or dry weight (dw), although sometimes the methods result in sediment concentrations being expressed on a volumetric basis. Concentrations in water are usually expressed relative to volume (mL).
- Sediment samples may have been collected as grab samples or cores and may or may not have been combined to make composite samples. Similarly, water samples may have been collected using pumps or bottles and may be composited.
- Some studies test measured portions of the sediments directly while others test sediment resuspended into a liquid to mimic the mobilised sediment fraction.
- The summary results might be from one sampling occasion or compiled from multiple sampling occasions during a period of months or years.
- The efficiency of microorganism recovery and detection may differ between sediment and water, and between sediment types.
- The detection methods may target viable microorganisms (culturable, e.g. CFU or PFU) or may use PCR-based methods that do not distinguish live/dead microorganisms.

However, the intent of including these examples is to emphasise that sediments tend to contain higher numbers of faecal-associated microorganisms compared to overlying water, although this is not consistent across all studies.

Table 3. The prevalence and/or concentrations of faecal-associated microorganisms in paired sediment and water samples collected during field studies

Study summary	Conclusion and references
A survey of the lower Hudson River Estuary (New York, USA) found the concentrations of enterococci and *E. coli* were, in general, at least one order of magnitude higher in surface sediments (MPN/100 g DW) compared to the overlying water (MPN/100 mL water).	(O'Mullan *et al.*, 2019) • FIB present at higher concentrations in sediments compared to overlying water
A study in Canada found that, even in a 'pristine' stream flowing mainly through mountains and forests, the concentration of *E. coli* in the sediment was 433 times higher than the water. In a stream affected by agriculture, the sediment concentration of *E. coli* was only seven times higher than the water. However, this discrepancy is partly explained by the water samples collected from sites along the pristine stream containing much lower concentrations of *E. coli* (<100 CFU/100 mL) compared to water collected along the agricultural stream (>100 CFU/100 mL).	(Pandey *et al.*, 2018) • FIB present at higher concentrations in sediments compared to overlying water
From 21 samples taken along four transects across the Conwy Estuary (Wales), the overall average concentration of *E. coli* in the sediment (5.9 x 10^3 CFU/100 g ww) was 281 times higher than in the water, and the concentration of total coliforms (1.3 x 10^5 CFU/100 g ww) was 433 times higher in the sediment compared to the water.	(Perkins *et al.*, 2014) • FIB present at higher concentrations in sediments compared to overlying water
The concentrations of faecal coliforms, faecal streptococci and faecal markers (somatic coliphages and F-specific coliphages) were all higher in sediment samples from a recreational area of the Ria de Aveiro coastal lagoon (Portugal) compared to paired water samples. For example, at one point in time the concentration of faecal coliforms was 240 MPN/100 mL in the water and 1,200 MPN/100 g in the sediment. At a site near industrial activities, sediment concentrations of these faecal indicators/markers were not consistently higher than those measured in the water samples.	(Alcântara and Almeida, 1995) • FIB and faecal markers present at higher concentrations in sediments compared to overlying water, except near industrial sites
In a study of freshwater, estuarine and marine sites in the Cook Inlet (Alaska), the concentrations of faecal coliforms were significantly higher in sediment than water. The concentrations of enterococci were also higher in sediment compared to water, but the difference was not significant.	(Norman *et al.*, 2013) • Faecal coliforms, but not enterococci, were present at higher concentrations in sediments compared to overlying water
A study of ten faecal-contaminated sites in the Apies River and tributaries (Gauteng Province, South Africa), examined 1116 water and 1116 sediment samples collected during the wet and dry season. There was little difference between water and sediment samples, in both dry and wet seasons: – *E. coli* (range, MPN/100 mL): water 5.1×10^0–3.4×10^3, sediment 5.1×10^0–6.3×10^3 during dry season; water 5.8×10^1–8.8×10^4, sediment 2.4×10^3–1.3×10^5 during wet season.	(Abia *et al.*, 2016) • Prevalence or concentration of *E. coli* and pathogenic bacteria similar between water and sediments in faecal-contaminated sites

– *V. cholerae* (prevalence, n=10 sites): water 60%, sediment 60% during dry season; water 100%, sediment 100% during wet season. – *Salmonella* spp. (prevalence, n=10 sites): water 60%, sediment 60% during dry season; water 100%, sediment 100% during wet season. – *Shigella* spp. (prevalence, n=10 sites): water 30%, sediment 30% during dry season; water 60%, sediment 50% during wet season. The same sites were almost always positive and if a target microbe was found in sediment it was also found in the water.	
A one-year study of sample sites along two UK estuaries tested paired sediment and water samples for *E. coli* and intestinal enterococci. Graphical representations of their data show that these bacteria were more likely to be detected in water samples, but at times the concentrations in sediment samples were higher than in water (comparing concentration per 100 mL water with concentration per 100 g sediment). While the concentrations varied between sites and over time, the authors commented that, when sediments were positive for FIB, these were typically at concentrations 4 $\log_{10}$ higher than the overlying water column. Water and sediment samples were also tested for selected bacterial and viral pathogens. Using qPCR-based methods, *Salmonella* spp., *C. jejuni* and norovirus GII were each detected in some of the water samples, with the results indicating their concentrations were low (10–111 GC/100 mL *Salmonella* spp., <10 GC/100 mL for *C. jejuni* or norovirus GII). *Shigella* spp., HAV, HEV and norovirus GI were not detected in any water sample. In comparison, none of these pathogens were detected in sediment samples.	(Hassard *et al.*, 2017) • FIB more likely to be detected in water samples but when present in sediments, their concentrations were higher than the overlying water • Pathogenic bacteria and viruses present in water but not sediments
In the South Fork Broad River watershed (Georgia, USA), 15 sites were targeted for sampling. These were located either beside a treated wastewater outfall, or in an area characterised by agriculture or by forestry. From a total of 120 sediment and 120 water samples, it was found that culturable *E. coli* concentrations were several log higher in sediment samples (per 100 g) compared to water samples (per 100 mL), at all sites. The concentrations of culturable enterococci were similar between water and sediment samples. The relative prevalence values for pathogenic bacteria in water and sediment samples did not show a consistent pattern: – *Campylobacter*: 8% water, 33% sediment – *Listeria*: 68% water, 70% sediment – *Salmonella* (*invA*): 51% water, 7% sediment – STEC (*stx2*): 43% water, 61% sediment.	(Bradshaw *et al.*, 2016) • *E. coli*, but not enterococci, were present at higher concentrations in sediments compared to overlying water • Pathogenic bacteria were detected in water and sediments but the relative prevalence did not show a consistent trend
Using a molecular method that detects, quantifies and identifies bacterial RNA (which indicates the presence of live bacteria), *Enterococcus* and *E. coli* targets were more prevalent in freshwater sediment samples (86% and 81%, respectively) than in suspended sediment separated from water samples (51% and 39%, respectively). MST markers indicated faecal contamination from	(VanMensel *et al.*, 2023) • Concentrations of *Enterococcus* and *E. coli* RNA higher in bed sediments compared to

