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Evaluation of the suitability of selected contaminants for wastewater-based surveillance at the border

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	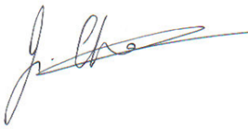	
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EXECUTIVE SUMMARY

Wastewater-based surveillance (WBS) is a useful tool for non-invasively screening arrivals at the New Zealand border en masse for a range of different biological and non-biological contaminants. A previous report prepared for the Ministry of Health assessed the logistics of conducting WBS at New Zealand's international airports, including sampling directly from inbound international aircraft and from airport wastewater networks. This current report extends this assessment by evaluating a wide range of different contaminants for their suitability for WBS.

Contaminants chosen for evaluation reflect both contaminants of international concern, as highlighted by the World Health Organization and United States Centers for Disease Control and Prevention (CDC), and interests of the Ministry of Health. Selected groups of contaminants include vector-borne diseases, for many of which incursions into New Zealand are likely underestimated due to a high rate of asymptomatic infections limiting clinical diagnosis; viral haemorrhagic fevers, which pose considerable risk due to the potential for severe, life-threatening infection and ability to be spread from person-to-person; other high-risk diseases of concern, including potential bioterrorism agents; vaccine-preventable diseases; sexually transmitted infections; and radioactive substances.

Several different representative contaminants within each selected group were evaluated for a range of different characteristics which impact on their suitability for WBS. For biological contaminants, these include symptoms of infection, and whether asymptomatic infections have been reported; how the contaminant is spread, including whether person-to-person transmission is known; global distribution of the contaminant; prevalence of case notifications in New Zealand; whether biomarkers of infection are excreted in urine and/or faeces; any previous WBS studies; and whether the infectious agent has been isolated from urine and/or faeces and therefore may pose a potential health hazard to anyone exposed to wastewater containing this contaminant (e.g., sample collectors, laboratory staff, wastewater treatment plant personnel). For radioactive substances, given the huge variety of radioisotopes people may be exposed to precluding assessment of all possibilities, this report focused on the main radioisotopes released during previous major nuclear incidents – iodine-131, caesium-134 and caesium-137, and polonium-210 due to its role in a high-profile poisoning incident in 2006.

The aim of this report is not to compare different surveillance methods for the various contaminants, or indeed to ascertain whether WBS is the best surveillance choice for a given contaminant, but rather to determine whether WBS may be suitable for a given contaminant based on the aforementioned characteristics.

Information identified in this report will be used to support the future development of a framework for guiding WBS at the border, which it is anticipated can be used to guide decision making in response to international outbreaks or contamination events involving not only the evaluated contaminants, but also other contaminants, including new/emerging contaminants, based on similarity to those evaluated in this report.

1. INTRODUCTION

A key role of border health in Aotearoa New Zealand is the detection of public health risks at the border, to take public health action to prevent harm to the health and wellbeing of the general public, international travellers and aircraft and ship crew. However, in many cases people infected with certain diseases or internally exposed to certain contaminants (e.g., radioisotopes) may show no symptoms when arriving at the border, and therefore not be detected by current surveillance methods. Furthermore, Aotearoa is a signatory to the International Health Regulations (IHR) 2005[1], consequently Aotearoa must 'strengthen, develop and maintain core surveillance and response capacities to detect, assess, notify and report public health events to the World Health Organization (WHO) and respond to public health risks and emergencies'.

Wastewater-based surveillance (WBS) is an ideal tool for screening arrivals at the border as it is non-invasive, can screen arrivals en masse and has already proven useful for monitoring diseases where a significant number of infected individuals are asymptomatic (e.g., COVID-19, polio). A previous report prepared for the Ministry of Health evaluated the logistics of conducting WBS at New Zealand airports. This report will build on that work by evaluating the suitability of a broad range of different contaminants for WBS at the border. Information from this report will then be used to support development of a framework which can be used to determine whether WBS at the border is suitable for a given contaminant.

This first step in development of the framework is to evaluate a wide range of different contaminants for their suitability for WBS. Information obtained from these evauations can then be used to guide rapid decision-making in response to international outbreaks/events not only for the evaluated contaminants but also for other related contaminants for which there may be insufficient knowledge (e.g., newly emerging diseases).

Several groups of contaminants were selected for evaluation in this report, including:

- Vector-borne diseases
- Viral haemorrhagic fevers
- Other high-risk diseases of concern (including potential bioterrorism agents)
- Vaccine-preventable diseases
- Sexually transmitted infections
- Radioactive substances

Selection of contaminants for consideration in each class was informed by diseases of concern identified by the World Health Organization (WHO)[2,3,4] and/or United States Centers

[1] https://www.tewhatuora.govt.nz/our-health-system/border-health/border-health-legislation-policy-and-planning/international-health-regulations Accessed 20 March 2024
[2] https://www.who.int/news-room/fact-sheets/detail/vector-borne-diseases Accessed 15 August 2023
[3] https://www.who.int/teams/immunization-vaccines-and-biologicals/diseases Accessed 15 August 2023
[4] https://www.who.int/health-topics/sexually-transmitted-infections Accessed 15 August 2023

for Disease Control and Prevention (CDC)[5,6], and interests of the Ministry of Health. Considerations included burden of disease, prevention and treatment options, legal requirements for notification, and potential of climate change to increase potential risks. Many of the chosen candidates feature in a recent study co-authored by Dr. Anthony Fauci, the Former Director of the United States National Institute of Allergy and Infectious Diseases, which highlighted global examples of emerging and re-emerging infectious diseases (Figure 1). Antimicrobial resistance (AMR) is not included in this report due to the complexities associated with AMR surveillance warranting a separate report.

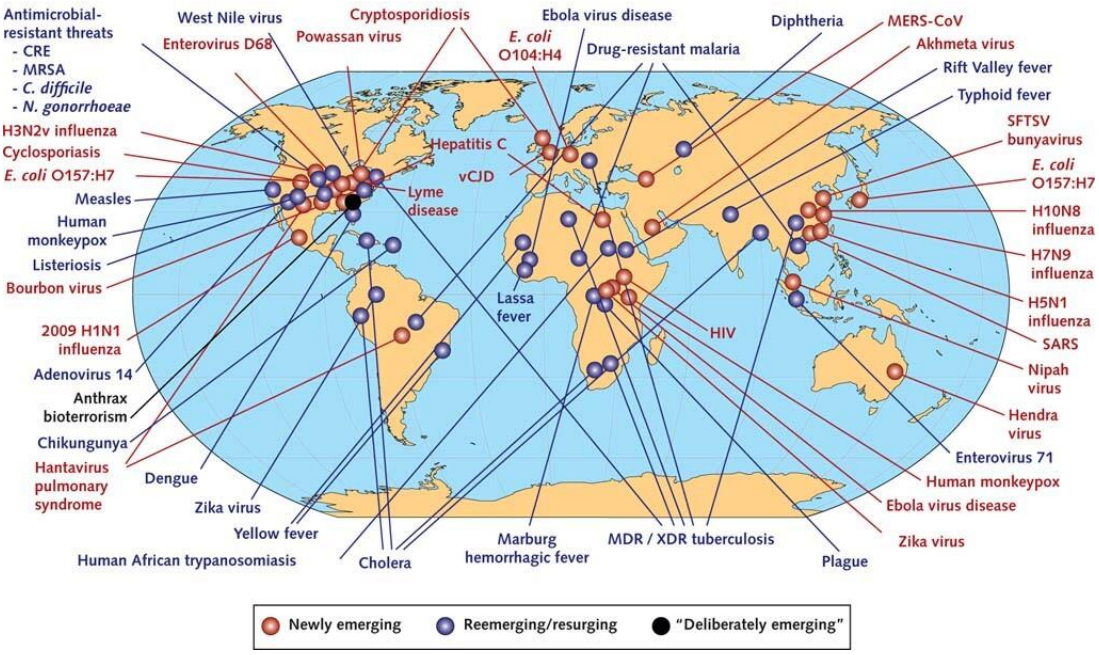

Figure 1 Global examples of emerging and re-emerging infectious diseases

Reproduced from Paules et al. (2017).

To assess whether border WBS is suitable for a given contaminant, this report will evaluate several key criteria including:

- Symptoms: are cases likely to display overt symptoms, or be asymptomatic? For contaminants where affected individuals are likely to display obvious symptoms WBS may be less useful. However, even for contaminants where all affected individuals generally display symptoms, there may be a lag period between exposure and symptom development during which biomarker may be shed. As such, the contaminant may be detectable in wastewater prior to symptom development.
- Transmission: how is the contaminant spread between individuals? This will provide insight into the likelihood of local transmission after border incursion.
- Global distribution: could inform selection of flights for surveillance.
- Case notifications in New Zealand: how common is border incursion?

[5] https://www.cdc.gov/vhf/about.html Accessed 15 August 2023
[6] https://emergency.cdc.gov/agent/agentlist-category.asp Accessed 15 August 2023

- Excretion of biomarkers: are biomarkers of exposure shed in urine and/or faeces?
- Has the contaminant been assessed using WBS? A summary of infectious diseases which have been monitored using WBS is provided in Appendix Table 26.
- If the contaminant is present in aircraft/airport wastewater, does it pose a potential hazard to sample collectors, laboratory staff, wastewater treatment plant personnel or the public (through exposure to untreated or insufficiently treated wastewater)?

A recent study by Jones et al. (2023) assessed the likelihood of identifying SARS-CoV-2 cases entering the United Kingdom based on the likelihood a passenger will defecate on the flight. This study provides valuable insight into the likelihood of detecting contaminants for which biomarkers are shed in faeces. However, there are many contaminants for which biomarkers of exposure are shed in urine. Currently there are no studies assessing the likelihood of passengers urinating on a flight, although it might be speculated that passengers are more likely to urinate than defecate on a flight leading to increased chances of detection. Additionally, as noted by Jones et al, where a disease causes diarrhoea, this may also increase the chances of and infected person defecating on a flight (unless they have taken anti-diarrhoea medication).

As noted above, aside from the well-known role of WBS in monitoring for COVID-19 and polio, WBS has also been applied to a wide range of other infectious diseases. Studies include both targeted PCR screening approaches (e.g., RT-qPCR) and untargeted metagenomics approaches. Of particular importance for this report is the study of Spurbeck et al. (2023) who used both untargeted metagenomics and the Illumina respiratory pathogen and AMR targeted sequencing panel to screen 28 wastewater samples collected in Ohio, United States. This panel targets 282 respiratory pathogens which includes 187 bacteria, 42 viruses, 53 fungi and 1,218 AMR alleles (Spurbeck et al., 2023). Using these two approaches this study identified several of the contaminants being evaluated in this report, as will be discussed in the relevant sections below.

2. VECTOR-BORNE DISEASES

The term vector-borne disease (VBD) refers to any illness caused by bacteria, viruses and parasites transmitted by vector organisms such as insects[7]. Viral diseases transmitted by arthropod vectors (e.g., mosquitoes, ticks, fleas, sandflies) are specifically referred to as arboviruses (**ar**thropod-**bo**rne **virus** of vertebrates) (Casals, 1971). According to the WHO, VBD accounts for more than 17% of all infectious diseases and causes over 700,000 deaths annually[7]. A non-exhaustive summary of VBDs collated by the WHO indicating the type of pathogen and vector organism is presented in Table 1.

Table 1 World Health Organization list of vector-borne diseases

Vector		Disease caused	Type of pathogen
Mosquito	*Aedes*	Chikungunya	Virus
		Dengue	Virus
		Lymphatic filariasis	Parasite
		Rift Valley fever	Virus
		Yellow Fever	Virus
		Zika	Virus
	Anopheles	Lymphatic filariasis	Parasite
		Malaria	Parasite
	Culex	Japanese encephalitis	Virus
		Lymphatic filariasis	Parasite
		West Nile fever	Virus
Aquatic snails		Schistosomiasis (bilharziasis)	Parasite
Blackflies		Onchocerciasis (river blindness)	Parasite
Fleas		Plague (transmitted from rats to humans)	Bacteria
		Tungiasis	Ectoparasite
Lice		Typhus	Bacteria
		Louse-borne relapsing fever	Bacteria
Sandflies		Leishmaniasis	Parasite
		Sandfly fever (phlebotomus fever)	Virus
Ticks		Crimean-Congo haemorrhagic fever	Virus
		Lyme disease	Bacteria
		Relapsing fever (borreliosis)	Bacteria
		Rickettsial diseases (eg: spotted fever and Q fever)	Bacteria
		Tick-borne encephalitis	Virus
		Tularaemia	Bacteria
Triatome bugs		Chagas disease (American trypanosomiasis)	Parasite
Tsetse flies		Sleeping sickness (African trypanosomiasis)	Parasite

List obtained from https://www.who.int/news-room/fact-sheets/detail/vector-borne-diseases.

[7] https://www.who.int/news-room/fact-sheets/detail/vector-borne-diseases Accessed 15 August 2023

In New Zealand, all arboviral diseases, malaria, typhus (rickettsial diseases) and plague are notifiable to a Medical Officer of Health and the Local Authority in New Zealand under the Health Act 1956[8]. As of November 2021, the only VBDs reported in New Zealand were mosquito-borne infections acquired overseas[9]. The ESR EpiSurv database keeps a record of all vector-borne illnesses notified in New Zealand[10]. However, as some vector-borne illnesses may cause only mild or no symptoms, thus not necessitating medical assessment allowing for diagnosis, the true prevalence of these diseases could be much higher[9].

In 2022, Lee et al published a study assessing the potential of WBS to study arboviral diseases (Figure 2). This study primarily focused on dengue virus, zika virus, West Nile virus and yellow fever virus, reviewing information on excretion of these viruses in urine, and developing a model to estimate the volume of municipal wastewater that would need to be processed to detect these viruses at variable shedding rates.

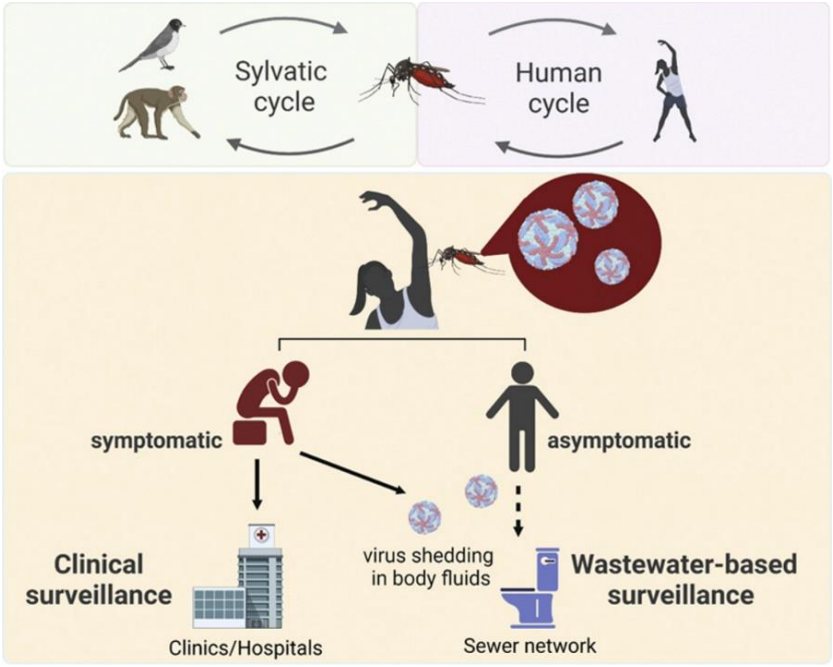

Figure 2 Role of wastewater-based surveillance in monitoring for vector-borne diseases

Reproduced from Lee et al. (2022).

This section will focus on 14 of the most common VBDs, evaluating their suitability for border WBS. In addition to surveillance of vector borne diseases and epidemic preparedness, prevention of vector borne diseases remains crucial for public health. Prevention includes vaccination when appropriate, and for all diseases, surveillance and control of vectors[11].

[8] https://www.health.govt.nz/system/files/documents/pages/schedule-of-notifiable-diseases-updated-jun22.pdf Accessed 15 August 2023

[9] https://www.ehinz.ac.nz/assets/Factsheets/Released_2021/MosquitoBorneDisease_released112021.pdf Accessed 4 April 2024

[10] https://www.esr.cri.nz/digital-library/notifiable-disease-dashboard/. Accessed 4 April 2024

[11] Pests of public health significance – Health New Zealand | Te Whatu Ora Accessed 15 November 2023

2.1 DENGUE

2.1.1 Transmission

Dengue is an acute febrile illness caused by four related enveloped single-stranded RNA viruses of the *Flavivirus* genus (family *Flaviviridae*, serotypes DEN-1, DEN-2, DEN-3 and DEN-4) and is primarily transmitted by *Aedes* mosquitoes[12]. Dengue is not spread directly from person-to-person[13].

2.1.2 Prevention

As of 2022, there is a single licensed dengue vaccine, Dengvaxia®, with other candidates undergoing phase III clinical trials (Torres-Flores et al., 2022).

2.1.3 Geographical distribution

Dengue is endemic in the tropics and subtropics, occurring in more than 100 countries worldwide[12], as shown in Figure 3.

According to the WHO "more than 3.9 billion people in over 129 countries are at risk of contracting dengue, with an estimated 96 million symptomatic cases and an estimated 40,000 deaths every year"[14]. There are also an estimated 290 million asymptomatic cases annually (Bhatt et al., 2013).

2.1.4 New Zealand epidemiology

Annual notifications of dengue infections in New Zealand between 2006 – 2021 are shown in Figure 4[15]. Notifications fluctuated during this time, peaking at 294 cases in 2018. The dramatic reduction from 222 cases in 2019 to only 50 cases in 2020 and 7 cases in 2021 is likely due to the COVID-19 associated border closure. Two species of *Aedes* mosquito are present in New Zealand[16].

2.1.5 Symptoms

Around 40 – 80% of dengue infections are asymptomatic[12]. Where symptoms do develop, they are generally mild to moderate and begin within 5 – 7 days after exposure[17]. The most common symptom is fever, which may be accompanied by nausea, vomiting, headache, rash, and pain in the joints, bone, muscles and/or eyes[18]. Symptoms generally last 2 – 7 days[18]. In around 1 in 20 cases, severe, life-threatening symptoms may develop including internal bleeding, organ impairment, and shock or respiratory distress[19].

[12] https://wwwnc.cdc.gov/travel/yellowbook/2020/travel-related-infectious-diseases/dengue Accessed 23 August 2023
[13] https://www.who.int/news-room/questions-and-answers/item/dengue-and-severe-dengue Accessed 23 August 2023
[14] https://www.who.int/news-room/fact-sheets/detail/vector-borne-diseases Accessed 23 August 2023
[15] https://www.esr.cri.nz/expertise/public-health/infectious-disease-intelligence-surveillance/ Accessed 4 April 2024
[16] https://www.ehinz.ac.nz/indicators/border-health/high-risk-pests-intercepted/ Accessed 8 April 2024
[17] https://wwwnc.cdc.gov/travel/yellowbook/2024/infections-diseases/dengue#clinical Accessed 23 August 2023
[18] https://www.cdc.gov/dengue/symptoms/index.html Accessed 23 August 2023
[19] https://www.cdc.gov/dengue/healthcare-providers/clinical-presentation.html Accessed 4 April 2024

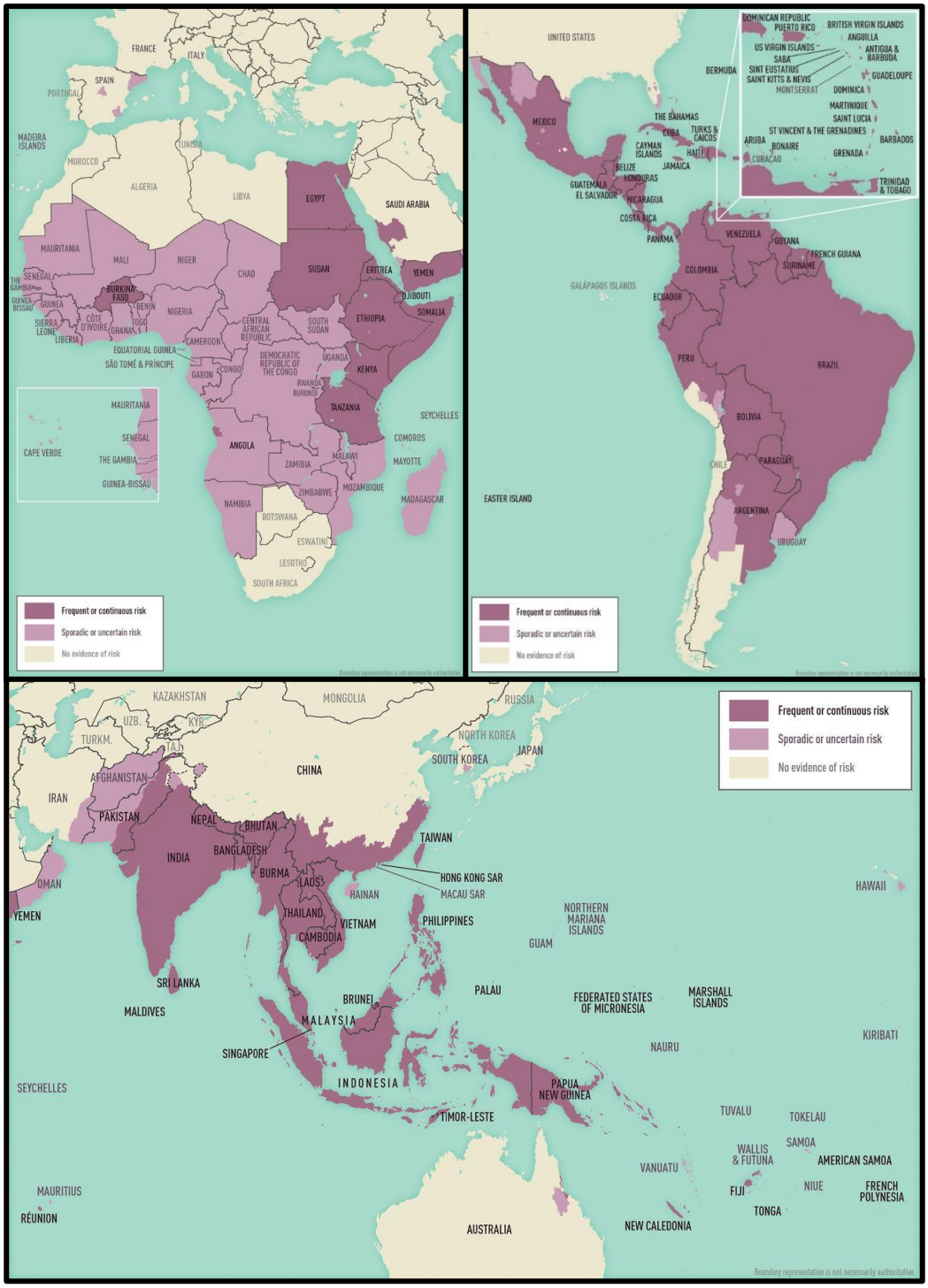

Figure 3 Dengue risk around the world Reproduced from https://wwwnc.cdc.gov/travel/yellowbook/2024/infections-diseases/dengue (last reviewed 1 May 2023). Dark purple, frequent or continuous risk; light purple, sporadic or uncertain risk; yellow, no evidence of risk.

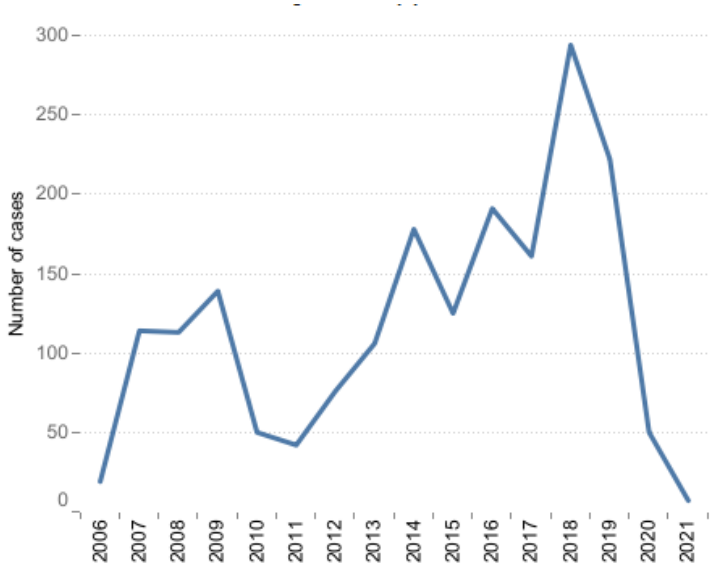

Figure 4 Number of reported dengue cases in New Zealand 2006 - 2021

Reproduced from https://www.esr.cri.nz/digital-library/notifiable-disease-dashboard/.

2.1.6 Excretion of biomarkers of infection

Several studies have identified dengue virus RNA in urine, as summarised in Table 2. Additionally, RNA from dengue virus serotypes 2 and 3 has been shown to be stable in wastewater at 6°C for at least 21 days, so may be suitable for WBS (Chandra et al., 2021) (Figure 5).

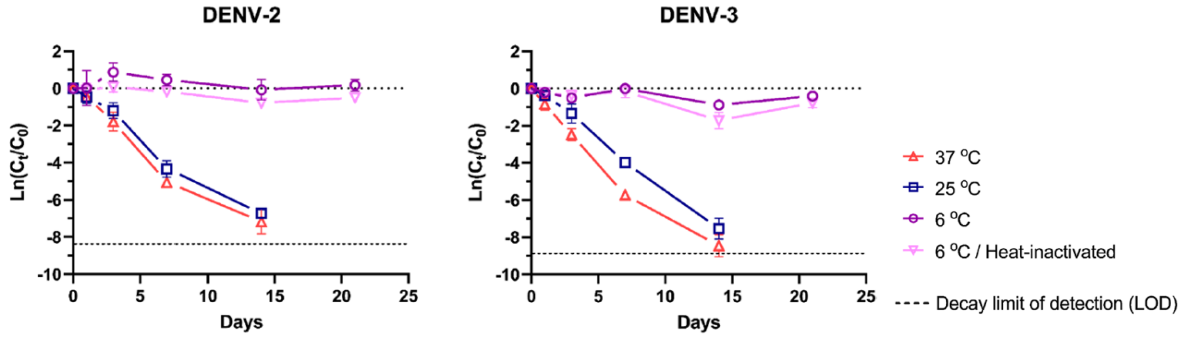

Figure 5 Decay of dengue virus serotypes 2 and 3 RNA in wastewater

Reproduced from Chandra et al. (2021).

Wolfe et al. (2024) detected dengue virus RNA in wastewater solids from three different wastewater treatment plants in Florida, USA. They estimated detection was possible with as few as 4.23 laboratory confirmed dengue cases per million people.

Table 2 Summary of studies assessing excretion of dengue virus RNA in urine

Study participants	% positive patients	Shedding dynamics (no. of samples)	Reference
118 (442 samples)	41.6 (of total samples)	• 13.6% (3/22) positive within 2 days after fever onset • 40.4% (80/198) positive days 3 – 5 after fever onset • 47.4% (63/133) positive days 6 – 7 after fever onset • 49.3% (37/75) positive in week 2 after fever onset • 7.1% (1/14) positive in week 3 after fever onset	Andries et al. (2015)
53 (77 samples)	45.2	• 25% (2/8) positive days 0 – 3 after fever onset • 32% (7/22) positive days 4 – 5 after fever onset • 52% (11/21) positive days 6 – 7 after fever onset • 78% (7/9) positive days 8 – 9 after fever onset • 80% (4/5) positive days 10 – 11 after fever onset • 50% (2/4) positive days 12 – 13 after fever onset • 60% (3/5) positive days 14 – 16 after fever onset • 0% (0/3) positive >16 days after fever onset	Hirayama et al. (2012)
2	100	• 100% positive day 2, 100% negative day 9 PSO	Poloni et al. (2010)
21 (22 samples)	52.4	• 75% (3/4) positive within 4 days of symptom onset • 25% (1/4) positive days 5 – 7 PSO • 100% (6/6) positive days 11 – 21 PSO • 33% (2/6) positive days 22 – 37 PSO • 0% (2/2) positive 60 or more days PSO	Van den Bossche et al. (2015)
13 (49)	84.6	• 25% (1/4) positive days 2 – 3 PSO • 55% (6/11) positive days 4 – 5 PSO • 69% (9/13) positive days 6 – 7 PSO • 73% (8/11) positive days 8 – 9 PSO • 75% (3/4) positive days 10 – 11 PSO • 75% (3/4) positive days 12 – 13 PSO • Negative on days 20 (1/1) and 34 (1/1) PSO	Korhonen et al. (2014)
1	100	• Positive day 7, 8 and 14 PSO • Negative day 25 PSO	Mizuno et al. (2007)

PSO, post symptom onset.

However, the authors note that this may be due to the methodology employed in this study, which included extended sample storage prior to analysis, and processing of low volumes of wastewater (50 mL) (Thakali et al., 2022). Subsequent studies have optimised methodology for recovery and quantification of dengue virus from wastewater using spiked samples (Chandra et al., 2023; Chen et al., 2023).

Lee et al. (2022) assessed the feasibility and sensitivity limits of WBS for dengue virus and estimated that the load of dengue virus shed to wastewater was between 80,000 – 20,000,000 genome copies per infected person per day based on 0.8 – 2 L of urine shed daily. Based on this, they estimated the sensitivity of detection for the dengue virus, based on varying volumes of wastewater processed (50 – 10,000 mL) and a limit of detection of 50 genome copies recovered per mL of wastewater processed (Figure 6).

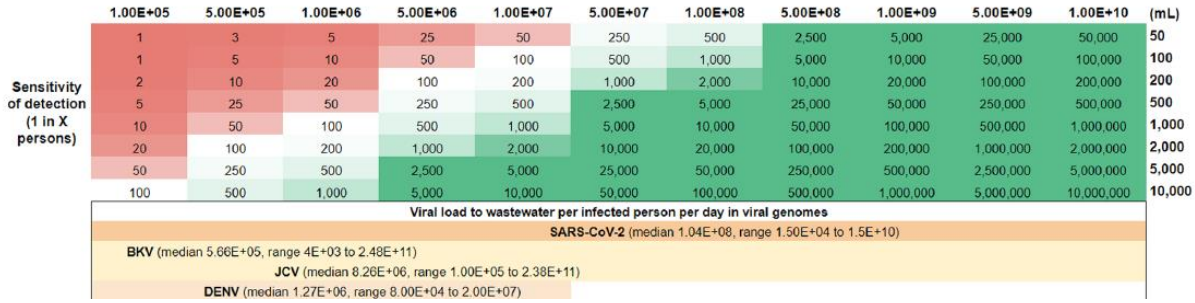

Figure 6 Sensitivity of detection of dengue virus in wastewater

Reproduced from Lee et al. (2022). SARS-CoV-2, and the BKV and JCV polymoviruses are presented as examples of viruses predominantly shed in faeces (SARS-CoV-2) and urine (BKV and JCV). DENV, dengue virus. Values across the top indicate the viral load to wastewater per infected person per day, which are given as a range. Volume of wastewater analysed is on the righthand y axis.

2.1.7 Potential health hazard if present in wastewater

No information suggesting the dengue virus could be transmitted through contact with wastewater (e.g., while sampling, processing samples in the laboratory, or at the WWTP) was identified during preparation of this report. This includes studies by Andries et al. (2015) and Hirayama et al. (2012) who unsuccessfully attempted to isolate infectious virus from urine. RNA from dengue virus serotypes 2 and 3 has been found to persist in wastewater for over 20 days at 6°C and around 15 days at 25°C and 37°C (Chandra et al., 2021), although it is unclear if this is indicative of survival of infectious virus. However, given dengue is not known to be transmitted from person-to-person[20], the presence of the dengue virus in aircraft/airport wastewater is unlikely to pose a health hazard to people collecting or processing wastewater samples, or to WWTP staff.

[20] https://www.who.int/news-room/questions-and-answers/item/dengue-and-severe-dengue Accessed 23 August 2023

2.2 YELLOW FEVER

2.2.1 Transmission

Yellow fever is caused by an enveloped single-stranded RNA virus of the genus *Flavivirus* (family *Flaviviridae*) which is primarily transmitted through the bite of infected *Aedes* and *Haemagogus* mosquitoes[21]. It is not transmitted from person-to-person[22].

2.2.2 Prevention

An effective, single-dose vaccine is available for yellow fever[23].

2.2.3 Geographical distribution

According to the WHO, as of 2023, yellow fever is endemic in 34 countries in Africa and 13 countries in Central and South America[23]. Maps showing areas with risk of transmission of yellow fever where vaccination is recommended in Africa[24] and South America[25] are shown in Figure 7, Figure 8.

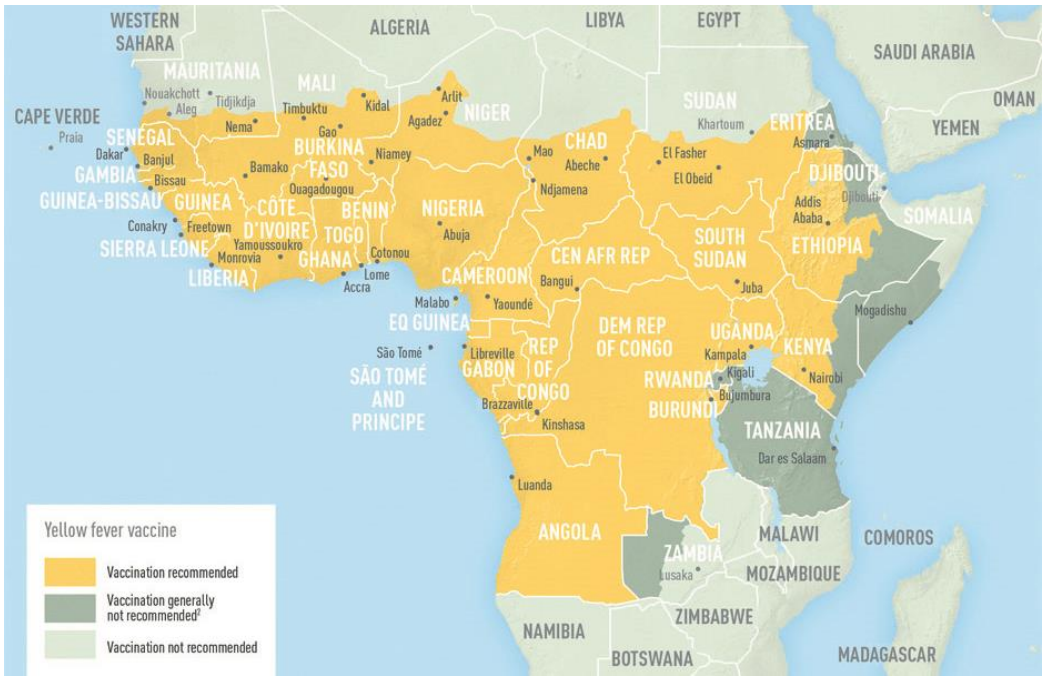

Figure 7 Countries in Africa with risk of yellow fever virus transmission

Reproduced from https://www.cdc.gov/yellowfever/maps/africa.html. Correct as of August 2018.

[21] https://wwwnc.cdc.gov/travel/yellowbook/2020/travel-related-infectious-diseases/yellow-fever Accessed 24 August 2023
[22] https://www.health.ny.gov/diseases/communicable/yellow_fever/fact_sheet.htm Accessed 24 August 2023
[23] https://www.who.int/news-room/fact-sheets/detail/yellow-fever Accessed 24 August 2023
[24] https://www.cdc.gov/yellowfever/maps/africa.html Accessed 24 August 2023
[25] https://www.cdc.gov/yellowfever/maps/south_america.html Accessed 24 August 2023

Figure 8 Countries in South America with risk of yellow fever virus transmission

Reproduced from https://www.cdc.gov/yellowfever/maps/south_america.html. Correct as of May 2018.

2.2.4 New Zealand epidemiology

As of June 2023, there has never been a case of yellow fever detected in New Zealand[26].

2.2.5 Symptoms

The incubation period for yellow fever is 3 – 6 days after exposure, and most cases are asymptomatic[27]. Where symptoms do develop, they may include nausea, vomiting, loss of appetite, fever, headache and muscle pain, and generally last only 3 – 4 days[27]. However, in a small percentage of patients a second, more serious toxic phase develops around 24 hours after initial symptoms resolve[27]. During this phase patients develop high fever, and there are effects on multiple organs including the liver and kidneys, often leading to jaundice (yellowing of the skin and eyes – to which the disease owes its name), abdominal pain and vomiting, dark urine and in some cases bleeding (haemorrhaging) from the eyes, nose,

[26] https://www.health.govt.nz/our-work/diseases-and-conditions/communicable-disease-control-manual/yellow-fever Accessed 24 August 2023
[27] https://www.who.int/news-room/fact-sheets/detail/yellow-fever Accessed 24 August 2023

mouth and stomach[28]. Approximately 50% of patients who enter this toxic phase will die within 7 – 10 days[28].

2.2.6 Excretion of biomarkers of infection

RNA of the yellow fever virus has been shown to persist in wastewater for several days (Figure 9), so could potentially be assessed using WBS (Chandra et al., 2021).

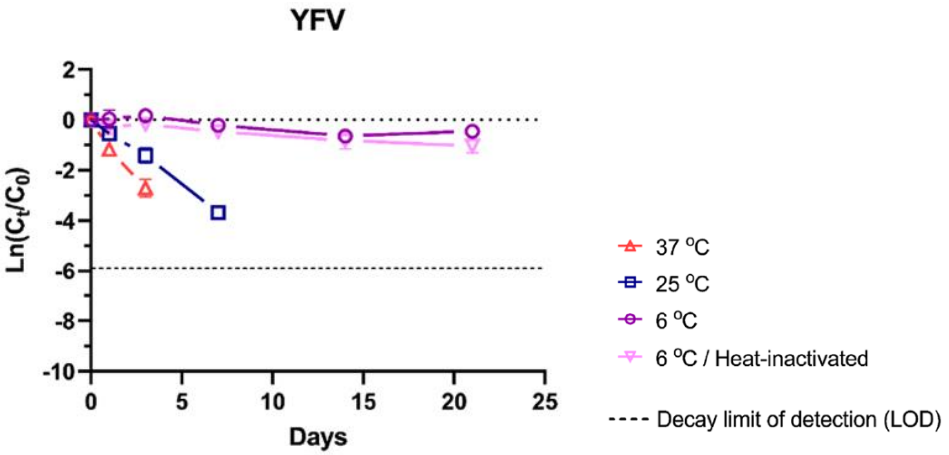

Figure 9 Decay of yellow fever virus RNA in wastewater

Reproduced from Chandra et al. (2021).

Lee et al. (2022) assessed the feasibility and sensitivity limits of WBS for the yellow fever virus and estimated that the load of yellow fever virus shed to wastewater was between 24,000 – 1.86 x 10^{10} genome copies per infected person per day based on 0.8 – 2 L of urine shed daily. Based on this, they estimated the sensitivity of detection for the yellow fever virus, based on varying volumes of wastewater processed (50 – 10,000 mL) and a limit of detection of 50 genome copies recovered per mL of wastewater processed (Figure 10).

Chandra et al. (2023) subsequently developed optimised methodology for recovery and quantification of yellow fever virus from wastewater using spiked samples. Several studies have identified yellow fever virus RNA in urine, as summarised in Table 3. Infectious yellow fever virus has also been isolated from human urine (Barbosa et al., 2018; Li et al., 2019; Phan et al., 2020). However, it is important to note that the yellow fever 17D virus used in the live attenuated yellow fever vaccine has also been detected in urine, with viral RNA of the vaccine strain being detected up to 25 days post-vaccination (Domingo et al., 2011). As such, any positive detection in wastewater would need to consider whether this was due to excretion of viral RNA by a recently vaccinated traveller.

2.2.7 Potential health hazard if present in wastewater

As noted above infectious yellow fever virus has been isolated from human urine (Barbosa et al., 2018; Li et al., 2019; Phan et al., 2020), so where an infected individual urinates on a plane or at the airport there could be a potential health hazard posed to people collecting or

[28] https://www.who.int/news-room/fact-sheets/detail/yellow-fever Accessed 24 August 2023

processing aircraft/airport wastewater samples, or to WWTP staff. However, as the yellow fever virus is not known to be transmitted from person-to-person[29], infection via exposure to wastewater containing urine of infected individuals is considered unlikely.

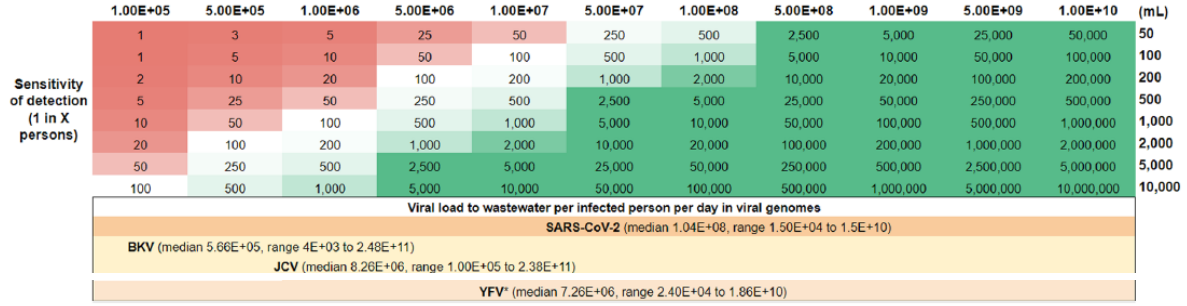

Figure 10 Sensitivity of detection of yellow fever virus in wastewater

Adapted from Lee et al. (2022). SARS-CoV-2, and the BKV and JCV polymoviruses are presented as examples of viruses predominantly shed in faeces (SARS-CoV-2) and urine (BKV and JCV). Values across the top indicate the viral load to wastewater per infected person per day, which are given as a range.

Table 3 Summary of studies assessing excretion of yellow fever virus RNA in urine

Study participants	% positive patients	Shedding dynamics (no. of samples)	Reference
1	100	• Positive 10 days PSO; viral load 9.3×10^6 RNA copies/mL • Positive three weeks PSO; viral load 3.3×10^3 RNA copies/mL	Barbosa et al. (2018)
60	25	• 41% (11/27) positive in acute phase (days 1 – 15 PSO) • 12% (4/33) positive in convalescent phase (days 22, 28, 66 and 69 PSO)	de Rezende et al. (2022)
1	100	• Samples taken on days 5 – 8, 13, 24, 31 and 45 PSO all positive	Phan et al. (2020)
4	100	• Patient 1: negative day 4 PSO, positive days 6 – 9 • Patient 2: positive days 15 and 19 • Patient 3: positive days 10 and 14 • Patient 4: positive days 7, 8, 10, 11, 14, 17, 20 and 32	Li et al. (2019)
1	100	• Samples taken on days 9, 17, 20 and 24 PSO all positive • Samples taken on days 31 and 45 PSO negative	Reusken et al. (2017)

PSO, post symptom onset.

[29] https://www.health.ny.gov/diseases/communicable/yellow_fever/fact_sheet.htm Accessed 24 August 2023

2.3 ZIKA

2.3.1 Transmission

Zika is caused by an enveloped single-stranded RNA virus of the genus *Flavivirus* (family *Flaviviridae*) and is primarily transmitted via *Aedes* mosquitoes[30]. However, it can also be transmitted from mother to child during pregnancy or birth, through sexual contact, blood transfusions, possibly organ transplantation and potentially through breast milk[30] (Figure 11).

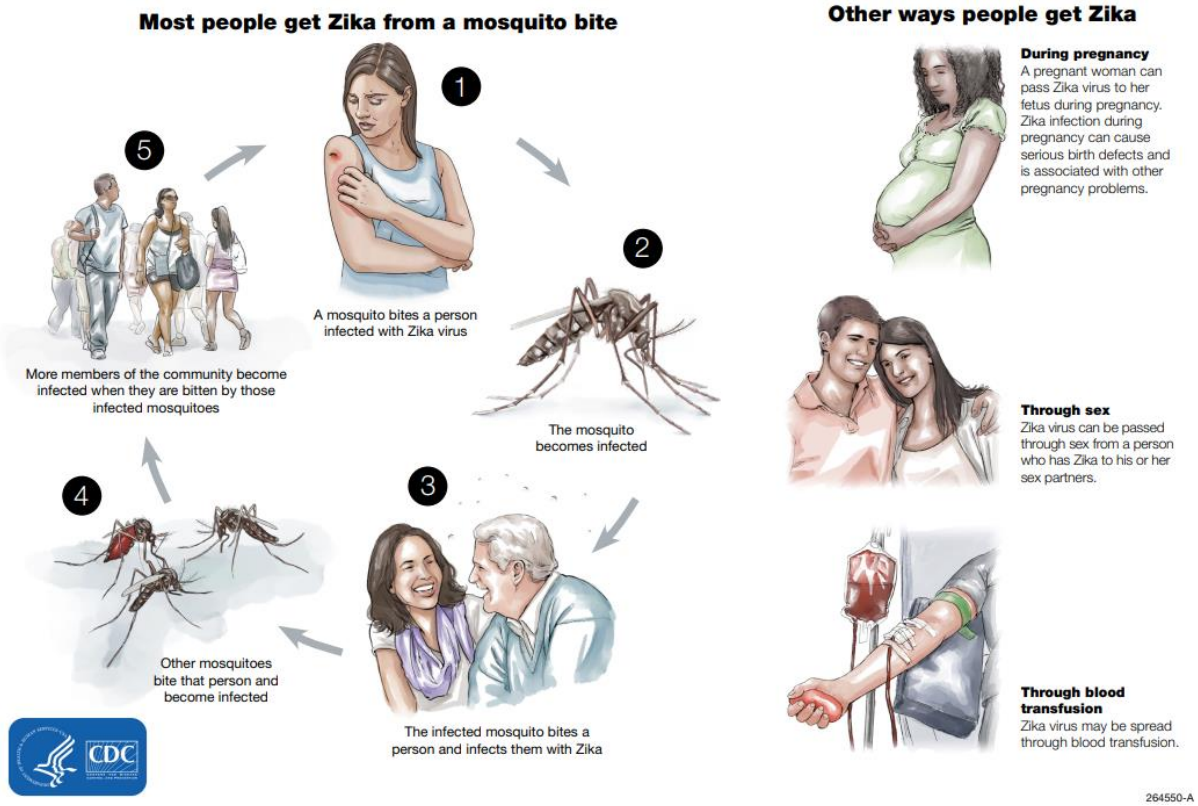

Figure 11 Modes of transmission of Zika virus

Reproduced from https://www.cdc.gov/zika/prevention/transmission-methods.html.