geese, dogs and gulls. RNA markers for a range of pathogenic bacteria were not detected. Further analyses showed that low energy sites with fine sediment had higher RNA concentrations.	suspended sediments separated from water • RNA from pathogenic bacteria not detected
The concentration of viruses was higher in the top 2 cm of sediments compared to overlying water at seven coastal canals and four oyster beds in the Galveston Bay area (Texas, USA). The method for measuring viral concentrations ensured that only viable viruses were detected, although only viruses able to grow in buffalo green monkey kidney cells could be detected. Some viruses were able to be identified and all were enteroviruses. Enteroviruses are unable to multiply outside the host, so the researchers concluded that the sediment offered protection from viral inactivation.	(LaBelle *et al.*, 1980) • Infectious enteroviruses present at higher concentrations in sediments compared to overlying water
At two sites receiving treated wastewater (salinity 2–20 ppt) in Galveston Bay (Texas, USA), 15 samples of the 'fluffy' (flocculant) uppermost sediment (filtered from water), 35 compact sediment samples and 35 water samples were tested for infectious faecal-associated viruses. The highest viral abundance was found in the 'fluffy' sediments at the sediment/water interface: – Enteroviruses 3–12 PFU/250 L water, 39–398 PFU/kg fluffy sediment, 7–10 PFU/kg compact sediment (respective prevalence 14%, 47% and 6%) – Rotaviruses 119–1000 PFU/250 L water, 800–3800 PFU/kg fluffy sediment, 1200 PFU/kg compact sediment (respective prevalence 16%, 40% and 12%) Coxsackievirus, Poliovirus and Echovirus were also detected in all three matrices.	(Rao *et al.*, 1986b; Rao *et al.*, 1984) • Infectious rotaviruses and enteroviruses present at higher concentrations in the uppermost sediment layer compared to deeper sediments and overlying water
The concentrations of enteric viruses were higher in sediment samples compared to water samples from the freshwater Peri lagoon and associated Sangradouro River (southern Brazil), collected during wet and dry seasons, although the prevalence was higher in water samples. The viral recovery rates were approximately 10% from water and 46% from sediments. In summer, human adenovirus DNA was detected in 71% of water samples (concentration of infectious particles was in the range $4x10^3$–$1.1x10^4$ PFU/L) and 38% of sediment samples ($1.3x10^3$–$8x10^4$ PFU/kg). In winter, human adenovirus DNA was detected in 63% of water samples and 38% of sediment samples but infectious viruses were not detected in either matrix. The concentration of human adenovirus DNA was higher in sediment samples ($3.1x10^8$–$6.01x10^9$ GC/kg) compared to water samples ($8.9x10^5$–$1.7x10^8$ GC/L). Rotavirus species A was detected using PCR-based methods in the surface water and sediment samples, but more often and at higher concentrations in the water samples compared to the sediment samples. During summer, the prevalence of rotavirus in the water and sediments were 21% and 8%, respectively, and these values were 46% and 13% during winter. HAV RNA was only detected in water samples during summer (46%) and winter (13%), and not in sediments.	(Elmahdy *et al.*, 2016) • Enteric viruses were more likely to be detected in water samples but when present in sediments, their concentrations were higher than the overlying water

There are fewer data available for protozoan parasites. *Cryptosporidium* spp. oocysts and norovirus RNA (GI and GII) were detected in water samples collected from freshwater, estuarine and marine sites in the Cook Inlet (Alaska), but not paired sediment samples (Norman *et al.*, 2013). *Giardia* spp. cysts were more prevalent in water samples compared to paired sediment samples, and present at higher concentrations in the water. In another study, the prevalence of *Cryptosporidium* spp. oocysts in samples of water from the Apies River (South Africa) was 30%, which was similar to paired sediment samples (28%) (Mphephu *et al.*, 2021). Based on the concentration ranges reported, the oocysts concentrations were similar in water (4.6–5.6 $\log_{10}$ oocysts/L) and sediment (4.9–5.8 oocysts/L).[16] However, the authors report that at most sample sites, the concentration was between one- and four-fold higher in sediments compared to water samples (as determined through microscopy). Further analyses confirmed the presence of *C. parvum* and *C. hominis*.

Natural aquatic environment inhabitants

The relative abundance of *Vibrio* spp. in paired water and sediment samples has also been investigated in some studies. These results also suggest that *Vibrio* spp. can be present at higher numbers in sediments:

- From 21 samples taken along four transects across the Conwy Estuary (Wales), *Vibrio* spp. were detected at each sampling site at an average concentration of 7.8 x 10^3 CFU/100 mL water compared to 5.4 x 10^5 CFU/100 g ww sediment (58 times higher) (Perkins *et al.*, 2014).
- Compared to water samples, *Vibrio* spp. were present more often and in higher concentrations (1–3 times more abundant) in sediment samples taken at 10 beaches along the Central Wadden Sea coast and within two connected estuaries (Böer *et al.*, 2013). For example, on a per site basis, the mean concentration of *V. alginolyticus* was in the ranges $1.5\text{x}10^3$–$2.9\text{x}10^5$ CFU/100 g sediment and $6\text{x}10^1$–$8.4\text{x}10^4$ CFU/100 mL water, and the mean concentration of *V. parahaemolyticus* was in the ranges $7.6\text{x}10^2$–$1.6\text{x}10^5$ CFU/100 g sediment and $3.6\text{x}10^1$–$6.3\text{x}10^3$ CFU/100 mL water.
- The prevalence of *Vibrio* spp. was higher in sediment compared to water samples collected from freshwater, estuarine and marine sites in the Cook Inlet (Alaska) (Norman *et al.*, 2013). For the five estuarine sites located upstream of a wastewater outlet, *Vibrio* spp. were detected in 46% of the water samples (n=13) and 67% of the sediment samples (n=12).
- A one-year study of multiple sample sites along two UK estuaries tested paired sediment and water samples for *Vibrio* spp. using PCR and culture methods (Hassard *et al.*, 2017). Culturable presumptive *Vibrio* spp. were detected in almost all sediment samples at concentrations at times exceeding 7-log CFU/100 g. The results for water are not available in a form enabling direct comparison, but the available analyses indicate that *Vibrio* spp. were also detected in at least some of the water samples from both estuaries, at all sampling occasions.
- Using divers, water and sediments were collected from three sites at coastal locations in Denmark, Germany and Finland, and tested for *Vibrio* spp. using molecular methods (Fernández-Juárez *et al.*, 2024). A diverse range of *Vibrio* spp. were detected but overall, the concentration of *Vibrio* spp. genes in the sediment (per g) was 100-fold

[16] The volume of sediments analysed was determined by the volume of fluid displaced by sediment.

higher than in the water (per mL). The marker gene for *V. vulnificus* (*vvhA*) was present in sediments at concentrations 1,000-fold higher than the water.

A study of *Pseudomonas aeruginosa* distribution in a pool of the Mississippi River (Wisconsin and Minnesota, USA) found a higher prevalence in sediments and aufwuchs swabs (surface growth on submerged objects) compared to water (Pellett *et al.*, 1983). However, these bacteria were also detected in almost half of the fish slime/faeces or plant samples taken from this pool, demonstrating that they were well adapted to freshwater environments.

NZ studies

During 2018, samples of sediment and water were taken from two sites in each of three Canterbury rivers, with these sites being located upstream and downstream of intensive dairy farming areas (Davis *et al.*, 2021). The concentration of presumptive *E. coli* was consistently higher in the sediment compared to the water samples, with the units for both sample types expressed as CFU/100 mL.[17] For example, in samples from the Rangitata River taken upstream of the dairying area during autumn, the *E. coli* concentrations were 20 CFU/mL in water and 7,100 CFU/mL in sediment. Downstream of the dairying area these concentrations were 175 CFU/mL and 273,300 CFU/mL for the water and sediment, respectively. Molecular methods were used to determine the presence of genes associated with STEC virulence (*stx1*, *stx2* and *eae*) and STEC serotype (O157 *rfbE* and O26 *wzy*). Overall, these genes were detected more often in sediment compared to paired water samples (and more often downstream of the intensive dairying areas).

A second Canterbury study, of two freshwater tributaries, found that the concentrations of *E. coli* in sediments were similar to those measured in paired water samples (Van Hamelsveld *et al.*, 2019). All results were reported as log (CFU/mL) and it is assumed this reflects the initial volume of diluted sediment (100 g in 100 mL laboratory media).

In Christchurch, paired water and surface sediment samples were collected during the period 2011–2013 from three sites along the Avon River, Christchurch, during and after discharge of untreated human sewage resulting from the earthquakes (Devane *et al.*, 2019; Devane *et al.*, 2014). Samples were analysed for *E. coli*, *C. perfringens*, F-Specific RNA bacteriophage, *Campylobacter* spp., *Giardia* spp. and *Cryptosporidium* spp. The microbial concentrations are reported as CFU/100 mL water and CFU/g dw sediment, so are not easily compared.[18] It can be observed that sediment *E. coli* concentrations in both matrices were higher at two sites below the sewage discharge point, during the sewage discharge period (2011), compared with one site above this discharge point. The samples taken during 2013 showed that the concentrations of *E. coli* in water and sediments were lower than measured during 2011, except for samples of sediments from one site (the cause was not determined). *Campylobacter* spp. were detected more often in water samples compared to sediment samples with the results indicating that the presence of these bacteria was related to sewage discharges and they did not accumulate in the sediments. In contrast, *Cryptosporidium* spp. and *Giardia* spp. may have accumulated in the sediments, since these were detected months after the major sewage discharges ceased and at higher

[17] 2 g of wet sediment was agitated in 3 mL of water and used to prepare four dilutions, with each then filtered and the filters tested for *E. coli*. It is assumed that the concentration has been calculated based on the original mixture of sediment and water.

[18] Dry weight is used to minimise variability associated with water content when the research is intended to compare sediment samples between sites or sampling times, rather than to compare the concentrations of microorganisms in sediment and water.

concentrations than during discharges (although the difference was not significant). However, undocumented sewage discharges may have affected this study's results.

During 1991/92, enteroviruses were detected in the top 2–3 cm of marine sediments collected beside a wastewater outfall from an Auckland treatment plant (Green and Lewis, 1999). The highest concentration of viable enteroviruses was 33 PFU/100 g sediment. Further PCR testing showed the presence of hepatitis A virus in sediments throughout the year. The concentrations in water were not reported in this study.

A survey of 18 freshwater sites in Southland indicated that, at some sites, the *E. coli* concentration was probably higher in the sediment (CFU/g dw) compared to the water (*E. coli* per 100 mL) (Rusinol and Moriarty, 2013). The different units make this comparison difficult. The highest *E. coli* concentration (18,286 CFU/g dw) was in a fine sand sediment. The water from this site did not contain an elevated *E. coli* concentration relative to water samples from other sites. Regarding this site, the authors comment that "This result suggests that when the sediment is disturbed by recreational activity, *E. coli* will be resuspended in the water column. It is that likely that this will change the water from being acceptable for recreation contact to being unacceptable. The result also highlights the lack of correlation between river water and sediment quality during base flow."