2.3.2 Prevention

As of May 2023, there are no approved vaccines for Zika, however, several candidates are in clinical trials (Essink et al., 2023)[31].

The WHO recommends abstinence or safe sex practices of 3 months and 2 months for men and women respectively returning from areas with active Zika transmission[32].

2.3.3 Geographical distribution

Although the Zika virus was first identified in Uganda in 1947, it rose to prominence in 2015 due to a large epidemic in Brazil and was declared a Public Health Emergency of

[30] https://wwwnc.cdc.gov/travel/yellowbook/2024/infections-diseases/zika Accessed 24 August 2023
[31] https://www.manchester.ac.uk/discover/news/first-human-trial-of-new-zika-vaccine-begins/ Accessed 24 August 2023
[32] https://www.who.int/news-room/fact-sheets/detail/zika-virus Accessed 24 August 2023

International Concern (PHEIC) in February 2016 due to a causal link between Zika virus and congenital malformations[33]. A map showing areas with risk of Zika infection as of 25 July 2022[34] is shown in Figure 12.

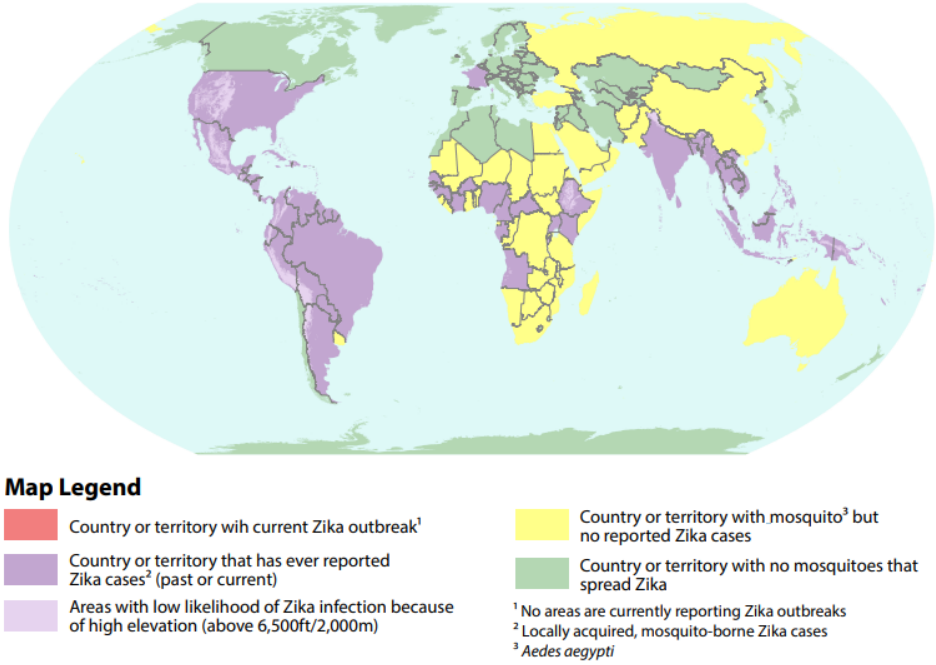

Figure 12 Areas of risk for Zika virus infection (2022)

Reproduced from https://wwwnc.cdc.gov/travel/files/zika-areas-of-risk.pdf Correct as of 6 December 2023.

2.3.4 New Zealand epidemiology

Annual notifications of zika infections in New Zealand between 2006 – 2021 are shown in Figure 13. Notifications spiked in 2014 and peaked at 100 cases in 2016, before dropping to 11 cases in 2017[35].

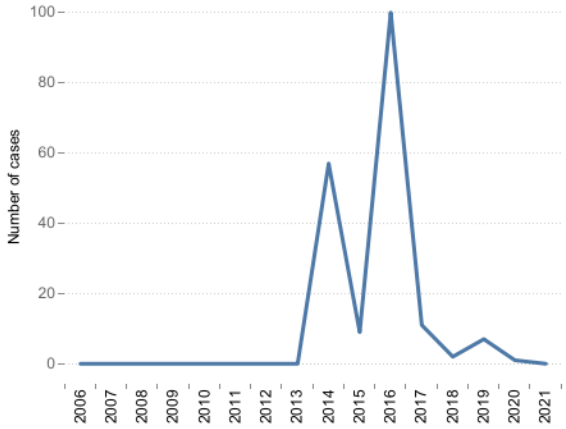

Figure 13 Number of reported Zika virus cases in New Zealand 2006 - 2021
Reproduced from https://www.esr.cri.nz/digital-library/notifiable-disease-dashboard/.

[33] https://www.who.int/news-room/fact-sheets/detail/zika-virus Accessed 24 August 2023
[34] https://wwwnc.cdc.gov/travel/files/zika-areas-of-risk.pdf Accessed 8 April 2024
[35] https://www.esr.cri.nz/expertise/public-health/infectious-disease-intelligence-surveillance/ Accessed 4 April 2024

2.3.5 Symptoms

The incubation period for Zika virus is 3 – 14 days and most infections are asymptomatic[36]. However, Zika can be passed on even before symptom onset[37]. Where symptoms do develop, they are typically mild, lasting for 2 – 7 days and include fever, rash, headache, conjunctivitis, muscle and joint pain and malaise[38]. However, some cases have been associated with the rare neurological disorder Guillain-Barré syndrome, neuropathy (damage to the nerves) and myelitis (inflammation of the spinal cord)[38]. Additionally, infection during pregnancy may result in congenital malformations, including microcephaly, miscarriage, stillbirth, or preterm birth[38]. Zika virus can persist in semen and vaginal secretions[39].

2.3.6 Excretion of biomarkers of infection

The Zika virus can persist in wastewater for days to weeks (Figure 14) so could potentially be assessed using WBS (Chandra et al., 2021; Muirhead et al., 2020; Zhu et al., 2023). Lee et al. (2022) assessed the feasibility and sensitivity limits of WBS for Zika and estimated the load of virus shed to wastewater was between 80,000 – 2.0 x 10^8 genome copies per infected person per day based on 0.8 – 2 L of urine shed daily. Based on this, they estimated the sensitivity of detection for Zika virus, based on varying volumes of wastewater processed (50 – 10,000 mL) and a limit of detection of 50 genome copies recovered per mL processed (Figure 15).

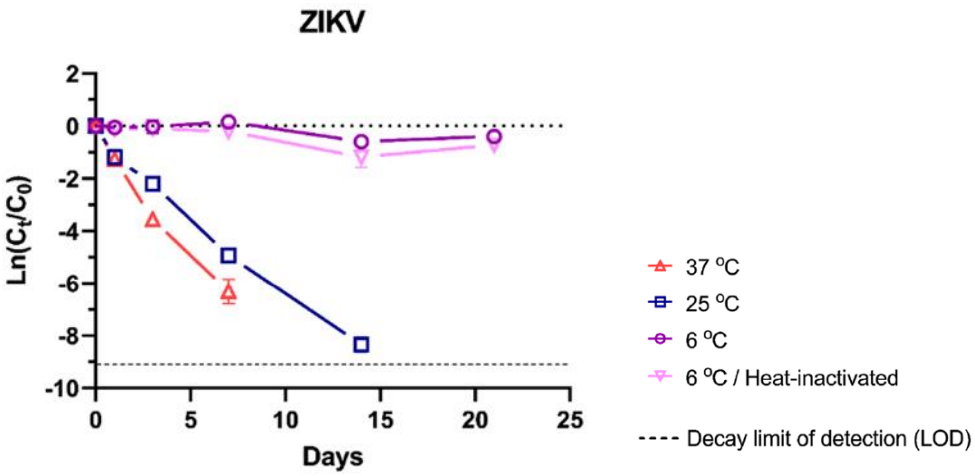

Figure 14 Decay of zika virus RNA in wastewater

Reproduced from Chandra et al. (2021).

[36] https://www.who.int/health-topics/zika-virus-disease Accessed 24 August 2023
[37] https://www.cdc.gov/zika/prevention/transmission-methods.html Accessed 24 August 2023
[38] https://www.who.int/news-room/fact-sheets/detail/zika-virus Accessed 24 August 2023
[39] https://www.gov.uk/guidance/zika-virus-preventing-infection-by-sexual-transmission Accessed 24 August 2023

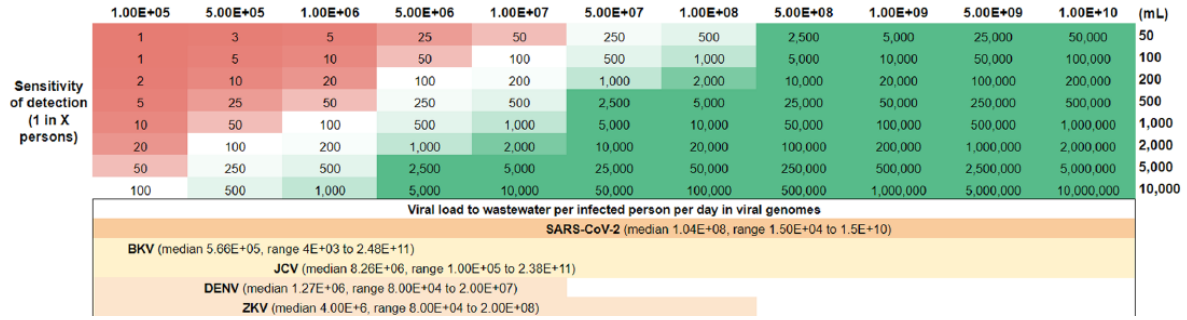

Figure 15 Sensitivity of detection of Zika virus in wastewater

Adapted from Lee et al. (2022). SARS-CoV-2, and the BKV and JCV polymoviruses are presented as examples of viruses predominantly shed in faeces (SARS-CoV-2) and urine (BKV and JCV). DENV, dengue virus; ZKV, Zika virus. Values across the top indicate the viral load to wastewater per infected person per day, which are given as a range.

Chandra et al. (2023) have subsequently developed optimised methodology for recovery and quantification of Zika virus from wastewater using spiked samples. Additionally, Chen and Bibby (2023) have developed a model-based framework to assess the feasibility of monitoring Zika virus using WBS. This framework uses Monte Carlo simulations to generate distributions for total Zika virus RNA shedding by infected individuals and the process limit of detection, allowing the probability of detecting Zika virus RNA in wastewater to be calculated for different infection rates. Additionally, Wong et al. (2024) have shown that WBS can be used to identify Zika hotspots, whereby wastewater and mosquito surveillance showed good geographic and temporal concordance in identifying affected areas in Singapore.

Infectious Zika virus has been isolated from human urine (Bonaldo et al., 2016; Fonseca et al., 2014; Zhang et al., 2016), and several studies have detected Zika virus RNA in urine as summarised in Table 4.

2.3.7 Potential health hazard if present in wastewater

As noted above, RNA of the Zika virus has been shown to persist in wastewater for long periods (up to 28 days at 35°C) (Chandra et al., 2021; Muirhead et al., 2020; Zhu et al., 2023), although it is unclear if this is representative of infectious virus. Infectious virus has been reported in human urine (Bonaldo et al., 2016; Fonseca et al., 2014; Zhang et al., 2016), so where an infected individual urinates on a plane or at the airport there could be a potential health hazard posed to people collecting or processing aircraft/airport wastewater samples, or to WWTP staff. However, further work is needed to assess this.

Table 4 Summary of studies assessing excretion of Zika virus RNA in urine

Study participants	% positive patients	Shedding dynamics (no. of samples)	Reference
70	93	• Positive samples detected from day 0 – 20 of symptom onset • 95% positive (52/55) within first 5 days of symptom onset • 82% (9/11) positive after 5 days PSO	Bingham et al. (2016)
9	44	• Positive samples taken on days 1, 3 (2 samples) and 5 PSO • Negative samples taken on days 1, 2 (3 samples) and 5 • Viral loads ranged from 102 copies/mL - 2.68×10^5 copies/mL	Bonaldo et al. (2016)
1	100	• Positive from day 3 – 13 PSO	Zhang et al. (2016)
6	100	• Samples positive from < 5 days to > 10 days PSO	Gourinat et al. (2015)
9	Unclear	• RNA detected 4 days PSO until up to 14 days PSO • Negative day 2 PSO	Campos et al. (2016)
2 (both suffering from Guillain-Barré syndrome)	100	• Patient 1 positive day 15 post onset of neurological symptoms, negative on day 21 • Patient 2 positive days 5, 15 and 21 post onset of neurological symptoms	Rozé et al. (2016)
1	100	• Positive day 6 PSO	Fonseca et al. (2014)
1	100	• Positive day 5, 6 and 11 PSO • Negative days 18 and 32 PSO	Chan et al. (2017)

PSO, post symptom onset.

2.4 JAPANESE ENCEPHALITIS

2.4.1 Transmission

Japanese encephalitis is a vector-borne viral zoonosis caused by Japanese Encephalitis Virus (JEV), an enveloped single-stranded RNA virus of the genus *Flavivirus* (family *Flaviviridae*) and transmitted by the bite of *Culex* mosquitoes[40]. The virus exists in a cycle between *Culex* mosquitoes and vertebrate animal hosts (predominantly pigs and wading birds)[40] (Figure 16). Humans (and horses) are dead-end hosts as they do not develop sufficiently high concentrations of virus for infection of new mosquitoes[40]. The virus is not transmitted from person-to-person or by touching infected animals or eating infected animal products[41].

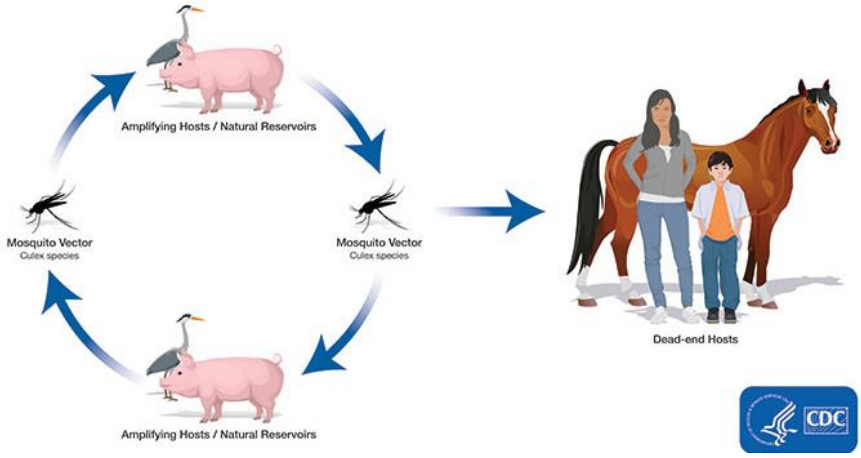

Figure 16 Japanese encephalitis virus transmission cycle

Reproduced from https://www.cdc.gov/japaneseencephalitis/transmission/index.html

2.4.2 Prevention

Several vaccines exist for Japanese encephalitis, including three inactivated vaccines and one live attenuated vaccine[42].

2.4.3 New Zealand epidemiology

Japanese encephalitis has never been reported in New Zealand, although it has been found in Australia[43], where on 4 March 2022 it was declared a Communicable Disease Incident of National Significance[44], with 24 cases and three deaths attributed to Japanese encephalitis virus infection in Australia in 2022 (Yakob et al., 2022). Several species of *Culex* mosquito, both native and introduced, are present in New Zealand[45].

[40] https://www.cdc.gov/japaneseencephalitis/transmission/index.html Accessed 24 August 2023
[41] https://www.health.nsw.gov.au/Infectious/factsheets/Pages/japanese_encephalitis.aspx Accessed 24 August 2023
[42] https://www.who.int/teams/health-product-policy-and-standards/standards-and-specifications/vaccine-standardization/japanese-encephalitis Accessed 24 August 2023
[43] https://www.vetcouncil.org.nz/Web/News/Articles/2022/Japanese_encephalitis.aspx Accessed 24 August 2023
[44] https://www.health.gov.au/diseases/japanese-encephalitis Accessed 24 August 2023
[45] https://teara.govt.nz/en/sandflies-and-mosquitoes/page-2 Accessed 8 April 2024

2.4.4 Geographic distribution

JEV is found in Asia, Oceania, Australia, Pakistan and from Japan to India[46] (Figure 17).

Figure 17 Global distribution of Japanese encephalitis virus

Reproduced from https://www.cdc.gov/japaneseencephalitis/maps/index.html. As of 7 April 2023.

2.4.5 Symptoms

Most cases of Japanese encephalitis are asymptomatic or have only mild symptoms[47]. However, a small percentage of cases (> 1%) develop neurological illness (encephalitis) around 5 – 15 days after infection[48]. Initial symptoms may include fever, headache and vomiting, followed by neurological symptoms such as disorientation, tremors, seizures and coma[47,48]. Approximately 20 – 30% of patients who develop encephalitis die and 30 – 50% of survivors have long-term cognitive, neurological or psychiatric symptoms[48].

2.5.6 Excretion of biomarkers of infection

Japanese encephalitis virus RNA has been detected in archived wastewater samples from two Australian WWTPs using targeted PCR (Fanok et al., 2023), with JEV detections occurring during a timeframe that coincided with a cluster of acute encephalitis cases and JEV detections in mosquitoes.

[46] https://www.ecdc.europa.eu/en/japanese-encephalitis/facts Accessed 24 August 2023
[47] https://www.cdc.gov/japaneseencephalitis/index.html Accessed 24 August 2023
[48] https://www.cdc.gov/japaneseencephalitis/symptoms/index.html Accessed 24 August 2023

Infectious Japanese encephalitis virus has been isolated from human urine (Huang et al., 2017). Viral RNA has also been detected in urine from an infected patient from days 14 – 26 PSO (not detected on day 28) (Huang et al., 2017). However, a separate study of urine samples collected from 52 patients between 3 – 9 days after symptom onset failed to detect any viral RNA (Zhao et al., 2013). Bharucha et al. (2019) also failed to detect viral RNA in urine collected from 41 patients and note that this could be due to the observed rapid degradation of viral RNA at 4°C and -80°C.

2.5.7 Potential health hazard if present in wastewater

Given infectious Japanese encephalitis virus has been isolated from human urine (Huang et al., 2017), where an infected individual urinates on a plane or at the airport there could be a potential health hazard posed to people collecting or processing aircraft/airport wastewater samples, or to WWTP staff. However, as no person-to-person transmission has been documented[49], this is considered unlikely.

2.5 WEST NILE FEVER

2.5.1 Transmission

West Nile fever (WNF) is a viral disease caused by an enveloped single-stranded RNA virus of the genus *Flavivirus* (family *Flaviviridae*) and is predominantly transmitted to humans via the bite of *Culex* mosquitoes (Clark & Schaefer, 2023). WNF is closely related to Japanese encephalitis[50] and exists in a cycle between mosquitoes and bird hosts which amplify the virus to high levels allowing for infection of other mosquitoes when they bite an infected bird[51] (Figure 18). WNF is not transmitted by direct contact with infected animals or people[52].

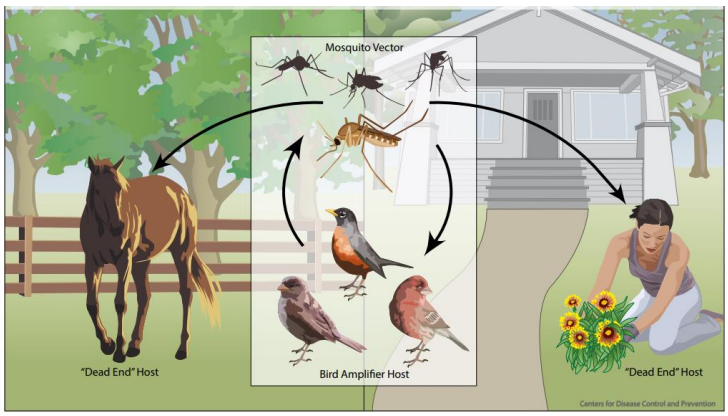

Figure 18 West Nile virus transmission cycle

Reproduced from
https://www.cdc.gov/westnile/resources/pdfs/13_240124_west_nile_lifecycle_birds_plainlanguage_508.pdf

[49] https://www.health.nsw.gov.au/Infectious/factsheets/Pages/japanese_encephalitis.aspx Accessed 24 August 2023
[50] https://www.cdc.gov/japaneseencephalitis/transmission/index.html Accessed 24 August 2023
[51] https://www.cdc.gov/westnile/resources/pdfs/13_240124_west_nile_lifecycle_birds_plainlanguage_508.pdf Accessed 24 August 2023
[52] https://doh.wa.gov/you-and-your-family/illness-and-disease-z/west-nile-virus Accessed 24 August 2023

2.5.2 Prevention

Although there are vaccines for West Nile virus for horses, no licensed human vaccines are currently available (Saiz, 2020).

2.5.3 Geographical distribution

West Nile fever is commonly found in Europe, Africa, the Middle East, West Asia and North America[53] (Figure 19). Outbreaks generally occur along major bird migratory routes[53]. A strain of West Nile virus known as Kunjin virus is endemic in Australia[54], although cases are rare (43 cases since 1991)[55].

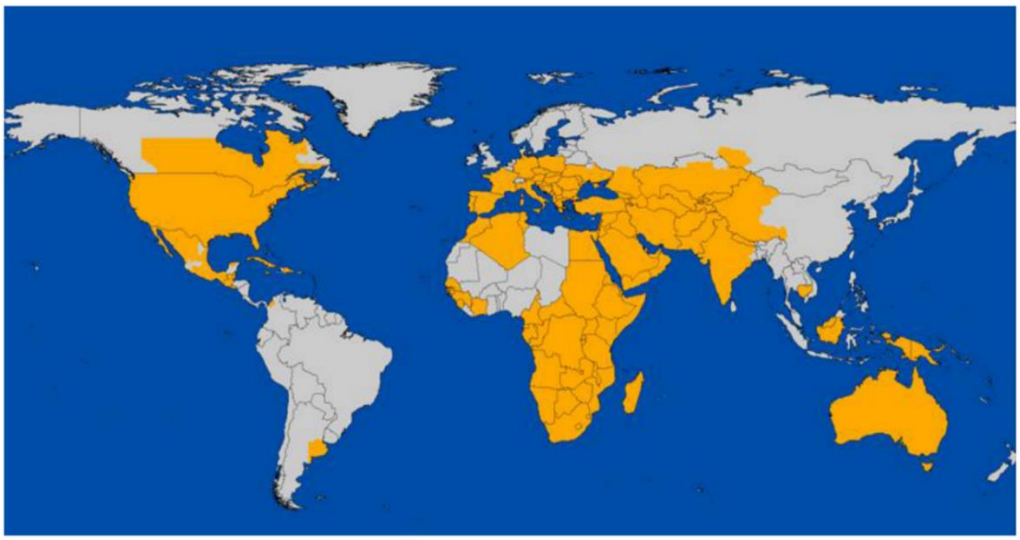

Figure 19 Global distribution of West Nile virus (2006)

Reproduced from Reisen (2013).

2.5.4 New Zealand epidemiology

West Nile virus has never been reported in New Zealand[56].

2.5.5 Symptoms

The incubation period for West Nile fever is generally 2 – 6 days but can range from 2 – 14 days, or up to several weeks where an individual is immunocompromised[57]. Approximately 80% of cases are asymptomatic[58]. Where symptoms do develop, they often include fever with headache, joint pain and body ache, vomiting, diarrhoea and in some cases a rash[58]. Most individuals experiencing these symptoms recover completely, although fatigue and

[53] https://www.who.int/news-room/fact-sheets/detail/west-nile-virus Accessed 24 August 2023
[54] https://www.dpi.nsw.gov.au/animals-and-livestock/horses/health-and-disease/west-nile-virus Accessed 24 August 2023
[55] https://www.betterhealth.vic.gov.au/health/conditionsandtreatments/west-nile-virus Accessed 24 August 2023
[56] https://www.mpi.govt.nz/dmsdocument/51988-Surveillance-Magazine-Vol-49-No-2-June-2022 Accessed 20 June 2023
[57] https://www.cdc.gov/westnile/healthcareproviders/healthCareProviders-ClinLabEval.html Accessed 24 August 2023
[58] https://www.cdc.gov/westnile/symptoms/index.html Accessed 24 August 2023

weakness may persist for weeks - months[59]. In approximately 1/150 infections, severe illness such as meningitis or encephalitis will develop[60]. Symptoms of severe illness may include headache, high fever, stiff neck, muscle weakness, disorientation, stupor, vision loss, convulsions/tremors, numbness and paralysis[60]. Approximately 1 in 10 people who develop severe illness will die, and for the remainder, recovery may take weeks – months and some central nervous system effects may be permanent[60].

2.5.6 Excretion of biomarkers of infection

No studies directly assessing the presence of West Nile virus in wastewater were identified during the preparation of this report. However, Lee et al. (2022) have assessed the feasibility and sensitivity limits of WBS for West Nile virus and estimated that the load of virus shed to wastewater was between 800,000 – 2.0 x 10^{10} genome copies per infected person per day based on 0.8 – 2 L of urine shed daily. Based on this, they estimated the sensitivity of detection for West Nile virus, based on varying volumes of wastewater processed (50 – 10,000 mL) and a limit of detection of 50 genome copies recovered per mL of wastewater processed (Figure 20).

Infectious West Nile virus has been isolated from human urine (Barzon et al., 2014; Papa et al., 2014) and several studies have detected viral RNA in urine, as summarised in Table 5.

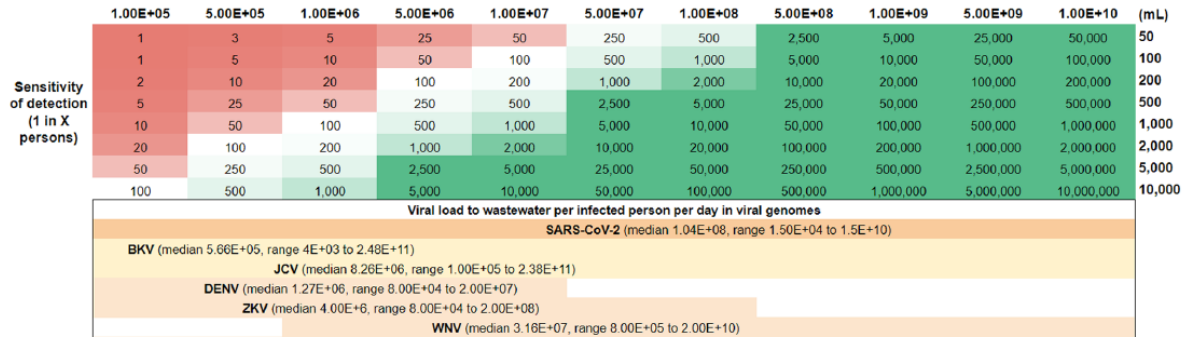

Figure 20 Sensitivity of detection of West Nile virus in wastewater

Adapted from Lee et al. (2022). SARS-CoV-2, and the BKV and JCV polymoviruses are presented as examples of viruses predominantly shed in faeces (SARS-CoV-2) and urine (BKV and JCV). DENV, dengue virus; ZKV, Zika virus; WNV, West Nile virus. Values across the top indicate the viral load to wastewater per infected person per day, which are given as a range.

2.5.7 Potential health hazard if present in wastewater

As noted above, infectious West Nile virus has been isolated from human urine (Barzon et al., 2014; Papa et al., 2014), so where an infected individual urinates on a plane or at the airport there could be a potential health hazard posed to people collecting or processing aircraft/airport wastewater samples, or to WWTP staff. However, as this virus is not transmitted directly from person-to-person[61] this is considered unlikely.

[59] https://www.cdc.gov/westnile/healthcareproviders/healthCareProviders-ClinLabEval.html Accessed 24 August 2023
[60] https://www.cdc.gov/westnile/symptoms/index.html Accessed 24 August 2023
[61] https://doh.wa.gov/you-and-your-family/illness-and-disease-z/west-nile-virus Accessed 24 August 2023

Table 5 Summary of studies assessing excretion of West Nile virus RNA in urine

Study participants	% positive patients	Shedding dynamics (no. of samples)	Reference
17	100	• Positive samples obtained from 2 – 21 days PSO • Viral load ranged from < 100 copies/mL (on day 21) – 1.5×10^7 copies/mL	Barzon et al. (2014)
1	100	• Positive 8 days PSO • Negative days 11 – 15 PSO	Tonry et al. (2005)
1	100	• Positive days 7, 10, 20 and 30 PSO • Negative 50 days PSO	Velasco et al. (2020)
48	58.3	• Positive samples collected from days 3 – 19 PSO • Viral load from 17 - 2.2×10^8 copies/mL • Samples collected days 34 and 35 negative	Lustig et al. (2016)
35	40	• 45% (9/20) positive in first week of illness • 33% (5/15) positive in second week of illness	Papa et al. (2014)
95	50.5	• RNA detected from days 1 – 41 PSO • 53% (34/64) positive in first 10 days from symptom onset • 33% (7/21) positive days 11 – 20 PSO • 70% (7/10) positive days 20+ (days 21, 22, 28, 31, 35, 39, 41)	Gdoura et al. (2022)
9	100	• 26% (10/38) positive, all positive samples collected within 18 days PSO • Negative days 19 - 144 DPO	(Gorchakov et al., 2019)

PSO, post symptom onset.

2.6 RIFT VALLEY FEVER

2.6.1 Transmission

Rift Valley fever (RFV) is an acute viral haemorrhagic fever caused by an enveloped single-stranded RNA virus of the *Phlebovirus* genus (family *Bunyaviridae*)[62] (Boshra et al., 2011). Rift Valley fever is most often seen in domesticated livestock (e.g., sheep, cattle, goats, camels, buffalo) in eastern and southern Africa[62]. However, it can also cause disease in humans and is transmitted by mosquitoes (and in rare cases other biting insects), or acquired through contact with blood, bodily fluid or tissue of infected animals[63] (Figure 21). No person-to-person transmission has ever been documented[63].

2.6.2 Prevention

Although a vaccine for RFV has been developed it is not licensed or commercially available, only being used to protect laboratory and veterinary workers at high risk of exposure[64].

2.6.3 Geographical distribution

In addition to southern and eastern Africa, cases have also been reported in other parts of Africa, and in Saudi Arabia and Yemen[65], as shown in Figure 22. The RFV status of other countries is unknown[65], although it has been speculated that the emergence of RFV in the Middle East, Comoros Archipelago and northern Egypt suggests the geographical range of this virus may be increasing (Mansfield et al., 2015). There have been several documented human outbreaks of RFV, as summarised in Table 6.

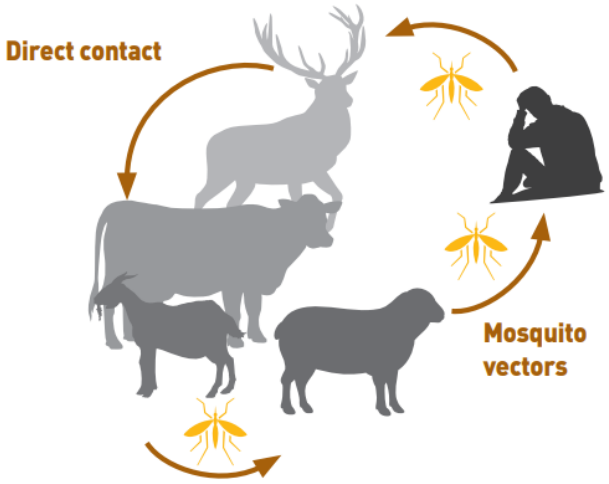

Figure 21 Modes of transmission of Rift Valley fever

Reproduced from https://www.mpi.govt.nz/dmsdocument/51436-Rift-Valley-Fever-fact-sheet.

[62] https://www.cdc.gov/vhf/rvf/about.html Accessed 23 August 2023
[63] https://www.cdc.gov/vhf/rvf/transmission/index.html Accessed 23 August 2023
[64] https://www.who.int/teams/health-product-policy-and-standards/standards-and-specifications/vaccine-standardization/rift-valley-fever Accessed 23 August 2023
[65] https://www.cdc.gov/vhf/rvf/outbreaks/distribution-map.html Accessed 23 August 2023

Figure 22 Distribution of Rift Valley fever

Reproduced from https://www.cdc.gov/vhf/rvf/outbreaks/distribution-map.html (last reviewed 8 June 2023). Blue, countries reporting endemic RFV and substantial outbreaks; green, countries reporting few cases, periodic isolation of virus or serologic evidence of infection; brown, RFV status unknown.

2.6.4 New Zealand epidemiology

As of August 2023, no cases of Rift Valley fever have ever been notified in New Zealand.

2.6.5 Symptoms

The incubation period of RFV is around 2 – 6 days following exposure[66]. Most infections are asymptomatic, or individuals experience only mild symptoms such as fever, back pain, weakness and dizziness, and typically recover within 2 – 7 days[66]. However, around 8 – 10% of infected individuals develop much more severe symptoms which may include:

- Ocular disease, where lesions develop on the eyes around 1 – 3 weeks after symptom onset, which may lead to permanent vision loss[66].
- Encephalitis (< 1% of cases) which develops 1 – 4 weeks after symptom onset, causing headache, coma or seizures. Although death from Rift Valley fever encephalitis is rare, the neurological effects may be severe and long-lasting[66].

[66] https://www.cdc.gov/vhf/rvf/symptoms/index.html Accessed 24 August 2023

Table 6 Outbreaks of Rift Valley fever since 2000

Year	Countries affected	No. confirmed/suspected cases	Case fatality rate (%)	Reference
2016 - present	Uganda	4	0	Shoemaker et al. (2019)
2019	Mayotte Island (French Island in the Comoros Archipelago)	142	0	Youssouf et al. (2020)
2018	Kenya	26	23	
2017	Gambia*	1	100	
2016	Angola[#]	1	0	Liu et al. (2017)
2016	Niger	348	9.5	
2015	Mauritania	31	42	Boushab et al. (2016)
2013 - 2014	Senegal (related cases in animals in Mauritania)	11	0	Sow et al. (2016)
2012	Mauritania	41	32	Sow et al. (2014)
2009 - 2011	South Africa (related cases in animals in Namibia)	302	8	Archer et al. (2013) Monaco et al. (2013)
2010	Mauritania	30	10	Faye et al. (2014)
2010	South Africa	172	9	
2006 - 2007	Kenya, Tanzania and Somalia	392 Kenya 309 Tanzania	26 Kenya 47 Tanzania	Nguku et al. (2010) Mohamed et al. (2010)
2000	Saudi Arabia and Yemen	884 Saudi Arabia 1,087 Yemen	14 Saudi Arabia 11 Yemen	Shoemaker et al. (2002)

Data from https://www.cdc.gov/vhf/rvf/outbreaks/summaries.html. * Reported in Senegal after medical evacuation of patient from Gambia. [#]Reported in China in a patient who had returned from working in Angola.

- Haemorrhagic fever (< 1% of cases) which typically begins around 2 – 4 days after disease onset with jaundice followed by vomiting blood, bleeding from the gums, nose, and skin, and bloody stool. Around 50% of haemorrhagic cases are fatal, with death usually occurring 3 – 6 days after symptom onset[67].

2.6.6 Excretion of biomarkers of infection

No studies assessing the presence of the Rift Valley fever virus in wastewater were identified during preparation of this report.

Infectious Rift Valley fever virus has been isolated from human urine (Li et al., 2019). Viral RNA has also been detected in a urine sample from an infected individual taken 74 days after the onset of symptoms (Haneche et al., 2016). In the same study, viral RNA was not detectable 117 days after symptom onset, and viral RNA could not be detected in a stool sample taken 82 days after symptom onset.

2.6.7 Potential health hazard if present in wastewater

As noted above, infectious Rift Valley fever virus has been isolated from human urine (Li et al., 2019), so where an infected individual urinates on a plane or at the airport there could be a potential health hazard posed to people collecting or processing aircraft/airport wastewater samples, or to WWTP staff. However, as no person-to-person transmission has ever been documented[68], this is unlikely.

2.7 CRIMEAN-CONGO HAEMORRHAGIC FEVER

2.7.1 Transmission

Crimean-Congo haemorrhagic fever is a viral illness caused by an enveloped single-stranded RNA virus of the *Nairovirus* genus (family *Bunyaviridae*) (Wang et al., 2012) . Crimean-Congo haemorrhagic fever is primarily transmitted by *Hyalomma* ticks but can also be transmitted via contact with tissues of infected animals, with hosts including a range of wild and domestic animals (including livestock)[69]. Person-to-person transmission may also occur where there is close contact with infected blood, bodily fluids or tissues[69] (Figure 23). Cases of vertical transmission from mother to baby have also been reported, and sexual transmission may also occur (reviewed by Portillo et al. (2021)).

2.7.2 Prevention

There is currently no vaccine for Crimean-Congo haemorrhagic fever [70].

[67] https://www.cdc.gov/vhf/rvf/symptoms/index.html Accessed 24 August 2023
[68] https://www.cdc.gov/vhf/rvf/transmission/index.html Accessed 24 August 2023
[69] https://www.who.int/news-room/fact-sheets/detail/crimean-congo-haemorrhagic-fever Accessed 24 August 2023
[70] https://www.who.int/news-room/fact-sheets/detail/crimean-congo-haemorrhagic-fever Accessed 24 August 2023

2.7.3 Geographical distribution

Crimean-Congo haemorrhagic fever is endemic in Africa, Asia, the Balkans and the Middle East[71], as shown in Figure 24. There are an estimated 10,000 – 15,000 cases of Crimean-Congo haemorrhagic fever annually, with around 500 of these being fatal[72]

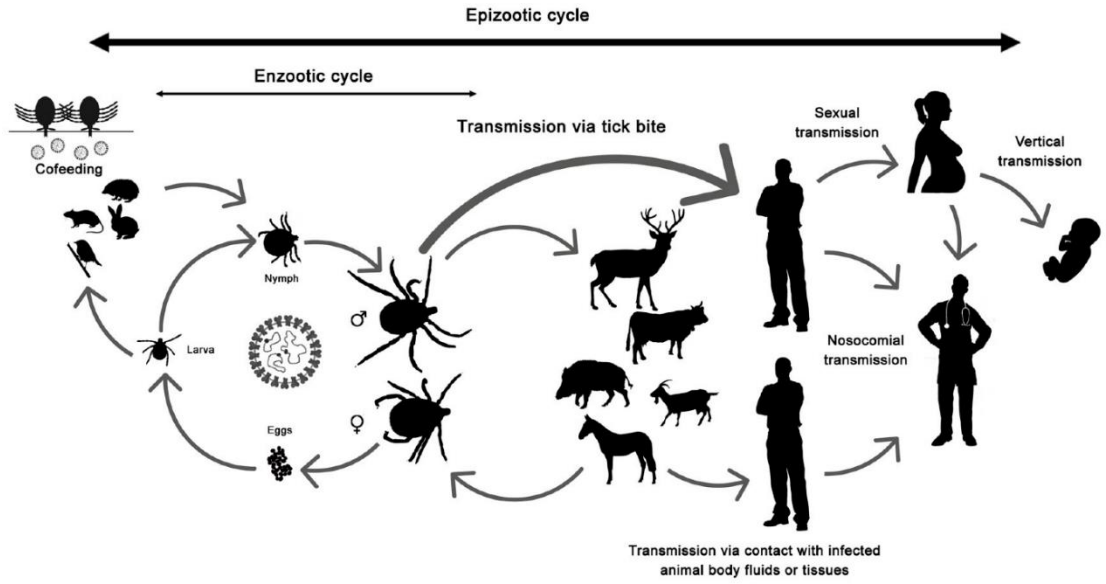

Figure 23 Routes of transmission of Crimean-Congo haemorrhagic fever

Reproduced from Portillo et al. (2021).

2.7.4 New Zealand epidemiology

There has never been a reported case of Crimean-Congo haemorrhagic fever in New Zealand[73].

2.7.5 Symptoms

The incubation period for Crimean-Congo haemorrhagic fever is generally 3 – 7 days and approximately 80% of cases are asymptomatic or only display mild symptoms[70]. Where symptoms develop, they start suddenly with high fever, back and joint pain, headache, vomiting and stomach pain[74]. Patients also commonly exhibit flushed faces with red eyes and throat, and petechiae (red spots) on the roof of the mouth[74]. Some cases may also exhibit jaundice and changes in sensory perception and mood[74]. Around day four of the illness, patients may start to haemorrhage, evidenced by severe nosebleeds, large areas of severe bruising and bleeding from injection sites, which may last for around two weeks[74]. In past outbreaks, 9 – 50% of patients hospitalised due to Crimean-Congo haemorrhagic fever have died[74].

[71] https://www.who.int/health-topics/crimean-congo-haemorrhagic-fever Accessed 24 August 2023
[72] https://www.ecdc.europa.eu/en/crimean-congo-haemorrhagic-fever/facts/factsheet Accessed 24 August 2023
[73] https://www.health.govt.nz/our-work/diseases-and-conditions/communicable-disease-control-manual/viral-haemorrhagic-fevers Accessed 24 August 2023
[74] https://www.cdc.gov/vhf/crimean-congo/symptoms/index.html Accessed 24 August 2023

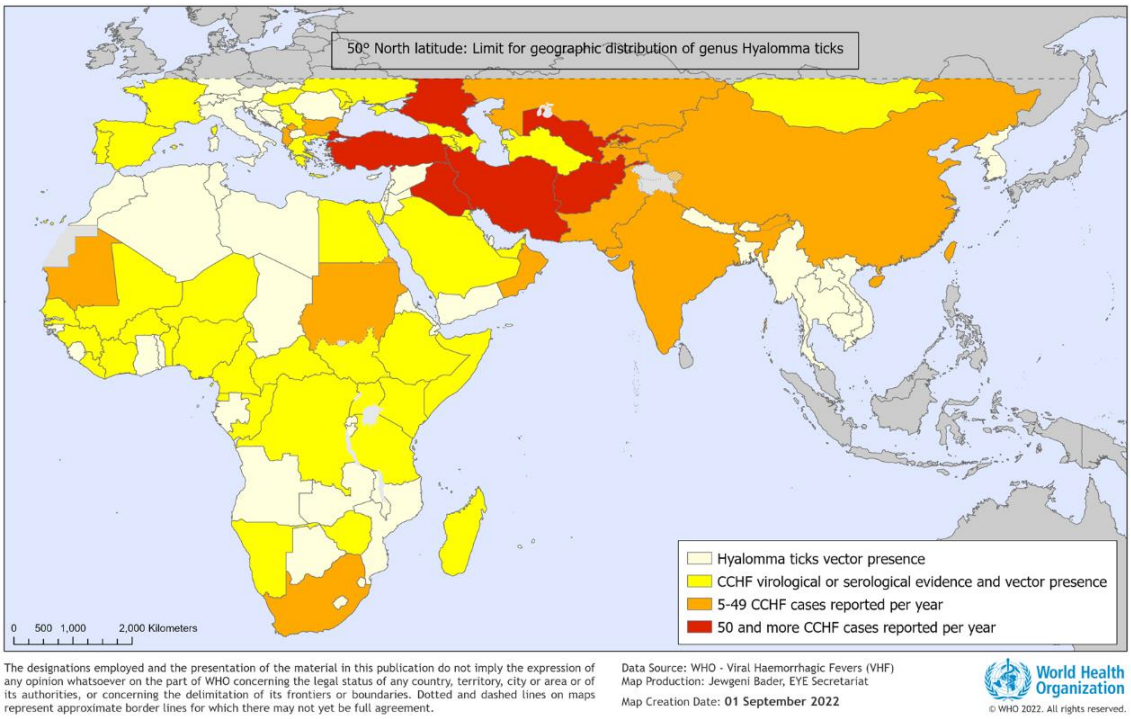

Figure 24 Global distribution of Crimean-Congo haemorrhagic fever (2022)

Reproduced from https://www.who.int/health-topics/crimean-congo-haemorrhagic-fever

2.7.6 Excretion of biomarkers of infection

No WBS studies assessing the presence of the Crimean-Congo haemorrhagic fever virus in wastewater were identified during preparation of this report. Several studies have identified RNA of the Crimean-Congo haemorrhagic fever virus in urine, as summarised in Table 7.

2.7.7 Potential health hazard if present in wastewater

No information relating to potential transmission of Crimean-Congo haemorrhagic fever virus via wastewater (e.g., while sampling, processing samples in the laboratory, or at the WWTP) was identified during preparation of this report. However, as transmission via infected bodily fluids may occur[75], the potential for infection via wastewater should be considered.