5.2 PHYSICAL RESUSPENSION OF SEDIMENT

Natural resuspension by water turbulence

Rainfall events and storms increase water turbulence in aquatic environments, which resuspends sediment. A study of water from a river estuary in North Carolina (USA) reported that 14% of *E. coli* were attached to suspended particles, but during periods of runoff and sediment resuspension this increased to 68% (Fries *et al.*, 2008). During a study in Adelaide (Australia), samples of sediment and water were taken from a beach near the outlet from a river, each day for 10 days following a rain event (Craig *et al.*, 2004). The concentration of faecal coliforms peaked in both sample types during the rainfall event (>1×10^6 CFU per 100 g sediment or per 100 mL water) but decreased faster in the water compared to the sediment during the following days.[19] However, this study did not separate the microbial contributions from incoming rainwater and resuspended sediment. Another study, which monitored estuarine water quality during storm events, concluded that the measured increase of *E. coli* and enterococci concentrations during these events was mainly due to overland flow, with resuspended sediments only making a minor contribution (Stumpf *et al.*, 2010).

A second study in Australia, conducted in the upper reaches of a tidally-influenced estuary (Yarra River, Victoria), found a negative correlation between the *E. coli* concentration in water and the tidal level (Jovanovic *et al.*, 2017). At low tide, the concentration of *E. coli* in the water tended to be highest. They attributed this relationship to higher flow velocities during low tide causing sediment resuspension, although were not able to confirm this with water velocity measurements and did not consider dilution. Bed and sediment resuspension was also proposed as the cause of increased *E. coli* concentrations in the water in the lower part of the estuary, but this was only detected when the effect of wet weather events was removed. In laboratory studies using sediment cores from different points along the Yarra River, both gentle agitation of the cores (mimicking tidal movement) and vigorous shaking (mimicking storm events or other deep sediment disturbances such as dredging) increased

[19] The T_{90} value for the water was calculated as 1.3 days, and was 1.7 days for the sediment.

E. coli concentrations in the overlying water by up to 20 times, even when these disturbances were carried out more than two weeks after the cores were put into storage (Schang *et al.*, 2018).

A study of an estuary in India (Tapi estuary, Gujarat) reported that bacterial concentrations were higher during the monsoon period compared to periods before and after (Borade *et al.*, 2014). However, the results are not consistent on this point and suggest that both water and sediment concentrations are affected by the monsoon events, with sediment resuspension contributing to change. Using faecal coliforms as an example, the average concentrations in water and sediment pre-monsoon were 29 CFU/mL (range ND-200 CFU/mL) and 2000 CFU/g (range ND-7000 CFU/g), respectively. During the monsoon, the water concentrations slightly increased (mean 94 CFU/mL, range ND-360) and the sediment concentrations decreased (mean 500 CFU/g, range ND-2000). High water flows and dilution from high water volumes likely contributed, and it is difficult to determine the impact of resuspended sediment. Post-monsoon concentrations were 26 CFU/mL water (range ND-90 CFU/mL) and 562 CFU/g sediment (range ND-1000 CFU/g).

However, some studies have measured increased FIB concentrations during a rising storm, ahead of the peak water flow, which has been interpreted as bacteria in the sediment being resuspended by accelerating currents (Pachepsky and Shelton, 2011). A study in Canada (Swan Creek, Ontario) inoculated tracer *E. coli* into the sediment of a small alluvial stream to monitor resuspension (Jamieson *et al.*, 2005). During the following months they found that the tracer and suspended solids both increased in the water column during the rising limb of storm events, providing evidence of bacterial resuspension with the sediments.

Artificial resuspension experiments

A person wading in water approximately 20 cm deep increased the concentration of enterococci in the water immediately surrounding the wader (O'Mullan *et al.*, 2019). In ten trials, water samples were taken before and after a sampler entered the water at a site located along a river estuary in New York (USA). The wading caused visible turbidity in the water and the mean increase in enterococci was 114 MPN/100 mL water. The researchers noted that this exceeded a local microbiological action value of 60 MPN/100 mL.

Similarly, at a recreational site along the Tacarigua River (Trinidad and Tobago), a pair of water and sediment samples were taken before two people waded in the area for two minutes, after which a second water sample was taken (Phillip *et al.*, 2009). This experiment was repeated on four different occasions and each time, the post-disturbance water samples contained higher concentrations of *E. coli* and total suspended solids. The mean concentration of *E. coli* in the sediments (per g) was 70 times higher than measured in undisturbed water (per 100 mL), and sediment disturbance caused a 4-fold increase in the concentration of *E. coli* in the water. More widely, the concentration of *E. coli* or faecal coliforms in water samples collected when recreational users were present were significantly higher than those collected when no one was in the water, and there were also weakly positive correlations between these concentrations and the number of people in the water.

Two studies have investigated the effect of sediment disturbance on water quality through inserting part of a cylinder into the sediment, vigorously stirring the upper layer of sediment within the cylinder then collecting a water sample containing the resuspended sediments. The first was a study in NZ, which evaluated the water quality of 30 rivers in Canterbury prior to and after this artificial sediment disturbance (Pattis *et al.*, 2023). At each site, the microbial concentrations were compared between a composite sample of river water taken upstream of the sampler's position, and a composite of stirred sediment subsamples, during three visits. A stirring stick was used to resuspend the sediments within the cylinder, with the depth of sediment disturbance ranging from 2–6 cm. In general, the prevalence and concentrations of *E. coli*, enterococci and *C. perfringens* spores were higher in the stirred sediment samples although this was not consistent between sites. For example, in 45 samples from 23 rivers the concentration of *E. coli* in stirred sediment was between 133% and 17,100% higher than the paired water samples. *Campylobacter* spp. were detected at least once in every river. For 37 samples, the concentration of *Campylobacter* spp. was >110% higher in the resuspended sediment sample compared to the paired water sample. Considering all 90 samples, *C. perfringens* were detected in 9 water samples and 75 stirred sediment samples, clearly indicating that these spores had settled into the sediment. *Cryptosporidium* spp. and *Giardia* spp. were also detected in stirred sediment samples, but paired water samples were not tested for these protozoa. The authors commented that "While 71% of water samples ($n = 64$) met NZ Recreational Water guidelines prior to stirring, only 39% of samples ($n = 35$) met the guidelines after stirring."

The second study utilised a paint-mixing drill to disturb the top 5–6 cm of sediment within a cylinder for 45 seconds, with water samples taken within the cylinder before and 30 seconds after mixing (Wilson *et al.*, 2016). This study was conducted at several sites around a freshwater recreational beach alongside a lake in Missouri (USA). The concentrations of *E. coli* in the water after mixing were significantly higher than that measured before sediment disturbance. The sediment mixing increased *E. coli* water concentrations by two or three orders of magnitude. More widely, the researchers in this study identified that an important source of *E. coli* in the water was bathers resuspending sediments that had been contaminated with avian faeces. This was confirmed using avian MST markers.

A field study in South Africa found that, after a 1 m^2 riverbed area was physically raked, the *E. coli* concentration in downstream water was 7.9 times higher than the concentration before raking (Abia *et al.*, 2017). The *E. coli* concentrations within the water 2 m downstream from the disturbance returned to baseline levels within 80 seconds of the raking. At another point in the river, the movement of cattle caused visible sediment resuspension and the downstream *E. coli* concentration to increase by 6.5 times before quickly returning to baseline (no cattle defecation was observed).

During dredging of the Mississippi River (Wisconsin, USA), the concentrations of faecal coliforms in water samples were higher relative to samples taken four days prior to, and five days after, the dredging operation (Grimes, 1975). This was attributed to the suspension and redistribution of sediments and previously sediment-bound bacteria. The greatest increase in faecal coliform concentrations were detected in samples taken immediately downstream from the dredging operation and along prevailing water current routes.

A temporal study of a recreational beach in the USA found a significant and positive correlation between the number of bathers in the water, the water turbidity and the concentration of viable *C. parvum* oocysts (Sunderland *et al.*, 2007). While the increased turbidity suggests sediment resuspension was a contributing factor, direct water contamination from bathers could not be eliminated as a source of *C. parvum* and sediment samples were not tested.

Large scale flumes were used to mimic FIB deposition and resuspension after sewage contamination events in a medium-sized freshwater river in Germany (Walters *et al.*, 2014). While noting that the sediments used were coarse, the results demonstrated that increased bed shear stress resulted in increases in the total suspended solids and FIB in the water column. In another study, artificially induced high flow events through a freshwater creek mobilised *E. coli* in upstream sediments and spread these bacteria through downstream reaches (Cho *et al.*, 2010). While the upstream sediments were dominated by sand, the mud (clay + silt) fractions of these sediments had higher *E. coli* concentrations and it was assumed that these muddy sediments were predominantly mobilised.

A study in the Topehaehae Stream in NZ involved opening a dam to release water from a reservoir to create artificial floods through a cattle farming area (Muirhead *et al.*, 2004). However, fine sediments were only present at one sample point in the stream and the results were not informative for this current review.

Hydrodynamic models

Hydrodynamic models that investigate the role of sediment settlement and resuspension on the concentration of FIB in water show that resuspended sediment contributes to an increase in bacterial concentrations in the water and allows bacteria to be redistributed to other parts of the aquatic system. These models can incorporate assumptions for the ratio of bacteria attached to sediment against those that are free-floating, called the partition coefficient, and the rate of bacterial adsorption/desorption from sediment particles (Droppo *et al.*, 2011; Gao *et al.*, 2011). They can also incorporate equations to describe the exchange of bacteria between the water column and sediments, and decay (death) of bacteria in both matrices. A numerical model developed to investigate the movement of bacteria between the sediment and water predicted that, under conditions that favour sediment resuspension, the concentration of bacteria in the water is strongly affected by the concentration of bacteria in the sediment (Gao *et al.*, 2011). They did not find the partition coefficient had a significant effect. When investigating initial settling of bacteria from the water column, the partition coefficient was significant, since bacteria attached to particles would settle faster. The settling velocity rate was also important, with larger particles settling at a faster rate compared to smaller particles.

Some of these findings have been confirmed through models developed to describe different aquatic systems.

From a model developed to describe the Tamsui River estuarine system in Taiwan, the sediment settling velocity had the strongest effect on the concentration of faecal coliforms (*E. coli*) in the water, with a decrease in settling velocity resulting in an increase in faecal coliform concentration (Chen and Liu, 2017). The effect of settling velocity was stronger than the concentration of faecal coliforms in the sediment. The partition coefficient also exerted a strong effect on the concentration of faecal coliforms in the water. Bacteria associated with suspended sediment are more likely to settle out of the water compared to their planktonic counterparts.

In another study, of the South Nations River in Ontario, Canada, the concentration of live and dead bacteria in sediments was measured using a live/dead stain and microscopy (Droppo *et al.*, 2011). The samples were taken from the sediment bed, and separately from river water using centrifugation. The results are not reported but were used by the researchers to investigate the movement of bacteria through the aquatic system. The model results showed that the flow rates (and associated sediment shear stress) in this system usually supported sediment deposition rather than resuspension but also showed how conditions could cause sediment erosion and downstream re-deposition.

A study in Europe has investigated correlations between physicochemical factors in marine environments and the concentration of genetic markers for *Vibrio* spp. and *V. vulnificus* in waters and sediments (Fernández-Juárez *et al.*, 2024). Crucially, they identified sea surface wave height, turbidity, phosphorous concentrations and sediment concentrations of *Vibrio* spp. gene copies as significant predictors for *Vibrio* spp. and/or *V. vulnificus* water abundance (alongside sea surface temperatures). This suggested that sediment resuspension increased concentrations of *Vibrio* spp. and *V. vulnificus* in the water column. Further investigations found a positive correlation between *Vibrio* spp. gene abundance in the water and the abundance of other phyla which were known to preferentially inhabit marine sediments, plus a negative correlation with Secchi depth (water clarity).