[75] https://www.who.int/news-room/fact-sheets/detail/crimean-congo-haemorrhagic-fever Accessed 24 August 2023

Table 7 Summary of studies assessing excretion of Crimean-Congo haemorrhagic fever RNA in urine

Study participants	% positive patients	Shedding dynamics (no. of samples)	Reference
18	67	• RNA detected from days 3 – 16 PSO • 0% (0/2) positive days 1 – 2 • 36.4% (8/22) samples positive days 3 – 5 PSO • 50% (28/56) samples positive days 6 – 9 PSO • 69% (20/29) samples positive days 10 – 14 PSO • 11% (1/9) samples positive days 15 – 19 PSO	Yagci-Caglayik et al. (2020)
3	67	• Patient 1 positive day 4 PSO; viral load 7×10^3 copies/mL • Patient 2 positive day 7 PSO; viral load 1×10^4 copies/mL • Patient 3 negative on day 7 PSO	Bodur et al. (2010)
1	100	• Positive day 3 PSO using RT-qPCR • Using colorimetric RT-LAMP RNA also detected days 8 and 13 of convalescence	Febrer-Sendra et al. (2023)
5	100	• Patient 1 positive day 36 PSO • Patient 2 positive days 6 and 19 PSO • Patient 3 positive day 1 PSO • Patient 4 positive day 1 PSO, negative days 10 and 25 PSO • Patient 5 positive day 25 PSO, negative days 4, 11, 15, 18, 34 and 40 PSO	Thomas et al. (2012)

PSO, post symptom onset; LAMP, loop-mediated isothermal amplification

2.8 CHIKUNGUNYA

2.8.1 Transmission

Chikungunya is a viral disease caused by an enveloped single-stranded RNA virus of the genus *Alphavirus* (family *Togaviridae*) which is predominantly transmitted through the bite of *Aedes* mosquitos[76]. It is not spread from person-to-person[77].

2.8.2 Prevention

There is currently no vaccine available for chikungunya[77].

2.8.3 Geographic distribution

Chikungunya is predominantly found in Africa, Asia and the America's, although there have been sporadic outbreaks in other countries[77,78]. The global distribution of chikungunya as of October 2020[79] is shown in Figure 25. In 2023, as of December, ~460,000 cases and over 360 deaths had been reported internationally, with most of these cases reported in South America[80].

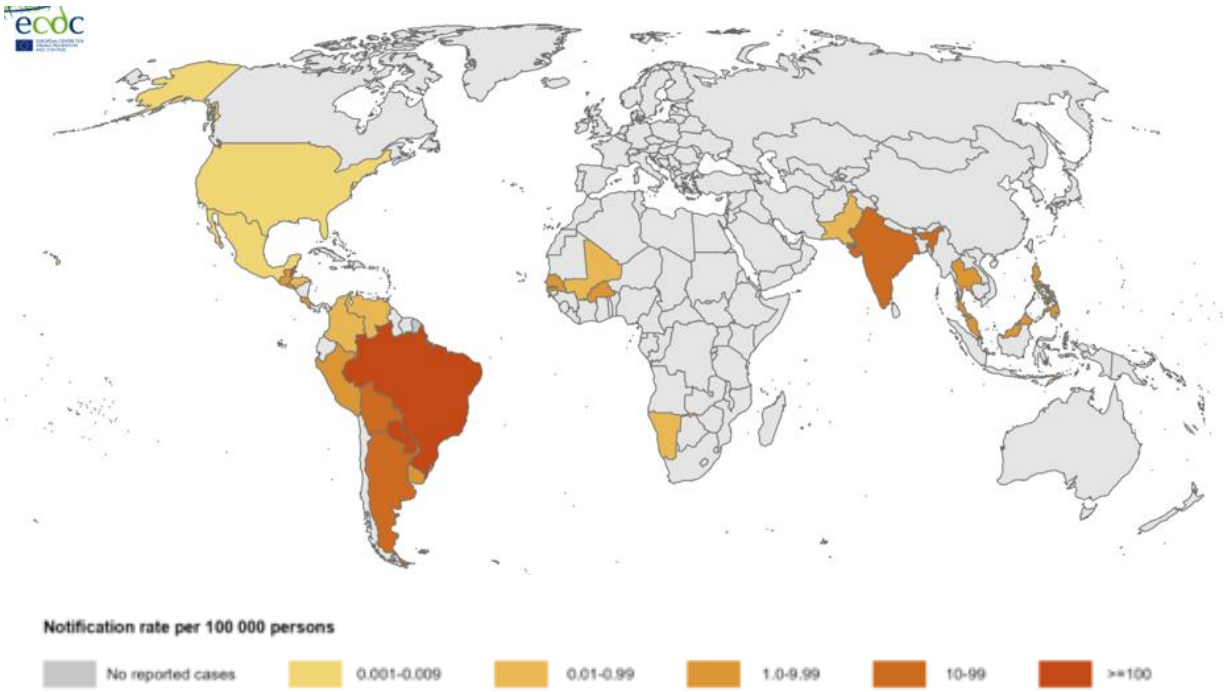

Figure 25 Global distribution of reported Chikungunya cases

Reproduced from https://www.ecdc.europa.eu/en/publications-data/12-month-chikungunya-virus-disease-case-notification-rate-100-000-population-3. Notification rate per 100,000 persons in last 12 months. Correct as of 21 March 2024.

[76] https://www.who.int/news-room/fact-sheets/detail/chikungunya Accessed 24 August 2023
[77] https://www.paho.org/en/topics/chikungunya. Accessed 24 August 2023
[78] https://www.cdc.gov/chikungunya/geo/chikungunya-in-the-us.html Accessed 24 August 2023
[79] https://www.ecdc.europa.eu/en/publications-data/12-month-chikungunya-virus-disease-case-notification-rate-100-000-population-3 Accessed 8 A
[80] https://www.precisionvaccinations.com/chikungunya-outbreaks. Accessed 8 April 2024

2.8.4 New Zealand epidemiology

Annual notifications of chikungunya infections in New Zealand between 2006 – 2021 are shown in Figure 26. Notifications spiked between 2014 – 2017, peaking at 48 cases in 2015[81]. Only 5 cases were notified in 2020 and no cases were notified in 2021. However, this is likely to have been impacted by the COVID-19 associated border closures.

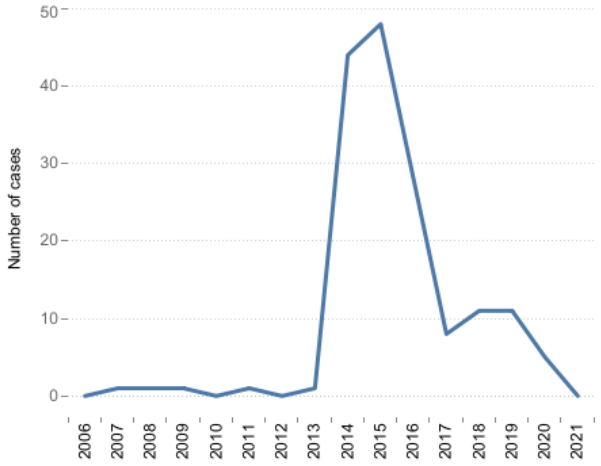

Figure 26 Number of reported chikungunya cases in New Zealand 2006 - 2021

Reproduced from https://www.esr.cri.nz/digital-library/notifiable-disease-dashboard/.

2.8.5 Symptoms

Approximately 3 – 28% of chikungunya infections are asymptomatic[82]. Where individuals develop symptoms, the incubation period is typically 3 – 7 days[82]. Symptoms of chikungunya include sudden onset high fever (typically > 39°C) and joint pain, with fevers typically lasting for a week or less. Joint pain is often severe and debilitating, affecting multiple joints particularly in the hands and feet. Other symptoms include headache, nausea, vomiting, conjunctivitis and myalgia (muscle ache/pain). A rash may also develop after the onset of fever. This is generally maculopapular (a rash with both flat and raised parts) and affects the trunk and extremities and in some cases the palms, soles of the feet and face[82]. The acute symptoms of chikungunya generally resolve within 7 – 10 days[82]. However, some patients may experience a relapse of rheumatological symptoms in the months after infection, and up to 80% of patients may experience prolonged fatigue and joint pain for months to years after infection[82]. Cases of chikungunya are, however, rarely fatal[83].

[81] https://www.esr.cri.nz/expertise/public-health/infectious-disease-intelligence-surveillance/ Accessed 4 April 2024
[82] https://wwwnc.cdc.gov/travel/yellowbook/2024/infections-diseases/chikungunya Accessed 4 April 2024
[83] https://www.cdc.gov/chikungunya/symptoms/index.html Accessed 24 August 2023

2.8.6 Excretion of biomarkers of infection

The chikungunya virus has been detected in wastewater samples collected in Portugal using targeted PCR (Monteiro et al., 2023), and collected in India using metagenomics (Stockdale et al., 2023). In the study by Monteiro et al. (2023), 273 archived wastewater samples collected from May 2022 to April 2023 from 10 WWTPs across Portugal detected chikungunya virus in 11% of samples, despite the fact that autochthonous (locally acquired) cases had not been detected in Portugal during the study period.

Several studies have also identified RNA of the chikungunya virus in urine, as summarised in Table 8.

Table 8 Summary of studies assessing excretion of chikungunya viral RNA in urine

Study participants	% positive patients	Shedding dynamics (no. of samples)	Reference
152	23 (30% of females, 9,6% of males)	• RNA detected from day 0 of symptom onset up to 95 days PSO • Median time till RNA no longer detectable of 25.3 days PSO	Martins et al. (2022)
32	6	• 8% (2/24) positive during first week PSO • Positive samples collected days 3 and 5 PSO • 0% (0/8) positive after first week PSO	Musso et al. (2016)
1	100	• Urine positive 30 days PSO	Bandeira et al. (2016)
6	100	• Unclear what stage of infection samples were taken but patients were symptomatic	Salles et al. (2021)

PSO, post symptom onset.

2.8.7 Potential health hazard if present in wastewater

No information suggesting the chikungunya virus could be transmitted through contact with wastewater (e.g., while sampling, processing samples in the laboratory, or at the WWTP) was identified during preparation of this report. Given chikungunya is not transmitted from person to person[84], infection via exposure to aircraft/airport wastewater containing this virus is considered unlikely.

[84] https://www.paho.org/en/topics/chikungunya Accessed 24 August 2023

2.9 ROSS RIVER VIRUS DISEASE

2.9.1 Transmission

Ross River virus disease is a viral infection caused by an enveloped single-stranded RNA virus of the genus *Alphavirus* (family *Togaviridae*) (Harley et al., 2001), Ross River virus disease is transmitted to humans via the bite of infected mosquitoes, most commonly *Culex annulirostris*, *A. vigilax* and *A. notoscriptus*[85]. It does not spread from person-to-person[86]. Ross River virus has been identified in a range of different animals, although the exact role different species play in the infection cycle is unclear (Stephenson et al., 2018).

2.9.2 Prevention

There is currently no vaccine for Ross River virus disease[87].

2.9.3 Geographic distribution and prevention

Ross River virus is endemic in Australia and Papua New Guinea and has caused notable outbreaks in several Pacific Islands[88] (Figure 27). It is the most prevalent mosquito-borne infection in Australia (Stephenson et al., 2018), with an average of 4,653 cases reported annually (Qian et al., 2021).

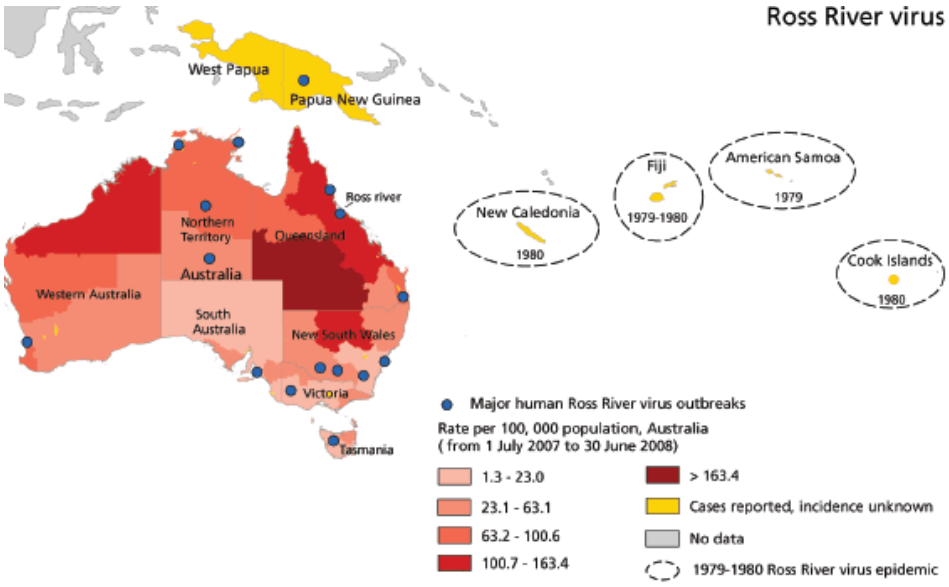

Figure 27 Distribution of Ross River virus (2011)

Reproduced from https://oncohemakey.com/91-barmah-forest-ross-river-virus-disease/. Last updated 14 February 2011.

[85] http://conditions.health.qld.gov.au/HealthCondition/condition/14/217/120/ross-river-virus Accessed 25 August 2023
[86] https://www.health.nsw.gov.au/Infectious/factsheets/Pages/ross-river-fever.aspx Accessed 25 August 2023
[87] https://wwwnc.cdc.gov/travel/diseases/ross-river-virus-disease Accessed 25 August 2023
[88] https://oncohemakey.com/91-barmah-forest-ross-river-virus-disease/ Accessed 25 August 2023

2.9.4 New Zealand epidemiology

Annual notifications of Ross River virus infections in New Zealand between 2006 – 2021 are shown in Figure 28[89]. During this time there were generally less than five cases annually, with the highest number of reported cases (seven) in 2017.

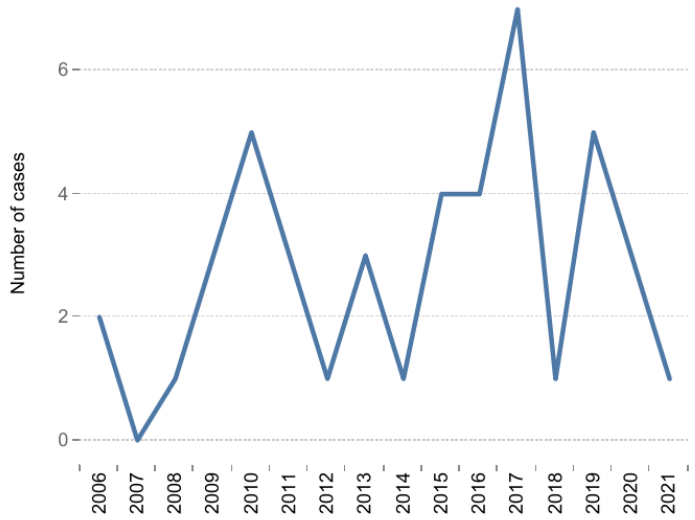

Figure 28 Number of reported Ross River fever cases in New Zealand 2006 - 2021

Reproduced from https://www.esr.cri.nz/digital-library/notifiable-disease-dashboard/.

2.9.5 Symptoms

The incubation period for Ross River disease is generally 7 – 9 days but can range from 3 – 21 days from the time of infection, and many cases are asymptomatic[90]. Where symptoms do develop, they may include fever, rash, fatigue and painful, swollen joints[90]. Due to the joint inflammation and pain, it is sometimes called epidemic polyarthritis[91]. Although most people recover for Ross River disease within a few weeks, in some cases symptoms may persist for months[92]. No deaths from Ross River disease have ever been reported[90].

2.9.6 Excretion of biomarkers of infection

No WBS studies assessing the presence of Ross River virus RNA in wastewater were identified during preparation of this report. No studies assessing the presence of biomarkers of Ross River virus infection in urine or faeces were identified during preparation of this report. However, the Victorian Infectious Diseases Reference Laboratory conducts PCR testing for Ross River virus using urine and faeces as optional specimens implying viral nucleic acid is detectable in these excreta[93].

[89] https://www.esr.cri.nz/digital-library/notifiable-disease-dashboard Accessed 4 April 2024
[90] https://www.cdc.gov/ross-river-virus/symptoms-diagnosis-treatment/index.html Accessed 25 August 2023
[91] https://arthritisaustralia.com.au/types-of-arthritis/ross-river-virus Accessed 25 August 2023
[92] https://www.healthdirect.gov.au/ross-river-virus Accessed 25 August 2023
[93] https://www.vidrl.org.au/resources/test-handbook/tests/ross-river-virus-pcrsee-alphavirus-genotyping-pcr Accessed 25 August 2023

2.9.7 Potential health hazard if present in wastewater

No information relating to potential transmission of Ross River virus via wastewater (e.g., while sampling, processing samples in the laboratory, or at the WWTP) was identified during preparation of this report. Given this disease is not transmitted from person-to-person[94], infection via contact with contaminated wastewater is considered unlikely.

2.10 PLAGUE

2.10.1 Transmission

Plague is caused by the bacterium *Yersinia pestis* which is carried by fleas, often found on small mammals such as rats, and can be transmitted to humans via bites of infected fleas, contact with infected bodily fluids or tissues, or inhalation of respiratory droplets from people with pneumonic plague[95].

2.10.2 Prevention

Although several different candidate plague vaccines have been developed or are in development, there is currently no licensed plague vaccine available (Sun & Singh, 2019), but some are in clinical trials[96,97].

Plague is treated with antibiotics under the guidance of an infectious diseases physician. After 48 hours of appropriate antimicrobial treatment the risk of transmission is substantially reduced. Public health management of cases and contacts is required, including restriction whilst infectious and antibiotic prophylaxis for contacts[98].

2.10.3 Geographical distribution

Plague is found on all continents, except for Oceania, but is currently most common in the Democratic Republic of the Congo, Madagascar and Peru[95]. The global distribution of natural plague foci (co-occurrence of the bacteria, an animal reservoir and a vector[95]) is shown in Figure 29[99].

[94] https://www.health.nsw.gov.au/Infectious/factsheets/Pages/ross-river-fever.aspx Accessed 25 August 2023
[95] https://www.who.int/news-room/fact-sheets/detail/plague Accessed 24 August 2023
[96] https://www.clinicaltrialsarena.com/news/dynavax-plague-vaccine-trial/ Accessed 24 August 2023
[97] https://www.ox.ac.uk/news/2021-07-26-phase-i-trial-begins-new-vaccine-against-plague Accessed 24 August 2023
[98] https://www.tewhatuora.govt.nz/for-the-health-sector/health-sector-guidance/communicable-disease-control-manual/plague/#management-of-case Accessed 24 March 2024
[99] https://cdn.who.int/media/images/default-source/health-topics/plague/plague-map-2016 Accessed 24 August 2023

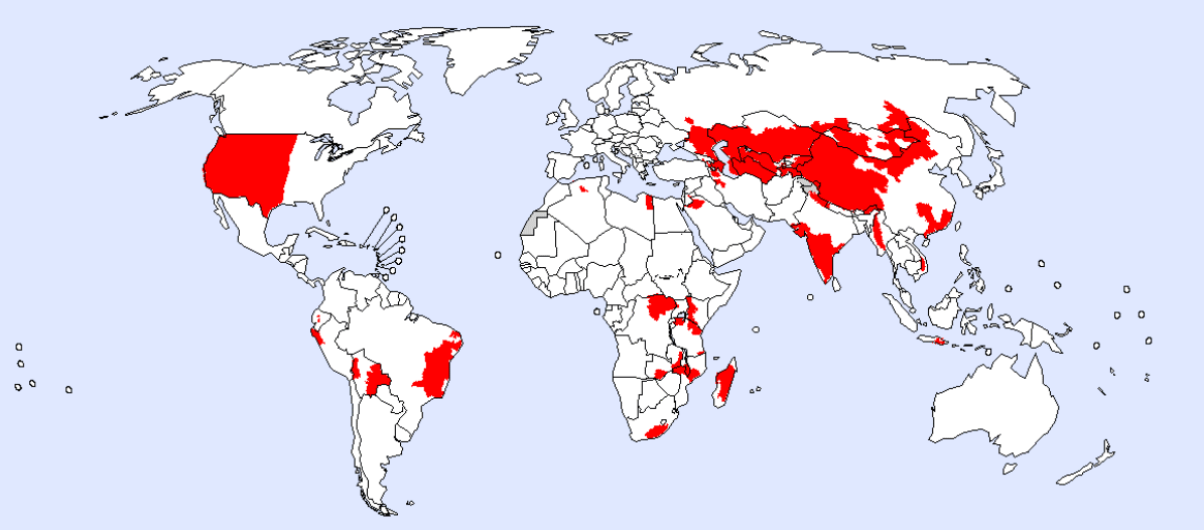

Figure 29 Global distribution of natural plague foci (2016)

Reproduced from https://cdn.who.int/media/images/default-source/health-topics/plague/plague-map-2016. Red, areas with potential plague natural foci based on historical data and current information.

2.10.4 New Zealand epidemiology

An outbreak of plague occurred in Auckland between 1900 – 1911 with 21 cases and 9 deaths[100,101]. No cases of plague have been reported in New Zealand since 1911, although both flea species known to transmit plague are present in New Zealand[101].

2.10.5 Symptoms

There are three main types of plague: bubonic plague, septicaemic plague and pneumonic plague[102]. Bubonic plague is the most common form[103] and generally develops as the result of a bite from an infected flea, with an incubation period of around 2 – 8 days[102]. The plague bacteria multiply in a lymph node close to the bite site, resulting in it becoming painful and swollen into what is referred to as a bubo[103,103]. The bacteria may spread to other sites in the body and more buboes may develop[102]. Where the bacteria travel to the lungs they can cause pneumonic plague[102]. The bubo may also erupt into an open, pus-filled sore[103]. Other symptoms of infection include headache, fever, chills, and weakness[102]. The fatality rate for bubonic plague ranges from 30 – 60%[103,103]. Bubonic plague can be spread from person-to-person via contact with pus from buboes[101].

Pneumonic plague is the most serious form and can develop from inhalation of infectious droplets (e.g., respiratory droplets from an infected person) or from systemic spread of the bacterial infection from untreated bubonic or septicaemic plague to the lungs[102]. The incubation period for pneumonic plague is only 1 – 3 days and symptoms include headache, fever, weakness and rapid onset of pneumonia with cough, shortness of breath, chest pain and in some cases production of watery or bloody sputum[102]. If left untreated pneumonic

[100] https://teara.govt.nz/files/27772-enz.pdf Accessed 24 August 2023
[101] https://www.tewhatuora.govt.nz/for-the-health-sector/health-sector-guidance/communicable-disease-control-manual/plague Accessed 8 April 2024
[102] https://www.cdc.gov/plague/symptoms/index.html Accessed 24 August 2023
[103] https://www.who.int/news-room/fact-sheets/detail/plague Accessed 24 August 2023

plague can be rapidly fatal[104]. People infected with pneumonic plague are contagious from the onset of respiratory symptoms until after at least 48 hours of treatment[105].

Septicaemic plague develops when plague bacteria multiply in the blood and can be a complication of bubonic or pneumonic plague or can occur independently via a flea bite with no formation of buboes[106]. The incubation period for septicaemic plague is unclear[107]. Symptoms include abdominal pain, fever and chills, bleeding into the skin and organs, extreme weakness and shock[108]. Septicaemic plague is often fatal[104].

Asymptomatic *Y. pestis* infections have been noted to be "rare to non-existent"[109].

2.10.6 Excretion of biomarkers of infection

Y. pestis has been detected in municipal wastewater in Ohio, USA using metagenomics (Spurbeck et al., 2023). A targeted PCR assay is available for detection of *Y. pestis* in water samples, but has not yet been applied to WBS (Kane et al., 2019). No studies reporting detection of *Y. pestis* DNA in urine or faeces were identified during preparation of this report. However, a commercial kit is available for detecting *Y. pestis* DNA in urine[110]. Other species of *Yersinia* have been detected in wastewater (Falcão et al., 2004) and isolated from stool (Doraiswamy et al., 1977; Yeung, 2021) and urine (Le Guern et al., 2018).

2.10.7 Potential health hazard if present in wastewater

No information relating to potential transmission of *Y. pestis* via contact with wastewater (e.g., while sampling, processing samples in the laboratory, or at the WWTP) was identified during preparation of this report. As such, further work is needed to determine whether the presence of this pathogen in wastewater may pose a hazard to people working with aircraft/airport wastewater.

2.11 TYPHUS

2.11.1 Transmission

Typhus, also known as typhus fever, refers to a group of related vector-borne bacterial diseases transmitted by fleas, lice and chiggers[111]. There are at least four types of typhus: epidemic (louse-borne) typhus, scrub typhus (also known as tsutsugamushi disease), murine (flea-borne) typhus (also known as urban typhus or endemic typhus), and flea-borne spotted fever typhus. All are caused by bacteria in the family *Rickettsiaceae*[111]. Epidemic typhus is caused by the bacterium *Rickettsia prowazekii* and is spread by infected body lice[112]. Scrub typhus is caused by the bacterium *Orientia tsutsugamushi* and is spread by infected chiggers (a type of mite)[113]. Murine typhus is caused by the bacterium *Rickettsia typhi* and is

[104] https://www.who.int/news-room/fact-sheets/detail/plague Accessed 24 August 2023
[105] https://infectioncontrol.ucsfmedicalcenter.org/sites/g/files/tkssra4681/f/wysiwyg/pneumonic%20plague%20GUIDELINES.pdf Accessed 24 August 2023
[106] https://emergency.cdc.gov/agent/plague/factsheet.asp Accessed 24 August 2023
[107] https://www.cdc.gov/plague/faq/index.html Accessed 24 August 2023
[108] https://emergency.cdc.gov/agent/plague/factsheet.asp Accessed 24 August 2023
[109] https://www.nmhealth.org/publication/view/help/1009/ Accessed 2 October 2023
[110] https://am-diagnostics.co.uk/product/zena-max-yersinia-pestis/ Accessed 24 August 2023
[111] https://www.cdc.gov/typhus/index.html Accessed 24 August 2023
[112] https://www.cdc.gov/typhus/epidemic/index.html Accessed 24 August 2023
[113] https://www.cdc.gov/typhus/scrub/index.html Accessed 24 August 2023

spread by infected fleas through bites, breathing in flea dirt, or rubbing flea dirt into the eyes[114]. Spotted fever typhus is caused by *Rickettsia felis* and spread by cat fleas (*Ctenocephalides felis*) (Brown & Macaluso, 2016). Typhus is not spread from person-to-person[115].

2.11.2 Prevention

There is currently no vaccine for any of the types of typhus[112,113,114].

2.11.3 Geographic distribution

Epidemic typhus outbreaks are generally associated with wars and other catastrophic events that result in poor sanitary conditions that lead to lice infestations, although it has been speculated to have a potentially worldwide distribution (Fournier & Raoult, 2020). Cases of epidemic typhus reported since 1997 (up to 2020) are shown Figure 30. Most cases of scrub typhus occur in South and East Asia, and certain parts of the Pacific rim (Figure 31), although its distribution is noted to be expanding (Elliott et al., 2019). Murine typhus is distributed worldwide but is more prevalent in tropical and subtropical climates[116]. *R. felis* has been detected in fleas worldwide (Brown & Macaluso, 2016; Parola, 2011).

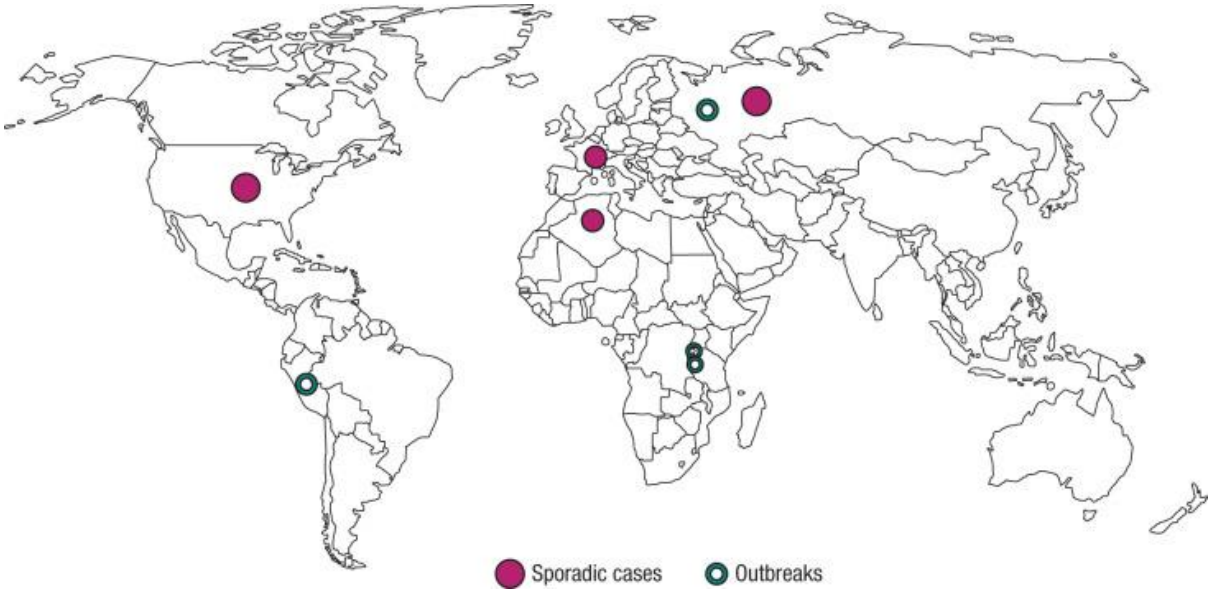

Figure 30 Global distribution of epidemic typhus (2020)

Reproduced from Fournier and Raoult (2020).

[114] https://www.cdc.gov/typhus/murine/index.html Accessed 24 August 2023
[115] https://www.vdh.virginia.gov/epidemiology/epidemiology-fact-sheets/typhus/ Accessed 24 August 2023
[116] https://www.cdc.gov/typhus/healthcare-providers/index.html Accessed 24 August 2023

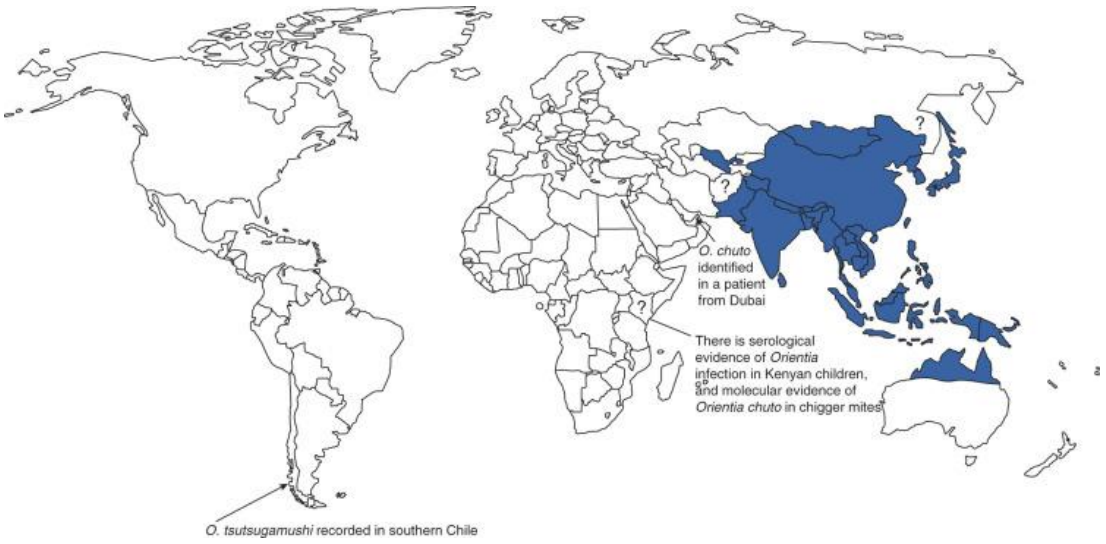

Figure 31 Global distribution of scrub typhus (2020)

Reproduced from Newton and Day (2020).

Figure 32 Global distribution of clinical diagnosis of *Rickettsia felis* infections (yellow stars) and arthropods infected with *R. felis* (red circles).

Reproduced from Parola (2011)

2.11.4 New Zealand epidemiology

Rickettsial diseases are notifiable in New Zealand[117] and case numbers reported between 2001 to 2020 can be seen in Figure 33. *Rickettsia typhi* is known to be endemic in some regions of New Zealand[118]. No cases of epidemic typhus (*R. prowazekii*) have been reported in New Zealand between 1997 and 2021[119].

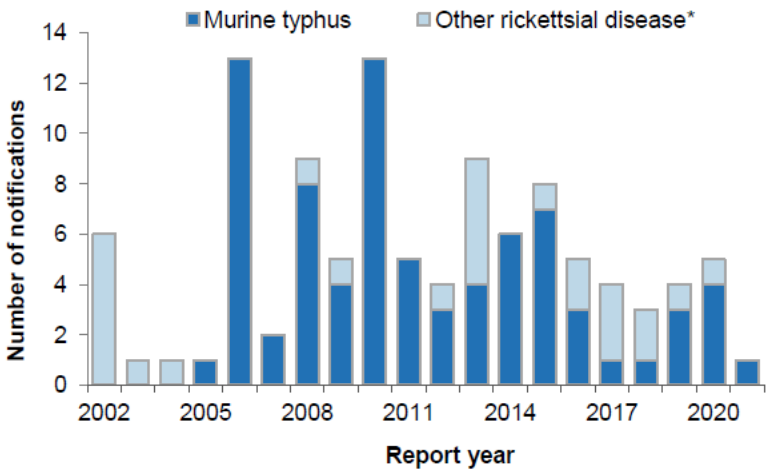

Figure 33 Number of reported cases of rickettsial disease in New Zealand 2006 – 2021

Reproduced from https://www.esr.cri.nz/digital-library/notifiable-diseases-annual-surveillance-summary-2021 *Includes all other diseases caused by organisms of the *Rickettsia* genus except epidemic typhus (*R. prowazekii*).

2.11.5 Symptoms and antibiotic treatment

The incubation period for epidemic typhus is around 10 – 14 days (Bechah et al., 2008). Patients often experience 1 – 3 days of malaise before the onset of fever and severe headache (Bechah et al., 2008). Other symptoms may include chills, rash, cough, nausea, vomiting, body and muscle aches and joint pain, rapid breathing, confusion, seizures and coma[120] (Bechah et al., 2008). With early doxycycline antibiotic treatment people usually recover quickly[120]. Without treatment, up to 60% of cases are fatal, but with antibiotic treatment the fatality rate is around 4% (Bechah et al., 2008). In some cases, people remain infected but asymptomatic after recovery from their initial illness, and relapse months or years later in what is known as Brill-Zinsser disease[120]. Relapse often occurs when the immune system is weakened (e.g., due to medication, illness or old age) and generally exhibits similar but milder symptoms to the initial illness[120].

The incubation period for scrub typhus is around 6 – 21 days (Rapsang & Bhattacharyya, 2013) after which headache, fever, muscle ache, cough and gastrointestinal symptoms

[117] https://www.health.govt.nz/system/files/documents/pages/schedule-of-notifiable-diseases-updated-jun22.pdf Accessed 24 August 2023
[118] https://www.health.govt.nz/our-work/diseases-and-conditions/communicable-disease-control-manual/rickettsial-diseases Accessed 24 August 2023
[119] https://www.esr.cri.nz/digital-library/notifiable-diseases-annual-surveillance-summary-2021/ Accessed 8 April 2024
[120] https://www.cdc.gov/typhus/epidemic/index.html Accessed 24 August 2023

develop (Rapsang & Bhattacharyya, 2013). A primary lesion forms at the bite site, enlarges, undergoes necrosis and crusts over to form a flat black eschar (Rapsang & Bhattacharyya, 2013). Nearby lymph nodes often become enlarged and tender, and later in infection there is generalised enlargement of all lymph nodes (Rapsang & Bhattacharyya, 2013). Symptoms may become more severe and a flat rash may develop on the trunk (Rapsang & Bhattacharyya, 2013). If left untreated, meningoencephalitis may develop, leading to confusion and coma[121], and there may be signs of cardiac dysfunction (Rapsang & Bhattacharyya, 2013). Untreated patients may remain febrile for up to 2 weeks and require another 4 – 6 weeks to convalesce, and up to 30% of cases may be fatal (Rapsang & Bhattacharyya, 2013). In some cases, infections may be asymptomatic (Prakash, 2017).

The incubation period for murine typhus is generally 7 – 14 days (Peniche Lara et al., 2012). Symptoms include headache, fever, musculoskeletal pain, and, in 60-70% of cases, a maculopapular rash that appears around 5 days after symptom onset on the trunk and extremities and lasts for around 4 days (Peniche Lara et al., 2012). Most cases are mild and resolve within 10 – 14 days (Peniche Lara et al., 2012). In up to 10% of cases there may be additional symptoms including renal failure, hepatitis (liver inflammation), pneumonitis, or meningoencephalitis (Peniche Lara et al., 2012). In around 2 – 4% of cases severe symptoms may develop including shock, respiratory distress, excessive bleeding, abnormal blood clotting, neurological symptoms and multi-organ failure (Peniche Lara et al., 2012). However, the mortality rate for murine typhus is usually 1% or less (Peniche Lara et al., 2012). Asymptomatic infections have also been reported (Angelakis et al., 2010).

Spotted fever typhus has similar symptoms to murine typhus which include high fever, headache, myalgia, and rash (Angelakis et al., 2016; Maina et al., 2012). A limited number of severe infections have been described which include photophobia, hearing loss, signs of meningitis, and severe respiratory insufficiency (Angelakis et al., 2016).

2.11.6 Excretion of biomarkers of infection

Rickettsia prowazekii has been detected in wastewater in Ohio, USA using metagenomics (Spurbeck et al., 2023). No studies assessing the presence of biomarkers of typhus infection in urine or faeces were identified during preparation of this report, however Keita et al (2015) isolated *Rickettsia* spp. of the spotted fever group and *R. felis* from 4.4% of 451 faecal samples.

2.11.7 Potential health hazard if present in wastewater

No information relating to potential transmission of any of the three bacterial species responsible for scrub, murine or epidemic typhus via wastewater (e.g., while sampling, processing samples in the laboratory, or at the WWTP) was identified during preparation of this report. Given these diseases are all vector-borne and not known to be transmitted from person-to-person[122], infection via this route is considered unlikely.

[121] https://www.cdc.gov/typhus/scrub/index.html Accessed 24 August 2023
[122] https://www.vdh.virginia.gov/epidemiology/epidemiology-fact-sheets/typhus/ Accessed 24 August 2023

2.12 TULARAEMIA

2.12.1 Transmission

Tularaemia, also known as rabbit fever, is a zoonotic disease caused by the bacterium *Francisella tularensis*[123]. Tularaemia can be transmitted by the bite of several different insects including ticks, deer flies, mosquitoes, lice, midges, fleas and mites (Dinc et al., 2017). It can also be transmitted by breathing in *F. tularensis* bacteria, eating or drinking infected food/water, and direct contact with infected animals[124]. *F. tularensis* is very infectious, which has raised concerns it could be used as a bioweapon[124]. Tularaemia is not known to be transmitted from person to person[124]. Tularaemia has been identified in several different animal species, with rodents, hares and rabbits being particularly susceptible[125]. The transmission cycle of tularaemia is shown in Figure 34.

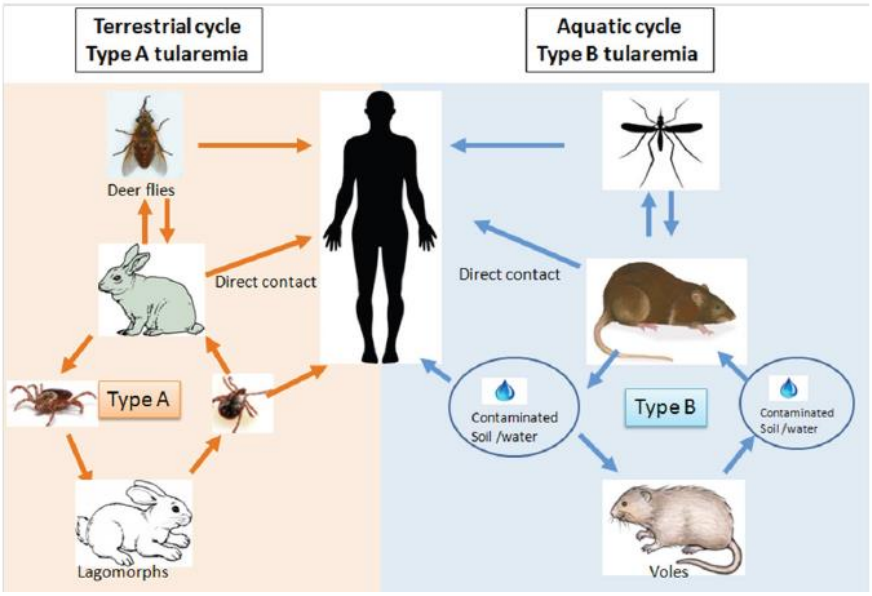

Figure 34 Transmission cycle of tularaemia

Reproduced from Dinc et al. (2017).

2.12.2 Prevention

There is currently no safe, fully licensed vaccine available for protection against tularaemia, although candidates are in development[126].

2.12.3 Geographic distribution

Type A tularaemia is caused by *F. tularensis* subspecies *tularensis*, which is mainly present in North America and is the most virulent[127] and type B is caused by *F. tularensis* subspp. *holarctica* which is present in the entire Northern hemisphere and Australia (Maurin, 2020). The distribution of the two types can be seen in Figure 35. Tularaemia was identified in Australia in 2003 (Whipp et al., 2003) but case reports remain rare[128].

[123] https://emergency.cdc.gov/agent/tularemia/faq.asp Accessed 25 August 2023
[124] https://emergency.cdc.gov/agent/tularemia/facts.asp Accessed 25 August 2023
[125] https://www.cdc.gov/tularemia/index.html Accessed 25 August 2023
[126] https://www.utsa.edu/today/2020/02/story/tularemia-vaccine.html Accessed 25 August 2023
[127] https://www.ecdc.europa.eu/en/tularaemia/facts Accessed 25 August 2023
[128] https://www.health.gov.au/diseases/tularaemia Accessed 25 August 2023

2.12.4 New Zealand epidemiology

No reports of tularaemia in New Zealand were identified during preparation of this report.

2.12.5 Symptoms

The incubation period for tularaemia is generally 3 – 5 days but ranges from 1 – 14 days[129], and some infected individuals may be asymptomatic[130]. Symptoms of tularaemia vary depending on the route of infection as shown in Table 9. Appropriate and timely antibiotic treatment is recommended[129].

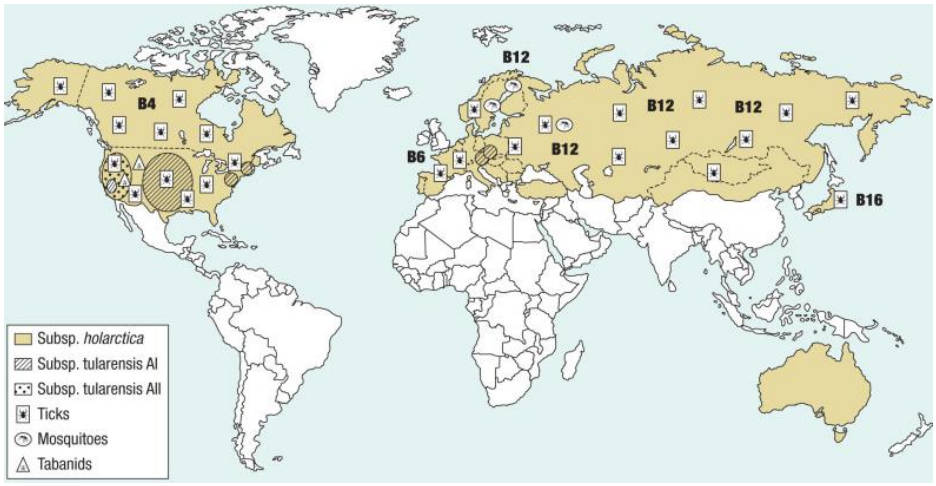

Figure 35 Global distribution of tularaemia

Reproduced from Maurin (2020). Fawn, regions with *F. tularensis,* grouped by subsp. *tularensis* (type AI and AII strains, dashed and dotted shading) and subsp. *holarctica* (type B strains, bold type).

Table 9 Clinical forms of tularaemia

Form	Route of acquisition
Ulceroglandular or glandular	Vector-borne and direct contact (touching infected animals or material contaminated with *F. tularensis*)
Oculoglandular	Touching the eye with contaminated fingers or possibly from infective dust
Oropharyngeal	Ingesting contaminated food or water
Respiratory	Inhaling contaminated dust or laboratory-acquired infection
Typhoidal	Unknown (probably oral or respiratory)

Reproduced from WHO (2007).

Ulceroglandular and glandular tularaemia is the most common form, often accounting for >95% of cases in Europe (WHO, 2007). These forms are transmitted via insect bites or by direct or indirect contact with infected animals (e.g., direct handling, bites or handling of materials contaminated by an infected animal) (WHO, 2007). Infected individuals will develop fever and a small papule will form at the site of infection, which then progresses into a pustule/ulcer surrounded by inflammation (WHO, 2007). In some cases multiple papules and pustules may develop (WHO, 2007). The ulcer(s) heal, leaving a small scar (WHO, 2007). In some cases an ulcer may not be detectable (glandular tularaemia) (WHO, 2007). A

[129] https://emergency.cdc.gov/agent/tularemia/faq.asp Accessed 25 August 2023
[130] https://rarediseases.org/rare-diseases/tularemia/ Accessed 2 October 2023

few days after the onset of fever a regional lymph node will start to become enlarged, tender, palpable and in some cases visible with the skin overlying the lymph node becoming red and swollen (WHO, 2007). If treatment is started within the week of symptom onset the lymph node swelling will resolve, however, if treatment is delayed or not given there is a high chance (30-40%) of the lymph nodes becoming infected and pus-filled (WHO, 2007).

Oculoglandular tularaemia is rare (<1% of cases) and occurs when *F. tularensis* enters the eye (e.g., from touching the eyes with contaminated fingers) (WHO, 2007). Symptoms include fever, unilateral conjunctivitis, swollen eyelids, excessive tear formation, sensitivity to light and thick, coloured discharge (WHO, 2007). The lymph node in front of the ears may also become enlarged and tender, altering the contour of the cheek (WHO, 2007).

Oropharyngeal tularaemia occurs when *F. tularensis* is ingested via contaminated food or water (WHO, 2007). Symptoms include inflammation and ulceration of the oral mucosa and pharyngitis (WHO, 2007). The lymph nodes in the neck (often on one side) will also become infected and enlarged (WHO, 2007).

Respiratory tularaemia occurs when *F. tularensis* is inhaled, often during farm-based activities (WHO, 2007). Symptoms may appear similar to pneumonia (cough, increased respiration rate, chest pain, high fever), or non-specific (e.g., nausea and vomiting with no respiratory symptoms) (WHO, 2007). In type A disease, symptoms start 3 – 5 days after exposure and include chills, cough (dry or productive), high fever, pharyngitis, headache, laboured breathing, chest pain, drowsiness, weakness and profuse sweating (WHO, 2007). Without antibiotics 30 – 60% of patients die (WHO, 2007). In type B disease, pneumonia may not develop (WHO, 2007), and the disease is non-lethal (Tärnvik & Berglund, 2003).

The cause of typhoidal (septicaemic) tularaemia[131] is unclear but includes cases with no lesions on the skin or mucous membranes, or lymph node enlargement (WHO, 2007). Symptoms include exhaustion, weight loss, fever, and in some cases lung involvement[131].

2.12.6 Excretion of biomarkers of infection

Francisella tularensis has been detected in municipal wastewater in Ohio, USA (Spurbeck et al., 2023) and in wastewater collected from residential dormitories and other locations within the University of Miami, USA (Tierney et al., 2023) using metagenomics. However, no studies reporting the presence of infectious *F. tularensis* or its genomic material in urine or faeces were identified during preparation of this report.

2.12.7 Potential health hazard if present in wastewater

No information relating to potential transmission of *F. tularensis* via wastewater (e.g., while sampling, processing samples in the laboratory, or at the WWTP) was identified during preparation of this report. However, *F.* tularensis has been shown to persist for prolonged time periods in water microcosms: bacteria remained culturable after 7 days in 37°C water, 6 weeks at 18°C, and 11 weeks at 4°C (Brunet et al., 2022). Given that *F. tularensis* can spread through respiratory droplets and is highly infectious[132], further work is needed to determine whether its presence in wastewater poses a health hazard to people working with aircraft/airport wastewater samples, or to WWTP staff. In particular, the potential for transmission via wastewater aerosols should be considered.

[131] https://www.columbia-lyme.org/tularemia Accessed 25 August 2023
[132] https://emergency.cdc.gov/agent/tularemia/facts.asp Accessed 25 August 2023

2.13 MALARIA

2.13.1 Transmission

Malaria is a life-threatening parasitic infection caused by five different *Plasmodium* species – *P. falciparum*, *P. vivax*, *P. malariae*, *P. ovale* and *P. knowlesi*, and spread by female *Anopheles* mosquitoes[133]. Malaria does not spread from person-to-person but may be spread by contaminated needles or blood transfusion[133].

2.13.2 Prevention

A malaria vaccine (RTS,S) that acts against *P. falciparum* has been developed and is being distributed to children throughout Africa[134].

Preventing insect bites, using screens and nets as well as appropriate antimalarial drugs are important for prevention[135].

2.13.3 Global distribution and burden of disease

Of the five *Plasmodium* species, *P. falciparum* is the deadliest and is the most prevalent in Africa, and *P. vivax* is the most prevalent outside of sub-Saharan Africa[133]. In 2021 there were an estimated 247 million cases of malaria globally, resulting in around 619,000 deaths, with 95% of cases and 96% of deaths occurring in Africa[133]. Regions in which malaria transmission is known to occur[136] are shown in Figure 36.

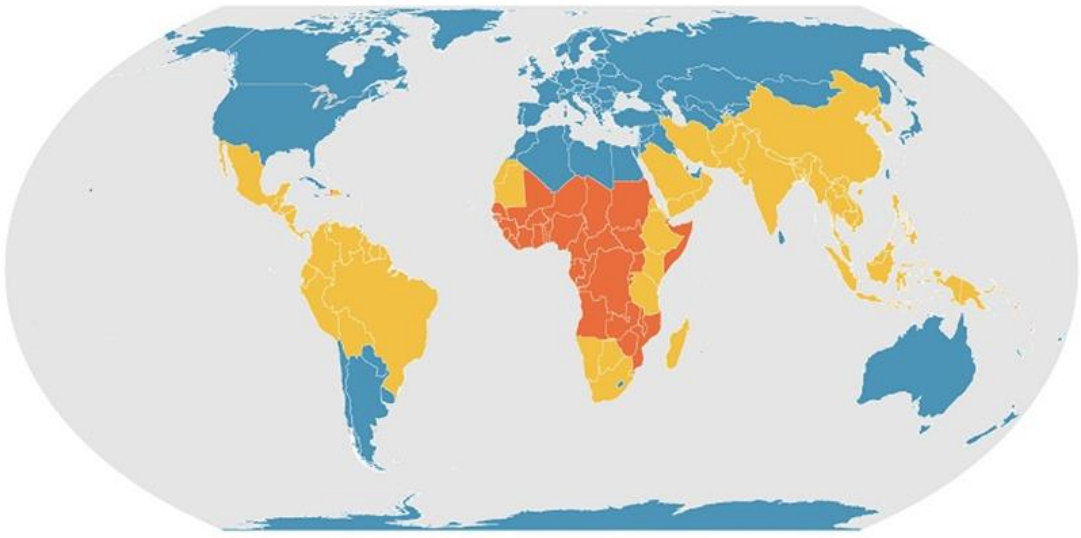

Figure 36 Areas of the world where malaria transmission occurs

Reproduced from https://www.cdc.gov/malaria/about/distribution.html. Last reviewed April 2020. Orange, countries with malaria transmission throughout; yellow, countries with transmission in some places; blue, countries where transmission is not known to occur.

[133] https://www.who.int/news-room/fact-sheets/detail/malaria Accessed 24 August 2023
[134] https://www.who.int/news-room/questions-and-answers/item/q-a-on-rts-s-malaria-vaccine Accessed 24 August 2023
[135] https://www.who.int/publications/i/item/guidelines-for-malaria Accessed 25 March 2024
[136] https://www.cdc.gov/malaria/about/distribution.html Accessed 24 August 2023

2.13.4 New Zealand epidemiology

Annual notifications of malaria infections in New Zealand between 2006 – 2021 are shown in Figure 37. Notifications peaked at 52 cases in 2011 but only 17 and 8 cases were notified in 2020 and 2021 respectively, likely due to the COVID-19 associated border closures.

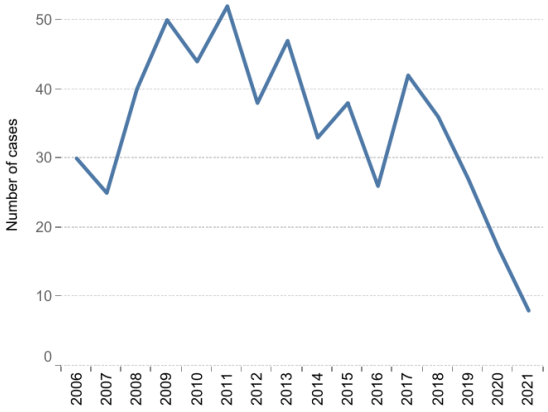

Figure 37 Number of reported malaria cases in New Zealand 2006 - 2021

Reproduced from https://www.esr.cri.nz/digital-library/notifiable-disease-dashboard/.

2.13.5 Symptoms

The incubation period of malaria ranges from 7 – 30 days[137]. Asymptomatic infections have been reported, with a recent study reporting 19% of 232 asymptomatic individuals tested in Nigeria were infected with *P. falciparum* (Ibrahim et al., 2023). Symptoms of malaria infection include fever, chills, headache, fatigue and muscle aches[138]. Anaemia and jaundice may also develop due to a loss of red blood cells[138]. If left untreated, severe symptoms such as seizures, mental confusion, kidney failure, coma and ultimately death may occur[138]. Severe malaria is almost always fatal if left untreated (Walter & John, 2022). However, with timely and appropriate treatment the death rate is generally low (< 2%) (Walter & John, 2022).

2.13.6 Excretion of biomarkers of infection

Plasmodium spp. has been detected in wastewater in Ohio, USA using metagenomics (Spurbeck et al., 2023), but it is unclear if it is a species that causes malaria in humans. *P. falciparum*, *P. vivax*, *P. malariae*, and *P. ovale* have been detected in both hospital and municipal wastewater in Turkey using metagenomics, while *P. knowlesi* was present in WWTP samples but absent from hospital wastewater (Gündoğdu et al., 2023). Plasmodium species, including *P. malariae*, *P. vivax*, and *P. falciparum* have also been detected in New Zealand municipal wastewater using a metagenomics approach, likely due shedding of *Plasmodium* oocyts by infected hosts, given there is no local transmission in Aotearoa due to absence of *Anopheles* spp. mosquitoes (Ariyadasa et al., 2023).

P. falciparum DNA has been detected in faeces of infected patients using PCR (Jirků et al., 2012), and *Plasmodium* spp. DNA (including *P. falciparum*) has also been detected in

[137] https://www.cdc.gov/malaria/about/disease.html Accessed 24 August 2023
[138] https://www.cdc.gov/malaria/about/faqs.html Accessed 24 August 2023

children in Uganda (Al-Shehri et al., 2019) and Gabon (Imboumy-Limoukou et al., 2023). *P. falciparum, P. malariae* and *P. ovale wallikeri* DNA has been detected in faeces of rural Cameroonians (Loy et al., 2018).

2.13.7 Potential health hazard if present in wastewater

No information suggesting malaria can be transmitted via contact with wastewater (e.g., while sampling, processing samples in the laboratory, or at the WWTP) was identified during preparation of this report. Given that malaria is primarily transmitted by mosquitoes, transmission via contaminated wastewater is considered unlikely.

2.14 LEISHMANIASIS

2.14.1 Transmission

Leishmaniasis is a parasitic disease caused by obligate intracellular protozoa of the genus *Leishmania*[139]. More than 20 different species can cause infection in humans[139]. The *Leishmania* parasite is transmitted to humans via the bite of infected female phleobotomine sand flies[140] (Figure 38) and can infect more than 70 different animal species[140]. Some *Leishmania* species can also be spread via contaminated needles and blood transfusions, and transmission from a pregnant mother to her unborn foetus has also been reported[141]. Leishmaniasis is associated with poverty, malnutrition and poor housing[142].

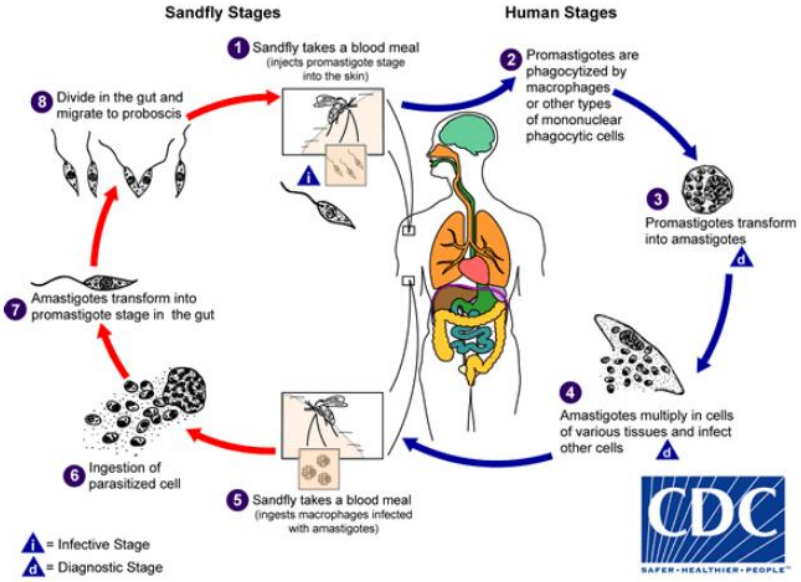

Figure 38 Transmission cycle of leishmaniasis

Reproduced from https://www.cdc.gov/dpdx/leishmaniasis/index.html

[139] https://www.cdc.gov/dpdx/leishmaniasis/index.html Accessed 24 August 2023
[140] https://www.who.int/news-room/fact-sheets/detail/leishmaniasis Accessed 24 August 2023
[141] https://www.cdc.gov/parasites/leishmaniasis/gen_info/faqs.html Accessed 24 August 2023
[142] https://www.who.int/news-room/questions-and-answers/item/leishmaniasis Accessed 12 December 2023

2.14.2 Prevention

There is currently no vaccine available to protect against leishmaniasis (Malvolti et al., 2021).

Other control strategies depend on the setting but may include early detection and treatment of cases, vector (and in some cases reservoir host) control, environmental management and improving the social determinants of health, e.g., housing and poverty[143].

2.14.3 Geographic distribution

There are three main forms of Leishmaniasis: visceral, cutaneous and mucocutaneous (or mucosal)[143], which will be described in more detail below. Visceral leishmaniasis is the most serious and is most common in India, Brazil and east Africa, with an estimated 50,000 – 90,000 new cases worldwide every year[143]. Cutaneous leishmaniasis is the most common and occurs mostly in the Middle East, central Asia, the Mediterranean basin and the Americas, with an estimated 600,000 – 1 million new cases worldwide every year[143]. The mucocutaneous form is most common in Peru, Bolivia, Brazil and Ethiopia[143]. The global distribution of the different forms (as of 2012) is shown in Figure 39.

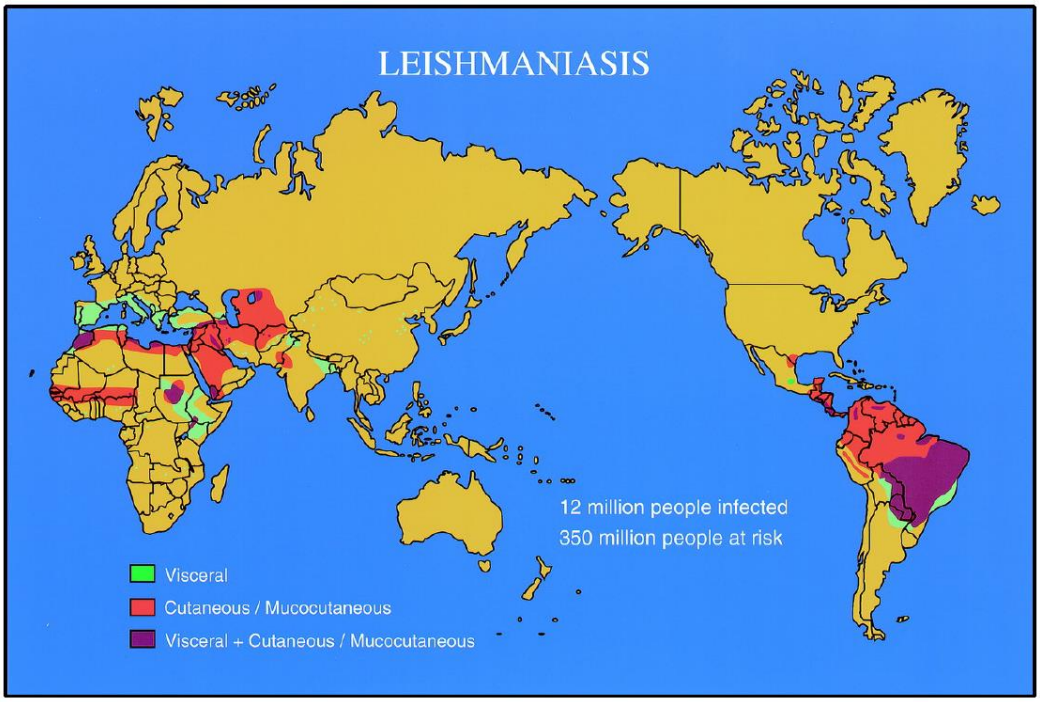

Figure 39 Global distribution of Leishmaniasis (2012)

Reproduced from Bowles et al. (2015).

2.14.4 New Zealand epidemiology

Leishmania parasites are not found in New Zealand[144].

[143] https://www.who.int/news-room/fact-sheets/detail/leishmaniasis Accessed 24 August 2023
[144] https://dermnetnz.org/topics/leishmaniasis Accessed 24 August 2023

2.14.5 Symptoms

The incubation period for visceral leishmaniasis can range anywhere from 10 days – 24 months (average of 2 – 6 months)[145]. Symptoms range from mild to severe and include enlargement of the spleen (seen in most patients), anaemia, leucopenia (low white blood cell count), weight loss, fever, and enlargement of the liver[146,145]. Patients may also exhibit respiratory problems, diarrhoea and vomiting, malnutrition, jaundice, fluid build-up in the abdomen, bleeding from the nose and mouth, and in some cases lower limb oedema (swelling)[145]. Over 95% of cases are fatal if untreated[146].

The incubation period for cutaneous leishmaniasis ranges from 2 weeks to several months, with some cases reportedly developing three years after infection (Piscopo & Mallia Azzopardi, 2007). Sores develop on the skin (papules, nodules or ulcers), may be painful and may be accompanied by swelling of nearby glands[147]. In over 90% of cases, it takes 3 – 18 months for the sores to heal (Piscopo & Mallia Azzopardi, 2007).

The incubation period for mucocutaneous leishmaniasis is generally 1 – 3 months but it may also develop years after a cutaneous ulcer has healed (Piscopo & Mallia Azzopardi, 2007). Lesions mostly commonly form on the mucosa of the nasal septum, which may result in its perforation and may extend to the roof of the mouth and the pharynx[148]. This infection may extend to the uvula (the soft flap of tissue that hangs at the back of the mouth), resulting in its swelling and eventual amputation[148]. Lesions on the nasal mucosa can cause bleeding, runny nose and obstruction; lesions on the larynx and pharynx can cause hoarseness, pain, abnormal voice and swallowing difficulties[148].

Approximately 20 – 60% of leishmaniasis infections in endemic areas are thought to be asymptomatic (Ibarra-Meneses et al., 2022).

2.14.6 Excretion of biomarkers of infection

Several *Leishmania* species were detected in rural wastewater in Turkey using a metagenomics approach (Gündoğdu et al., 2023). *Leishmania* species were present in both untreated and treated wastewater, suggesting these bacterial species may be resistant to wastewater treatment (Gündoğdu et al., 2023). In contrast, metagenomic profiling of New Zealand wastewater collected at various stages of the treatment process found that the abundance of Euglenozoa, a phylum comprising *Leishmania*, decreased through the treatment process (Ariyadasa et al., 2023). Several studies have identified *Leishmania* DNA in urine from patients with both visceral and cutaneous leishmaniasis, as summarised in Table 10.

2.14.7 Potential health hazard if present in wastewater

Potentially infectious, viable *Leishmania infantum* amastigotes have been isolated from human urine (de Costa Lima et al., 2018). As such, where an infected individual urinates on a plane or at the airport there could be a potential health hazard posed to people collecting or processing aircraft/airport wastewater samples, or to WWTP staff. However, as leishmaniasis is primarily transmitted by mosquitoes this is considered unlikely.

[145] https://www3.paho.org/hq/index.php Accessed 24 August 2023
[146] https://www.who.int/news-room/fact-sheets/detail/leishmaniasis Accessed 24 August 2023
[147] https://www.cdc.gov/parasites/leishmaniasis/gen_info/faqs.html Accessed 24 August 2023
[148] https://www.paho.org/en/topics/leishmaniasis/cutaneous-and-mucosal-leishmaniasis Accessed 24 August 2023

Table 10 Summary of studies assessing excretion of *Leishmania* DNA in urine

Study participants	% positive patients	Other notes	Reference
37	• 86.9% (20/23) of patients with cutaneous leishmaniasis positive • 92.8% (13/14) of patient with visceral leishmaniasis positive	• Detected DNA from *L. infantum*, *L. major* and *L. tropica*	Mirzaei et al. (2018)
30	20	• *L. infantum* DNA detected in 6/30 urine samples of patients with visceral leishmaniasis	de Costa Lima et al. (2018)
11	100	• *L. infantum* DNA detected in all urine samples of patients with visceral leishmaniasis using three different extraction protocols	da Silva et al. (2014)
86	21	• *Leishmania* DNA detected in 18/86 urine samples of patients with cutaneous leishmaniasis • 75% (6/8) of patients with mucocutaneous involvement were positive • 15% (12/78) of patients with isolated cutaneous disease were positive	Veland et al. (2011)
17	88.2	• *L. infantum* DNA detected in 15/17 urine samples of patients suffering a clinical episode of visceral leishmaniasis • *Leishmania* DNA detected in 14/55 urine samples collected during the asymptomatic phase post-treatment	Fisa et al. (2008)
30	97	• *Leishmania* DNA detected in 29/30 urine samples of patients with visceral leishmaniasis	Motazedian et al. (2008)

PSO, post symptom onset.

3. VIRAL HAEMORRHAGIC FEVERS

Viral haemorrhagic fevers (VHFs) are a group of several diseases caused by RNA viruses from four families (*Arenaviridae*, *Bunyaviridae*, *Filoviridae* and *Flaviviridae*)[149]. Although symptoms of infection by these different viruses vary, they are all capable of causing 'viral haemorrhagic fever', a condition affecting multiple organs, resulting in damage to the cardiovascular system and reducing "the body's ability to function on its own"[149]. As the name suggests, VHF infection may cause bleeding or haemorrhaging, and in some cases severe, life-threatening disease, with most having no known cure or vaccine[149].

The viruses which cause VHFs are found naturally in certain host animal or insect populations[149]. As such, outbreaks of these diseases generally occur in geographical areas where the host populations reside, when humans encounter an infected animal or insect host[149]. Some VHFs are then able to spread from person-to-person[149]. VHFs have been identified as bioterrorism agents with the potential for large numbers of casualties[150].

This section will focus on VHFs listed on the US CDC website[149]. Some of the listed diseases are also VBDs so have been discussed in Chapter 3. As many of these diseases are newly emerging, there is often little information available on their excretion in urine and/or faeces. As such, this section will consider the most prevalent or well-studied VHFs: Lassa fever, Ebola, Marburg HF (haemorrhagic fever) and Hantavirus.

Table 11 Example viral haemorrhagic fevers by family

VHF virus family			
Arenaviruses[151]	Bunyaviruses[152]	Filoviruses[153]	Flaviviruses[154]
Argentine HF	Crimean-Congo HF	Ebola	Alkhurma HF
Bolivian HF	Hantavirus Pulmonary Syndrome	Marburg HF	Kyasanur Forest Disease
Chapare HF			
Sabia-associated HF	HF with renal syndrome		Omsk HF
Venezuelan HF	Rift Valley fever		Tick-borne encephalitis
Lassa fever			
Lujo HF			
Lymphocytic choriomeningitis			

[149] https://www.cdc.gov/vhf/about.html Accessed 25 August 2023
[150] https://www.tewhatuora.govt.nz/for-the-health-sector/health-sector-guidance/communicable-disease-control-manual/viral-haemorrhagic-fevers/ Accessed 26 March 2024
[151] https://www.cdc.gov/vhf/virus-families/arenaviridae.html Accessed 25 August 2023
[152] https://www.cdc.gov/vhf/virus-families/bunyaviridae.html Accessed 25 August 2023
[153] https://www.cdc.gov/vhf/virus-families/filoviridae.html Accessed 25 August 2023
[154] https://www.cdc.gov/vhf/virus-families/flaviviridae.html Accessed 25 August 2023

3.1 LASSA FEVER

3.1.1 Transmission

Lassa fever is a zoonotic acute viral haemorrhagic illness caused by an enveloped single-stranded RNA virus of the genus *Mammarenavirus* (family *Arenaviridae*)[155]. The Lassa virus is transmitted to humans via *Mastomys* rodents (or multimammate rats), which act as an animal reservoir for the virus and do not develop disease but shed the virus in their urine and faeces[155]. Humans become infected via contact with food or objects contaminated with rodent urine or faeces, then the virus may be transmitted from person-to-person via contact with blood, bodily secretions, urine or faeces of an infected individual[155]. Cases of sexual transmission have also been reported[155].

3.1.2 Prevention

There is currently no vaccine available for Lassa fever, although there are candidates in clinical trials (Sulis et al., 2023).

3.1.3 Geographical distribution

Lassa fever is endemic to several countries in West Africa, including Guinea, Nigeria, Liberia and Sierra Leone[156] (Figure 40). Other countries which have reported cases, or serological evidence of infections, include Benin, Burkina Faso, Côte d'Ivoire, Ghana, Mali and Togo[155].

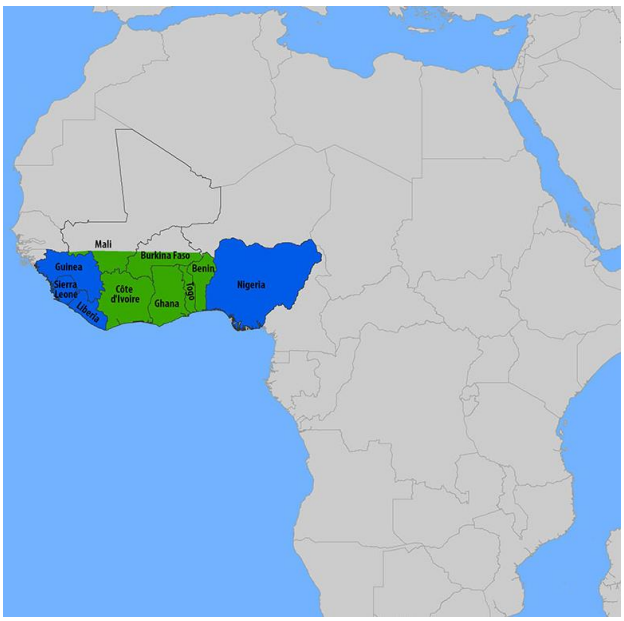

Figure 40 Distribution of Lassa fever in West Africa

Reproduced from https://www.cdc.gov/vhf/lassa/outbreaks/index.html. Blue, countries reporting endemic disease and substantial outbreaks; green, countries reporting few cases, periodic isolation of virus, or serologic evidence of infection; grey, status unknown.

[155] https://www.who.int/news-room/fact-sheets/detail/lassa-fever Accessed 25 August 2023
[156] https://www.cdc.gov/vhf/lassa/outbreaks/index.html Accessed 25 August 2023

3.1.4 New Zealand epidemiology

There has never been a reported case of Lassa fever in New Zealand[157].

3.1.5 Symptoms

The incubation period for Lassa fever ranges from between 6 – 21 days after exposure, and approximately 80% of infections are asymptomatic[155]. People are not thought to be contagious before symptom onset[158] Where symptoms develop, they usually start gradually with fever, weakness and malaise, and may progress to other symptoms including sore throat, cough, chest and abdominal pain, headache, nausea, vomiting, diarrhoea and/or muscle pain[159]. In severe cases, patients may develop swelling of the face, fluid build-up in the lung cavity, and start to haemorrhage from the nose, mouth, gastrointestinal tract or vagina, leading to low blood pressure[159]. In the later stages of these severe infections, disorientation, shock, tremors, seizures and coma may develop[159]. Approximately 15 – 20% of all patients hospitalised due to Lassa fever will die, although this represents only approximately 1% of all Lassa virus infections[160]. The exception is infections during late pregnancy, where maternal and/or foetal death occurs in more than 80% of all third trimester infections[159]. Approximately 1 in 3 cases of Lassa fever result in some degree of hearing loss, which in many cases is permanent[160]

3.1.6 Excretion of biomarkers of infection

No WBS studies assessing the presence of Lassa virus in wastewater were identified during preparation of this report. Infectious Lassa fever virus has been isolated from human urine (Choi et al., 2018; Kitching et al., 2009; Lunkenheimer et al., 1990; Monath & Casals, 1975) and several studies have identified Lassa virus RNA in urine, as summarised in Table 12. Viral RNA has also been detected in faeces (day 11 PSO) with a viral load of 4.4×10^4 copies/mL (Grahn et al., 2016).

3.1.7 Potential health hazard if present in wastewater

As noted above, infectious Lassa virus has been isolated from human urine (Choi et al., 2018; Kitching et al., 2009; Lunkenheimer et al., 1990; Monath & Casals, 1975) so where an infected individual urinates on a plane or at the airport there could be a potential health hazard posed to people collecting or processing aircraft/airport wastewater samples, or to WWTP staff. The potential hazard posed by Lassa virus in wastewater has been assessed by Shaffer et al. (2023) who spiked Lassa virus into raw municipal wastewater and monitored the persistence of infectious virus (Figure 41). The T_{90} values for the two Lassa virus isolates tested, which represents the time taken for a 90% reduction in viable virus concentration, were 1.2 and 1.8 days (Shaffer et al., 2023). This suggests excreted Lassa virus discharged to the wastewater network may remain infectious for at least a day.

[157] https://www.health.govt.nz/our-work/diseases-and-conditions/communicable-disease-control-manual/viral-haemorrhagic-fevers Accessed 25 August 2023
[158] https://www.cdc.gov/vhf/lassa/pdf/what-you-need-to-know-about-lassa-508.pdf Accessed 25 August 2023
[159] https://www.who.int/news-room/fact-sheets/detail/lassa-fever Accessed 25 August 2023
[160] https://www.cdc.gov/vhf/lassa/symptoms/index.html Accessed 25 August 2023

Table 12 Summary of studies assessing excretion of Lassa fever virus RNA in urine

Study participants	% positive patients	Shedding dynamics (no. of samples)	Reference
1	100	• Positive day 5, 8, 10, 12, 14 and 15 of hospitalisation • Positive 8-, 16- and 30-days post hospital discharge • Negative 51 days post discharge	Choi et al. (2018)
159 (995 samples)	34	• 34% (37/110) positive directly after hospital discharge • 20% (27/138) positive 0.5 months post hospital discharge • 6% (9/145) positive 1 month post hospital discharge • 0.7% (1/138) positive 3 months post hospital discharge • 0% positive 6, 9-, 12-, 18- and 24-months post hospital discharge (n = 133, 122, 99, 63 and 47)	Thielebein et al. (2022)
5	80	• Positive samples obtained on days 12, 15, 32 and 40 PSO (1 patient each day) • Negative day 62 PSO	Lunkenheimer et al. (1990)
1	100	• Positive days 28, 35 and 42 PSO, negative days 58, 72 and 78 • Viral load from $4.6 \times 10^2 – 5.7 \times 10^3$ copies/mL	Grahn et al. (2016)

PSO, post symptom onset.

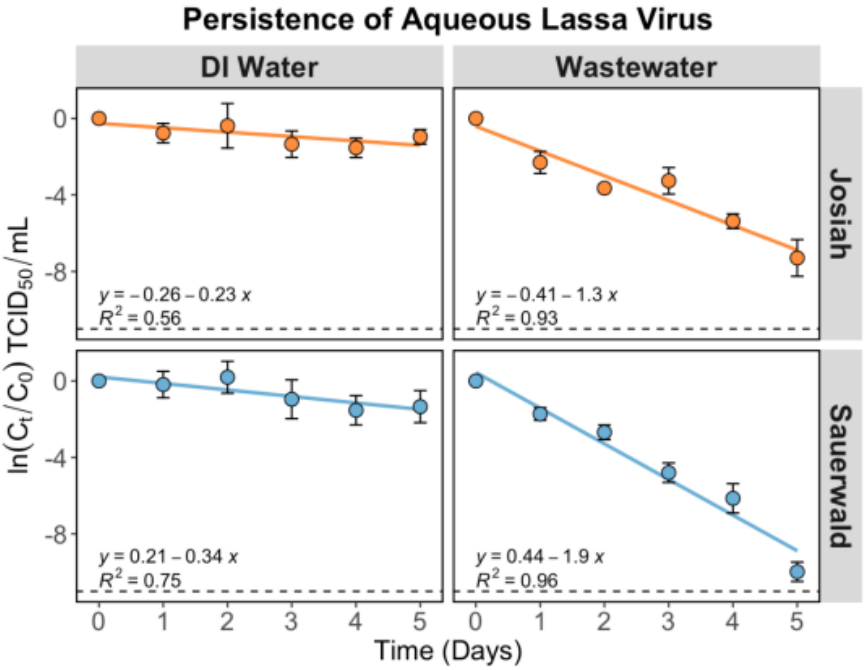

Figure 41 Persistence of Lassa virus in deionized (DI) water and raw municipal wastewater

Reproduced from Shaffer et al. (2023). Josiah and Sauerwald are different Lassa virus strains.

3.2 EBOLA VIRUS DISEASE

3.2.1 Transmission

Ebola virus disease is a severe, often-fatal zoonotic illness caused by enveloped single-stranded RNA viruses of the genus *Ebolavirus* (family *Filoviridae*) (Zhang et al., 2014). There are four species known to cause disease in humans - *Zaire ebolavirus*, *Sudan ebolavirus*, *Bundibugyo ebolavirus*, and *Taï Forest ebolavirus* (Vetter et al., 2016). A fifth species, *Reston ebolavirus*, appears to only cause asymptomatic infection in humans (Vetter et al., 2016). These viruses are named after the Ebola River in the Democratic Republic of the Congo (formerly Zaire), the site where they were first discovered in 1976[161].

Ebola virus is thought to be transmitted to humans from an infected animal such as a fruit bat or non-human primate[162], particularly when preparing, cooking and eating infected animals[163]. Infected humans can then transmit the virus person-to-person through contact with infected blood or bodily fluid (e.g., urine, faeces, vomit, saliva, semen, breast milk, amniotic fluid) or objects contaminated with bodily fluids[162]. It may also be transmitted in semen from a man who has recovered from the illness as the virus is known to persist in the testicles[162]. Ebola virus is not known to be transmitted through food but as noted above may be transmitted during handling and consumption of infected wild animals[162].

[161] https://www.cdc.gov/vhf/ebola/about.html Accessed 25 August 2023
[162] https://www.cdc.gov/vhf/ebola/transmission/index.html Accessed 25 August 2023
[163] https://www.who.int/news-room/fact-sheets/detail/ebola-virus-disease Accessed 25 August 2023

3.2.2 Prevention

There are currently two Ebola vaccines for protection against *Zaire ebolavirus* – the first of these, Ervebo, is recommended by the WHO Strategic Advisory Group of Experts (SAGE) as part of a "broader set of Ebola outbreak response tools"[164], and exhibits a "rapid antibody response in 14 days after a single dose"[165]. The second vaccine is delivered in two doses 8 weeks apart and as such is not suitable as part of a rapid outbreak response[166].

3.2.3 Geographical distribution

The first Ebola outbreaks occurred in remote areas of Central Africa close to tropical rainforests[167]. Outbreaks primarily occur on the African continent[168] (Table 13, Figure 42). In 2014 – 2016 there was a large outbreak in West Africa which spread to Guinea, Sierra Leone and Liberia[167]. Ebola has been detected outside of Africa, including in Italy, the United Kingdom, Spain, the United States, but all cases have been either in laboratory workers, travellers returning from affected areas, or local healthcare workers treating them (Table 13).

3.2.4 New Zealand epidemiology

There has never been a case of Ebola in New Zealand[169].

3.2.5 Symptoms and treatment

The incubation period for Ebola virus disease is around 2 – 21 days from exposure, and people are not infectious prior to symptom onset[170]. Symptom onset is often sudden and may include fever, headache, sore throat, fatigue and muscle pain, followed by development of a rash, vomiting, diarrhoea and internal and external haemorrhaging (bleeding)[170]. On average, 50% of Ebola virus cases are fatal, but this varies and in past outbreaks has ranged from 25 – 90%[171]. However, new treatments have greatly improved chances of survival when patients are treated early[172]. Asymptomatic Ebola infections have been reported but their prevalence is unclear (Dean et al., 2016; Kelly et al., 2022; Mbala et al., 2017).

3.2.6 Excretion of biomarkers of infection

Metagenomic analysis of wastewater collected in Uganda in 2016 revealed a single read which matched Ebola virus, although this was not confirmed by PCR (O'Brien et al., 2017). No other WBS in which Ebola was detected in wastewater were identified during preparation of this report. Studies assessing the presence of Ebola virus RNA in urine and faeces mostly have very small study sizes, but do demonstrate shedding for at least 2 weeks post symptom onset (Table 14).

[164] https://www.who.int/news/item/12-11-2019-who-prequalifies-ebola-vaccine-paving-the-way-for-its-use-in-high-risk-countries Accessed 25 August 2023
[165] https://www.cdc.gov/vhf/ebola/clinicians/vaccine/index.html Accessed 25 August 2023
[166] https://www.who.int/news-room/questions-and-answers/item/ebola-vaccines Accessed 25 August 2023
[167] https://www.who.int/health-topics/ebola Accessed 25 August 2023
[168] https://www.cdc.gov/vhf/ebola/about.html Accessed 25 August 2023
[169] https://www.health.govt.nz/our-work/diseases-and-conditions/communicable-disease-control-manual/viral-haemorrhagic-fevers Accessed 25 August 2023
[170] https://www.who.int/news-room/fact-sheets/detail/ebola-virus-disease Accessed 25 August 2023
[171] https://www.paho.org/en/topics/ebola-virus-disease Accessed 25 August 2023
[172] https://www.afro.who.int/health-topics/ebola-disease Accessed 25 August 2023

3.2.7 Potential health hazard if present in wastewater

The Ebola virus is known to be transmitted via contact with urine and faeces from infected individuals[173], and infectious Ebola virus has been isolated from urine (Kreuels et al., 2014). As such, where an infected individual urinates or defecates on a plane or at the airport there could be a potential health hazard posed to people collecting or processing aircraft/airport wastewater samples, or to WWTP staff.

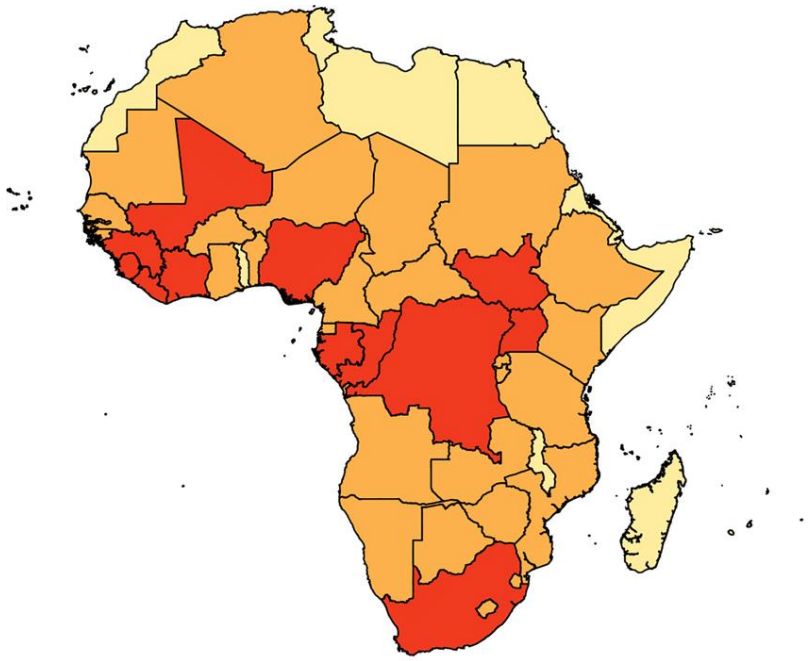

Figure 42 Ebola virus risk level for African countries based on history of outbreaks

Reproduced from Skrip and Galvani (2016). Red, high risk of future outbreak based on having at least one documented outbreak since 1976; orange, moderate risk due to having borders contiguous with high-risk countries; yellow, low risk due to no history of Ebola cases and no shared borders with high-risk countries.

[173] https://bestpractice.bmj.com/patient-leaflets/en-gb/html/1415888264941/Ebola Accessed 25 August 2023

Table 13 Summary of Ebola outbreaks since 1976

Year	Countries affected	Species	Additional information	Reported cases	% fatal
2022	Uganda	*Sudan ebolavirus*		164	34
	Democratic Republic of the Congo	*Zaire ebolavirus*		1	100
	Democratic Republic of the Congo	*Zaire ebolavirus*		5	100
2021	Democratic Republic of the Congo	*Zaire ebolavirus*		11	82
	Democratic Republic of the Congo	*Zaire ebolavirus*		12	50
	Guinea	*Zaire ebolavirus*		23	52.2
2020	Democratic Republic of the Congo	*Zaire ebolavirus*		130	42.3
2018	Democratic Republic of the Congo, Uganda	*Zaire ebolavirus*		3,470	66
	Democratic Republic of the Congo	*Zaire ebolavirus*		54	61
2017	Democratic Republic of the Congo	*Zaire ebolavirus*		8	50
2014	Democratic Republic of the Congo	*Zaire ebolavirus*		69	71
	Guinea, Liberia, Sierra Leone	*Zaire ebolavirus*	West African Epidemic	28,610	39
	Italy	*Zaire ebolavirus*	Healthcare worker infected in Sierra Leone	1	0
	Mali	*Zaire ebolavirus*	Introduced by traveller from Guinea	8	75
	Nigeria	*Zaire ebolavirus*	Introduced by traveller from Liberia	20	40
	Senegal	*Zaire ebolavirus*	Introduced by an infected traveller	1	0
	Spain	*Zaire ebolavirus*	Healthcare worker treating patient from Sierra Leone	1	0
	United Kingdom	*Zaire ebolavirus*	Healthcare worker infected in Sierra Leone	1	0
	United States	*Zaire ebolavirus*	Travellers infected in West Africa and two US nurses who treated them	4	25
2012	Uganda	*Sudan ebolavirus*		6	50
	Democratic Republic of the Congo	*Bundibugyo ebolavirus*		38	34
	Uganda	*Sudan ebolavirus*		11	36
2011	Uganda	*Sudan ebolavirus*		1	100
2008	Democratic Republic of the Congo	*Zaire ebolavirus*		32	47
	Philippines	*Reston ebolavirus*	Infected by pigs in a slaughterhouse	6 asymptomatic	0
2007	Uganda	*Bundibugyo ebolavirus*		131	32
	Democratic Republic of the Congo	*Zaire ebolavirus*		264	71

2005	Democratic Republic of the Congo	*Zaire ebolavirus*		12	83
2004	Russia	*Zaire ebolavirus*	Lab worker working on a vaccine	1	100
	Sudan	*Sudan ebolavirus*		17	41
2003	Democratic Republic of the Congo	*Zaire ebolavirus*		35	83
	Democratic Republic of the Congo	*Zaire ebolavirus*		143	89
2001	Democratic Republic of the Congo	*Zaire ebolavirus*		59	75
	Gabon	*Zaire ebolavirus*		65	81
2000	Uganda	*Sudan ebolavirus*		425	53
1996	Russia	*Zaire ebolavirus*	Lab worker working on an experimental treatment	1	100
	Philippines	*Reston ebolavirus*	In monkeys in export facility	0	0
	United States	*Reston ebolavirus*	In monkeys from Philippines in QF	0	0
	South Africa	*Zaire ebolavirus*	Healthcare worker infected in Gabon and nurse who treated him.	2	50
	Gabon	*Zaire ebolavirus*		60	75
	Gabon	*Zaire ebolavirus*		31	68
1995	Democratic Republic of the Congo	*Zaire ebolavirus*		315	81
1994	Côte D'Ivoire	*Taï Forest ebolavirus*	Scientist who conducted autopsy on infected chimpanzee	1	0
	Gabon	*Zaire ebolavirus*		51	61
1992	Italy	*Reston ebolavirus*	In monkeys from Philippines in QF	0	0
1989	Philippines	*Reston ebolavirus*	Outbreak in macaques in a primate export facility	3 asymptomatic	0
	United States	*Reston ebolavirus*	Via monkeys from Philippines in QF	4 asymptomatic	0
1979	Sudan	*Sudan ebolavirus*		34	65
1977	Democratic Republic of the Congo	*Zaire ebolavirus*		1	100
1976	United Kingdom	*Zaire ebolavirus*	Lab infection from a contaminated needle	1	0
	Sudan	*Sudan ebolavirus*		284	53
	Democratic Republic of the Congo	*Zaire ebolavirus*		318	88

Information obtained from https://www.cdc.gov/vhf/ebola/history/chronology.html. *Reston ebolavirus* does not cause disease in humans. Multiple incidences in the same country during a given year represent separate outbreaks. Democratic Republic of the Congo was formerly known as Zaire. QF, quarantine facility

Table 14 Summary of studies assessing excretion of Ebola virus RNA in urine and/or faeces

Study participants	% positive patients	Shedding dynamics (faeces)	Shedding dynamics (urine)	Reference
1	100	• Positive day 7 – 9, 12 – 13 PSO	• Positive from day 6 – 13 PSO	Schibler et al. (2015)
1	100	• Positive days 22 and 25 PSO • Negative days 28, 30 and 32 PSO	• Positive days 22, 25 and 28 PSO • Negative days 30 and 32 PSO	Mora-Rillo et al. (2015)
1	100	• Not tested	• Positive day 16 PSO	Moreau et al. (2015)
2	50	• Not tested	• Patient 1 negative day 12 PSO • Patient 2 positive days 6 – 9, 11; negative days 12 – 15 PSO	Liddell et al. (2015)
2	100	• Not tested	• Detectable from day 17 until at least day 28 PSO in 1 patient	Lyon et al. (2014)
9 urine (5 acute, 4 convalescent) 4 faeces (acute)	0 urine 50 faeces	• 50% positive – samples collected 4 – 12 days PSO	• 0% positive – 7 samples collected in acute phase (5 – 22 days PSO); 4 samples collected in convalescent phase (8 – 40 days PSO)	Bausch et al. (2007)
28	100	• 0% (0/79) positive for virus isolation Samples not tested by PCR	• 0% (0/95) positive for virus isolation Samples not tested by PCR.	Rowe et al. (1999)
7	100	• 14% (1/7) patients positive from rectal swab (positive 22 and 29 PSO, negative 25 and 33 days PSO)	• 0% (0/7) positive. Samples collected 11-33 days PSO	Rodriguez et al. (1999)
7	100	• Not tested	• Samples positive from day 0 up to at least 30 days PSO in some cases	Janvier et al. (2016)
1	100 faeces 100 urine	• Positive days 6, 7, 9, 12, 15 – 19 PSO	• Positive days 5 – 7, 22, 25, 26, 28 PSO	Wolf et al. (2015)
330 faeces (558 samples) 593 urine (1875 samples) **Long-term detection study**	0% faeces 0.3% urine	• 0% (0/558) positive 0 – 24 months post hospital discharge • No samples tested during hospitalisation	• 2.3% (3/128) of samples positive within 3 months of hospital discharge • 0% (0/1747) samples positive 3 – 24 months post hospital discharge • No samples tested during hospitalisation	Keita et al. (2019)

PSO, post symptom onset.