6. ILLNESS FROM EXPOSURE TO AQUATIC SEDIMENTS

Summary

No outbreak reports within the scope of this review were located, where ingestion of water with resuspended sediments during recreation was confirmed as the cause of infection. Of the notified gastrointestinal illnesses reported in NZ during 2023, and considering the completion of risk factor information, exposure to recreational water was the most often reported risk factor among giardiasis cases.

From a quantitative risk assessment considering a faecal-contaminated freshwater system and illness from pathogenic *E. coli* through recreational contact, it was estimated that sediment disturbance increased the probability of infection between 0–4% and 63%.

6.1 RECREATIONAL WATER CONTACT AS A RISK FACTOR FOR GASTROINTESTINAL ILLNESS, NZ

Case reports recorded in NZ's notifiable disease database, EpiSurv, can capture information on exposure to recreational water as a risk factor for illness, although other risk factors can be reported. It is important to note that publicly available data on these cases does not provide information on the type of water they were exposed to, which could be environmental waters (rivers, lakes, estuaries, beaches, etc.) or constructed recreational areas such as swimming pools, spas and water parks.

Table 4 summarises this information for notifiable gastrointestinal diseases reported to EpiSurv during 2023 (ESR, 2025). Cases can also be notified to EpiSurv under the general category of 'Acute Gastroenteritis' if there is a suspected common source, or the case is in a high-risk category (e.g., food handler or early childhood service worker) or illness is caused by an infectious agent of public health importance. During 2023 there were 461 acute gastroenteritis cases, for whom information on recreational water contact was known for 345. Of the 345 cases, 21% had reported recreational water contact as a risk factor (ESR, 2025).

There were 786 outbreaks reported during 2023 (ESR, 2025). "Waterborne" was the primary mode of transmission for six of these outbreaks, involving 146 cases, but this includes outbreaks from contaminated drinking water.

These EpiSurv data indicate the pathogenic microorganisms that could be transmitted to people in contact with water for recreation. Data presented in Section 4.3 show that these pathogens can be found in aquatic sediments.

Table 4. Notified gastrointestinal illnesses in NZ during 2023: Reported cases and recreational exposure to water as a risk factor

CAUSATIVE ORGANISM	NOTIFIED CASES	RATE PER 100,000	PERCENTAGE REPORTING RECREATIONAL WATER CONTACT[1]	PERCENTAGE OF CASES WHO ANSWERED THIS QUESTION[2]
Campylobacteriosis	6089	116.6	34.7	18.3
Giardiasis	897	17.2	31.0	48.5
Pathogenic *E. coli* infection (STEC)	1006	19.3	22.1	62.1
Cryptosporidiosis	831	15.9	21.6	59.0
Salmonellosis	827	15.8	19.3	63.8
Yersiniosis	1408	27.0	17.0	47.3
Shigellosis	122	2.3	16.7	68.9

Source: ESR (2025)

[1] The percentage of cases answering 'yes' based on the total number of cases that provided information on recreational water contact.

[2] The percentage of cases that provided information on recreational water contact.

6.2 OUTBREAKS

There are many outbreak reports where illnesses have occurred after recreational contact with contaminated water, including after storm events. However, it is difficult to identify outbreaks resulting from localised sediment resuspension. No relevant outbreak reports were located.

6.3 QUANTITATIVE MICROBIAL RISK ASSESSMENT (QMRA)

A QMRA centred on the faecal-contaminated Apies River in the Gauteng Province of South Africa has considered the health risk from sediment resuspension during the dry season, caused by increased disturbance from people using this river as a water source (Abia *et al.*, 2016). The researchers calculated the probability of infection for each of ten sites along the river and some tributaries. Assuming 8% of the *E. coli* present in the water were pathogenic, the incidental ingestion of 1 ml of undisturbed water had a probability of infection in the range 0–4% depending on the site. This increased to as high as 63% for one site when it was assumed that sediment disturbance increased the concentration of *E. coli* by 2-log. If the undisturbed water was being used as drinking water (which, in this region it commonly is), the probability of infection was 6–84% from consumption of 100 mL. This increased to 67–97% when sediment was resuspended.

7. THE IMPACT OF CLIMATE CHANGE

Summary

Aquatic sediments and the microbes within these are likely to be impacted by climate change-induced increases in temperature, changes to rainfall/run-off and erosion patterns, increased coastal sea levels and changes in the frequency of severe weather events.

These changes will not necessarily negatively affect the survival of FIB and pathogenic microorganisms. Based on the information reviewed in this document, increased sedimentation may prolong their survival, although warmer temperatures and/or changes to oxygen concentrations are likely to have varied effects. An increased frequency of severe weather events will create more opportunities for sediment resuspension.

QMRA models are needed to predict the impact of climate change on faecal-associated pathogenic microbes in sediments, and the resultant impact on human disease in NZ.

The aquatic ecosystems considered in this review are complex and interconnected with the wider catchment and/or marine environment, and many are also interconnected with human infrastructure and activities. The sediment and associated microbiota are just one part of these much larger systems. Changes in NZ's environment in response to global climate change will cause localised effects on aquatic systems, which will likely impact sediment microbiota, but it is beyond this current review to consider this in detail. However, there are some general considerations that fall within the scope of this review.

Aside from the overall increase in temperature, and increased periods of warmer-than-average temperatures, two of the larger environmental changes that will impact aquatic sediments are changes to rainfall/run-off patterns (which also alter erosion patterns) and increased coastal sea levels (Elliott *et al.*, 2019). Interlinked with these are changes in the frequency of severe weather events, which affects the frequency of terrestrial flooding and marine storm surges.

Increasing human pressure on freshwater resources also tends to reduce and degrade freshwater flows through aquatic systems. Across NZ, the average river flows in some regions are expected to increase by more than 5%, and in others this is predicted to decrease by more than 5% (MFE, 2020). NZ lakes are increasingly stratified, promoting algal blooms near the surface, reducing light penetration and depleting oxygen in deeper waters. As freshwater inputs into coastal aquatic systems decrease and tidal ranges increase, saline waters can extend further inland and hypoxic conditions develop (Biguino *et al.*, 2023). High nutrient loads accelerate hypoxic conditions, and these can also promote algal blooms, which reduce water clarity.