It has previously been noted that “it remains unknown if Ebola virus may be transmitted via wastewater” (Bibby et al., 2015). However, a study in which the Ebola virus was spiked into wastewater found it was relatively stable, with infectious virus still present after 8 days at 20°C (Bibby et al., 2015). A subsequent 2017 study investigated the aerosolisation of Ebola virus surrogates in toilets, a lab-scale wastewater treatment aeration basin and converging sewer pipes (Lin & Marr, 2017). This study found that although toilets generated large numbers of aerosols they were of very small total volume so it was concluded that the chance of aerosolising viruses when flushing was “expected to be low” (Lin & Marr, 2017). In contrast, they found that viable virus was able to be aerosolised from the aeration basin and converging sewer pipes (to a lesser extent) (Lin & Marr, 2017). However, the amount of virus aerosolised will obviously depend on the viral load being discharged to the wastewater network, which will be influenced by the number of infected individuals. Additionally, this study assessed a standard flush toilet, which in comparison to aircraft toilets uses considerably more water during flushing (up to 19 litres versus <2 litres (Eaton & Gilpin, 2023)). As such, it might be speculated that the risk of aerosolising Ebola virus when flushing an aircraft toilet would be even lower than for standard flush toilets.

A Bayesian belief network model has also been developed to assess the risk posed to wastewater workers from Ebola virus present in wastewater (Zabinski et al., 2018). This model can be used to assess scenarios of ingestion.

3.3 MARBURG VIRUS DISEASE

3.3.1 Transmission

Marburg virus disease is a severe zoonotic haemorrhagic fever caused by a enveloped single-stranded RNA virus of the genus *Marburgvirus* (family *Filoviridae*) (Zhang et al., 2014) which infects humans and non-human primates[174]. It was first identified during two large outbreaks in Marburg and Frankfurt in Germany, and Belgrade in Yugoslavia (now Serbia) in 1967 which were associated with laboratory work with African green monkeys imported from Uganda[175], and is closely related to the Ebolaviruses[174].

The Egyptian cave-dwelling fruit bat, *Rousettus aegyptiacus* (family *Pteropodidae*), is an animal reservoir for Marburg virus[174]. However, it is unclear how the virus spreads from bats to humans, although it is known to be present in bat urine, faeces and oral secretions[176]. Once a human is infected, the virus can be transmitted from person-to-person via blood or bodily fluids (e.g., urine, faeces, saliva, vomit, semen, breast milk, sweat, amniotic fluid), or objects contaminated with bodily fluids from an infected person[176]. Similar to Ebola virus, it may also be passed in semen from a man who has already recovered from the illness due to persistence of the virus in the testicles[176]. People can also be infected when handling infected non-human primates or via contact with their bodily fluids[176].

[174] https://www.cdc.gov/vhf/marburg/about.html Accessed 25 August 2023
[175] https://www.who.int/news-room/fact-sheets/detail/marburg-virus-disease Accessed 25 August 2023
[176] https://www.cdc.gov/vhf/marburg/transmission/index.html Accessed 25 August 2023

3.3.2 Prevention

There is currently no approved vaccine available for Marburg virus, but several candidates are in development[177], including one undergoing human trials[178].

3.3.3 Geographical distribution

Aside from the 1967 cases, outbreaks have been restricted to sub-Saharan Africa[179] (Table 15). However, the geographic range of the *R. aegyptiacus* bat is much broader so more people may be at risk[180] (Figure 43). Recently, there have been two outbreaks in Tanzania (21 March – 31 May 2023) and Equatorial Guinea (13 Feb – 8 June 2023)[179].

3.3.4 New Zealand epidemiology

There has never been a reported case of Marburg virus in New Zealand[181].

3.3.5 Symptoms

The incubation period for Marburg virus disease ranges from 2 – 21 days[182], and the virus is not transmitted during the incubation period[183]. Symptoms start abruptly with high fever, severe headache, severe malaise and often muscle aches and pain[182]. On the third day, abdominal pain/cramping, nausea, vomiting and severe watery diarrhoea may develop[182]. Patients often appear ghost-like with "drawn features, deep-set eyes, expressionless faces, and extreme lethargy" [182]. Days 5 – 7 after symptom onset, severe haemorrhaging from the gums, nose, vagina, gastrointestinal tract and puncture sites (e.g., from intravenous lines or blood-test sites) may develop, patients generally have sustained high fevers and may show symptoms of central nervous dysfunction including confusion, aggression and irritability[182]. Where death occurs, this is generally 8 – 9 days after symptom onset after severe blood loss and shock[182]. The average case fatality rate of Marburg virus disease is around 50% but varies depending on the strain and how the case is managed[182]. No asymptomatic cases of Marburg virus infection have been documented (Kortepeter et al., 2020).

3.3.6 Excretion of biomarkers of infection

No WBS studies assessing the presence of Marburg virus in wastewater were identified during preparation of this report. Marburg virus has been isolated from human urine and visualised using immune-fluorescence (Martini, 1973). However, no studies have specifically assessed detection of Marburg virus in urine or faeces using PCR. Given this virus is transmissible via contaminated urine and faeces[184], infectious virus must be present in these excreta during at least some stage of the infection.

[177] https://www.ecdc.europa.eu/en/infectious-disease-topics/z-disease-list/ebola-virus-disease/facts/factsheet-about-marburg-virus Accessed 25 August 2023
[178] https://www.nih.gov/news-events/news-releases/marburg-vaccine-shows-promising-results-first-human-study Accessed 25 August 2023
[179] https://www.cdc.gov/vhf/marburg/outbreaks/chronology.html
[180] https://www.cdc.gov/vhf/marburg/about.html Accessed 25 August 2023
[181] https://www.health.govt.nz/our-work/diseases-and-conditions/communicable-disease-control-manual/viral-haemorrhagic-fevers Accessed 25 August 2023
[182] https://www.who.int/news-room/fact-sheets/detail/marburg-virus-disease Accessed 25 August 2023
[183] https://africacdc.org/disease/marburg-virus-disease-mvd/ Accessed 25 August 2023
[184] https://www.cdc.gov/vhf/marburg/transmission/index.html Accessed 25 August 2023

3.3.7 Potential health hazard if present in wastewater

The Marburg virus is transmitted via contact with urine and faeces of infected individuals[184], and has been isolated from urine (Martini, 1973). As such, where an infected individual urinates or defecates on a plane or at the airport there could be a potential health hazard posed to people collecting or processing aircraft/airport wastewater samples, or to WWTP staff.

Table 15 Summary of Marburg virus disease outbreaks

Year	Countries affected	Reported cases	Reported deaths
2023	Tanzania	9	6 (67%)[185]
	Equatorial Guinea	40	35 (88%)[185]
2022	Ghana	3	2 (67%)
2021	Guinea	1	1 (100%)
2017	Uganda	4	3 (75%)
2014	Uganda	1*	1 (100%)
2008	Netherlands (contracted in Uganda)	1	1 (100%)
2008	USA (contracted in Uganda)	1	0
2007	Uganda	4	1 (25%)
2004-2005	Angola	252	227 (90%)
1998-2000	Democratic Republic of the Congo	154	128 (83%)
1990	Russia (laboratory contamination)	1	1 (100%)
1987	Kenya	1	1 (100%)
1980	Kenya	2	1 (50%)
1975	South Africa (contracted in Zimbabwe)	3	1 (33%)
1967	Germany and Yugoslavia (lab workers handling monkeys imported from Uganda)	31	7 (23%)

Data from https://www.cdc.gov/vhf/marburg/outbreaks/chronology.html. *8 others developed symptoms but did not test positive.

[185] https://www.afro.who.int/countries/united-republic-of-tanzania/news/marburg-virus-disease-outbreak-tanzania-declared-over Accessed 25 August 2023

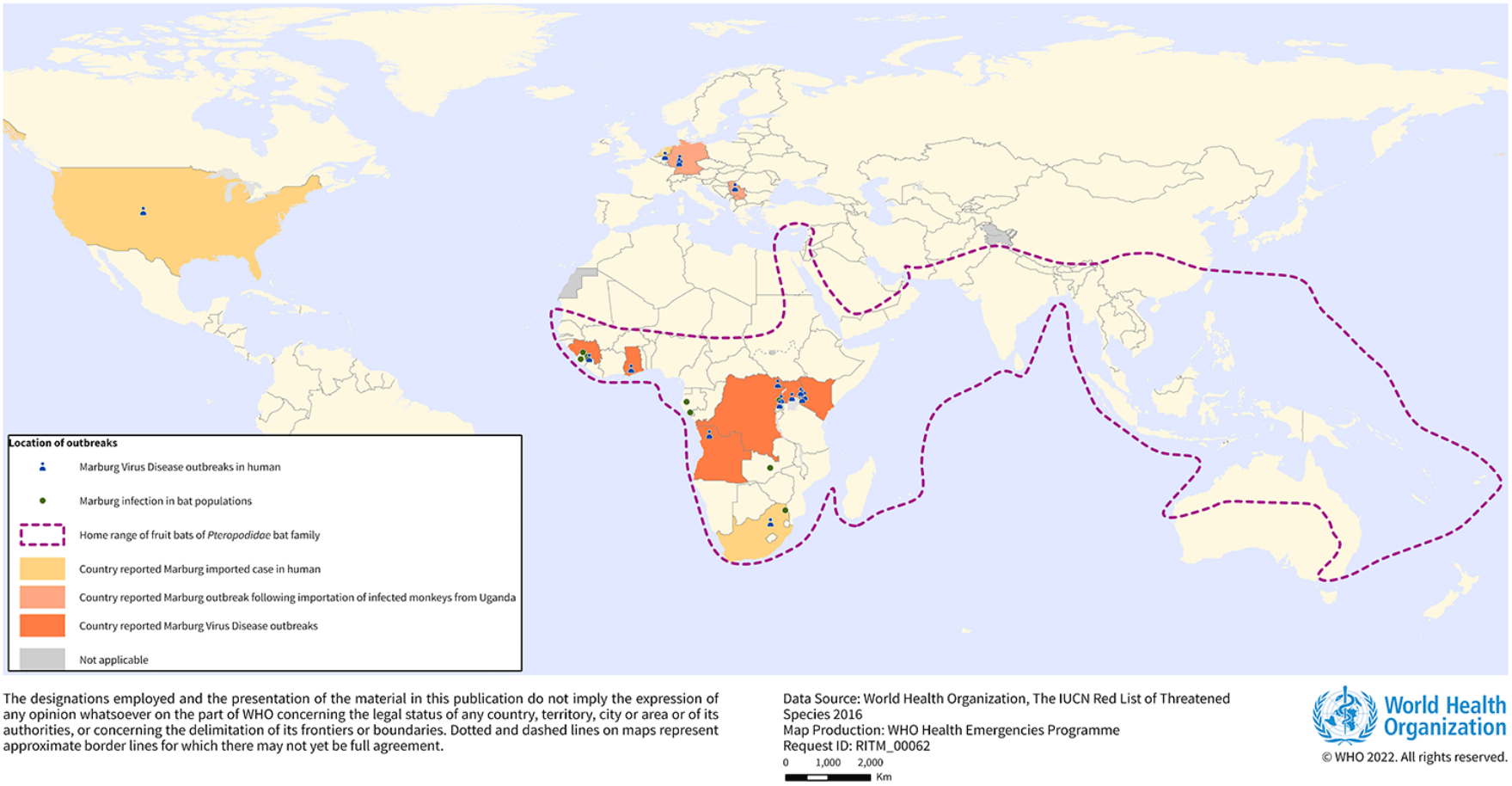

Figure 43 Global distribution of Marburg virus disease outbreaks (2022)

Reproduced from https://cdn.who.int/media/images/default-source/health-topics/marburg-virus-disease/ritm00062_marberg_distribution_20230323.png

3.4 HANTAVIRUS

3.4.1 Transmission

Hantavirus is an emerging zoonotic illness caused by several enveloped single-stranded RNA viruses of the genus Hantavirus (family *Bunyavirus*)[186] which are transmitted by rodents via their urine, faeces and saliva[187]. People are mainly infected when they breathe in air contaminated with virus by stirring up of rodent nesting materials or materials contaminated with their urine or faeces[187]. These viruses may also be transmitted through bites from infected rodents, eating food contaminated with rodent urine, faeces or saliva, or touching contaminated materials then touching the nose or mouth[187], or through the eyes or broken skin[188]. Some reports from Argentina and Chile have suggested that the hantavirus strain Andes virus can be transmitted from person-to-person, but a systematic review found that the balance of evidence does not support this claim (Toledo et al., 2022).

3.4.2 Prevention

There is no vaccine for Hantavirus infection[189].

3.4.3 Geographical distribution

Hantaviruses cause two diseases in humans - hantavirus pulmonary syndrome (HPS), which occurs in the Americas, and haemorrhagic fever with renal syndrome (HFRS), which occurs in Europe and Asia (Toledo et al., 2022) (Figure 44).

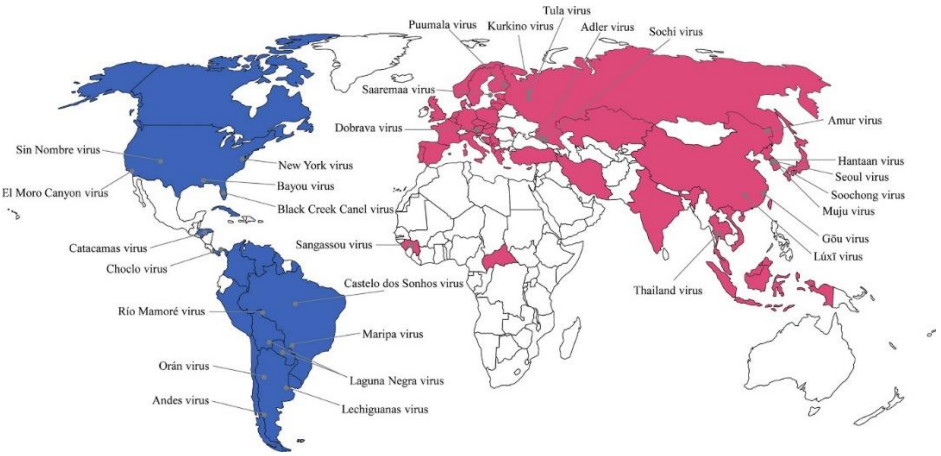

Figure 44 Global distribution of HPS and HFRS

Reproduced from Kim et al. (2021). Blue hantavirus pulmonary syndrome (HPS); pink, haemorrhagic fever with renal syndrome (HFRS). Names indicate different viral strains found in those regions.

3.4.4 New Zealand epidemiology

There has never been a reported case of Hantavirus infection in New Zealand[190].

[186] https://www.cdc.gov/hantavirus/technical/hanta/virology.html Accessed 25 August 2023
[187] https://www.cdc.gov/hantavirus/hps/transmission.html Accessed 25 August 2023
[188] https://www.cdc.gov/hantavirus/hfrs/index.html Accessed 25 August 2023
[189] https://www.cdc.gov/hantavirus/hps/diagnosis.html Accessed 25 August 2023
[190] https://www.health.govt.nz/our-work/diseases-and-conditions/communicable-disease-control-manual/viral-haemorrhagic-fevers Accessed 25 August 2023

3.4.5 Symptoms

Symptoms of HPS develop 1 – 8 weeks after exposure, although the exact incubation period is unknown due to the small number of HPS cases[191]. Asymptomatic HPS infection is considered to be rare[192]. All cases of HPS initially present with fever, muscle aches and fatigue[191]. Up to 50% of cases may also present with chills, headaches, dizziness, nausea, vomiting, diarrhoea and abdominal pain[191]. Around 4 – 10 days after the initial symptoms develop, the disease enters the late phase which presents with coughing and shortness of breath due to the lungs filling with fluid[191]. At this stage the disease progresses rapidly, requiring hospitalisation and in many cases ventilation within 24 hours[192]. Approximately 38% of HPS cases are fatal[191].

Symptoms of HFRS generally develop within 1 – 2 weeks after exposure but may take as long as 8 weeks before they develop[193]. Infections may also be asymptomatic (Romero & Anjum, 2022). Symptoms of HFRS develop suddenly and include fever, chills, intense headaches, nausea, abdominal pain and blurred vision[193]. Patients may also appear flushed and have a rash and/or inflamed/red eyes[193]. Patients may then develop acute kidney failure, vascular leakage, low blood pressure and shock, with the severity of symptoms varying depending on the virus strain, with the Hantaan and Dobrava viruses often causing particularly severe symptoms[193]. Other severe complications include meningoencephalitis (inflammation of the brain and meninges), acute disseminated encephalomyelitis (inflammation of the brain and spinal cord), seizures, abnormal blood clotting, haemorrhage, perimyocarditis (inflammation of the tissue around the heart and the heart muscle), pulmonary oedema (excess fluid in the lungs) and multi-organ failure (Zou et al., 2016). Classic HFRS usually exhibits five phases: febrile (fever) phase (3 – 7 days), hypotensive (low blood pressure) phase (hours – 2 days), oliguric (low urinary output) phase (3 – 7 days), diuretic phase (increased urination) (days – weeks), and the convalescent (recovery) phase (2 – 3 months) (Zou et al., 2016). Complete recovery from HFRS may take weeks - months[193]. The mortality rate for HFRS varies from <1% - 15% depending on the virus strain (Romero & Anjum, 2022).

3.4.6 Excretion of biomarkers of infection

No WBS studies assessing the presence of Hantavirus in wastewater were identified during preparation of this report. Hantavirus RNA has been detected in the urine of four Korean soldiers suffering from HFRS in samples taken 4, 7, and 8 (2 samples) days after symptom onset (Cho et al., 2021). Infectious hantavirus (Andes strain) has also been isolated from the urine of patients suffering from acute HPS (Godoy et al., 2009).

3.4.7 Potential health hazard if present in wastewater

Given infectious hantavirus has been isolated from human urine (Godoy et al., 2009), and transmission from animal urine has been documented, where an infected individual urinates on a plane or at the airport there could be a potential health hazard posed to people collecting or processing aircraft/airport wastewater samples, or to WWTP staff.

[191] https://www.cdc.gov/hantavirus/hps/symptoms.html Accessed 25 August 2023
[192] https://www.cdc.gov/hantavirus/technical/hps/clinical-manifestation.html Accessed 25 August 2023
[193] https://www.cdc.gov/hantavirus/hfrs/index.html Accessed 25 August 2023

4. OTHER HIGH-RISK DISEASES

This section will consider the suitability of WBS for detection of high-risk diseases arriving at the border. Diseases to be considered are those which if introduced into New Zealand would pose a considerable threat to the health of our communities, with selection guided by the CDCs list of potential bioterrorism agents/diseases[194] and the WHO Public Health Emergencies of International Concern (PHEIC) (Figure 45).

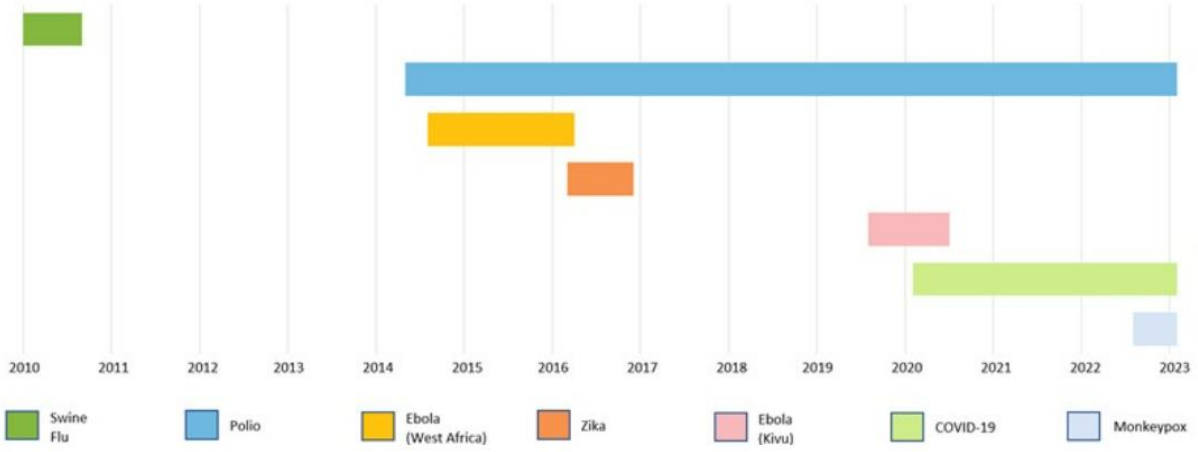

Figure 45 Summary of Public Health Emergencies of International Concern declarations since 2010

Reproduced from https://www.ehinz.ac.nz/indicators/border-health/overseas-infectious-diseases-of-concern/

4.1 SMALLPOX

4.1.1 Transmission

Smallpox is an infectious disease caused by the variola virus, an enveloped double-stranded DNA virus of the genus *Orthopoxvirus* (family *Poxviridae*)[195]. There are two strains of the variola virus – variola major and variola minor, with variola major being the most common and severe (~30% mortality versus 1% for variola minor)[196]. Smallpox is considered "one of the most devastating diseases known to humanity" [196] with an estimated 300 million deaths in the 20th century (Henderson, 2011). Health Assembly declared that smallpox had been eradicated[197], becoming the only human disease to be eradicated thus far[198].

[194] https://emergency.cdc.gov/agent/agentlist-category.asp Accessed 25 August 2023
[195] https://wwwnc.cdc.gov/travel/yellowbook/2024/infections-diseases/smallpox-other-orthopoxvirus-associated-infections Accessed 29 August 2023
[196] https://www.who.int/teams/health-product-policy-and-standards/standards-and-specifications/vaccine-standardization/smallpox Accessed 29 August 2023
[197] https://www.cdc.gov/smallpox/index.html Accessed 29 August 2023
[198] https://www.who.int/news-room/spotlight/history-of-vaccination/history-of-smallpox-vaccination Accessed 29 August 2023

There are two laboratories in the world that officially store and handle the variola virus, under supervision of the WHO – the CDC in Atlanta, Georgia, USA and the State Research Center of Virology and Biotechnology (VECTOR Institute) in Koltsovo, Russia[199].

It is possible that smallpox could be used as a bioterrorism agent, particularly given many people born since the disease was declared eradicated are unlikely to have been vaccinated[200]. The United States CDC note that "there is credible concern that in the past some countries made the virus into weapons, which may have fallen into the hands of terrorists or other people with criminal intentions"[200].

Smallpox can be transmitted from person-to-person in aerosols and respiratory droplets (e.g., from coughing and sneezing) (Milton 2012), by direct contact with smallpox sores, or indirectly via materials (e.g., clothing and bedding) or objects contaminated with fluid from these sores[201]. In rare cases it has also been reported to spread through the air in enclosed settings[201].

4.1.2 Prevention

Effective vaccines resulted in the elimination of smallpox in 1980 (Henderson, 2011).

4.1.3 Geographical distribution

The last naturally occurring instance of smallpox was in Somalia in 1977 (Henderson, 2011).

4.1.4 New Zealand epidemiology

New Zealand had a significant smallpox outbreak in 1913 with 55 deaths[202]. Smallpox was eradicated from New Zealand over 100 years ago[203].

4.1.5 Symptoms

The incubation period for smallpox ranges from 7 – 19 days, and during this period an infected person is not infectious[204]. There are no known asymptomatic cases of smallpox[205]. Initial symptoms of smallpox infection include high fever, head and body aches and in some cases vomiting[201204]. This stage of the infection usually lasts for 2 – 4 days and infected individuals may be contagious during this period[204]. Next, a rash of small red spots starts in the mouth and on the tongue, and the fever persists[201204]. These spots develop into sores which open and release copious amounts of virus into the mouth and throat[201204]. At this time, a skin rash appears, first on the face then spreading to the arms and legs, followed by the hands and feet, and the entire body within 24 hours, the fever starts to subside, and the infected person may feel temporarily better[204]. Around four days after the spots appear, they develop into sores filled with thick, opaque fluid and often appear to have a dent in the centre[201204]. The fever may also recur at this stage[204]. The sores develop into pustules which crust over after about five days[204]. By around two weeks after the rash appears, the majority of spots will have formed scabs[204]. The scabs then start to fall off, with most gone by three weeks after the rash began – infected individuals are still infectious during this stage[204]. Around four weeks after the rash appeared, all scabs are likely gone, and the person is

[199] https://www.cdc.gov/smallpox/history/history.html Accessed 29 August 2023
[200] https://www.cdc.gov/smallpox/bioterrorism/public/threat.html Accessed 29 August 2023
[201] https://www.cdc.gov/smallpox/transmission/index.html Accessed 29 August 2023
[202] https://newsroom.co.nz/2019/01/29/smallpox-a-disease-in-deep-freeze/ Access 9 April 2024
[203] https://ourworldindata.org/smallpox Access 9 April 2024
[204] https://www.cdc.gov/smallpox/symptoms/index.html Accessed 29 August 2023
[205] https://my.clevelandclinic.org/health/diseases/10855-smallpox Accessed 29 August 2023

considered no longer contagious[206]. In some infections, life-threatening interstitial pneumonitis (scarring of the lungs that makes it difficult to breathe) and tubulointerstitial nephritis (inflammation of the tubules of the kidneys and the surrounding tissue) may develop (Martin, 2002). As noted above, the mortality rate of variola major is around 30%, and around 1% for variola minor[207]. Many survivors of smallpox infection are left with deep pitted scars, known as pockmarks[207].

4.1.6 Excretion of biomarkers of infection

No WBS studies assessing the presence of the smallpox virus in wastewater were identified during preparation of this report. However, infectious smallpox virus has been isolated from urine (Sarkar et al., 1973). No other studies reporting biomarkers of smallpox infection in urine of faeces were identified during preparation of this report.

4.1.7 Potential health hazard if present in wastewater

Given infectious smallpox virus has been isolated from urine (Sarkar et al., 1973), where an infected individual urinates on a plane or at the airport there could be a potential health hazard posed to people collecting or processing aircraft/airport wastewater samples, or to WWTP staff.

4.2 MPOX

4.2.1 Transmission

Mpox is a zoonotic illness caused by an enveloped double-stranded DNA virus of the genus *Orthopoxvirus* (family *Poxviridae*), the same genus as smallpox (Lansiaux et al., 2022). Mpox (formerly known as monkeypox) was first identified in laboratory monkeys in 1958, and the first human case was reported in the Democratic Republic of the Congo in 1970[208]. Mpox has recently risen to prominence due to a 2022-2023 outbreak affecting numerous non-endemic countries[209]. Mpox can be transmitted to humans from infected animals via bites, scratches, direct contact with dead animals or consuming contaminated meat[208]. It can also be passed person-to-person via direct contact with infectious lesions on the skin, mouth or genitals (e.g., during sexual contact), contact with contaminated clothing or objects, or via respiratory droplets/aerosols during prolonged close contact (e.g., from talking/breathing)[208].

4.2.2 Prevention

A vaccine has been developed and is available in New Zealand to eligible people[210].

4.2.3 Geographical distribution

Mpox is endemic in many parts of Africa including Gabon, Côte d'Ivoire, the Democratic Republic of the Congo, Cameroon, Liberia, Nigeria, Sierra Leone, and the Central African

[206] https://www.cdc.gov/smallpox/symptoms/index.html Accessed 29 August 2023
[207] https://www.who.int/teams/health-product-policy-and-standards/standards-and-specifications/vaccine-standardization/smallpox Accessed 29 August 2023
[208] https://www.who.int/news-room/fact-sheets/detail/monkeypox Accessed 29 August 2023
[209] https://www.who.int/emergencies/disease-outbreak-news/item/2022-DON390 Accessed 29 August 2023
[210] https://www.beehive.govt.nz/release/monkeypox-vaccination-available-eligible-people-next-week Accessed 29 August 2023

Republic[211], and has increased in prevalence since 1980 when the smallpox vaccination programme ceased[211]. During the 2022-2023 outbreak it has been reported in numerous non-endemic countries[211].

4.2.4 New Zealand epidemiology

As of January 2024, there have been 51 confirmed cases, including cases of local transmission[212].

4.2.5 Symptoms

The incubation period for mpox is around 3 – 17 days[213]. Some cases may be asymptomatic (Abbasi, 2022). Common symptoms of infection include fever, sore throat, headache, back pain and muscle aches, low energy and swollen lymph nodes[214]. Typically, these symptoms occur first, followed by development of a rash that starts on the face and spreads across the body[214]. The rash begins as flat sores which develop into fluid-filled blisters that may be painful or itchy[214]. These sores form a dip in the centre then dry up and form a crust which eventually falls off[214]. The rash may appear anywhere on the body and consist of a few to hundreds of spots[214]. In some cases, infected individuals may have swelling of the rectum or pain/difficulty when urinating[214]. People are contagious until all sores have crusted over, fallen off and a new layer of skin formed[214]. However, many cases in the 2022-2023 outbreak are not presenting with classic symptoms[211]. In around 50% of cases the rash appears before or together with other symptoms and may not spread across the body, and the first lesion may be in the anus, groin or in/around the mouth[214].

Mpox can develop into a serious infection, with complications including abscesses; pneumonia; corneal infections (leading to loss of vision); severe dehydration/malnutrition due to vomiting, diarrhoea and pain/difficulty swallowing; sepsis; encephalitis; myocarditis; and inflammation of the urinary passages (urethritis), genitals (head of penis) or rectum (proctitis)[214]. It is particularly dangerous for immunocompromised individuals, including those with HIV[214]. In September 2022, the death rate from mpox was estimated to be around 0.04%[215].

4.2.6 Excretion of biomarkers of infection

The mpox virus has been detected in municipal wastewater using targeted PCR in France (Wurtzer et al., 2022), the Netherlands (de Jonge et al., 2022), Poland (Gazecka et al., 2023) and several states in the United States (reviewed in Adams et al., 2024). Wastewater testing for mpox has also been piloted in New Zealand [216]. Mpox has also been detected in wastewater collected at Schiphol airport, Amsterdam (de Jonge et al., 2022) and Fiumicino airport, Rome (La Rosa et al., 2023), and the University of Miami hospital (Sharkey et al., 2023). Chen and Bibby (2022) estimated that mpox could be detected in US municipal wastewater when 7 infected people were present in a population of 100,000.

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211 https://www.who.int/emergencies/disease-outbreak-news/item/2022-DON390 Accessed 29 August 2023

212 https://www.esr.cri.nz/digital-library/monthly-notifiable-disease-surveillance-report-jan-2024/ Accessed 4 April 2024

213 https://www.cdc.gov/poxvirus/mpox/clinicians/clinical-recognition.html Accessed 29 August 2023

214 https://www.who.int/news-room/fact-sheets/detail/monkeypox Accessed 29 August 2023

215 https://www.nature.com/articles/d41586-022-02931-1 Accessed 29 August 2023

216 https://www.rnz.co.nz/news/national/478340/wastewater-testing-for-monkeypox-being-trialled-in-new-zealand-s-main-cities Accessed 4 April 2024

Mpox DNA has been identified in urine and faeces, with 75% of urine and 67% of faeces samples in a recent study being PCR positive (Peiró-Mestres et al., 2022). The US CDC have also noted that urine and faeces may contain infectious virus[217].

4.2.7 Potential health hazard if present in wastewater

Given infectious virus may be present in urine and faeces[217], where an infected individual urinates or defecates on a plane or at the airport there could be a potential hazard to people collecting or processing aircraft/airport wastewater samples, or to WWTP staff. However, "the stability of MPXV [mpox virus] in the environment is unknown and the presence of infectious MPXV [mpox virus] in wastewater has not yet been determined" (Atoui et al., 2023). As such, further work is needed to determine whether the presence of this pathogen in wastewater may pose a hazard to people working with aircraft/airport wastewater.

4.3 NIPAH VIRUS

4.3.1 Transmission

Nipah virus is an enveloped single-stranded RNA virus of the genus *Henipavirus* (family *Paramyxoviridae*) which causes a serious zoonotic illness transmitted via fruit bats (genus *Pteropus*)[218]. Nipah virus was first discovered in 1999 in a major outbreak in pigs in Malaysia and Singapore during which the disease was transmitted to humans, resulting in more than 100 deaths[218]. Nipah virus is transmitted to humans via close contact with infected animals or their bodily fluids (e.g., saliva, urine)[219]. Infection via consumption of foods contaminated by infected animals (e.g., fruit contaminated with bat saliva or urine) has also been reported[219]. Once a human is infected, the virus may then be passed from person-to-person via respiratory droplets and contaminated bodily fluids (e.g., urine, blood)[219].

4.3.2 Prevention

There is currently no approved vaccine against Nipah virus (de Wit et al., 2023).

4.3.3 Geographical distribution

Nipah virus infections have been reported in Bangladesh, India, Malaysia, Singapore and the Philippines, although the geographic distribution of the fruit bat hosts is much broader[220] (Figure 46).

4.3.4 New Zealand epidemiology

There have been no reported cases of Nipah virus in New Zealand.

4.3.5 Symptoms

The incubation period for Nipah virus is around 4 – 14 days following exposure and symptoms range from mild to severe[221], although some cases may be asymptomatic[222]. The disease initially presents with 3 -14 days of headache and fever, which may be accompanied by sore throat, cough and difficulty breathing[221]. In severe cases, patients may develop

[217] https://www.cdc.gov/poxvirus/mpox/if-sick/transmission.html Accessed 29 August 2023
[218] https://www.cdc.gov/vhf/nipah/about/index.html Accessed 29 August 2023
[219] https://www.cdc.gov/vhf/nipah/transmission/index.html Accessed 29 August 2023
[220] https://www.cdc.gov/vhf/nipah/outbreaks/distribution-map.html Accessed 29 August 2023
[221] https://www.cdc.gov/vhf/nipah/symptoms/index.html Accessed 29 August 2023
[222] https://www.who.int/news-room/fact-sheets/detail/nipah-virus Accessed 2 October 2023

encephalitis, leading to mental confusion, drowsiness, disorientation, seizures, and coma within 24 – 48 hours[221]. Approximately 40 – 75% of infections are fatal, and survivors may suffer from persistent convulsions and personality changes[221]. In some cases, symptoms, or death, may occur months or years after exposure, in what is known as dormant or latent infections[221].

4.3.6 Excretion of biomarkers of infection

No WBS studies assessing the presence of the Nipah virus in wastewater were identified during preparation of this report. Infectious Nipah virus has been isolated from urine (Chua et al., 2001; Goh et al., 2000). Viral RNA has also been detected in urine, with Chadha et al. (2006) identifying viral RNA in urine samples from 83% of patients (5/6). Positive samples were collected 5-, 8-, 9- and 10-days post symptom onset, whereas a sample collected on day 2 was negative.

4.3.7 Potential health hazard if present in wastewater

As infectious Nipah virus has been isolated from urine (Chua et al., 2001; Goh et al., 2000), and given that Nipah virus can be transmitted via the urine of infected individuals[223], where an infected individual urinates on a plane or at the airport there could be a potential health hazard posed to people collecting or processing aircraft/airport wastewater samples, or to WWTP staff. However, further work is needed to determine the stability and infectivity of Nipah virus in wastewater.

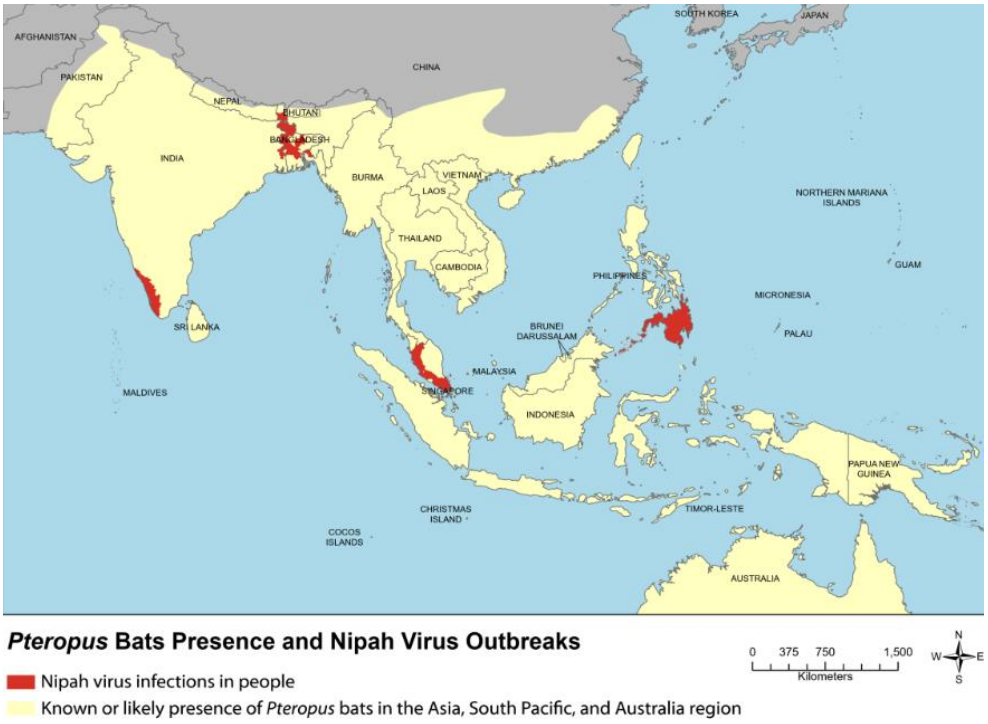

Figure 46 Distribution of Nipah virus outbreaks and *Pteropus* bats

Reproduced from https://www.cdc.gov/vhf/nipah/outbreaks/distribution-map.html

[223] https://www.cdc.gov/vhf/nipah/transmission/index.html Accessed 29 August 2023

4.4 HENDRA VIRUS DISEASE

4.4.1 Transmission

Hendra virus disease is a rare, often-fatal emerging zoonosis that affects humans and horses[224]. It is caused by the Hendra virus, an enveloped single-stranded RNA virus of the genus *Henipavirus* (family *Paramyxoviridae*)[225], the same genus as Nipah virus (Wang et al., 2021). The natural host of Hendra virus is flying foxes (fruit bats) of the *Pteropus* genus[225]. Infected flying foxes can transmit the virus to horses via contaminated urine, and horses, in turn, can transmit the virus to humans via their bodily fluids, excretions or tissues[226]. There is no evidence of direct transmission from flying foxes to humans or human-to-human transmission[227].

4.4.2 Prevention

There is no human vaccine against Hendra virus[228].

4.4.3 Geographical distribution

Hendra virus was first identified in the suburb of Hendra in Brisbane, Australia in 1994 in an outbreak among racehorses[229], in which a horse trainer died and stable-hand developed illness (Wang et al., 2021). As of December 2022, there has been another 65 'spill-over events' from flying foxes to horses, resulting in 106 equine deaths (Taylor et al., 2022). There have also been five additional human cases (all of whom had been in close contact with infected horses), of which three cases were fatal (Wang et al., 2021). It has been estimated that ~10% of people exposed to bodily fluids of infected horses will become infected (Middleton, 2014).

4.4.4 New Zealand epidemiology

There have been no reported cases of Hendra virus in New Zealand.

4.4.5 Symptoms

Symptoms of Hendra virus infection generally develop 5 – 21 days after exposure and include fever, sore throat, cough, headache and fatigue[230]. In more severe cases, meningitis or encephalitis may develop, causing high fever and drowsiness, and potentially leading to convulsions and coma[230]. Approximately 70% of human cases of Hendra virus infection are fatal[231].

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[224] https://www.who.int/health-topics/hendra-virus-disease Accessed 29 August 2023
[225] https://www.cdc.gov/vhf/hendra/index.html Accessed 29 August 2023
[226] https://www.cdc.gov/vhf/hendra/transmission/index.html Accessed 29 August 2023
[227] https://www.business.qld.gov.au/industries/farms-fishing-forestry/agriculture/biosecurity/animals/diseases/guide/hendra-virus Accessed 29 August 2023
[228] https://www.betterhealth.vic.gov.au/health/conditionsandtreatments/hendra-virus Accessed 29 August 2023
[229] https://www.who.int/health-topics/hendra-virus-disease Accessed 29 August 2023
[230] https://www.health.nsw.gov.au/Infectious/factsheets/Pages/hendra_virus.aspx Accessed 29 August 2023
[231] https://www.business.qld.gov.au/industries/farms-fishing-forestry/agriculture/biosecurity/animals/diseases/guide/hendra-virus Accessed 29 August 2023

4.4.6 Excretion of biomarkers of infection

No WBS studies assessing the presence of Hendra virus in wastewater were identified during preparation of this report. No studies assessing the presence of biomarkers of human Hendra virus infection in urine or faeces were identified during preparation of this report.

4.4.7 Potential health hazard if present in wastewater

No information relating to potential transmission of Hendra virus via wastewater (e.g., while sampling, processing samples in the laboratory, or at the WWTP) was identified during preparation of this report. As such, further work is needed to ascertain whether there is any additional health hazard associated with working with wastewater containing Hendra virus.

4.5 MIDDLE EAST RESPIRATORY SYNDROME CORONAVIRUS

4.5.1 Transmission

Middle East respiratory syndrome (MERS) is a viral respiratory disease caused by Middle East respiratory syndrome coronavirus (MERS-CoV) - an enveloped single-stranded RNA virus of the genus *Betacoronavirus* (family *Coronaviridae*) which is transmitted from dromedary camels to humans[232]. The MERS-CoV virus has been detected in camels in several countries in the Middle East, South Asia and Africa, and can be transmitted to humans via both direct and indirect contact, although the exact route of transmission is unclear[233]. Once a human is infected, person-to-person transmission is possible but predominantly occurs within households or in healthcare settings[233].

4.5.2 Prevention

There is currently no vaccine for MERS, but several candidates are in clinical development[233].

4.5.3 Geographical distribution

Between April 2012 to May 2023, there were 2,604 laboratory-confirmed cases of MERS-CoV globally, with 936 deaths (36% case fatality rate)[234]. During this period, 27 different countries reported cases, but the majority were in Saudi Arabia (84%)[235], with no cases detected outside of the Middle East since 2015[236]. As of 4 March 2024, no cases with an onset date in 2024 have been reported, the last reported case was in Saudi Arabia in October 2023[236]. The geographic distribution of MERS cases between April 2012 – February 2023 is shown in Figure 47. The incidence of MERS cases between 2021 – 2024 based on the original country of infection can be seen in Figure 48.

[232] https://www.who.int/health-topics/middle-east-respiratory-syndrome-coronavirus-mers Accessed 29 August 2023
[233] https://www.who.int/news-room/fact-sheets/detail/middle-east-respiratory-syndrome-coronavirus-(mers-cov) Accessed 29 August 2023
[234] https://www.emro.who.int/health-topics/mers-cov/mers-outbreaks.html Accessed 29 August 2023
[235] https://applications.emro.who.int/docs/WHOEMCSR662E-eng.pdf Accessed 29 August 2023
[236] https://www.ecdc.europa.eu/en/publications-data/distribution-confirmed-cases-mers-cov-place-infection-and-month-onset-march-4 Accessed 4 April 2024

4.5.4 New Zealand epidemiology

MERS is a notifiable disease in New Zealand, but no cases have ever been reported[237].

4.5.5 Symptoms

The incubation period for MERS-CoV ranges from 2 – 14 days and cases may be asymptomatic or display only mild respiratory symptoms[238]. However, most people display symptoms including fever, cough, shortness of breath and in some cases nausea/vomiting and diarrhoea, and many develop severe complications including pneumonia and kidney failure[238]. Approximately 30 – 40% of cases have been fatal[238].

MERS-CoV is thought to be contagious from the onset of fever until 10 days after the fever subsides[239].