A national model has been developed to predict the impact of climate change on erosion and suspended sediment loads in NZ (Neverman *et al.*, 2023). The model considers the contributions from three predominant erosion processes: mass movement, surficial erosion, and streambank erosion. It predicts that sediment loads will be primarily driven by mass movement erosion due to increasing storm frequency and magnitude. In some NZ areas, particularly in the North Island, it was predicted that the total sediment yield would change by at least 25% (RCP 2.6) or more than 100% (RCP 8.5) by 2090.[20] This will result in increased sedimentation in aquatic systems.

These changes will not necessarily negatively affect the survival of FIB and pathogenic microorganisms. Based on the information reviewed in this document, increased sedimentation in water bodies (and potentially increased nutrients) may prolong microbial survival, especially in conditions of reduced sunlight due to poor water clarity. Warmer temperatures and/or changes to oxygen concentrations may hasten the death of some faecal-associated microorganisms but may prolong the survival (or encourage the multiplication) of others. Climate change may also alter the environmental distribution of natural aquatic sediment inhabitants. Globally, the warming coastal marine environment has enabled *Vibrio* spp. to become more abundant and widespread, with a resultant increase in human infections (Baker-Austin *et al.*, 2017). This review shows that predation contributes to the decline of FIB populations, so climate change-driven effects on protozoan bacterial predators and zooplankton are likely to be important when considering FIB survival. For example, warmer water temperatures are expected to be favourable to free living amoeba (Ariyadasa *et al.*, 2025).

The information reviewed in this document also indicates that an increased frequency of severe weather events will create more opportunities for the water energy in aquatic systems to overcome sediment shear strength. The resulting resuspended sediment will carry microbes which previously resided in the sediment bed into the water column, noting that concentrations of microorganisms in these sediments are often many-fold higher than the overlying water.

QMRA models are needed to predict the impact of climate change on faecal-associated pathogenic microbes in sediments, and the resultant impact on human disease in NZ. More generally, cryptosporidiosis, giardiasis, campylobacteriosis and salmonellosis rates are expected to increase in NZ due to climate change (Britton *et al.*, 2010a; Britton *et al.*, 2010b; Grout *et al.*, 2024; McBride *et al.*, 2014). The contribution of recreational water exposure to these rates (including exposure from resuspended sediment) is likely to be lower compared to contributions from other exposures such as drinking water, food and animal contact, although research is needed to substantiate this hypothesis.

[20] To standardise climate change predictions across studies, Representative Concentration Pathways (RCPs) are used. RCPs are defined by the expected amount of atmospheric warming or cooling under different scenarios. RCP 2.6 represents a scenario of mitigations that reduce the annual rate of carbon dioxide emissions, minimising global surface temperature increase. RCP 8.5 represents a continual increase scenario, i.e., the current annual increase in the rate of carbon dioxide emissions continues.

8. CONCLUSION

In considering the microorganisms of interest for this review, the collated information shows that:

- Fine aquatic sediments provide an environment that prolongs the survival of microorganisms, although their survival depends on a range of extrinsic and intrinsic factors.
- Microorganisms attach to sediment particles and these initial attachments can become stronger as biofilms develop.
- The concentration of FIB and *Vibrio* spp. in sediments are almost always higher than the overlying water but this may not be the case for faecal-associated pathogenic bacteria, viruses and protozoan parasites.
- Laboratory studies suggest that the concentrations of FIB decrease at a similar rate to bacterial pathogens in sediment, but this is not supported by field studies except those completed near known human faecal point-sources (noting data are scarce, and continuous deposition will support positive correlations).
- Events that increase water energy can disturb sediments and this resuspension causes microbial concentrations to increase in the water.
- Studies have shown correlations (some weak) between the concentration of FIB in water, the presence/concentration of bathers and measures of water clarity that indicate the presence of suspended sediments.

Thus, pathogenic microorganisms in aquatic sediments do present a potential health risk to swimmers if they are disturbed, although most of the evidence for this comes from studies of FIB and epidemiological evidence is lacking. NZ's recreational water quality guidelines only require FIB indicators to be monitored in water samples. This does not account for microorganisms in the sediments and their potential resuspension, which may be one explanation for recreational water monitoring programs sometimes observing erratic FIB concentrations over time (Burton *et al.*, 1987; Weaver and Sinton, 2009). Sediments act as a microbial sink in aquatic environments and support longer microbial survival, so also provide a better indication of water quality and health risk over a longer period of time compared to water samples (LaBelle *et al.*, 1980). The risk to recreational swimmers in locations known for having water quality issues may be better assessed by measuring microorganisms in both sediment and water samples. Sediment sampling methods would need to be designed to take into account the heterogenous concentrations of the target microbes in an area.

This review has identified several important data gaps regarding the presence and survival of pathogenic microorganisms in aquatic sediments. A QMRA framework would help to quantify the risk to recreational swimmers under different scenarios, potentially focusing on representative microbial pathogens as informed by NZ infectious disease data. For example, *Cryptosporidium* spp. is a potential candidate due to its environmental persistence and importance as a waterborne pathogen in NZ. The scoping of this QMRA would identify priority data gaps. Additionally, NZ studies involving the collection of paired water and sediment samples in low energy aquatic environments popular for recreation, and testing these for FIB, selected pathogens and MST markers, would help to generate data towards assessing human health risk.

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APPENDIX A: SCOPE AND METHOD

A.1 Literature review scope

The literature review focused on:

- Studies of fine sediments in low wave energy environments (estuaries, rivers, harbours, lakes); see Section 2.
- Studies of faecal indicators (*E. coli*, enterococci, genetic markers) and/or pathogenic microorganisms likely to be in NZ sediments; see Section 3.
- Studies that involved paired sampling (sediment plus water, at the same place and time).
- Studies that involved multiple sample sites (spatial patterns) and/or sediment sampling over time (temporal patterns).