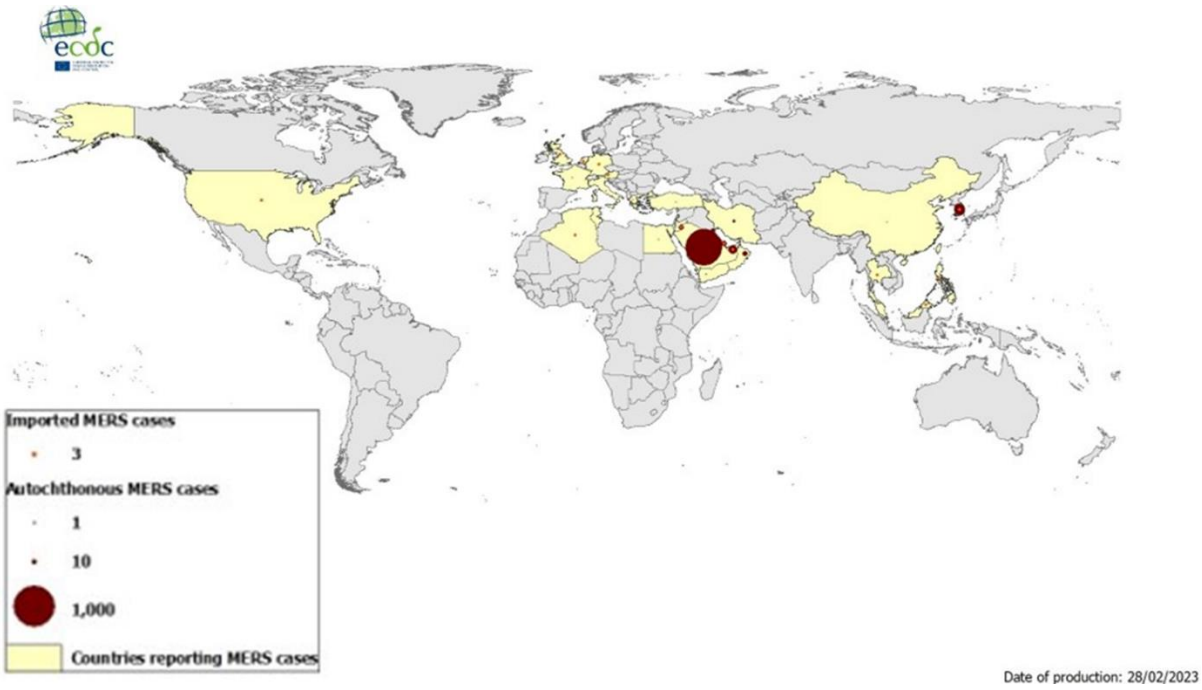

Figure 47 Global distribution of confirmed MERS cases by reporting country, April 2012 – February 2023

Adapted from https://www.ecdc.europa.eu/en/publications-data/geographical-distribution-confirmed-cases-mers-cov-reporting-country-april-2012-2

[237] https://www.health.govt.nz/our-work/diseases-and-conditions/communicable-disease-control-manual/middle-east-respiratory-syndrome-mers Accessed 29 August 2023
[238] https://www.cdc.gov/coronavirus/mers/about/symptoms.html Accessed 29 August 2023
[239] https://www.osha.gov/mers/medical-information Accessed 29 August 2023

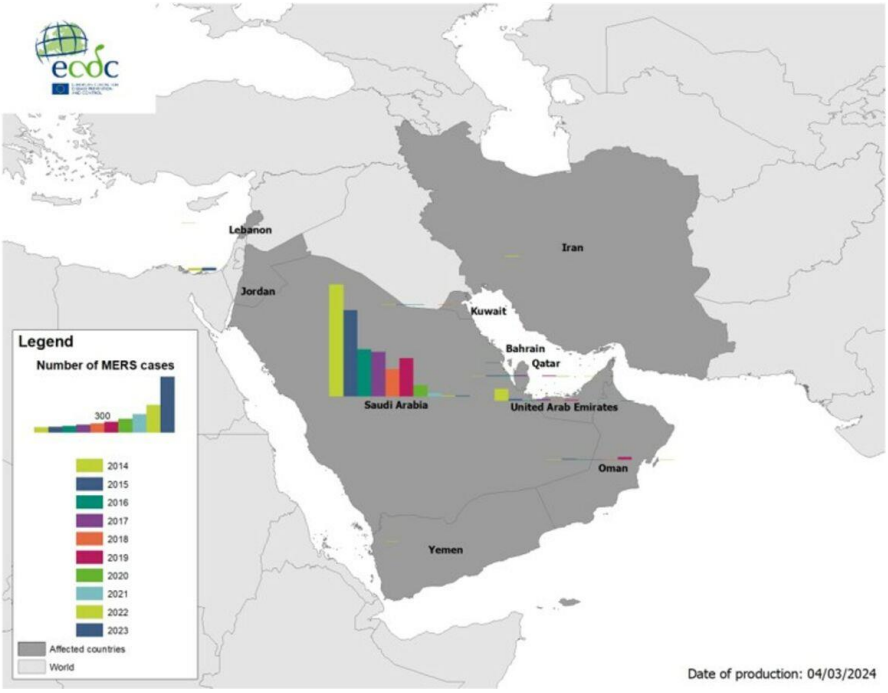

Figure 48 Global distribution of confirmed MERS cases by country of infection and year, April 2012 to March 2024

Reproduced from https://www.ecdc.europa.eu/en/publications-data/geographical-distribution-confirmed-mers-cov-cases-country-infection-and-year-21

4.5.6 Excretion of biomarkers of infection

No WBS studies assessing the presence of the MERS virus in wastewater were identified during preparation of this report.

MERS virus RNA has been detected in urine and faeces, as summarised in Table 16.

4.5.7 Potential health hazard if present in wastewater

No information relating to potential transmission of the MERS virus via wastewater (e.g., while sampling, processing samples in the laboratory, or at the WWTP) was identified during preparation of this report. Corman et al. (2016) unsuccessfully attempted to isolate infectious MERS virus from faeces with high MERS RNA concentrations. As noted above, although the MERS virus can be transmitted from person-to-person it generally only occurs within households or in healthcare settings[240]. As such, transmission via wastewater whilst collecting or processing aircraft/airport wastewater samples, or to WWTP staff may be less likely. However, further work is needed to assess the hazard posed by the presence of the MERS virus in aircraft/airport wastewater.

[240] https://www.who.int/news-room/fact-sheets/detail/middle-east-respiratory-syndrome-coronavirus-(mers-cov) Accessed 29 August 2023

Table 16 Summary of studies assessing excretion of MERS virus RNA in urine and faeces

Study participants	% positive patients	Shedding dynamics (faeces)	Shedding dynamics (urine)	Reference
1	100	• Positive days 12 and 16 PSO • Maximum viral load 1031 copies/g	• Positive days 12 and 13 PSO • Negative day 16 PSO • Maximum viral load 2691 copies/mL (day 13)	Drosten et al. (2013)
37	14.6% faeces 2.4% urine	• 12/82 positive • Maximum virus concentration 1.26 × 10^5 copies/mL • Average virus concentration 1.58 × 10^4 copies/mL	• 4/169 positive • Maximum virus concentration 5.01 × 10^2 copies/mL • Average virus concentration 1.26 × 10^2 copies/mL	Corman et al. (2016)
2	50		• Patient 1 positive days 20, 22, 27, 29 and 30 PSO • Patient 2 negative days 6, 9, 12, 15, 16, 23, 26, 28, 30 PSO	Poissy et al. (2014)

4.6 ANTHRAX

4.6.1 Transmission

Anthrax is a bacterial infection caused by *Bacillus anthracis*[241]. Anthrax bacteria are found naturally in soil and produce highly stable spores which can survive for decades in the environment[241]. These spores can infect domestic and wild animals who may transmit the infection to humans via contact with infected animals or contaminated animal products[241]. Anthrax infection, however, is not transmitted from person-to-person[241]. There are multiple different types of anthrax infection, depending on the route of exposure (e.g., cutaneous, inhalation, gastrointestinal, injection)[242].

Anthrax is noted by the US CDC to be one of the "most likely agents to be used in a biological attack"[243], and has been used as a weapon in the past including in a mail-based attack in the United States in 2001[243].

4.6.2 Prevention

There are two types of anthrax vaccines available for use in humans – a live attenuated vaccine and a cell free filtrate[244]. In the United States, a cell free filtrate vaccine (BioThrax™)[245] is approved for usage but is generally not administered to the general public but rather people at increased risk of exposure through their job (e.g., laboratory workers, military personnel, some people who handle animals/animal products)[246]. A human anthrax vaccine is also available in Australia in some cases for military or laboratory personnel but is not licensed for civilian use[247].

4.6.3 Geographical distribution

The geographic range of *B. anthracis* is "poorly understood" (Carlson et al., 2019), although it is known to be most common in the Caribbean, sub-Saharan Africa, Central and South America, central and southwestern Asia and southern and eastern Europe[241]. The global distribution of anthrax outbreaks (human, livestock and wildlife) between 2005 – 2016 can be seen in Figure 49.

4.6.4 New Zealand epidemiology

Anthrax is a notifiable disease in New Zealand[248], with the last human case reported in 1940 and the last outbreak in domestic animals reported in 1954[249].

[241] https://www.cdc.gov/anthrax/basics/index.html Accessed 29 August 2023
[242] https://www.cdc.gov/anthrax/symptoms/index.html Accessed 29 August 2023
[243] https://www.cdc.gov/anthrax/bioterrorism/index.html Accessed 29 August 2023
[244] https://cdn.who.int/media/docs/default-source/pvg/global-vaccine-safety/anthrax-vaccine-rates-information-sheet.pdf Accessed 29 August 2023
[245] https://www.fda.gov/media/71954/download Accessed 29 August 2023
[246] https://www.cdc.gov/vaccines/vpd/anthrax/public/index.html Accessed 29 August 2023
[247] http://conditions.health.qld.gov.au/HealthCondition/condition/14/33/8/anthrax Accessed 29 August 2023
[248] https://www.health.govt.nz/system/files/documents/pages/schedule-of-notifiable-diseases-updated-jun22.pdf Accessed 29 August 2023
[249] https://www.health.govt.nz/our-work/diseases-and-conditions/communicable-disease-control-manual/anthrax Accessed 29 August 2023

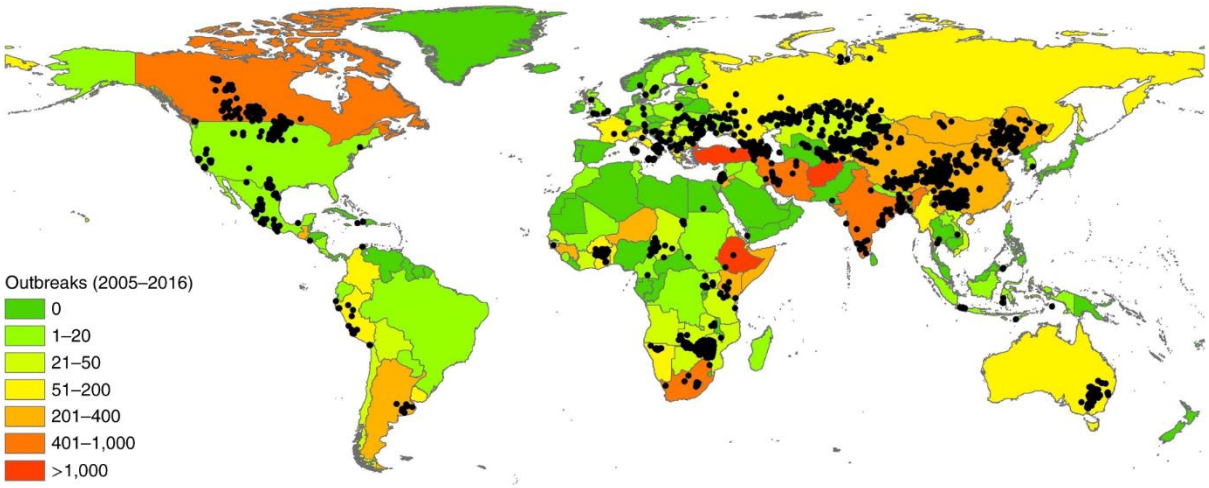

Figure 49 Global distribution of anthrax outbreaks

Reproduced from Carlson et al. (2019). Black dots indicate outbreak locations, based on data from January 2005 – August 2016.

4.6.5 Symptoms and treatment

Depending on the type of anthrax infection a person has acquired (cutaneous, inhalation, gastrointestinal, injection), the symptoms will vary, but with all types, where untreated, the infection may spread throughout the body causing severe illness and in some cases death[250]. Depending on the type of infection, the incubation time may vary from 1 day to more than 2 months[250].

Cutaneous anthrax infection is the most common form and is caused by spores penetrating the skin (e.g., via an open wound), with symptoms developing 1 – 7 days after exposure[251]. Initially a group of small blisters or itchy bumps form, often on the arms, hand, face or neck, and these may be surrounded by swelling[250]. A painless ulcer with a black centre then forms[250]. Without treatment, up to 20% of people with cutaneous anthrax infection will die, but with appropriate treatment survival is almost 100%[251].

Inhalation anthrax is the deadliest form and is most common in workplaces where there is exposure to anthrax spores in the air (e.g., tanneries, woollen mills, slaughterhouses)[251]. Symptoms of inhalation anthrax infection generally develop within a week of exposure but in some cases may take up to 2 months[251]. The infection starts in the lymph nodes of the chest and spreads throughout the body causing severe respiratory problems and shock[251]. Symptoms may include shortness of breath, fever and chills, chest pain, cough, sweats, body aches, extreme fatigue, nausea/vomiting/stomach pain, confusion or dizziness[250]. In the absence of treatment virtually all cases of inhalation anthrax are fatal, and even with appropriate treatment around 45% of patients will still die.

Gastrointestinal anthrax develops when a person consumes raw or uncooked meat of an infected animal, and symptoms generally begin 1 – 7 days after the meat is consumed[251]. This form of infection impacts the gastrointestinal tract, stomach and intestines and is fatal in

[250] https://www.cdc.gov/anthrax/symptoms/index.html Accessed 29 August 2023
[251] https://www.cdc.gov/anthrax/basics/types/index.html Accessed 29 August 2023

> 50% of cases in the absence of treatment and around 40% of patients with proper treatment[252]. Symptoms include sore throat/painful swallowing, hoarseness, swelling of the neck or neck glands, fever and chills, nausea, vomiting and diarrhoea (including bloody vomit and diarrhoea), stomach pain, swollen abdomen, red (flushed) face and eyes, headache, fainting[253]. Some cases may be asymptomatic (Chambers et al., 2023).

Injection anthrax has been reported in intravenous heroin users and appears to be similar to cutaneous anthrax except that the infection is generally deeper in the skin or muscle, more able to spread rapidly throughout the body, and harder to recognise and treat[252].

4.6.6 Excretion of biomarkers of infection

Bacillus anthracis has been identified in wastewater collected in Hong Kong (Li et al., 2015) and Ohio, USA (Spurbeck et al., 2023) using metagenomics. No studies reporting PCR detection of *B. anthracis* in urine or faeces were identified during preparation of this report. However, the WHO recommends culturing from faeces for diagnosis of suspected intestinal anthrax (WHO, 2008). Indeed, Nakanwagi et al. (2020) successfully cultured *B. anthracis* bacteria from the faeces of an individual suffering from gastrointestinal anthrax.

4.6.7 Potential health hazard if present in wastewater

Given *B. anthracis* has been cultured from faeces (Nakanwagi et al., 2020), where an infected individual defecates on a plane or at the airport there could be a potential health hazard posed to people collecting or processing aircraft/airport wastewater samples, or to WWTP staff. However, as anthrax is not transmitted from person-to-person[254], this is less likely.

4.7 TUBERCULOSIS

4.7.1 Transmission

Tuberculosis (TB) is a bacterial illness which most commonly affects the lungs and is most often caused by the bacterium *Mycobacterium tuberculosis*[255]. This species is part of the *Mycobacterium tuberculosis* complex (MTBC) which contains several other *Mycobacterium* species which can cause TB in humans or animals, including *M. africanum* which is known to cause TB in humans, most commonly in Western Africa (Mtetwa et al., 2022a).

Tuberculosis can be spread from person-to-person through the air when an infected person speaks, sings or coughs, but is not spread through direct contact such as shaking hands, kissing, sharing food/drink, or sharing linens[256]. Once the bacteria enter the throat and lungs, they can start to grow but may also enter the blood and move to other locations such as the spine, brain and kidneys[256]. Generally, only TB of the throat or lungs is considered contagious[256256].

[252] https://www.cdc.gov/anthrax/basics/types/index.html Accessed 29 August 2023
[253] https://www.cdc.gov/anthrax/symptoms/index.html Accessed 29 August 2023
[254] https://www.cdc.gov/anthrax/basics/index.html Accessed 29 August 2023
[255] https://www.cdc.gov/tb/topic/basics/default.htm Accessed 29 August 2023
[256] https://www.cdc.gov/tb/topic/basics/howtbspreads.htm Accessed 29 August 2023

4.7.2 Prevention

The Bacille Calmette-Guérin (BCG) vaccine, which was first administered in 1921 (Luca & Mihaescu, 2013), provides some protection against TB but it is often only administered in countries where the disease is common[257]. In New Zealand, the BCG vaccine is only available via the standard vaccination schedule to children 0 – 5 years old living in a household with someone with current, or a history of, TB; where a household member has lived in in a country with a high rate of TB (≥ 40 cases per 100,000 people) for 6 months or longer within the last 5 years; or where they will be living for 3 months or more in a country with a high rate of TB during their first 5 years[258].

4.7.3 Geographical distribution

Tuberculosis is found worldwide, but is most common in sub-Saharan Africa, Asia and Eastern Europe[259]. The estimated global incidence of TB in 2022 is shown in Figure 50.

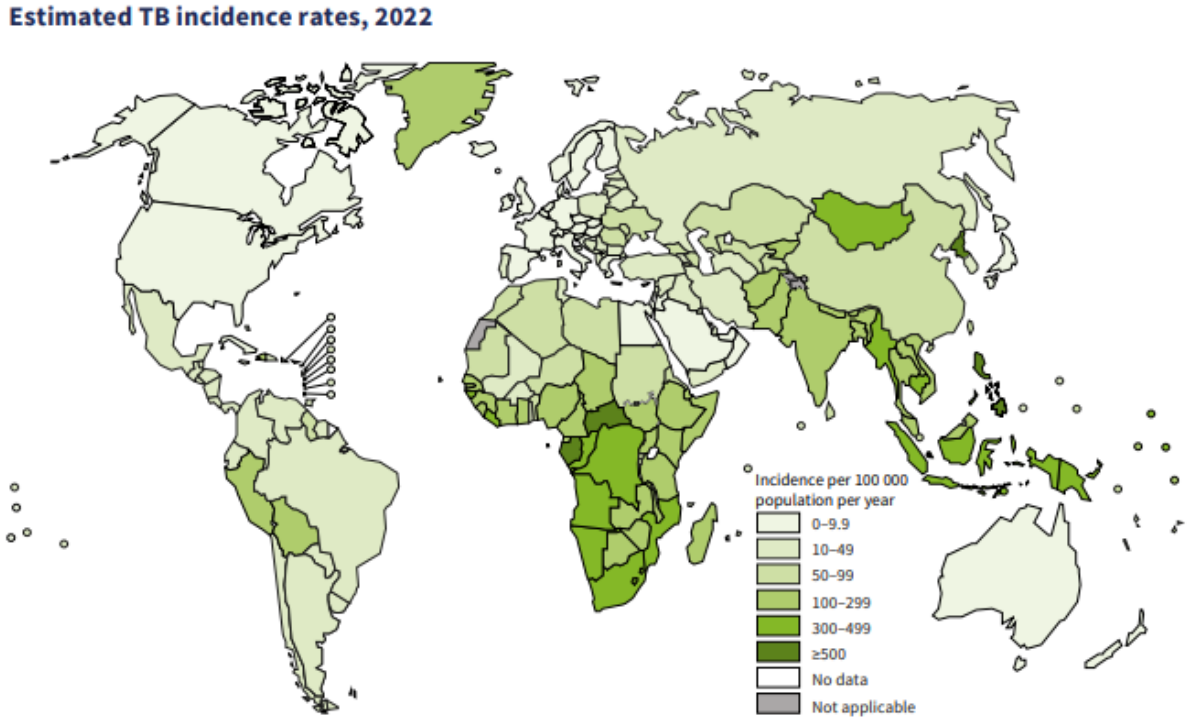

Figure 50 Estimated tuberculosis incidence rates (2022)

Reproduced from https://www.who.int/teams/global-tuberculosis-programme/tb-reports/global-tuberculosis-report-2023. Number of incident cases per 100,000 population per year.

[257] https://www.cdc.gov/tb/topic/basics/vaccines.htm Accessed 29 August 2023
[258] https://www.health.govt.nz/our-work/preventative-health-wellness/vaccine-information-healthcare-professionals/about-immunisation-new-zealand/bcg-vaccine-and-vaccinator-endorsement Accessed 29 August 2023
[259] https://wwwnc.cdc.gov/travel/diseases/tuberculosis Accessed 29 August 2023

4.7.4 New Zealand epidemiology

Tuberculosis is a notifiable disease in New Zealand[260] and ~300 cases are diagnosed in New Zealand every year (Figure 51), with ~80% of cases occurring in people born outside of New Zealand[261]. Of the cases in people born in New Zealand, ~50% are of Māori ethnicity[262] New Zealand is considered by the WHO to have a low incidence of TB[262].

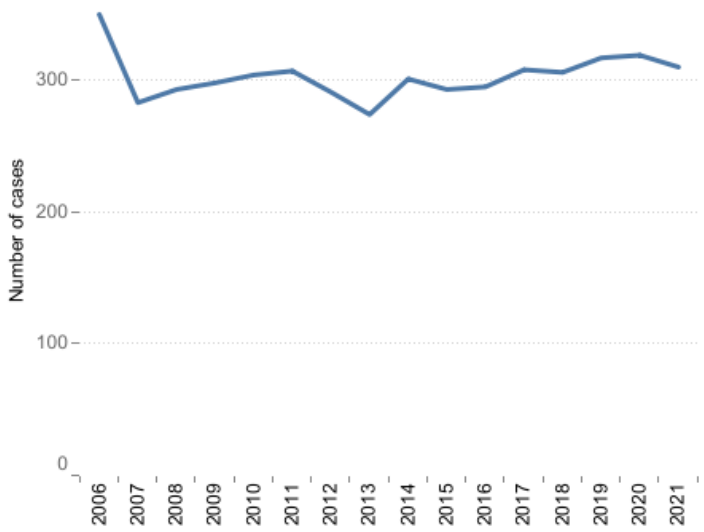

Figure 51 Number of reported tuberculosis cases in New Zealand 2006 - 2021

Reproduced from https://www.esr.cri.nz/digital-library/notifiable-disease-dashboard/.

4.7.5 Symptoms and treatment

Some people exposed to TB will develop symptoms within weeks of exposure, whereas others will not develop symptoms until years later, often when their immune system becomes weakened due to an unrelated reason[263]. People who are infected with TB but do not develop symptoms are said to have latent TB infection and are not contagious but may develop symptoms later in life if they do not receive treatment[264]. However, many people infected with TB never develop symptoms[263]. People with untreated pulmonary TB may be intermittently infectious for years. Children under 10 are generally not infectious[265]. People are typically considered non-infectious after at least two weeks of effective anti-TB treatment[265].

Tuberculosis usually affects the lungs and symptoms include a cough which lasts for 3 weeks or longer, chest pain, coughing up blood or sputum (phlegm that comes from deep

[260] https://www.health.govt.nz/system/files/documents/pages/schedule-of-notifiable-diseases-updated-jun22.pdf Accessed 29 August 2023
[261] https://www.health.govt.nz/your-health/conditions-and-treatments/diseases-and-illnesses/tuberculosis-disease Accessed 29 August 2023
[262] https://www.esr.cri.nz/digital-library/tuberculosis-in-new-zealand-annual-report-2020 Accessed 8 April 2024
[263] https://www.cdc.gov/tb/topic/basics/exposed.htm Accessed 29 August 2023
[264] https://www.cdc.gov/tb/topic/basics/tbinfectiondisease.htm Accessed 29 August 2023
[265] https://www.health.govt.nz/our-work/diseases-and-conditions/communicable-disease-control-manual/tuberculosis Accessed 29 August 2023

inside the lungs), fatigue/weakness, no appetite, weight loss, chills, fever and night sweats[266]. Approximately 50% of people with untreated TB will die, but the global case fatality rate in 2022 was 12.3%[267]. The TB bacteria may also affect other parts of the body including the brain, kidneys and spine[268].

4.7.6 Excretion of biomarkers of infection

Mycobacterium tuberculosis and *M. africanum* have been detected in wastewater in South Africa (Mtetwa et al., 2022a; Mtetwa et al., 2023), Ghana, Nigeria, Kenya, Uganda and Cameroon (Mtetwa et al., 2023) using targeted PCR. *Mycobacterium tuberculosis* has also been detected in urban wastewater in China (Fu et al., 2022) and Ohio, USA (Spurbeck et al., 2023) using metagenomics.

Mycobacterium tuberculosis has been cultured from the faeces of patients suffering from TB, and mycobacterial DNA has been identified in faeces as summarised in Table 17.

4.7.7 Potential health hazard if present in wastewater

Given *M. tuberculosis* has been cultured from human faeces (Kesarwani et al., 2022; Konno et al., 2019; Lin et al., 2009; Oramasionwu et al., 2013), where an infected individual defecates on a plane or at the airport there could be a potential health hazard posed to people collecting or processing aircraft/airport wastewater samples, or to WWTP staff. As these bacteria are known to be spread by the respiratory route, inhalation of wastewater aerosols containing these bacteria may be of particular concern. A recent study by Mtetwa et al. (2022b) has further investigated the potential health hazard posed by tuberculosis-causing bacteria present in wastewater concluding that there was a genuine risk of infection from this source (Mtetwa et al., 2022b).

[266] https://www.cdc.gov/tb/topic/basics/signsandsymptoms.htm Accessed 29 August 2023
[267] https://www.who.int/teams/global-tuberculosis-programme/tb-reports/global-tuberculosis-report-2023/tb-disease-burden/1-2-tb-mortality Accessed 4 April 2024
[268] https://www.cdc.gov/tb/publications/factsheets/general/tb.htm Accessed 29 August 2023

Table 17 Summary of studies assessing excretion of *M. tuberculosis* bacteria and its DNA in faeces

Study participants	% positive patients	No. samples culture positive	No. samples PCR positive	Reference
228	44	• 101/228		Oramasionwu et al. (2013)
13	54	• 7/13		Lin et al. (2009)
120	5 culture 27 PCR	• 6/120	• 24/90	Kesarwani et al. (2022)
22 (children with confirmed TB)	40 - 100		• 100% positive for cases with sputum smear-positive confirmed TB • 40% positive for cases with sputum smear-negative confirmed TB	Mesman et al. (2019)
187	40.6 culture 68.1 PCR	• 76/187	• 98/144 (using TRC Rapid®)	Konno et al. (2019)
129	78		• 101/129	Gaur et al. (2020)

4.8 LEPROSY

4.8.1 Transmission

Leprosy, also known as Hansen's disease, is a chronic infectious disease caused by the bacterium *Mycobacterium leprae*[269]. It is transmitted through droplets from the nose and mouth but prolonged, close contact with an infected person for a period of months is required to catch the disease[269]. It is not transmitted by casual contact (e.g., shaking hands, hugging)[269].

4.8.2 Prevention

In 2018 the WHO recommended the Bacille Calmette-Guérin (BCG) vaccine for areas where there is high leprosy burden (WHO, 2018). This vaccine has been used for more than 90 years to provide protection against the related bacterium *Mycobacterium tuberculosis* which causes tuberculosis (Luca & Mihaescu, 2013). However, data from clinical trials suggests the BCG vaccine provides variable protection against leprosy (18 – 90%) (Wang, 2023).

4.8.3 Geographical distribution

In 2019, more than 200,000 new cases of leprosy were reported to the WHO, with the highest reported case numbers in India, Brazil and Indonesia[270], as shown in Figure 52. In addition to new cases, there are an estimated 2 – 3 million worldwide living with leprosy-related disabilities[270].

4.8.4 New Zealand epidemiology

Leprosy is a notifiable disease in New Zealand (Yu et al., 2015), and case numbers reported between 2006 – 2021 can be seen in Figure 53.

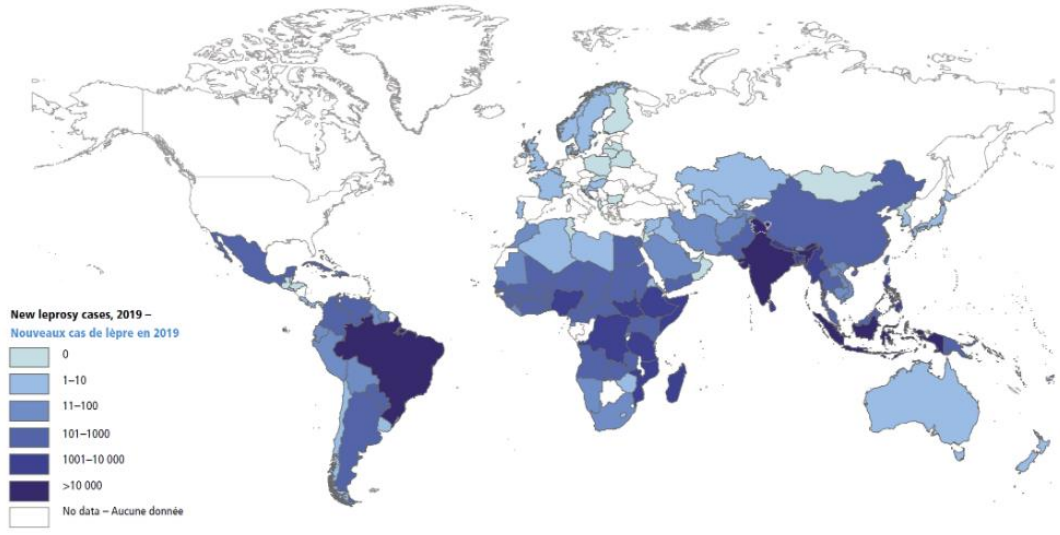

Figure 52 Global distribution of new leprosy cases (2019)

Reproduced from https://www.cdc.gov/leprosy/world-leprosy-day/index.html

[269] https://www.who.int/news-room/fact-sheets/detail/leprosy Accessed 29 August 2023
[270] https://www.cdc.gov/leprosy/world-leprosy-day/index.html Accessed 29 August 2023

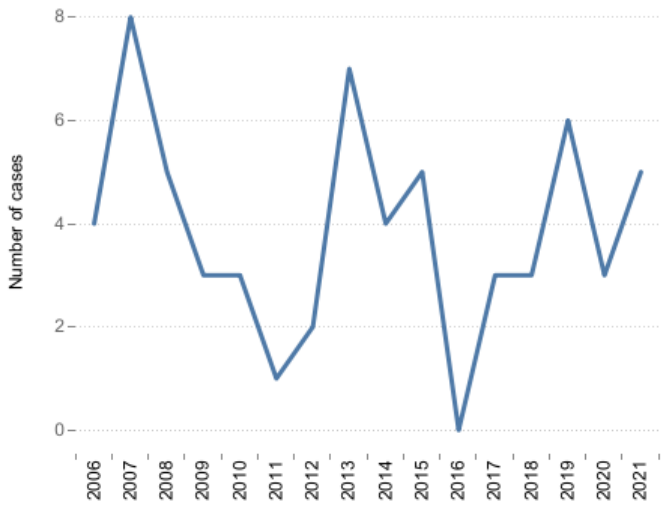

Figure 53 Number of reported leprosy cases in New Zealand 2006 - 2021

Reproduced from https://www.esr.cri.nz/digital-library/notifiable-disease-dashboard/.

4.8.5 Symptoms and treatment

The incubation period for leprosy is very long, ranging from 9 months to > 20 years[271]. There are two major types of leprosy – tuberculoid and lepromatous. For more than 90% of people infected with leprosy, their first symptom is numbness which starts with loss of temperature sensation and progresses to loss of sensitivity to light touch, pain, then deep pressure[272].

Patients with tuberculoid leprosy tend to display limited disease symptoms with development of only a few flat/slightly raised lesions on the skin which vary in size, are hairless, pale or slightly red and numb to the touch[273]. These patches also do not sweat, and affected nerves become thickened and tender to touch[272] The average incubation time for tuberculoid leprosy is 4 years[271].

Lepromatous leprosy is generally much more severe, and symptoms include swelling and thickening of limbs (especially the ankles and legs) which may develop ulcers, stuffy nose with discharge and bleeding, thickening of the forehead and earlobes, distortion of the nose and loss of eyebrows and eyelashes, widespread development of hypopigmented red macules which appear shiny and have normal sensation and progress to form nodules and plaques[272]. The bacteria may also affect the kidneys, liver, bones, testes and eyes leading to effects such as loss of digits, sterility, blindness and hepatitis[272]. The average incubation period for lepromatous leprosy is 8 years[271].

4.8.6 Excretion of biomarkers of infection

No WBS studies assessing the presence of *M. leprae* in wastewater were identified during preparation of this report.

[271] https://intel.cph.co.nz/media/47285/leprosy-protocol.pdf Accessed 29 August 2023
[272] https://dermnetnz.org/topics/leprosy Accessed 29 August 2023
[273] https://rarediseases.org/rare-diseases/leprosy/ Accessed 29 August 2023

M. leprae has been identified in faeces of a patient suffering from leprosy using microscopy, fluorescent in situ hybridisation and PCR (Millogo et al., 2021).

4.8.7 Potential health hazard if present in wastewater

Given *M. leprae* bacteria have been identified in faeces (Millogo et al., 2021), where an infected person defecates onboard an aircraft, or at the airport, these bacteria may be present in wastewater sampled for border WBS and therefore may pose a potential health hazard to people collecting or processing the wastewater samples, or to WWTP personnel. However, as prolonged close contact over months is generally required for person-to-person transmission of leprosy[274], transmission via contaminated wastewater is considered unlikely.

4.9 *CANDIDA AURIS*

4.9.1 Transmission

Candida auris is an emerging fungal pathogen which can cause severe illness, and has caused several outbreaks in healthcare settings particularly in patients who are immunosuppressed or have underlying medical conditions or invasive medical devices[275]. In 2022, *C. auris* is intrinsically resistant to many, and sometimes all, antifungal drugs and is recognised by the WHO as a critical priority pathogen (WHO, 2022). *C. auris* is most commonly spread in healthcare settings (nosocomial infections) via person-to-person transmission or contact with contaminated equipment or surfaces[276].

4.9.2 Prevention

There is currently no human vaccine to protect against *C. auris* infection (Gupta et al., 2022).

4.9.3 Geographical distribution

C. auris was first identified in discharge from the ear canal of a patient in Japan in 2009 (Umeyama et al., 2022). The global distribution of *C. auris* cases between 2009 and 6 October 2019 (prior to the COVID-19 pandemic) can be seen in Figure 54. During this period, more than 4,733 cases were reported across more than 33 countries (Chen et al., 2020). The WHO have noted that *C. auris* case numbers increased in many countries during the COVID-19 pandemic (WHO, 2022).

4.9.4 New Zealand epidemiology

As of 27 June 2023, one case, which was acquired overseas, has been reported in New Zealand[277].

4.9.5 Symptoms

Candida auris can cause a variety of different infections including urinary, respiratory, bloodstream and wound infections[278]. However, as this is an emerging disease and can be difficult to diagnose, the most observed symptoms are fever and chills presumed to be due

[274] https://www.who.int/news-room/fact-sheets/detail/leprosy Accessed 29 August 2023
[275] https://www.cdc.gov/fungal/candida-auris/index.html Accessed 29 August 2023
[276] https://www.cdc.gov/fungal/candida-auris/candida-auris-qanda.html Accessed 29 August 2023
[277] https://www.health.govt.nz/news-media/news-items/one-case-candida-auris-detected-new-zealand Accessed 29 August 2023
[278] https://www.health.state.mn.us/diseases/candidiasis/auris/basics.html Accessed 29 August 2023

to a bacterial infection but that do not resolve with antibiotics[279]. Diagnosis can also be complicated as *C. auris* is most commonly acquired in healthcare settings where people are already sick with other conditions[279]. This also makes estimation of mortality rates difficult, with reported mortality rates ranging from 0% to 72% (reviewed in Ahmad & Alfouzan, 2021). *Candida auris* may also asymptomatically colonise the skin, mouth, rectum or wounds in some people (Bradley, 2019).

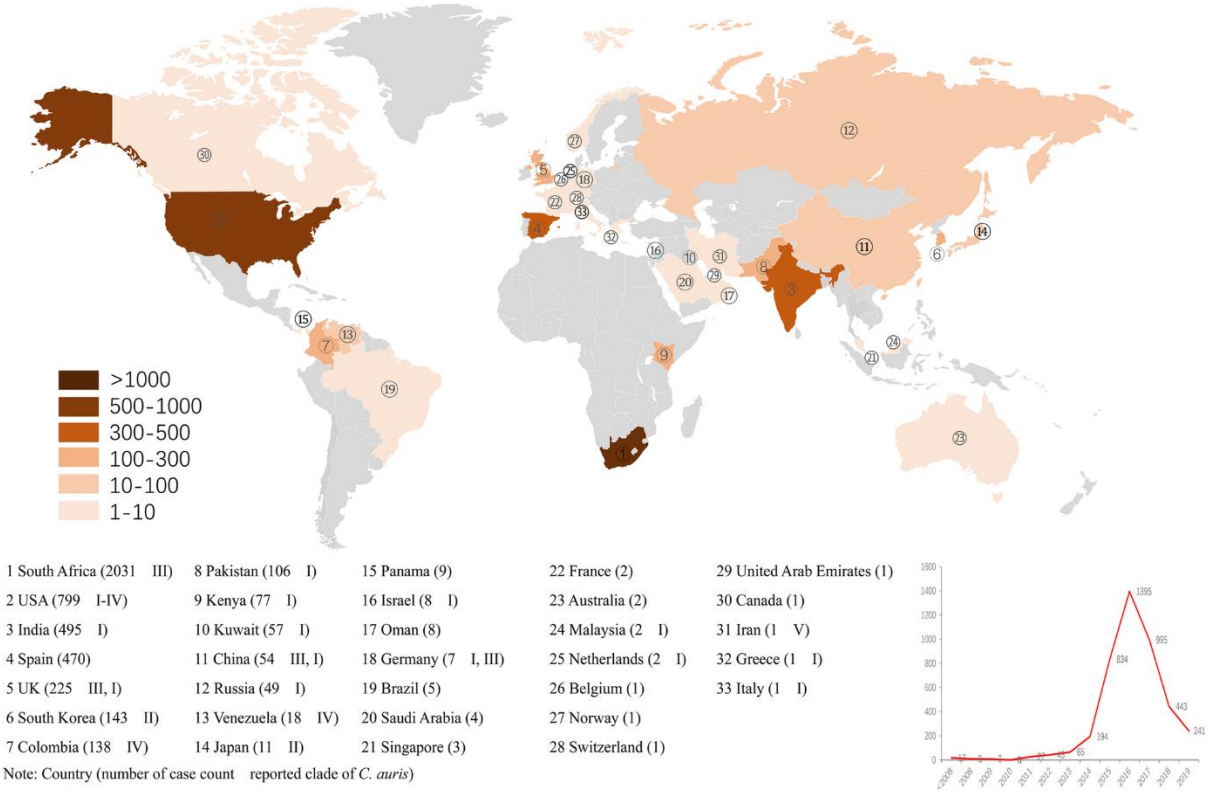

Figure 54 Global reported cases of *Candida auris* 2009 - 2019

Reproduced from Chen et al. (2020)

4.9.6 Excretion of biomarkers of infection

Candida auris has been detected in United States municipal and hospital wastewater in Nevada (Barber et al., 2023; Rossi et al., 2023) and Florida (Babler et al., 2023) using targeted PCR and culture-based detection. Zulli et al (2024) tested 13,842 wastewater samples collected from 190 wastewater treatment plants across 41 U.S. states and detected *C. auris* at 34% of WWTPs (*n* = 65) and 1.5% of samples using a targeted qPCR assay. Twelve states that did not report *C. auris* cases during the study period were found to have positive wastewater detections (Zulli et al., 2024). Several studies have reported isolation of *Candida auris* from urine, as summarised in Table 18.

[279] https://www.cdc.gov/fungal/candida-auris/c-auris-drug-resistant.html Accessed 29 August 2023

4.9.7 Potential health hazard if present in wastewater

Given *C. auris* has been isolated from urine and faeces, where an infected person urinates or defecates onboard an aircraft, or at the airport, fungal cells may be present in wastewater sampled for border WBS and therefore may pose a potential health hazard to people collecting or processing the wastewater samples, or to WWTP personnel. However, further work is needed to determine whether the presence of this pathogen in wastewater may pose a hazard to people working with wastewater.

Table 18 Summary of studies assessing presence of *Candida auris* in urine and stool

Study participants	% positive patients	Details	Reference
56	NA	• Isolated from urine of 27 patients	Khan et al. (2018)
NA	NA	• 73 *C. auris* strains isolated from patients with indwelling catheters • 10 *C. auris* strains isolated from mid-stream urine samples	Sayeed et al. (2019)
NA	NA	• Isolated from urine of 5 patients	Ruiz-Gaitán et al. (2018)
49	92	• Isolated from urine of 46/50 patients in ICU with *C. auris* infection	Barantsevich et al. (2019)
51	8	• 4/51 *C. auris* identifications initially made from positive urine cultures	Adams et al. (2018)
1-2	100	• Isolated from stool of 1/1 clinical specimens from known clinical cases • Isolated from urine of 2/2 clinical specimens from known clinical cases	Welsh et al. (2017)
NA	NA	• Among 128 clinical case-patients, 43 (34%) were identified via isolation from urine sample	Pacilli et al. (2020)
NA	NA	• Isolated in urine of 10/15 patients with *C. auris* infection	Tian et al. (2018)
NA	NA	• 3/417 stool samples from hospitalised patients positive for *C. auris* via PCR • 1/3 stool samples positive via PCR was able to be isolated (cultured)	Alam et al. (2019)

5. VACCINE-PREVENTABLE DISEASES

5.1 MEASLES

5.1.1 Transmission

Measles is a potentially life-threatening airborne disease caused by an enveloped single-stranded RNA virus of the genus *Morbillivirus* (family *Paramyxoviridae*) (Bellini et al., 1994). Measles is noted by the WHO to be "one of the world's most contagious diseases" and is spread in nasal and throat secretions during coughing, sneezing and breathing, with viral particles remaining infectious in the air and on surfaces for up to two hours[280]. It is estimated that one infected person can infect 9 out of 10 unvaccinated close contacts[280].

5.1.2 Prevention

In New Zealand, children are vaccinated against measles at 12 and 15 months using the MMR vaccine which protects against measles, mumps and rubella[281]. Approximately 95% of people who receive the MMR vaccine will become immune to measles after a single dose, and around 99% of people will be immune after two doses[282]. However, the number of New Zealand children receiving the MMR vaccine is declining, with those receiving the first dose decreasing from 95.1% for children born in 2017 to 88.9% for children born in 2020 (Hagedoorn et al., 2023).

5.1.3 Geographical distribution

Measles is found worldwide and is particularly common in regions of Africa, Asia and the Middle East, with an estimated 128,000 deaths globally in 2021[280].

5.1.4 New Zealand epidemiology

Measles is a notifiable disease in New Zealand[283] and cases reported between 2006 and 2021 can be seen in Figure 55. During this period case numbers peaked at 2,190 cases in 2019 predominantly due to a large outbreak in the Auckland region (Sonder & Ryan, 2020).

[280] https://www.who.int/news-room/fact-sheets/detail/measles Accessed 30 August 2023
[281] https://www.health.govt.nz/your-health/conditions-and-treatments/diseases-and-illnesses/measles Accessed 30 August 2023
[282] https://www.health.govt.nz/our-work/immunisation-handbook-2020/12-measles Accessed 30 August 2023
[283] https://www.esr.cri.nz/digital-library/measles-dashboard/ Accessed 9 April 2024

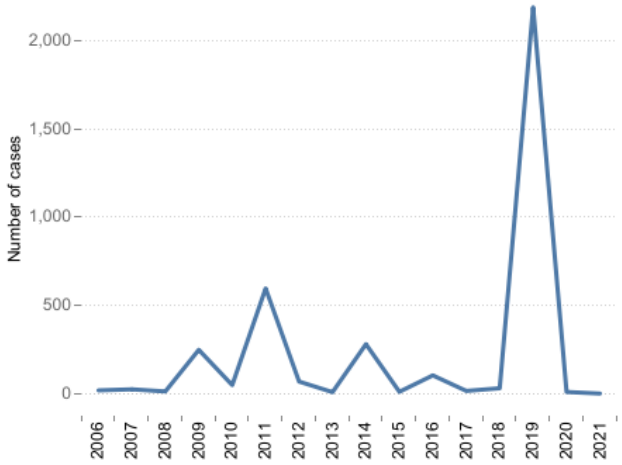

Figure 55 Number of reported measles cases in New Zealand 2006 - 2021

Reproduced from https://www.esr.cri.nz/digital-library/notifiable-disease-dashboard/.

5.1.5 Symptoms

The incubation period for measles generally ranges from 7 – 14 days after infection[284]. According to the United States CDC, there are no asymptomatic measles infections[285]. Symptoms of measles infection usually starts with high fever, runny nose, cough and red, watery eyes[284]. Two – three days later, tiny white spots known as Koplik spots appear inside the mouth[284]. Around 3 – 5 days after symptoms begin, the measles rash appears, generally starting as flat red spots around the hairline of the face and spreading down the body[284]. Raised bumps may appear on the flat spots, and the spots may join as they spread down the body[284]. As the rash appears, the infected person may spike a very high fever (> 40°C) [284]. Measles is particularly dangerous for children under 5, adults over 20, pregnant women and immunocompromised individuals[286]. Common complications of measles infection include diarrhoea (< 10% of cases) and ear infections (in ~10% of infected children)[286]. Severe complications include pneumonia (up to 1 in 20 infected children), encephalitis (~1 in 1,000 infected children) and complications during pregnancy (e.g., premature birth, low-birth-weight-baby)[286]. Between 1 to 3 children in every 1,000 who are infected with measles will die from respiratory or neurological complications[286]. Additionally, child survivors of measles encephalitis may be left deaf or with intellectual disabilities[286].

A very rare complication of measles which may occur 7 – 10 years after the original infection is subacute sclerosing panencephalitis (SSPE) which is a “fatal disease of the central nervous system”[286].

People infected with measles are generally contagious from four days before the rash develops until four days after the day the rash appears (total of nine days)[287].

[284] https://www.cdc.gov/measles/symptoms/signs-symptoms.html Accessed 30 August 2023
[285] https://www.cdc.gov/vaccines/pubs/pinkbook/meas.html Accessed 30 August 2023
[286] https://www.cdc.gov/measles/symptoms/complications.html Accessed 30 August 2023
[287] https://www.kidshealth.org.nz/measles Accessed 30 August 2023

5.1.6 Excretion of biomarkers of infection

A targeted PCR approach has been using to monitor the presence of measles virus in wastewater during an outbreak in the Netherlands (Benschop et al., 2017). More recently it has been sporadically detected in wastewater in England using targeted PCR (Kasprzyk-Hordern et al., 2023). It has also been retrospectively detected in a wastewater sample collected in India for SARS-CoV-2 monitoring (Stockdale et al., 2023).

Infectious measles virus has been isolated from human urine (Gresser & Katz, 1960), and several studies have identified viral RNA in urine, as summarised in Table 19. However, caution needs to be taken in interpretation of the detection of measles virus RNA in wastewater as it has also been shown to be detectable in the urine of recently vaccinated young adults (Rota et al., 1995), due to the measles vaccine being an attenuated live vaccine.

5.1.7 Potential health hazard if present in wastewater

Given infectious measles virus has been isolated from urine (Gresser & Katz, 1960), where an infected individual urinates on a plane or at the airport there could be a potential health hazard posed to people collecting or processing aircraft/airport wastewater samples, or to WWTP staff. However, as measles is primarily spread through nasal and throat secretions, further work is needed to ascertain whether the presence of this virus in wastewater poses a health hazard to those people collecting or processing samples, or to WWTP personnel.

Table 19. Summary of studies assessing excretion of measles virus RNA in urine

Study participants	% positive patients	Shedding dynamics (no. of samples)	Reference
89	57	• 51/89 samples collected within 7 days of the onset of rash were positive	Benamar et al. (2016)
50 samples	46 (of total samples)	• 67% (10/15) positive < 0 – 3 days post rash development • 53% (8/15) positive 4 – 7 days post rash development • 33% (2/6) positive 8 – 13 days post rash development • 29% (2/7) positive 14 – 20 days post rash development • 14% (1/7) positive > 21 days post rash development	Riddell et al. (2001)
65	86	• 88% (45/51) of patients sampled days 0 – 14 post rash development positive • 79% (11/14) of patients sampled days 15 – 33 post rash development positive	van Binnendijk et al. (2003)
6 (long-term clearance study)	50	• Positive samples detected 77, 101 and 115 days post rash development	Riddell et al. (2007)

5.2 MUMPS

5.2.1 Transmission

Mumps is a viral disease caused by an enveloped single-stranded RNA virus of the *Paramyxoviridae* family (Rubin et al., 2015), genus *Paramyxovirus* (Enders, 1996). Mumps is transmitted in airborne respiratory droplets and via direct contact with saliva or urine of infected individuals[288].

5.2.2 Prevention

Children in New Zealand are vaccinated against mumps at 12 and 15 months with the MMR vaccine[289]. A single dose is 64-66 % effective, and two doses is 83 – 88% effective at preventing mumps[288].

5.2.3 Geographical distribution

Mumps is found worldwide with an average of 500,000 cases annually[290].

5.2.4 New Zealand epidemiology

Mumps is a notifiable disease in New Zealand[291], and case notifications between 2006 and 2021 can be seen in Figure 56. Case numbers spiked to a high of 1,338 in 2017 then dropped off to 144 cases in 2020 and only 1 case in 2021, likely due at least in part to COVID-19 pandemic associated health measures.

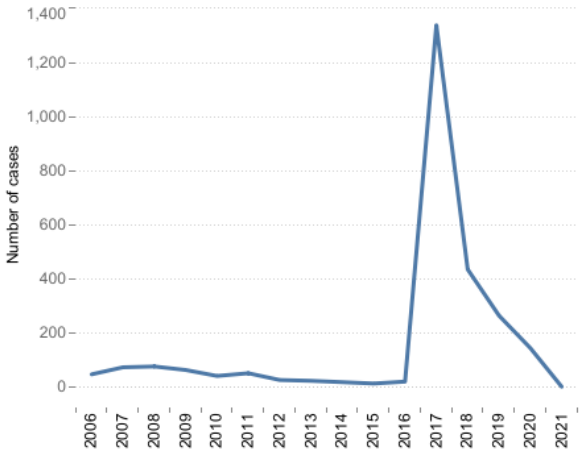

Figure 56 Number of reported mumps cases in New Zealand 2006 - 2021

Reproduced from https://www.esr.cri.nz/digital-library/notifiable-disease-dashboard/.

[288] https://www.health.govt.nz/our-work/immunisation-handbook-2020/14-mumps Accessed 30 August 2023
[289] https://www.health.govt.nz/your-health/conditions-and-treatments/diseases-and-illnesses/rubella Accessed 30 August 2023
[290] Chapter 15: Mumps; Epidemiology and Prevention of Vaccine-Preventable Diseases 14TH Edition (cdc.gov). Access 9 April 2024
[291] https://www.health.govt.nz/system/files/documents/pages/schedule-of-notifiable-diseases-updated-jun22.pdf Accessed 30 August 2023

5.2.5 Symptoms

The incubation period for mumps ranges from 12 – 25 days but is generally 16 – 18 days after infection[292]. At least 30% of mumps cases in children are asymptomatic[293]. Where symptoms do develop, they are often very mild[292]. The most well-known symptom of mumps infection is tender, puffy cheeks and a swollen jaw caused by swelling of the salivary glands under the ears (known as parotitis)[292]. Parotitis may be preceded by fever, headache, tiredness, loss of appetite and muscle aches[292]. Complications of mumps infection may include deafness, testicular atrophy or inflammation of the brain (encephalitis), pancreas (pancreatitis), testicles (orchitis), ovaries (oophoritis), breast tissue (mastitis) or tissue covering the brain and spinal cord (meningitis)[294]. Inflammation of the testicles may affect male fertility[294]. Death due to mumps infection is "exceedingly rare"[295].

People infected with mumps are the most contagious from 2 days before the onset of parotitis until 5 days after it has developed[296]. Although, the virus has been detected "in saliva from 7 days before to 9 days after the onset of parotitis", and cases of asymptomatic infection have also been found to be contagious[296].

5.2.6 Excretion of biomarkers of infection

The mumps virus has been detected in wastewater in China using high-throughput microfluidic-chip detection and confirmed using quantitative PCR (Fu et al., 2022). Mumps virus has been isolated from human urine (Krause et al., 2006; Tan et al., 2011), and viral RNA has been detected in urine as detailed in Table 20.

Table 20 Studies assessing excretion of mumps virus RNA in urine

Study participants	% positive patients	Shedding dynamics	Reference
100	30	• Unclear what stage of infection samples taken	Krause et al. (2006)
18	28	• Detected up to day 5 PSO	Tan et al. (2011)
155	43	• RNA detected up to 7 days PSO	Hatchette et al. (2009)

PSO, post symptom onset.

5.2.7 Potential health hazard if present in wastewater

Given the mumps virus has been isolated from urine (Krause et al., 2006; Tan et al., 2011), and given that the Ministry of Health notes that mumps can be spread via contact with urine of an infected person[297], where an infected individual urinates on a plane or at the airport there could be a potential health hazard posed to people collecting or processing aircraft/airport wastewater samples, or to WWTP staff, which needs to be taken into consideration.

[292] https://www.cdc.gov/mumps/about/signs-symptoms.html Accessed 30 August 2023
[293] https://intel.cph.co.nz/media/47434/mumps-protocol.pdf Accessed 30 August 2023
[294] https://www.cdc.gov/mumps/about/complications.html Accessed 30 August 2023
[295] https://www.cdc.gov/vaccines/pubs/surv-manual/chpt09-mumps.html Accessed 30 August 2023
[296] https://www.health.govt.nz/our-work/diseases-and-conditions/communicable-disease-control-manual/mumps Accessed 30 August 2023
[297] https://www.health.govt.nz/our-work/immunisation-handbook-2020/14-mumps Accessed 30 August 2023

5.3 RUBELLA

5.3.1 Transmission

Rubella is a viral illness caused by an enveloped single-stranded RNA virus of the genus *Rubivirus* (family *Matonaviridae*)[298]. The rubella virus is spread through respiratory droplets from the coughs and sneezes of infected people and can also be passed from a pregnant mother to her unborn foetus[299].

5.3.2 Prevention

In New Zealand, children are vaccinated against rubella at 12 and 15 months with the MMR vaccine[300]. Over 95% of people who receive the vaccine will be immune after a single dose, and almost 100% of people are immune after two doses[301].

5.3.3 Geographical distribution

Rubella is found worldwide and generally exhibits a seasonal pattern with epidemics every 5 – 9 years[298].

5.3.4 New Zealand epidemiology

Rubella is a notifiable disease in New Zealand[302], and reported cases between 2006 and 2021 can be seen in Figure 57. The last large Rubella outbreak in New Zealand was in 1995-1996[303].

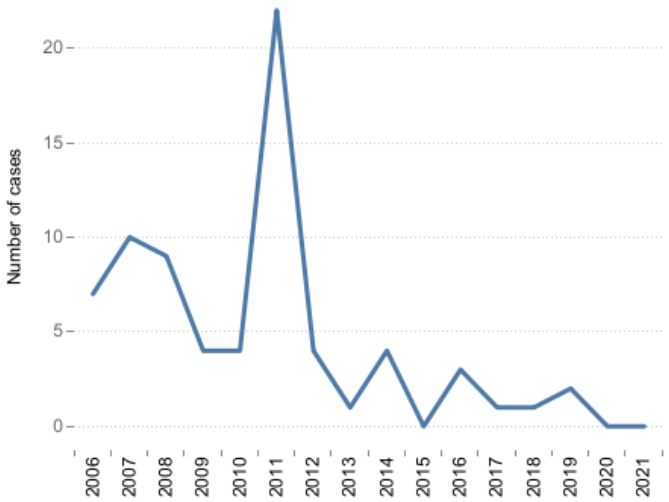

Figure 57 Number of reported rubella cases in New Zealand 2006 - 2021

Reproduced from https://www.esr.cri.nz/digital-library/notifiable-disease-dashboard/.

[298] https://www.who.int/teams/health-product-policy-and-standards/standards-and-specifications/vaccine-standardization/rubella Accessed 30 August 2023
[299] https://www.cdc.gov/rubella/about/transmission.html Accessed 30 August 2023
[300] https://www.health.govt.nz/your-health/conditions-and-treatments/diseases-and-illnesses/rubella Accessed 30 August 2023
[301] https://www.health.govt.nz/our-work/immunisation-handbook-2020/19-rubella Accessed 30 August 2023
[302] https://www.health.govt.nz/system/files/documents/pages/schedule-of-notifiable-diseases-updated-jun22.pdf Accessed 30 August 2023
[303] https://www.health.govt.nz/our-work/diseases-and-conditions/communicable-disease-control-manual/rubella Accessed 30 August 2023

5.3.5 Symptoms

The incubation period for rubella ranges from 12 – 23 days[304]. Approximately 25 – 50% of rubella infections are asymptomatic[305]. Children infected with rubella generally experience a mild illness, with few symptoms[305]. Where symptoms develop these typically start with a red rash which starts on the face and spreads across the body, lasting around three days[305]. In some cases, other symptoms may develop 1 – 5 days before the rash and include headache, cough, runny nose, swollen lymph nodes, low-grade fever, redness/swelling of the white of the eye (pink eye) and general discomfort[305]. Adults who become infected with rubella generally also develop mild illness, with a sore throat, rash, low-grade fever and in some cases pink eye, headache and general discomfort prior to developing the rash. Up to 70% of adult women who become infected with rubella may develop arthritis, which is rare in men and children[306]. Other complications include bleeding issues and brain infections[306]. Rubella is most serious for pregnant women, particularly during the first trimester, as it can cause miscarriage, stillbirth and birth defects such as heart problems, liver or spleen damage, intellectual disability or loss of hearing and eyesight[306]. People infected with rubella may be contagious from one week before to one week after rash appearance[307].

5.3.6 Excretion of biomarkers of infection

The rubella virus has been detected in sewage sludge in the United States using metagenomics (Bibby & Peccia, 2013). A recent publication also noted that the Texas Epidemic Public Health Institute (TEPHI) Wastewater Consortium is "working to detect vaccine-preventable viruses such as measles and rubella" (Clark et al., 2023). The WHO note that rubella virus can be detected in urine from one week before rash onset to two weeks after the rash appears[308]. Infectious rubella virus has been isolated from human urine (Kanbayashi et al., 2023), and rectal swabs (Green et al., 1965; Heggie & Robbins, 1964), suggesting it is likely also present in faeces. Kanbayashi et al. (2023) have also detected rubella virus RNA in urine (Table 21), and Mosquera et al. (2002) detected viral RNA in urine from a newborn infant born with congenital rubella syndrome 37 days after birth.

Table 21 Studies assessing excretion of rubella virus RNA in urine

Study participants	% positive patients	Shedding dynamics (no. of samples)	Reference
221	59.3	• 71.4% (30/42) positive day 0 PRO • 72.7% (48/66) positive day 1 PRO 61.3% (19/31) positive day 2 PRO 58.3% (14/24) positive day 3 PRO 50.0% (12/24) positive day 4 – 5 PRO • 35.3% (6/17) positive day 6 – 7 PRO • 9.1% (1/11) positive day 8 – 9 PRO • 16.7% (1/6) positive day 10 – 14 PRO • Viral load from 2 – 2,417 copies/mL	Kanbayashi et al. (2023)

PRO, post rash onset.

[304] https://www.cdc.gov/rubella/hcp.html Accessed 30 August 2023
[305] https://www.cdc.gov/rubella/about/symptoms.html Accessed 30 August 2023
[306] https://www.cdc.gov/rubella/about/complications.html Accessed 30 August 2023
[307] https://www.cdc.gov/rubella/hcp.html Accessed 30 August 2023
[308] https://www.who.int/teams/health-product-policy-and-standards/standards-and-specifications/vaccine-standardization/rubella Accessed 30 August 2023

5.3.7 Potential health hazard if present in wastewater

Given infectious rubella virus has been isolated from urine (Kanbayashi et al., 2023), where an infected individual urinates on a plane or at the airport there could be a potential health hazard posed to people collecting or processing aircraft/airport wastewater samples, or to WWTP staff. However, as rubella is primarily spread through respiratory droplets, further work is needed to determine whether its presence in wastewater poses a health hazard to people working with aircraft/airport wastewater samples, or to WWTP staff. In particular, the potential for transmission via wastewater aerosols should be considered as this organism is spread via respiratory droplets.

5.4 HEPATITIS

5.4.1 Transmission

Hepatitis is inflammation of the liver which can be caused by both viral infection and non-infectious agents[309]. There are five main hepatitis viruses – hepatitis A, B, C, D and E[309]. The hepatitis A virus is a non-enveloped single-stranded RNA virus of the genus *Hepatovirus* (family *Picornaviridae*) (Rasche et al., 2019). The hepatitis B virus is an enveloped partially double-stranded DNA virus of the genus *Orthohepadnavirus* (family *Hepadnaviridae*) (Rasche et al., 2019). The hepatitis C virus is an enveloped single-stranded RNA virus of the genus *Hepacivirus* (family *Flaviviridae*) (Rasche et al., 2019). The hepatitis D virus is an enveloped viroid-like single-stranded RNA virus of the genus *Deltavirus* and has not been assigned to a family (Rasche et al., 2019). The hepatitis E virus is a non-enveloped single-stranded RNA virus of the genus *Orthohepevirus* (family *Hepeviridae*) (Rasche et al., 2019).

Hepatitis A is primarily transmitted via the faecal-oral route, where an uninfected person consumes food or water contaminated with faeces from an infected person[310]. It can also be transmitted through close physical contact but is not spread by casual contact[310]. Hepatitis B is most commonly spread by exposure to infected bodily fluids such as saliva and semen, and blood (e.g., via needlestick injuries, piercing, tattooing, sexual contact, or sharing needles) and by perinatal transmission, where an infected mother transmits the virus to her baby during birth[311]. Hepatitis C is a blood-borne virus which can be transmitted through sharing needles/drug paraphernalia, inadequate sterilisation of medical equipment, and blood transfusion with contaminated blood, and less commonly via sexual contact and perinatal transmission[312]. It is not spread through casual contact (e.g., hugging and kissing), food/water or breast milk[312]. Transmission of hepatitis D occurs via contact with infected blood or through broken skin such as during tattooing or injection, perinatal transmission is also possible but is rare[313]. However, hepatitis D infection only occurs in people who are also infected with the hepatitis B virus[314]. Hepatitis E transmission occurs through the faecal-oral route via faecal contamination of food or water and may cause outbreaks where there is

[309] https://www.who.int/health-topics/hepatitis Accessed 30 August 2023
[310] https://www.who.int/news-room/fact-sheets/detail/hepatitis-a Accessed 30 August 2023
[311] https://www.who.int/news-room/fact-sheets/detail/hepatitis-b Accessed 30 August 2023
[312] https://www.who.int/news-room/fact-sheets/detail/hepatitis-c Accessed 30 August 2023
[313] https://www.who.int/news-room/fact-sheets/detail/hepatitis-d Accessed 30 August 2023
[314] https://www.cdc.gov/hepatitis/hdv/index.htm Accessed 30 August 2023

contamination of a drinking water supply[315]. Transmission may also occur via consumption of undercooked meat, particularly pork[315].

5.4.2 Prevention

In New Zealand, a hepatitis A vaccine is available but only recommended and funded for transplant patients, children with chronic liver disease and close contacts of hepatitis A cases[316]. In contrast, a vaccine against hepatitis B is administered at 6 weeks, 3 months and 5 months as part of a combined vaccine against diphtheria, pertussis, tetanus and *Haemophilus influenzae* type b as noted above[317]. There is currently no vaccine for hepatitis C[318] and D[319]. A vaccine for hepatitis E is licensed for usage in China but currently nowhere else in the world[320].

5.4.3 Geographical distribution

Hepatitis A is most common in low- and middle-income countries (Franco et al., 2012) and its global distribution can be seen in Figure 58. In 2012 it was noted that around 1.5 million cases of hepatitis A infection are reported globally every year, although it was thought that the infection rate may be up to ten times higher (Franco et al., 2012).

It is estimated that roughly one-third of the world's population has been infected with hepatitis B, and around 780,000 deaths are attributed to this disease worldwide every year (Jefferies et al., 2018). The global distribution of hepatitis B can be seen in Figure 59.

Hepatitis C is distributed worldwide, and in 2018 it was estimated that 71 million people had a chronic hepatitis C infection, with 399,000 deaths worldwide every year (Jefferies et al., 2018). The global distribution of hepatitis C can be seen in Figure 60.

Hepatitis D is distributed worldwide and in 2018 it was estimated that ~18 million people were infected globally (Jefferies et al., 2018). Rates of hepatitis D infection are speculated to be declining, due at least in part to hepatitis B immunisation (Jefferies et al., 2018). Global distribution of hepatitis D amongst people infected with hepatitis B is shown in Figure 61.

Hepatitis E is distributed worldwide, as shown in Figure 62. In 2018 it was estimated that globally approximately 20 million people are infected with hepatitis E every year, with around 44,000 deaths annually (Jefferies et al., 2018).

[315] https://www.who.int/news-room/fact-sheets/detail/hepatitis-e Accessed 30 August 2023
[316] https://www.health.govt.nz/our-work/immunisation-handbook-2020/8-hepatitis Accessed 30 August 2023
[317] https://www.health.govt.nz/our-work/immunisation-handbook-2020/9-hepatitis-b Accessed 30 August 2023
[318] https://www.cdc.gov/hepatitis/hcv/index.htm Accessed 30 August 2023
[319] https://www.cdc.gov/hepatitis/hdv/index.htm Accessed 30 August 2023
[320] https://www.who.int/news-room/fact-sheets/detail/hepatitis-e Accessed 30 August 2023

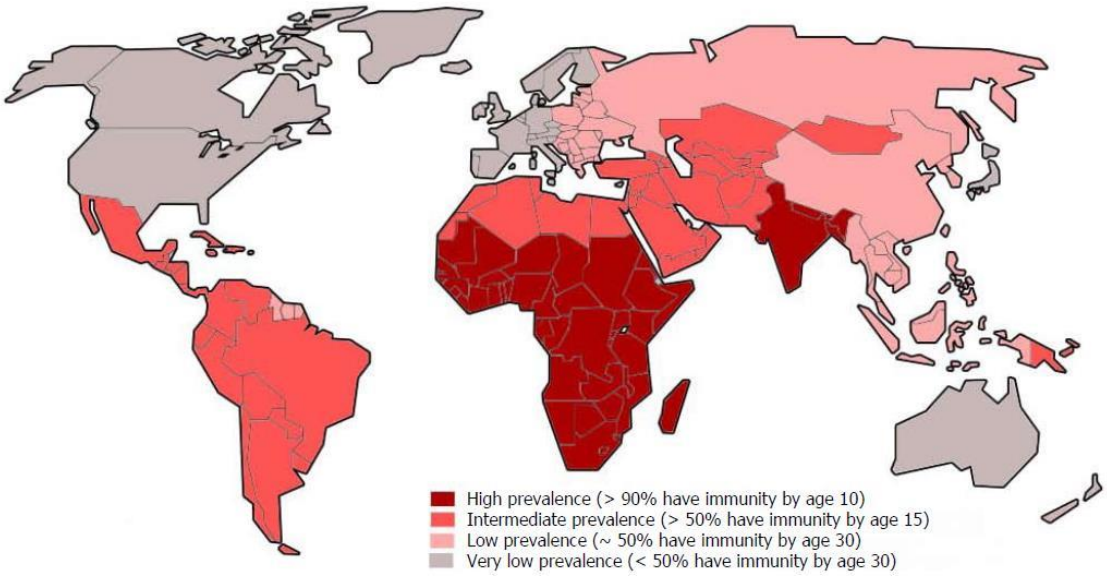

Figure 58 Global distribution of hepatitis A

Reproduced from Jefferies et al. (2018), data from Jacobsen (2018).

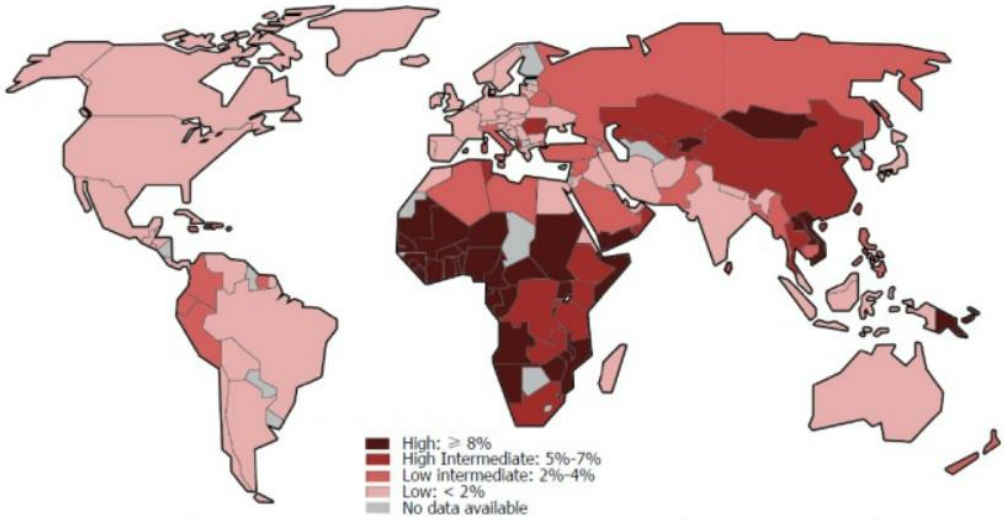

Figure 59 Global distribution of hepatitis B

Reproduced from Jefferies et al. (2018), data from Schweitzer et al. (2015).

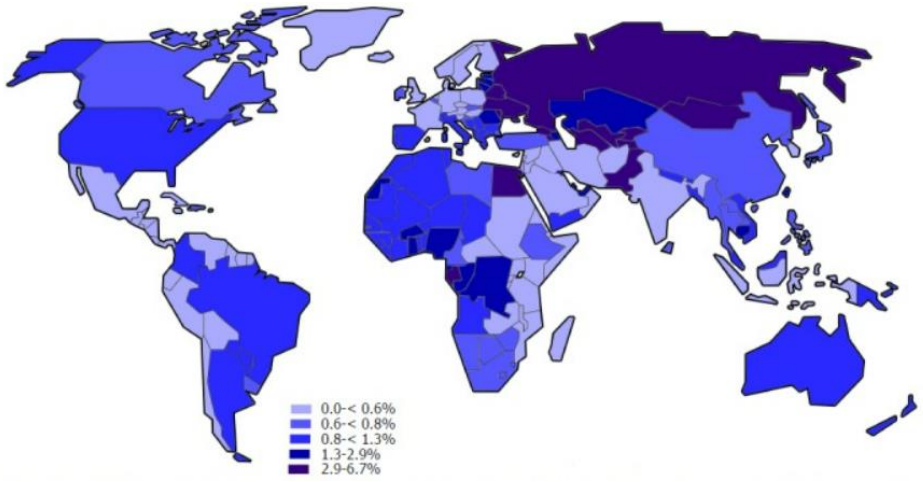

Figure 60 Global distribution of hepatitis C (% of population)

Reproduced from Jefferies et al. (2018), data from Gower et al. (2014).

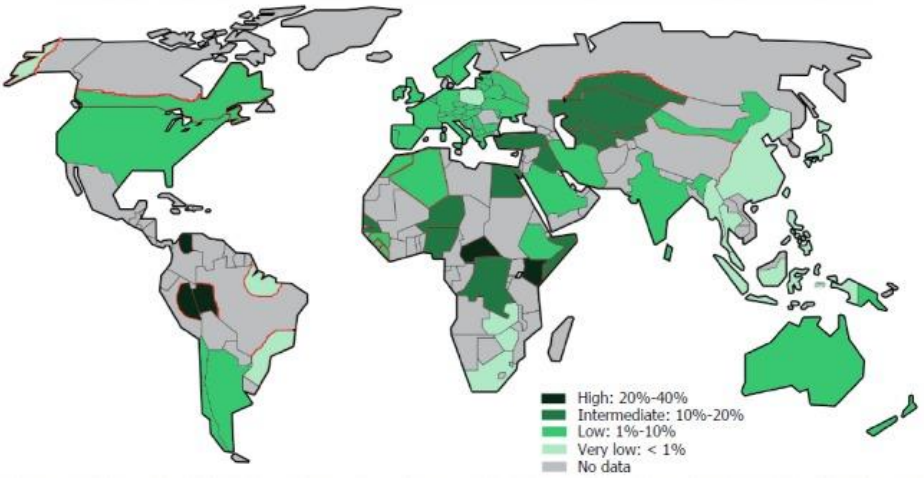

Figure 61 Global distribution of hepatitis D amongst the hepatitis B population

Reproduced from Jefferies et al. (2018), data from Wedemeyer and Manns (2010).

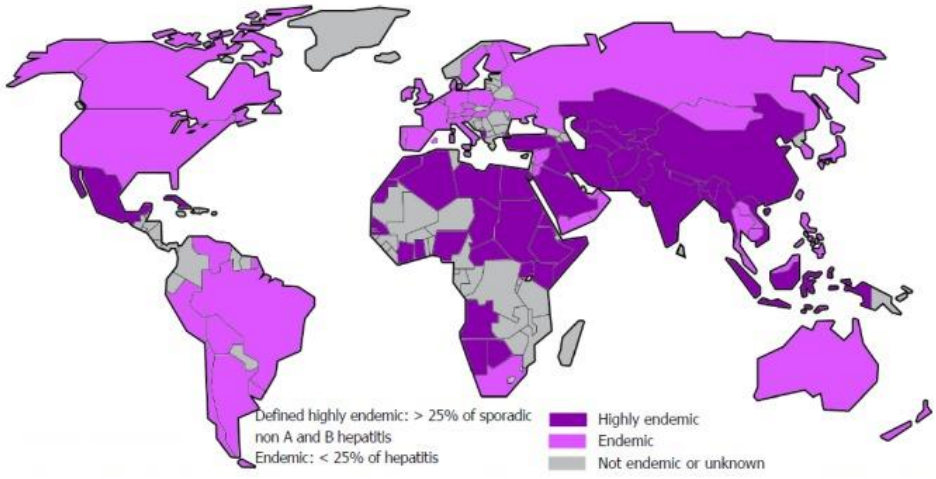

Figure 62 Global distribution of hepatitis E

Reproduced from Jefferies et al. (2018), data from WHO (2010).

5.4.4 New Zealand epidemiology

Viral hepatitis is notifiable in NZ and listed in the schedule of notifiable diseases as hepatitis A, hepatitis B, hepatitis C and hepatitis (viral) not otherwise specified (NOS), which includes hepatitis D and E[321]. Cases reported between 2006 and 2021 are shown in Figure 63 to Figure 66. There were 58 cases of hepatitis A in pre-COVID 2019, but only 8 cases in 2021[322] (Figure 63). Hepatitis B case numbers have been decreasing from a high of 72 in 2007 to 14 cases in 2021[322] (Figure 64). Hepatitis C case numbers have fluctuated between ~20 to 40 cases annually[322] (Figure 65). Of the 9 hepatitis cases 'not otherwise specified' in 2021[322] (Figure 66), 4 cases were hepatitis D and 7 cases were hepatitis E[323].

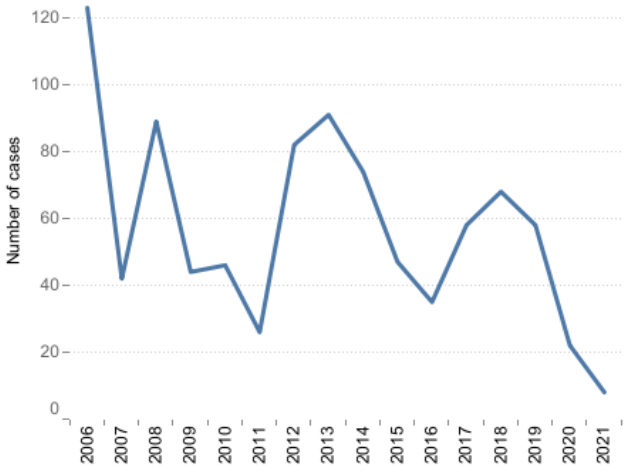

Figure 63 Number of reported hepatitis A cases in New Zealand 2006 - 2021

Reproduced from https://www.esr.cri.nz/digital-library/notifiable-disease-dashboard/.

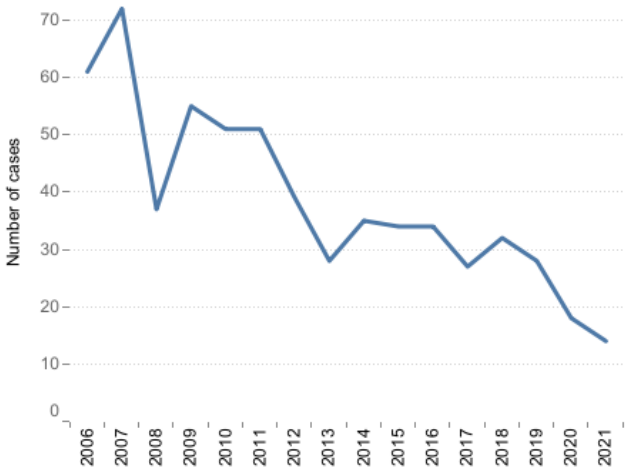

Figure 64 Number of reported hepatitis B cases in New Zealand 2006 - 2021

Reproduced from https://www.esr.cri.nz/digital-library/notifiable-disease-dashboard/.

[321] https://www.health.govt.nz/system/files/documents/pages/schedule-of-notifiable-diseases-updated-jun22.pdf Accessed 30 August 2023
[322] https://www.esr.cri.nz/digital-library/notifiable-disease-dashboard/ Accessed 30 August 2023
[323] https://www.esr.cri.nz/digital-library/notifiable-diseases-annual-surveillance-summary-2021/ Accessed 4 April 2024

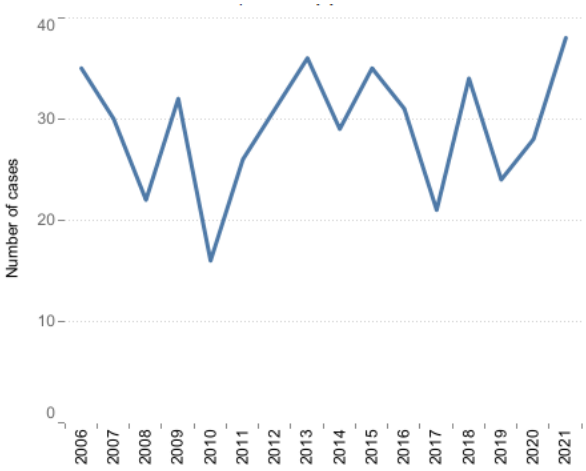

Figure 65 Number of reported hepatitis C cases in New Zealand 2006 - 2021

Reproduced from https://www.esr.cri.nz/digital-library/notifiable-disease-dashboard/.

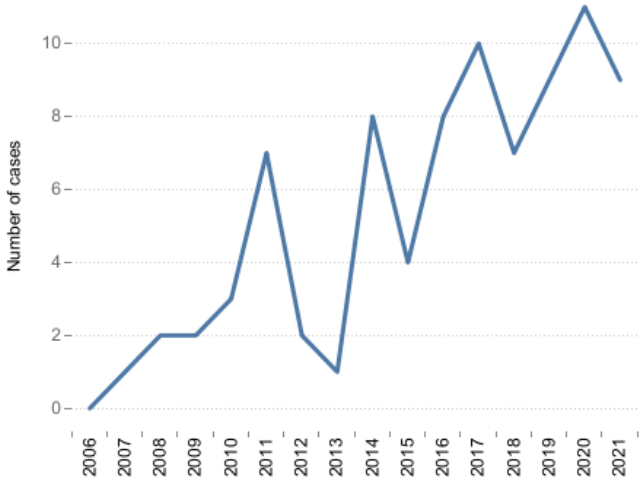

Figure 66 Number of reported hepatitis cases NOS in New Zealand 2006 - 2021

Reproduced from https://www.esr.cri.nz/digital-library/notifiable-disease-dashboard/. NOS, not otherwise specified; includes hepatitis D and E.

5.4.5 Symptoms

The incubation period for hepatitis A is generally 14 – 28 days[324]. Approximately 70% of cases in children under 6 are asymptomatic, but the likelihood of displaying symptoms increases with age, and ranges from mild to severe[324,325]. Symptoms of hepatitis A infection may include fever, nausea, diarrhoea, abdominal discomfort, loss of appetite, malaise, dark urine and jaundice[324]. Approximately 10% of children under 6 and 70% of older children and

[324] https://www.who.int/news-room/fact-sheets/detail/hepatitis-a Accessed 30 August 2023
[325] https://www.cdc.gov/vaccines/pubs/pinkbook/hepa.html Accessed 30 August 2023

adults will develop jaundice[324,325,]. In rare cases, hepatitis A may cause liver failure[326]. Hepatitis A is most contagious during the second half of the incubation period, before symptoms develop[327].

The incubation period for hepatitis B ranges from 60 – 150 days (average of 90)[328]. Most children under 5 and immunocompromised individuals will be asymptomatic, whereas up to 50% of children over 5 and adults will display symptoms of acute hepatitis B infection[329]. People infected with hepatitis B may be infectious 2 – 3 weeks before symptoms develop and for up to 2 – 3 months after recovery[330]. Asymptomatic people can also still transmit the virus[329]. Symptoms include fever, nausea, vomiting, loss of appetite, abdominal pain, fatigue, dark urine, jaundice, joint pain and clay-coloured bowel movements[329]. Symptoms usually last for weeks and in some cases up to 6 months[329]. Where the virus remains in the body after the initial illness the infection is considered chronic[329]. Most people suffering from chronic hepatitis B will have no symptoms[329]. In some cases, symptoms similar to the initial infection may arise and may be a signal of advanced liver disease[329]. One in 4 people whose chronic infection developed during childhood and 15% of people who became chronically infected as an adult will die from serious liver conditions (e.g., cirrhosis or liver cancer)[329].

The incubation period for hepatitis C is generally 2 – 12 weeks after exposure[331]. However, many people newly infected with hepatitis C are asymptomatic[331]. Where symptoms do develop, they are generally mild and non-specific, including nausea, vomiting, abdominal pain, fatigue, joint pain, loss of appetite, jaundice, fever, dark urine, light-coloured stool[331,332]. Similar to hepatitis B, chronic hepatitis C infection may develop[331]. This is often asymptomatic or displays generalised symptoms like depression and chronic fatigue[331]. Many individuals suffering from chronic hepatitis C infection will develop liver disease over a period of decades (e.g., cirrhosis, liver cancer), and the virus is often picked up during routine testing[331]. People suffering from acute hepatitis C infection are contagious from 1 or more weeks prior to symptom onset, and chronically infected people are thought to be contagious indefinitely[333].

The hepatitis D virus cannot multiply without the hepatitis B virus, so infections only occur as simultaneous infections (B and D together) or superinfection of a chronic hepatitis B patient with hepatitis D[334]. As such, hepatitis D is the rarest form, but is also the most severe[334]. However, the majority of infections are asymptomatic (Masood & John, 2022). The incubation period for hepatitis D superinfection is 2 – 8 weeks[334]. The symptoms of hepatitis D infection are similar to those for the other forms[334]. If infection occurs simultaneously with hepatitis B, the body is likely to clear the virus, but where it occurs as a superinfection in a chronic hepatitis B patient, chronic hepatitis D infection is likely to develop, increasing the

[326] https://www.niddk.nih.gov/health-information/liver-disease/viral-hepatitis/hepatitis-a Accessed 29 June 2023
[327] https://www.ecdc.europa.eu/en/hepatitis-A/facts Accessed 29 June 2023
[328] https://wwwnc.cdc.gov/travel/yellowbook/2024/infections-diseases/hepatitis-b Accessed 29 June 2023
[329] https://www.cdc.gov/hepatitis/hbv/bfaq.htm Accessed 29 June 2023
[330] https://www.health.govt.nz/our-work/immunisation-handbook-2020/9-hepatitis-b Accessed 29 June 2023
[331] https://www.cdc.gov/hepatitis/hcv/cfaq.htm Accessed 30 August 2023
[332] https://www.hepatitisfoundation.org.nz/liver-disease/hepatitis/hepatitis-c Accessed 30 August 2023
[333] https://www.health.ny.gov/diseases/communicable/hepatitis/hepatitis_c/fact_sheet.htm Accessed 30 August 2023
[334] https://www.hepatitisfoundation.org.nz/liver-disease/hepatitis/hepatitis-d Accessed 30 August 2023

risk of chronic liver disease[334]. People infected with hepatitis D are most infectious before the onset of symptoms[335].

The incubation period for hepatitis E is generally 15 – 60 days (average of 40 days) after exposure[336]. Many cases of hepatitis E infection are asymptomatic[336]. Where symptoms develop, they are similar to those for the other forms discussed above. In pregnant women, there is increased risk of severe illness including rapid liver failure (fulminant hepatitis) and death (10 – 30% risk for women in the third trimester)[336]. However, the overall case-fatality rate for hepatitis E is only 1%[336]. The disease is also particularly dangerous for people already suffering from chronic liver disease and people who have received an organ transplant and are taking immunosuppressive medication[336]. In some infections (specifically with genotype 3 strains) chronic hepatitis E infection may develop, but this is mainly in organ-transplant recipients[336]. Although the contagious period for hepatitis E is unknown, the virus has been found in stool from a week prior to onset of jaundice until 30 days after jaundice develops, and in chronically infected patients the virus is constantly shed[336].

5.4.6 Excretion of biomarkers of infection

Hepatitis A

The hepatitis A virus has been detected in urban wastewater in Argentina (Fantilli et al., 2023; Yanez et al., 2014), Brazil (Villar et al., 2007), China (Fu et al., 2022), France (Bisseux et al., 2018), Italy (La Rosa et al., 2014; Pellegrinelli et al., 2019), Kenya (Kiulia et al., 2010), Singapore (Aw & Gin, 2010), Sweden (Hellmér et al., 2014; Wang et al., 2020), Tunisia (Béji-Hamza et al., 2014; Gharbi-Khelifi et al., 2007; Ouardani et al., 2016), Uganda (O'Brien et al., 2017) and Detroit, USA (McCall et al., 2020) using targeted PCR.

Infectious hepatitis A virus has been detected in human faeces (Polish et al., 1999) and in sewage sludge and treated wastewater (Schlindwein et al., 2010), and hepatitis A diagnostic PCR is routinely performed using faeces[337]. Hepatitis A viral RNA has also been detected in faeces as detailed in Table 22.

Hepatitis B

The hepatitis B virus has been detected in urban wastewater in China using high-throughput microfluidic-chip detection (Fu et al., 2022). Viral DNA has been detected in faeces as detailed in Table 22 and in urine Komatsu et al. (2015). However, a study by Komatsu et al. (2015) found that faeces from patients with hepatitis B does not appear to be infectious, and Jain et al (2018) concluded that urine from hepatitis B patients was unlikely to be infectious.

Hepatitis C

The hepatitis C virus has been detected in urban wastewater in Detroit, USA (McCall et al., 2020), Taiwan (Kuo et al., 2023) and in numerous wastewater samples collected in India for SARS-CoV-2 monitoring (Stockdale et al., 2023). Infectious hepatitis C virus has been isolated from faeces (Heidrich et al., 2016) and viral RNA has been detected in faeces as detailed in Table 22 and in urine (Numata et al., 1993).

[335] https://www.health.vic.gov.au/infectious-diseases/hepatitis-d Accessed 30 August 2023
[336] https://www.cdc.gov/hepatitis/hev/hevfaq.htm Accessed 30 August 2023
[337] https://www.wellingtonscl.co.nz/for-referrers/microbiology/how-do-i-diagnose/hepatitis-a-virus-hav/ Accessed 30 August 2023

Hepatitis D

The hepatitis D virus has been detected in urban wastewater in China using high-throughput microfluidic-chip detection (Fu et al., 2022). However, no studies assessing the presence of viral RNA in urine or faeces were identified during preparation of this report.

Hepatitis E

The hepatitis E virus has been detected in urban wastewater in Argentina (Fantilli et al., 2023; Wassaf et al., 2014), France (Bisseux et al., 2018), Germany (Beyer et al., 2020), Italy (Alfonsi et al., 2018; Iaconelli et al., 2020), Israel (Ram et al., 2016), Sweden (Hellmér et al., 2014) and Switzerland (Masclaux et al., 2013) using targeted PCR; in China using high-throughput microfluidic-chip detection (Fu et al., 2022); Sweden using metagenomics (Wang et al., 2020); and the United States using microarrays and targeted PCR (Wong et al., 2013). Infectious virus has been isolated from human faeces (Takahashi et al., 2007; Zaki et al., 2009) and viral RNA has been detected in faeces, as detailed in Table 22. Viral RNA has also been detected in urine of a patient with chronic hepatitis E infection and 3/8 (38%) of patients with acute hepatitis E infection (Geng et al., 2016).

5.4.7 Potential health hazard if present in wastewater

As infectious hepatitis A (Polish et al., 1999), C (Heidrich et al., 2016) and E (Takahashi et al., 2007; Zaki et al., 2009) viruses have been isolated from faeces, where an infected individual defecates on a plane or at the airport there could be a potential health hazard posed to people collecting or processing aircraft/airport wastewater samples, or to WWTP staff. However, faeces from people with hepatitis B does not appear to be infectious (Komatsu et al., 2015). No information suggesting the hepatitis D virus could be transmitted through contact with wastewater (e.g., while sampling, processing samples in the laboratory, or at the WWTP) was identified during preparation of this report.

Arvanitidou et al. (2004) argued that there is epidemiological evidence for vaccinating WWTP workers against hepatitis A and B, as they found antibodies against the hepatitis A virus in 65.7% of WWTP workers versus 32.6% in the control group, and serological evidence of hepatitis B infection in 32.4% of the WWTP workers versus 5.8% in the control group.

Table 22 Summary of studies assessing excretion of hepatitis A, B, C and E viral nucleic acids in faeces

Virus	Study participants	% positive patients	Shedding dynamics	Reference
Hepatitis A	18	28	• 7 patients were screened 4 – 42 days post peak liver enzyme abnormalities – all negative • 6 patients were screened 4 – 21 days post peak liver enzyme abnormalities – all negative • 5/18 patients positive • One patient positive day 13, negative day 27 post peak liver enzyme abnormalities • Four patients positive 25 – 52 days post peak liver enzyme levels	Polish et al. (1999)
Hepatitis B	50 (chronic infections)	74	• Viral load 2.8 – 8.4 log copies/mL	Komatsu et al. (2015)
Hepatitis C	6 (chronic infections)	67	• Viral load up to 2.8×10^5 copies/mL	Beld et al. (2000)
Hepatitis E	11 (acute infections)	100	• For patient 1, detected up to day 121 PSO • For patients 2 – 11, detected up to days 14 – 33 (mean 22.4) PSO • Maximum viral load of 2.0×10^7 copies/mL	Takahashi et al. (2007)
Hepatitis E	10	60	• Patients included men (6), pregnant women (2) and children (2)	Ray et al. (1991)

5.5 PNEUMOCOCCAL DISEASE

5.5.1 Transmission

The term pneumococcal disease refers to infections caused by the bacterium *Streptococcus pneumoniae*, often referred to as pneumococcus[338]. Pneumococcus causes a range of different, and in some cases life-threatening, infections, including ear and sinus infections, pneumonia, meningitis and bacteraemia (blood infection) [339]. Where the bacteria are present in a normally sterile site (e.g., the blood, meninges, pleural fluid, cerebrospinal fluid or joints) the infection is referred to as invasive pneumococcal disease[340].

Pneumococcal bacteria spread from person-to-person via respiratory droplets and secretions (e.g., saliva and mucus), and it is possible for a person (often children) to carry the bacteria in their nose or throat and not become sick[341].