Initially, the review also focused on studies carried out in temperate climate zones relevant to NZ. Thus, studies carried out in the "temperate-without a dry season" (Cf) zone according to the Köppen-Geiger climate classifications were considered to be most relevant (Beck et al., 2018).[21] However, this was not strictly applied since some of the relevant data were scarce.

This review did not consider chemical hazards that may be present in aquatic sediments. A separate review is required to consider human exposure to chemical hazards that may be present in aquatic sediments and released during recreational activities. There are a range of chemicals that might be considered, including heavy metals, agrichemicals, natural (algal) toxins, persistent organic pollutants and others that might be discharged from specific industries, with urban wastewater outflows (e.g. from personal care products) and from other point sources (e.g. landfills). When considering environmentally relevant concentrations, only some of these exert acute adverse health effects. Most exert their effects through chronic (long term, repeated low level) exposure, which is most relevant to frequent swimmers.

Table 5 further clarifies the scope of this review.

Table 5. Scope of this review

ATTRIBUTE	SCOPE	REASON
Types of sediments		
Freshwater and coastal marine environments	In	Only low wave energy environments with fine aquatic sediments, such as estuaries, harbours, and freshwater rivers and lakes.
Intertidal and subtidal zones	In	Focusing on areas where people are likely to be in contact with water containing re-suspended fine sediments; studies of very deep water are less relevant, as are studies of contact with exposed sand.
Supratidal/dry zones	Out	Considered in an earlier review (King and Leonard, 2023).
Types of microbiological organisms		

[21] http://www.gloh2o.org/koppen/ (accessed 23 March 2023)

ATTRIBUTE	SCOPE	REASON
Faecal indicator micro-organisms: Enterococci, faecal coliforms, *E. coli*	In	Commonly used to indicate the presence of faeces, and thus the potential presence of pathogenic microorganisms
Pathogenic bacteria, fungi, viruses and protozoan parasites	In	Only those that are likely to be present in NZ aquatic sediments. Both those that are host-associated and natural water/sediment inhabitants.
Phytoplankton causing harmful algal blooms	Out	These are suspended in the water although may deposit in sediments after death. The hazard is the biotoxin (chemical hazard).
Microorganisms primarily causing diseases in people who have recently travelled overseas	Out	These are non-endemic diseases for NZ, e.g. typhoid, cyclosporiasis. It is acknowledged that these pathogens could be present in sewage as a result of infected cases being in NZ and so might temporarily enter aquatic environments.
Microorganisms causing tropical diseases	Out	See above.
Non-pathogenic microorganisms	Out	No risk to human health.
Sources of microbial pathogens		
Point source faecal contamination	In	Sporadic events or (semi)continuous e.g., broken sewer infrastructure, combined sewer/stormwater flows, sewage discharges, processing discharges. Also point-source contamination from concentrations of animals e.g., bird nesting grounds, stormwater from animal holding or processing sites.
Non-point source faecal contamination e.g. domestic and feral animals or runoff from agricultural land	In	Runoff from nearby land-based activities e.g., parking lots, agricultural land.
Resuspension of sediment into water by swimmers and other recreational users	In	Ingestion from swallowing water and/or contact with the water.
Resuspension of sediment through water movement (tides, inflows, low energy waves)	In	Ingestion from swallowing water and/or contact with the water.
Microorganisms in shellfish living in the aquatic sediments	Out	This is an extensive topic more suitable for separate review. Additionally, humans are exposed via eating the shellfish.
Literature subject matter		
Literature reviews	In	Effective method of collating evidence.
Studies of aquatic sediments in temperate climates*	In	Relevant to NZ climate.

ATTRIBUTE	SCOPE	REASON
Studies of aquatic sediments in extremely cold climates*	In	Not relevant to NZ but information used where more relevant studies are not available or where there are important findings.
Studies of aquatic sediments in tropical climates*	In	Information used where more relevant studies are not available, or where there are important findings (e.g., to inform on climate change).
Evidence of gastroenteric illness or other adverse reactions (e.g., skin irritation)	In	Evidence that microbial contamination of aquatic sediments is a potential health risk.
Survival of microorganisms in aquatic sediments compared to water	In	Microorganisms may survive longer and/or be present in higher concentrations in the sediment environment compared to the water column.
Prevalence/concentration of microorganisms in aquatic sediments in NZ	In	Shows whether microorganisms have been detected in sediments.
Prevalence/concentration of microorganisms in aquatic sediments in other countries	In	These data will be considered if there are no prevalence data available for NZ and more suitable data are not available (e.g., where there is evidence that the presence of these microorganisms presents a risk to human health).

* As guided by Zone C Köppen-Geiger climate classifications (Beck *et al.*, 2018), see also http://www.gloh2o.org/koppen/.

A.2 Review method

A reference library was established from relevant references collated through an earlier review of the health risks from sand (King and Leonard, 2023). This library was expanded, as described below.

Web of Science[22] and PubMed[23] are two citation search engines that together index peer reviewed scientific publications spanning the environment and human health. An exploratory search of both databases was conducted during January 2025, seeking relevant review and study articles. This provided articles covering a range of relevant topics including sediment resuspension, microbial distribution and survival in sediments, the impact of bather density on water quality, and water quality models that considered sediments. It was evident that a systematic search using combinations of keywords relevant to this review (e.g., sediment, pathogen, health, swim, bathing, resuspension, *Escherichia*, pathogen, recreation, etc.) would result in too many irrelevant citations and become inefficient.

Instead, the 134 articles compiled through the exploratory search were used to begin this review. As the review progressed, multiple literature searches were initiated using combinations of keywords relevant to the question being investigated. If a particularly relevant paper was located, the reference list for this paper, plus the 'cited by' and 'similar article' functions in PubMed, were used to locate further reports.

[22] https://www.webofscience.com published by Clarivate Analytics.
[23] https://pubmed.ncbi.nlm.nih.gov/ published by the National Center for Biotechnology Information, US National Library of Medicine.

As part of quality control, if a review cited results from a study of interest, the primary paper was usually retrieved to ensure the data were described correctly.

Additional web-based searches were also undertaken to locate relevant NZ data, as resources and time permitted. This included searches of NZ University library theses databases and regional council websites.