5.5.2 Prevention

There are two vaccines against *S. pneumoniae* approved for usage in New Zealand – the pneumococcal conjugate vaccine (PCV) and the polysaccharide pneumococcal vaccine (PPV)[342]. Children under 5 years of age are recommended to receive the PVC vaccine at six weeks, five months and twelve months[342]. The PPV vaccine is not suitable for children under the age of two[342].

5.5.3 Geographic distribution

Pneumococcal disease is found worldwide, and there are an estimated 14.5 million cases of serious pneumococcal infections reported every year, with approximately 826,000 deaths (Jimbo-Sotomayor et al., 2020). Invasive pneumococcal cases reported to the Pneumococcal Serotype Replacement and Distribution Estimation (PSERENADE) project (Knoll et al., 2021) can be seen in Figure 67.

5.5.4 New Zealand epidemiology

Invasive pneumococcal disease is notifiable in New Zealand[343], and cases reported between 2006 to 2021 can be seen in Figure 68. Cases peaked at 687 in 2009 but dropped to 468 in 2021[344].

[338] https://www.cdc.gov/pneumococcal/index.html Accessed 30 August 2023
[339] https://www.cdc.gov/pneumococcal/about/infection-types.html Accessed 30 August 2023
[340] https://www.health.govt.nz/our-work/diseases-and-conditions/communicable-disease-control-manual/invasive-pneumococcal-disease Accessed 30 August 2023
[341] https://www.cdc.gov/pneumococcal/about/risk-transmission.html Accessed 30 August 2023
[342] https://www.health.govt.nz/our-work/immunisation-handbook-2020/16-pneumococcal-disease Accessed 30 August 2023
[343] https://www.health.govt.nz/system/files/documents/pages/schedule-of-notifiable-diseases-updated-jun22.pdf Accessed 30 August 2023
[344] https://www.esr.cri.nz/expertise/public-health/infectious-disease-intelligence-surveillance/ Accessed 4 April 2024

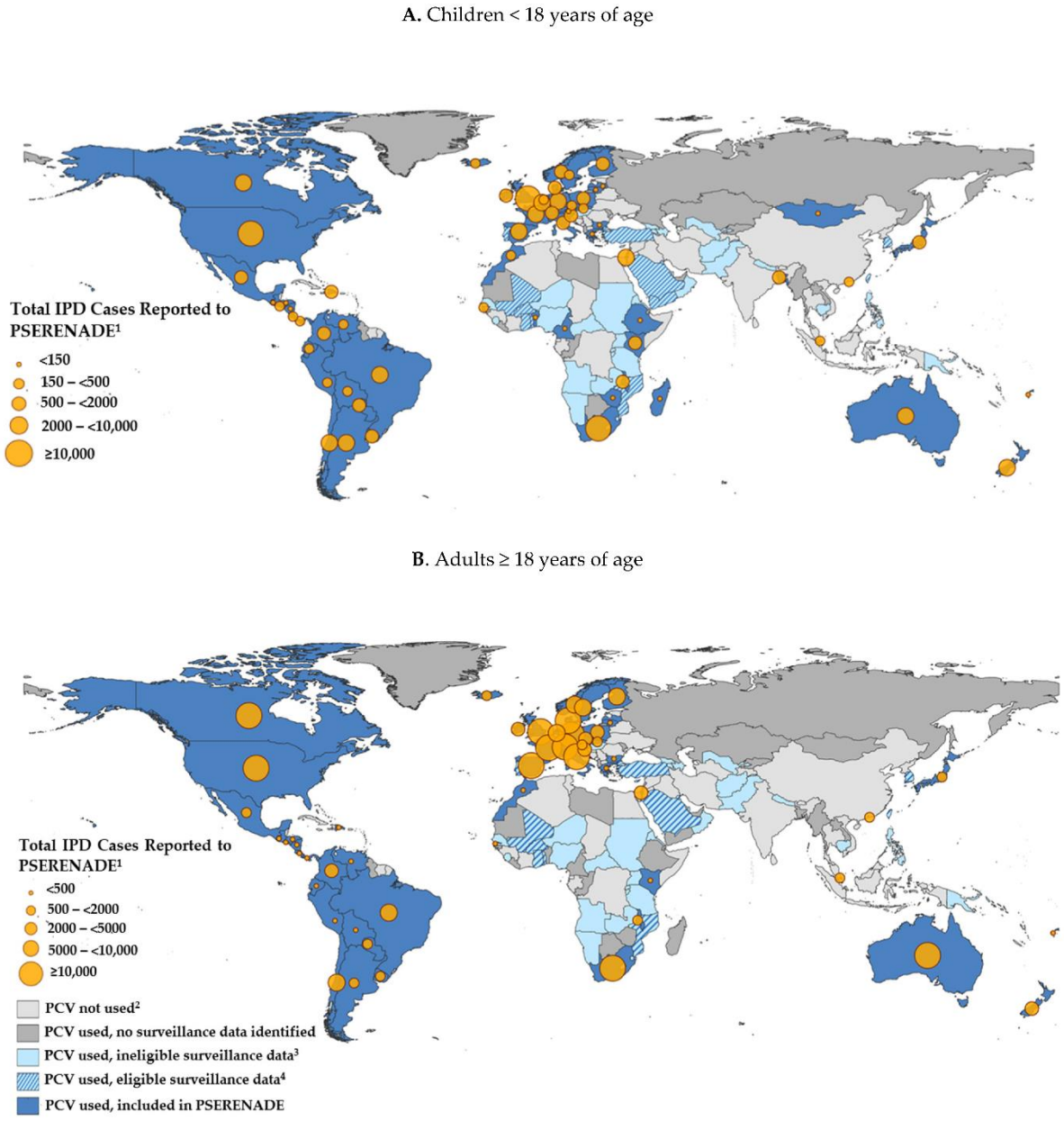

Figure 67 Invasive pneumococcal disease surveillance data

Reproduced from Knoll et al. (2021). PCV refers to the pneumococcal vaccine.

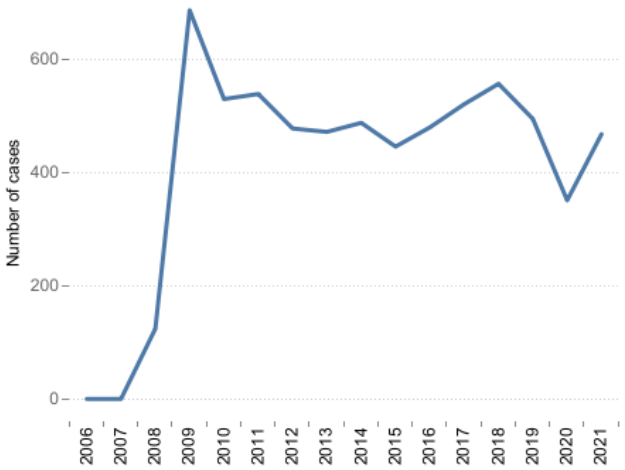

Figure 68 Number of reported invasive pneumococcal cases in New Zealand 2006 - 2021

Reproduced from https://www.esr.cri.nz/digital-library/notifiable-disease-dashboard/.

5.5.5 Symptoms

As noted above, pneumococcus bacteria can infect many different parts of the body, including the ears (otitis), sinuses (sinusitis), lungs (pneumonia), blood (bacteraemia) and lining of the brain and spinal cord (meningitis), with symptoms of infection differing depending on the part of the body infected[345]. People infected with pneumococcus are considered contagious for as long as the bacteria are found in their throat and nose[346].

Pneumococcus middle ear infections are the most common form and are often mild and characterized by fever, ear pain, a red swollen ear drum and sleepiness[347].

Pneumococcus sinus infections are often characterized by headache, stuffy or runny nose, loss of smell, facial pain/pressure and postnasal drip[347]. Complications are rare but may include formation of a painful abscess or infection of the surrounding tissue (e.g., bone, eyes)[347].

Pneumococcal pneumonia typically presents with cough, fever and chills, chest pain and rapid or difficulty breathing[347]. However, in older people the most common symptoms may be confusion and low alertness[347]. Complications include pericarditis (inflammation of the heart lining), empyema (infection of the chest cavity and area around the lungs) and endobronchial obstruction (blockage of the airways) with lung collapse and development of pus in the lungs[347]. Approximately 1 in 20 people who develop pneumococcal pneumonia will die[347].

[345] https://wwwnc.cdc.gov/travel/diseases/pneumococcal-disease-streptococcus-pneumoniae Accessed 30 August 2023

[346] https://www.vdh.virginia.gov/epidemiology/epidemiology-fact-sheets/streptococcus-pneumoniae-invasive-infection/ Accessed 30 August 2023

[347] https://www.cdc.gov/pneumococcal/about/symptoms-complications.html Accessed 30 August 2023

Blood infection, or bacteraemia, caused by pneumococcal bacteria may present with fever, chills and low alertness[348]. Approximately 1 in 30 children and 1 in 8 adults who develop pneumococcal bacteraemia will die, and many survivors may suffer the loss of limbs[348].

Pneumococcal meningitis is the most serious form and symptoms may include stiff neck, fever, headache, sensitivity to light and confusion[348]. Babies with pneumococcal meningitis may have low alertness, vomiting and poor eating/drinking[348]. Approximately 1 in 12 children and 1 in 6 older adults with pneumococcal meningitis will die, and survivors may suffer from long-term problems including developmental delays and hearing loss[348].

In response to invasive pneumococcal infection (e.g., pneumococcal pneumonia, bacteraemia and meningitis), sepsis, "the body's extreme response to an infection", may develop[348]. Symptoms of sepsis include high heart rate, shortness of breath, confusion/disorientation, extreme pain or discomfort, clammy/sweaty skin and fever/shivering or feeling very cold[348]. Complications of sepsis include organ damage (e.g., heart, lungs, brain) and kidney failure[348].

5.5.6 Excretion of biomarkers of infection

Streptococcus pneumoniae has been detected in urban wastewater in China (Fu et al., 2022), India (Madhukar et al., 2023) and the United States (Spurbeck et al., 2023) using metagenomics.

Streptococcus pneumoniae bacteria have been isolated from urine, although this was in studies of patients suffering from urinary tract infections, with which *S. pneumoniae* is not commonly associated (Burckhardt & Zimmermann, 2011; Juda et al., 2018). Bacterial DNA has also been detected in urine, as summarised in Table 23.

5.5.7 Potential health hazard if present in wastewater

Given *S. pneumoniae* bacteria have been isolated from urine (Burckhardt & Zimmermann, 2011; Juda et al., 2018), where an infected individual urinates on a plane or at the airport there could be a potential health hazard posed to people collecting or processing aircraft/airport wastewater samples, or to WWTP staff. However, as these bacteria are generally spread via respiratory secretions[349] this may be unlikely. Although, the potential for transmission via wastewater aerosols should be considered.

Table 23 Summary of studies assessing excretion of *Streptococcus pneumoniae* DNA in urine

Study participants	% positive patients	Details	Reference
227	2	• Samples collected at time of hospital admission	Murdoch et al. (2003)
256	2	• Samples collected at time of hospital admission • Median bacterial load 623 copies/mL	Werno et al. (2012)
16	100	• 100% of confirmed cases were PCR positive • Samples collected within 24 hours of hospital admission	Cima-Cabal et al. (2020)

[348] https://www.cdc.gov/pneumococcal/about/symptoms-complications.html Accessed 30 August 2023
[349] https://www.cdc.gov/pneumococcal/about/risk-transmission.html Accessed 30 August 2023

5.6 HAEMOPHILUS INFLUENZAE TYPE B (HIB)

5.6.1 Transmission

Haemophilus influenzae type b, Hib, is a life-threatening bacterial infection and is the second most common cause of bacterial pneumonia[350]. Over 90% of cases of invasive Hib (where the bacteria enter the blood stream, resulting in pneumonia, meningitis or sepsis) occur in children 5 and under[351]. The bacteria may also spread to the middle ear or sinuses leading to otitis media (middle ear infection) or sinusitis[351].

Hib is spread through respiratory droplets (e.g., from coughing and sneezing), and by prolonged close contact[352]. The bacteria can also be spread by asymptomatic individuals who are carrying the bacteria in their nose and throat[352].

5.6.2 Prevention

In New Zealand, children are vaccinated against Hib with a 6 in 1 combined vaccine for pertussis, diphtheria, tetanus, polio, hepatitis B and Hib at 6 weeks, 3 months and 5 months as discussed above, and with a Hib specific vaccine at 15 months[353]. Introduction of the Hib vaccine has almost eliminated this disease in countries where the vaccine is used[353].

5.6.3 Geographical distribution

Hib is found worldwide[354], but cases are almost eliminated in countries which vaccinate against Hib (Watt et al., 2009). The global distribution of child mortality due to Hib is shown in Figure 69, with the majority of deaths occurring in Africa and Asia (Watt et al., 2009).

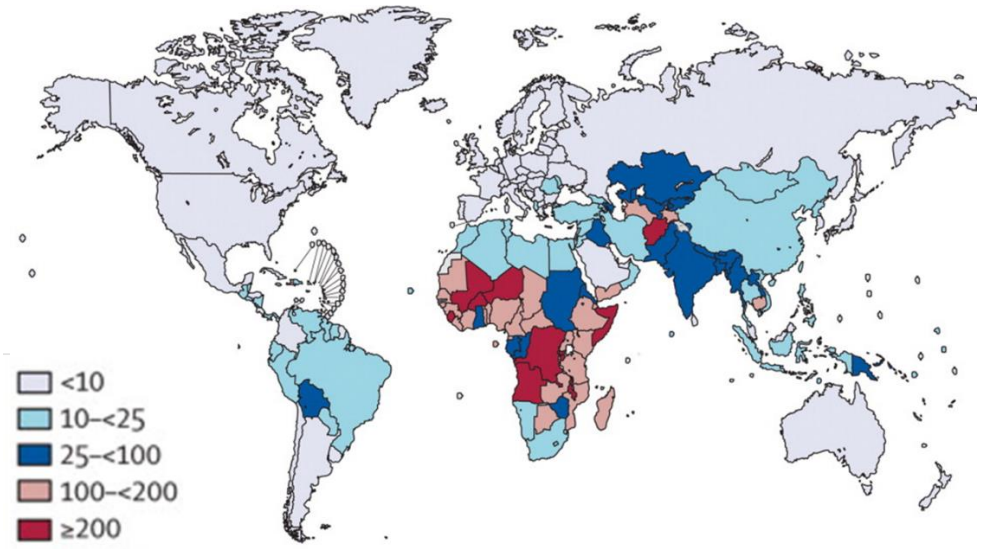

Figure 69 Global Hib mortality rate for children 1 – 59 months per 100,000 children (2009)

Adapted from Watt et al. (2009). Only includes HIV-negative Hib deaths.

[350] https://www.who.int/news-room/fact-sheets/detail/pneumonia Accessed 30 August 2023
[351] https://www.who.int/europe/news-room/fact-sheets/item/haemophilus-influenzae-type-b-(hib) Accessed 30 August 2023
[352] https://www.cdc.gov/hi-disease/about/causes-transmission.html Accessed 30 August 2023
[353] https://www.health.govt.nz/our-work/immunisation-handbook-2020/7-haemophilus-influenzae-type-b-hib-disease Accessed 30 August 2023
[354] https://www.cdc.gov/vaccines/pubs/pinkbook/hib.html Accessed 30 August 2023

5.6.4 New Zealand epidemiology

Hib is a notifiable disease in New Zealand[355], and between 2006 and 2021 there were generally less than 10 cases reported per year, except for a spike of 15 cases in 2007 (Figure 70)[356].

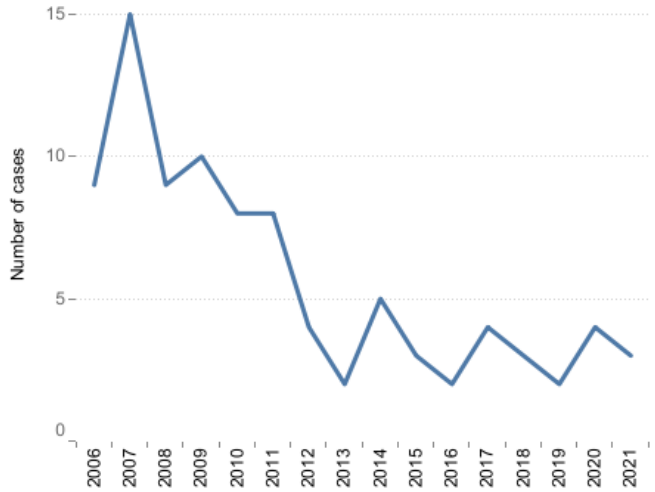

Figure 70 Number of reported *Haemophilus influenzae* type b cases in New Zealand 2006 – 2021

Reproduced from https://www.esr.cri.nz/digital-library/notifiable-disease-dashboard/.

5.6.5 Symptoms

The incubation period for Hib infection is generally 2 – 10 days from exposure[357]. Symptoms of Hib infection vary depending on what part of the body is infected[358]. Hib infection may present as meningitis, bacteraemia, pneumonia or epiglottitis ("infection and swelling in the throat that blocks the breathing passages")[358,359]. Symptoms of meningitis, bacteriaemia and pneumonia have been discussed above. Symptoms of epiglottitis include fever, noisy breathing, difficulty swallowing, drooling and difficulty breathing[358]. Complications may include inflammation of the heart, bones, joints and skin[358] Approximately 1 in 20 patients who develop meningitis and 1 in 100 patients who develop epiglottitis will die, and 1 in 3 survivors of meningitis will suffer from permanent nerve or brain damage[359].

[355] https://www.health.govt.nz/system/files/documents/pages/schedule-of-notifiable-diseases-updated-jun22.pdf Accessed 30 August 2023
[356] https://www.esr.cri.nz/expertise/public-health/infectious-disease-intelligence-surveillance/ Accessed 4 April 2024
[357] https://www.who.int/europe/news-room/fact-sheets/item/haemophilus-influenzae-type-b-(hib) Accessed 30 August 2023
[358] https://www.immune.org.nz/diseases/haemophilus-influenzae-type-b Accessed 30 August 2023
[359] https://www.health.govt.nz/your-health/conditions-and-treatments/diseases-and-illnesses/haemophilus-influenzae-type-b-hib Accessed 30 August 2023

In the absence of treatment, people infected with Hib are contagious for as long as the bacteria are present in discharge from their throat and nose, even if they are no longer experiencing symptoms[360,361].

5.6.6 Excretion of biomarkers of infection

Haemophilus influenzae has been detected in municipal wastewater collected in Ohio, USA (Spurbeck et al., 2023) and wastewater discharged from residential dormitories of the University of Miami, USA (Tierney et al., 2023) using metagenomics approaches.

Haemophilus influenzae type b bacteria have been isolated from urine from patients suffering from urinary tract infections, renal stones, epididymitis, orchitis, urethritis and prostatitis (Dingle & Clarridge, 2014; Stærk et al., 2018). No studies detailing isolation from urine of patients suffering from respiratory Hib infections were identified, however this may partially be attributed to the fact that *Haemophilus* species do not grow in standard bacterial culture media, so may go undetected in patients (Hansson et al., 2007). No studies reporting presence of *H. influenzae* DNA in urine or faeces were identified during preparation of this report.

5.6.7 Potential health hazard if present in wastewater

Given *H. influenzae* bacteria have been isolated from urine (Dingle & Clarridge, 2014; Stærk et al., 2018), where an infected individual urinates on a plane or at the airport there could be a potential health hazard posed to people collecting or processing aircraft/airport wastewater samples, or to WWTP staff. However, as these bacteria are generally spread via respiratory secretions or prolonged close contact this may be unlikely. Although, the potential for transmission via wastewater aerosols should be considered.

5.7 DIPHTHERIA

5.7.1 Transmission

Diphtheria is a bacterial illness caused by the bacterium *Corynebacterium diphtheriae*[362]. It is spread from person-to-person through respiratory droplets (e.g., from coughing and sneezing) and by direct contact with an infected person or contaminated objects/clothing[362]. There are two types of diphtheria – respiratory, which involves the nose, throat and tonsils and is generally the most severe form[363], and cutaneous which involves the skin and is generally the more contagious form[364].

5.7.2 Prevention

In New Zealand, children are vaccinated against diphtheria at 6 weeks, 3 months and 5 months of age (as a 6 in 1 combined vaccine for pertussis, diphtheria, tetanus, polio, hepatitis B and *Haemophilus influenzae* type b (Hib)), followed by a booster at 4 years old (a

[360] https://www.dshs.texas.gov/haemophilus-influenzae-including-hib Accessed 30 August 2023
[361] https://www.vdh.virginia.gov/epidemiology/epidemiology-fact-sheets/haemophilus-influenzae-type-b-hib-disease-haemophilus-b/ Accessed 30 August 2023
[362] https://www.who.int/news-room/questions-and-answers/item/diphtheria Accessed 30 August 2023
[363] https://www.stanfordchildrens.org/en/topic/default?id=diphtheria-in-children-90-P02511 Accessed 30 August 2023
[364] https://www.health.ny.gov/diseases/communicable/diphtheria/fact_sheet.htm Accessed 30 August 2023

4-in-1 combined vaccine for pertussis, tetanus, diphtheria and polio) and 11 years old (a combined vaccine for pertussis, tetanus and diphtheria)[365].

5.7.3 Geographical distribution

The disease continues to cause illness globally with the World Health Organization reporting 10,107 global cases of diphtheria in 2020[366].

5.7.4 New Zealand epidemiology

Diphtheria is a notifiable disease in New Zealand[367] and was common until the 1960s[368]. However, the last case of toxigenic respiratory diphtheria in New Zealand was in 1998, with cases notified since then all being cutaneous diphtheria[368]. Case notifications between 2006 and 2021 can be seen in Figure 71.

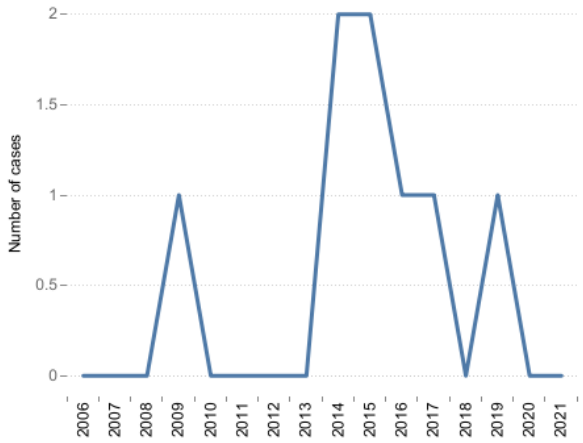

Figure 71 Number of reported diphtheria cases in New Zealand 2006 - 2021

Reproduced from https://www.esr.cri.nz/digital-library/notifiable-disease-dashboard/.

5.7.5 Symptoms

The incubation period for diphtheria is generally 2 – 5 days after exposure[369]. Asymptomatic infections have been reported[370], with one study finding 31% of infections in unvaccinated people were asymptomatic (Truelove et al., 2020). As noted above, diphtheria can infect both the respiratory tract and the skin[369]. Symptoms of respiratory diphtheria include sore throat, mild fever, weakness and swollen glands in the neck[369]. The diphtheria bacteria produce a toxin that destroys the tissue of the respiratory tract, forming a thick, grey coating

[365] https://www.health.govt.nz/our-work/immunisation-handbook-2020/15-pertussis-whooping-cough Accessed 30 August 2023
[366] https://www.cdc.gov/diphtheria/surveillance.html Accessed 9 April 2024
[367] https://www.health.govt.nz/system/files/documents/pages/schedule-of-notifiable-diseases-updated-jun22.pdf Accessed 30 August 2023
[368] https://www.health.govt.nz/our-work/immunisation-handbook-2020/6-diphtheria Accessed 30 August 2023
[369] https://www.cdc.gov/diphtheria/about/symptoms.html Accessed 30 August 2023
[370] https://www.health.govt.nz/our-work/immunisation-handbook-2020/6-diphtheria Accessed 30 August 2023

in the throat and nose 2 – 3 days after symptoms start[369]. This coating, known as a pseudomembrane, may make it difficult to swallow and breathe[369]. Where the diphtheria toxin enters the bloodstream, it can cause kidney failure or damage to the heart or nerves[369]. When untreated, approximately half of all respiratory diphtheria cases will be fatal, and even with treatment the mortality rate is around 1 in 10[369]. Untreated diphtheria cases may be contagious for up to four weeks, versus < 4 days for treated cases[371]. Diphtherial skin infections can present as open sores, or ulcers, but rarely cause severe disease[369].

5.7.6 Excretion of biomarkers of infection

Corynebacterium diphtheriae has been detected in municipal wastewater collected in Ohio, USA (Spurbeck et al., 2023) and wastewater discharged from residential dormitories at the University of Miami, USA (Tierney et al., 2023) using metagenomics approaches. No studies reporting detection of *C. diphtheriae* DNA in urine or faeces were identified during preparation of this report.

5.7.7 Potential health hazard if present in wastewater

No information suggesting *C. diphtheriae* can be transmitted through contact with wastewater (e.g., while sampling, processing samples in the laboratory, or at the WWTP) was identified during preparation of this report. Although it is primarily spread via respiratory droplets, it is also noted to be spread by contact with contaminated objects/clothing[372]. It is unclear if this includes objects/clothing contaminated with urine or faeces. As such, further work is needed to determine whether the presence of *C. diphtheriae* in wastewater may pose a hazard to people working with aircraft/airport wastewater. The potential for transmission via wastewater aerosols should be considered.

5.8 PERTUSSIS

5.8.1 Transmission

Pertussis, also known as whooping cough, is a highly infectious respiratory illness caused by the bacterium *Bordetella pertussis*[373]. Pertussis is spread from person-to-person through the air via respiratory droplets when an infected person sneezes or coughs, and by prolonged periods in close breathing space with an infected person[373].

5.8.2 Prevention

A vaccine is available to protect against pertussis and is administered in a combined vaccine against diphtheria, tetanus and polio (and hepatitis B and *Haemophilus influenzae* type B for the primary course)[374]. A booster is also recommended for pregnant women to provide passive immunity to the new-born infant[374].

[371] https://www.health.ny.gov/diseases/communicable/diphtheria/fact_sheet.htm Accessed 30 August 2023
[372] https://www.who.int/news-room/questions-and-answers/item/diphtheria Accessed 30 August 2023
[373] https://www.cdc.gov/pertussis/about/causes-transmission.html Accessed 30 August 2023
[374] https://www.health.govt.nz/our-work/immunisation-handbook-2020/15-pertussis-whooping-cough Accessed 30 August 2023

5.8.3 Geographical distribution

Pertussis is endemic worldwide, with the WHO reporting more than 151,000 cases globally in 2018[375] .

5.8.4 New Zealand epidemiology

Pertussis is a notifiable illness in New Zealand[376] and cases reported between 2006 and 2021 can be seen in Figure 72. Cases numbers peaked at 5,897 cases in 2012 then dropped dramatically to only 170 and 43 cases in 2020 and 2021 respectively, which has been attributed to public health measures associated with the COVID-19 pandemic[377].

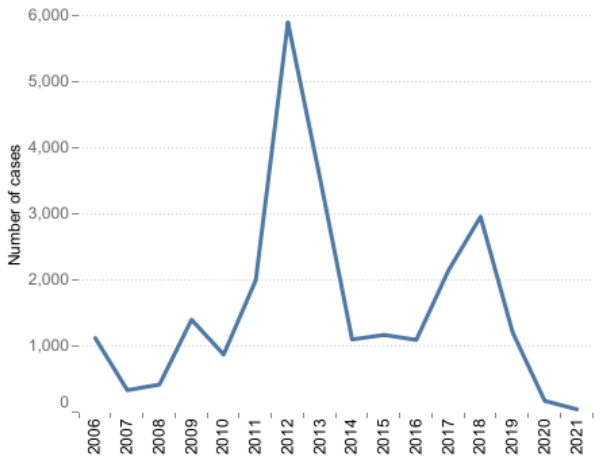

Figure 72 Number of reported pertussis cases in New Zealand 2006 - 2021

Reproduced from https://www.esr.cri.nz/digital-library/notifiable-disease-dashboard/.

5.8.5 Symptoms

The incubation period for pertussis is generally 5 – 10 days after exposure but may be as long as three weeks[378]. Cases of asymptomatic pertussis infection have been reported (Gill et al., 2021). People with pertussis may be contagious from the start of symptoms up until at least two weeks after the cough begins[378].

Early symptoms of pertussis infection may appear similar to a common cold and include low-grade fever, mild cough (not in babies), runny or stuffed nose and apnea (life-threatening pauses during breathing) and cyanosis (turning blue/purple) in babies/young children[378]. These symptoms may last for 1 – 2 weeks[378] These initial symptoms are followed around 1 – 2 weeks later by violent, uncontrolled coughing fits which may last for 1 – 6 weeks (up to 10 weeks) and become worse as the illness progresses[378]. During these coughing fits, infected individuals may struggle to breath, vomit, and make a high-pitched 'whoop' sound when they

[375] https://www.who.int/health-topics/pertussis Accessed 9 April 2024
[376] https://www.health.govt.nz/system/files/documents/pages/schedule-of-notifiable-diseases-updated-jun22.pdf Accessed 30 August 2023
[377] https://www.nzherald.co.nz/nz/two-whooping-cough-deaths-in-new-zealand-low-vaccination-rates-mean-spread-more-likely. Accessed 30 August 2023
[378] https://www.cdc.gov/pertussis/about/signs-symptoms.html Accessed 30 August 2023

inhale after coughing[378]. Many babies infected with pertussis, however, do not cough, instead they struggle to breath and may turn blue, with symptoms often appearing the same throughout the illness[378]. A schematic summarising the progression of pertussis symptoms can be seen in Figure 73.

Complications of pertussis infection in babies and children include pneumonia (1 in 5 cases), convulsions (1 in 50 cases), encephalopathy (brain disease; 1 in 150 cases) and death (1 in 100 cases)[379]. Approximately 1 in 3 cases of pertussis in babies < 1 year old will require hospitalisation[379]. Complications in teenagers and adults include pneumonia and cough-associated effects such as fainting, fracturing ribs, loss of bladder control and weight loss[379].

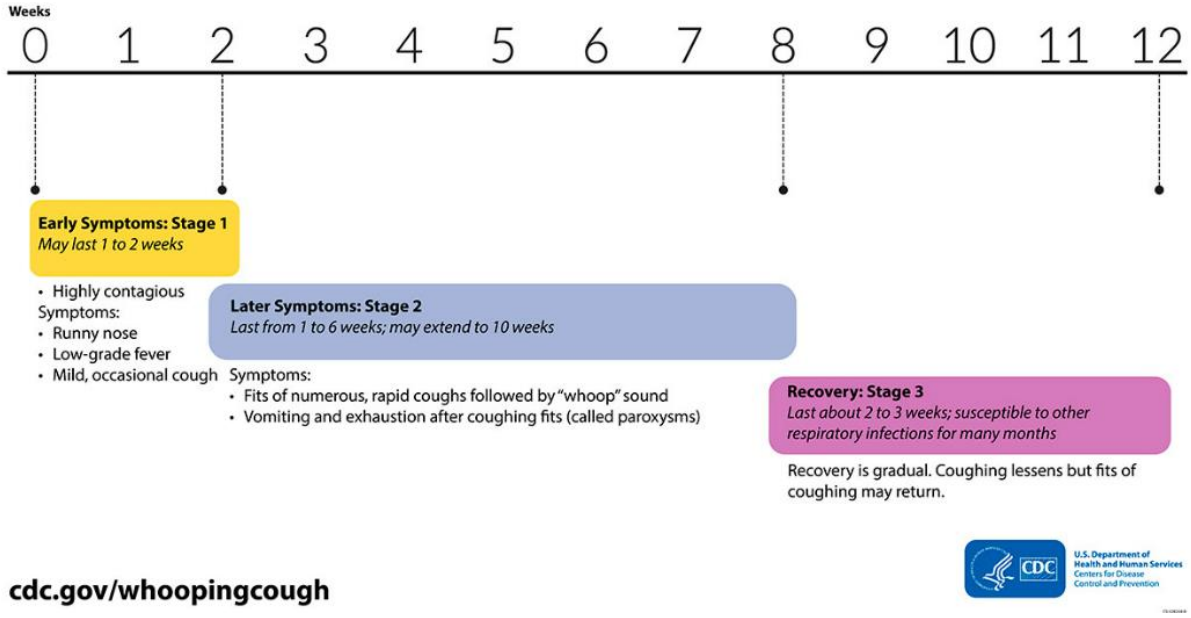

Figure 73 Pertussis disease progression

Reproduced from https://www.cdc.gov/pertussis/about/signs-symptoms.html

5.8.6 Excretion of biomarkers of infection

Bordetella pertussis has been detected in wastewater collected from the University of Miami, USA using metagenomics, including residential dormitories, the medical and marine campuses, and University hospital, as well as a regional Miami-Dade County wastewater treatment plant (Tierney et al., 2023). It has also been detected in municipal wastewater collected in Ohio, USA (Spurbeck et al., 2023) and urban wastewater collected in China (Fu et al., 2022) using metagenomic approaches.

No studies reporting detection of *B. pertussis* in urine or faeces were identified during preparation of this report. However, the Victorian Infectious Diseases Reference Laboratory

[379] https://www.cdc.gov/pertussis/about/complications.html Accessed 30 August 2023

note both urine and faeces as suitable specimens for *B. pertussis* PCR[380], implying that *B. pertussis* bacteria are present in these excreta.

5.8.7 Potential health hazard if present in wastewater

No information suggesting *B. pertussis* can be transmitted through contact with wastewater (e.g., while sampling, processing samples in the laboratory, or at the WWTP) was identified during preparation of this report. However, given pertussis is primarily spread via respiratory droplets and prolonged periods in close breathing space with an infected person[381], transmission via wastewater while collecting or processing aircraft/airport samples, or to WWTP staff less likely, although further work is needed to definitively ascertain the health hazard this poses, and any potential risk posed by wastewater aerosols.

[380] https://www.vidrl.org.au/resources/test-handbook/tests/bordetella-pertussis-pcr/ Accessed 30 August 2023
[381] https://www.cdc.gov/pertussis/about/causes-transmission.html Accessed 30 August 2023

6. SEXUALLY TRANSMITTED INFECTIONS

6.1 HUMAN IMMUNODEFICIENCY VIRUS (HIV)

6.1.1 Transmission

Human immunodeficiency virus, or HIV, is a retroviral infection which attacks the body's immune system and can lead to acquired immunodeficiency syndrome (AIDS)[382]. The HIV virus is an RNA virus of the genus *Lentivirus* (family *Retroviridae*)[383]. HIV is transmitted from person-to-person through bodily fluids including semen and vaginal fluids (e.g., sexual contact), blood (e.g., from sharing needles) and breast milk, and can be passed from mother to baby[382]. HIV cannot be spread through hugs, kisses or sharing food[382] (Figure 74).

Figure 74 Routes of transmission of HIV

Reproduced from https://www.cdc.gov/hiv/pdf/library/consumer-info-sheets/cdc-hiv-consumer-info-sheet-hiv-101.pdf

6.1.2 Prevention

There is currently no cure for HIV, but patients can be treated with antiretroviral drugs to prevent the virus replicating within the body[382]. People receiving antiretroviral treatment and with undetectable viral load do not transmit the virus via sexual contact[382]. There is currently no vaccine for HIV, although there are ongoing vaccine trials[384].

[382] https://www.who.int/news-room/fact-sheets/detail/hiv-aids Accessed 30 August 2023
[383] https://www.lsbio.com/research-areas/infectious-disease/retroviridae Accessed 30 August 2023
[384] https://www.infectiousdiseaseadvisor.com/home/topics/hiv-aids/is-there-an-hiv-vaccine/ Accessed 30 August 2023

6.1.3 Geographical distribution

HIV is found worldwide, with the majority of cases occurring in Africa[385]. In 2022 there were an estimated 1.3 million new HIV infections worldwide, and by the end of 2022, there were an estimated 39.0 million people living with HIV worldwide[386].

6.1.4 New Zealand epidemiology

There are approximately 3000 people in New Zealand receiving treatment for HIV, with 135 new cases notified in 2022[387]. Diagnoses of HIV between 2002 and 2022 in Aotearoa for various groupings is shown in Figure 75.

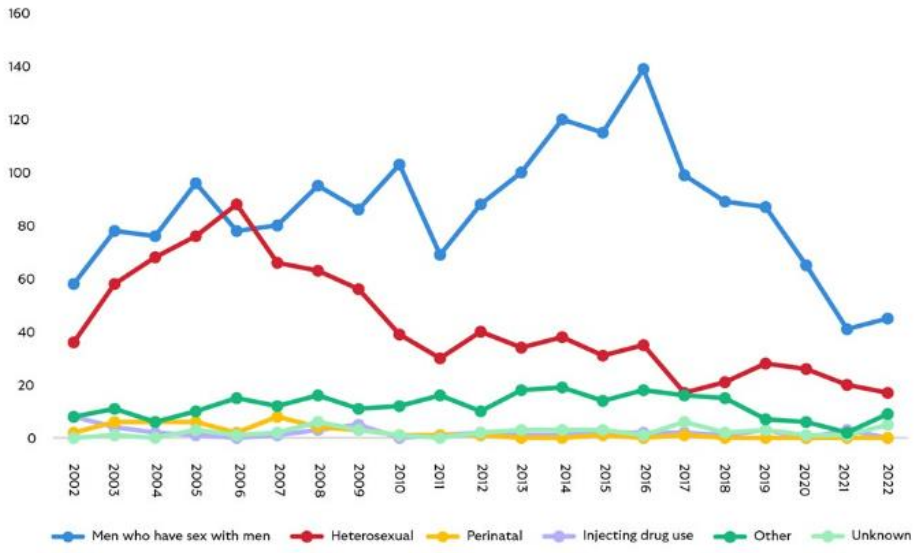

Figure 75 Local diagnoses of HIV in New Zealand 2002 - 2022

Reproduced from https://www.burnettfoundation.org.nz/learn/hiv/hiv-in-aotearoa/

6.1.5 Symptoms

Antibodies to HIV generally develop within 28 days of infection and during this period people may be asymptomatic but can still transmit the virus to other people, with the virus being most easily spread in the first few months after infection[388] due to rapid virus multiplication[389]. Where symptoms develop within the first few weeks after infection, they may be influenza-like and include headache, fever, sore throat and rash[388]. As the virus weakens the immune system other symptoms may appear including diarrhoea, weight loss, cough, swollen lymph nodes[388], fatigue, night sweats, muscle aches and mouth ulcers[389]. Without treatment, HIV infection generally advances to AIDS, the most advanced form of the infection, often after a period of several years[388]. In the absence of treatment, HIV infection

[385] https://www.afro.who.int/health-topics/hivaids Accessed 30 August 2023
[386] https://www.unaids.org/en/resources/documents/2022/UNAIDS_FactSheet Accessed 30 August 2023
[387] https://www.burnettfoundation.org.nz/learn/hiv/hiv-in-aotearoa/ Accessed 30 August 2023
[388] https://www.who.int/news-room/fact-sheets/detail/hiv-aids Accessed 30 August 2023
[389] https://hivinfo.nih.gov/understanding-hiv/fact-sheets/hiv-and-aids-basics Accessed 30 August 2023

can also increase susceptibility to tuberculosis, certain cancers (e.g., Kaposi's sarcoma, lymphomas), cryptococcal meningitis and severe bacterial infections, and can increase the severity of other infections including Mpox and hepatitis B and C[388].

6.1.6 Excretion of biomarkers of infection

HIV has been detected in United States municipal wastewater in Houston, TX (McCall et al., 2023; Terwilliger et al., 2022), the San Francisco Bay, CA area (Wolfe et al., 2024), and various locations in Florida and Michigan (Ansari et al., 1992) using targeted PCR. It has also been detected in sewage sludge in the US using metagenomics (Bibby & Peccia, 2013). A 1992 study found HIV-1 DNA proviral sequences in 66% (53/80) of urine samples from HIV-1-seropostive individuals, and HIV-1 RNA in 4.7% (2/43) urine samples (Li et al., 1992). In the Ansari et al. (1992) and Wolfe et al (2024) studies, both proviral DNA and viral RNA were detected in the wastewater samples, whereas Terwilliger et al. (2022) detected proviral DNA. The study by Wolfe et al (2024) found HIV-1 nucleic acid concentrations were orders of magnitude higher in wastewater solids than liquid wastewater.

6.1.7 Potential health hazard if present in wastewater

Infectious HIV has been shown to be stable in primary effluent wastewater for up to 6 hours, with a 1-log reduction in infectivity after 12 hours, 2-log reduction after 48 hours and > 3-log reduction after 72 hours (Casson et al., 1992). A separate study showed that it took 2.9 days in wastewater for a 10-fold reduction in HIV concentration (Slade et al., 1989). However, given that HIV is not transmitted by inhalation of aerosols or ingestion of contaminated water (Figure 74), transmission via contaminated wastewater is considered unlikely. Further research is needed to confirm this.

6.2 CHLAMYDIA

6.2.1 Transmission

Chlamydia is a bacterial infection caused by the bacterium *Chlamydia trachomatis*[390]. Chlamydia can be transmitted by sexual contact and passed from mother to baby during childbirth[390].

6.2.2 Prevention

There is currently no vaccine for chlamydia[392].

6.2.3 Geographical distribution

Chlamydia is the most common bacterial STI worldwide[391], and in 2020 the WHO estimated that there were 129 million new chlamydia infections globally[392].

[390] https://www.cdc.gov/std/chlamydia/stdfact-chlamydia-detailed.htm Accessed 30 August 2023
[391] https://www.paho.org/en/topics/chlamydia-infection Accessed 30 August 2023
[392] https://www.who.int/news-room/fact-sheets/detail/sexually-transmitted-infections-(stis) Accessed 30 August 2023

6.2.4 New Zealand epidemiology

Chlamydia is not a notifiable disease in New Zealand[393]. Estimated case numbers for 2014 – 2022 are shown in Figure 76. Case counts were relatively steady from 2014 to 2019 but fell in 2020, possibly due to COVID-19 public health measures affecting access to healthcare and testing[394].

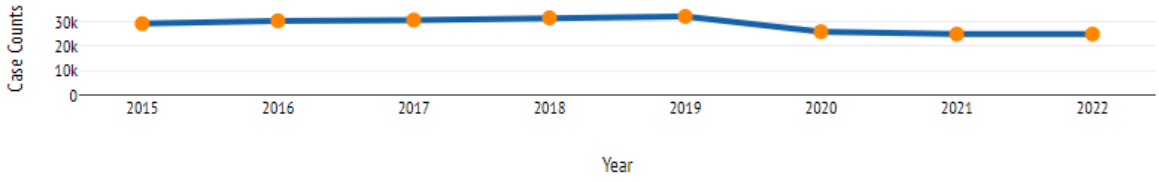

Figure 76 New Zealand national case counts for chlamydia 2014 - 2022

Reproduced from https://esr-cri.shinyapps.io/2022STIAnnualDashboard/. Accessed 8 April 2024.

6.2.5 Symptoms

The incubation period for chlamydia is generally 1 – 3 weeks, but most cases are asymptomatic[395]. However, the disease can still be spread in the absence of symptoms[396]. People with chlamydia are considered infectious until seven days after receiving treatment[397]

At least 50% of infected males experience no symptoms[395]. Where symptoms do develop, they most commonly include pain in the testicles and when urinating, burning or itching of the urethra, and/or watery, cloudy or white discharge from the penis[395]. If left untreated, swelling of the tubes that carry the sperm from the testicles (the epididymis) may develop, potentially leading to fertility problems[395].

At least 70% of infected females will have no symptoms[395]. Where symptoms do develop, they may include painful urination, pain during sex, pelvic or tummy pain, bleeding after sex and between periods, and unusual vaginal discharge[395]. If untreated, the infection can spread to the womb and cause pelvic inflammatory disease, a serious condition which can cause infertility, long-term pelvic or abdominal pain, formation of scar tissue that blocks the fallopian tubes and ectopic pregnancies[395].

Chlamydia can also affect the eyes if there is contact with infected semen or vaginal fluid, leading to conjunctivitis[395]. It may also infect the throat via unprotected oral sex, although this is uncommon and there are generally no symptoms[395]. The bacteria can also infect the rectum via unprotected anal sex, resulting in discomfort and rectal discharge[395].

6.2.6 Excretion of biomarkers of infection

A recent study reported in an Honours thesis identified *C. trachomatis* in wastewater samples collected from the University of Central Florida using targeted PCR (Chin Quee,

[393] https://www.rph.org.nz/health-professionals/notifiable-diseases/sti-notification-process-v2-january-2019-an.pdf Accessed 30 August 2023
[394] https://esr-cri.shinyapps.io/2022STIAnnualDashboard/ Accessed 8 April 2024
[395] https://www.nhs.uk/conditions/chlamydia/symptoms/ Accessed 30 August 2023
[396] https://www.cdc.gov/std/chlamydia/the-facts/chlamydia_2011_508.pdf Accessed 30 August 2023
[397] https://www.cdc.gov/std/chlamydia/stdfact-chlamydia.htm Accessed 30 August 2023

2023). It has also been detected in wastewater collected from various sites across the University of Miami, USA using metagenomics, including residential dormitories, the medical and marine campuses, and University hospital, and in municipal wastewater arriving at a Miami-Dade County wastewater treatment plant (Tierney et al., 2023). Using a metagenomics approach, Madhukar et al. (2023) detected *C. trachomatis* in wastewater collected from 16 of 17 open drainage sampling sites in an unidentified city in India.

DNA of *C. trachomatis* has also been detected in first void urine samples, with chlamydial loads of 156 – 2,515 copies/ml for men and 219 – 916 copies/ml for women (Wiggins et al., 2009). Bacterial loads in urine were found to be similar in symptomatic and asymptomatic women via counting of chlamydial elementary bodies (Thomas et al., 1998). Urine testing for chlamydia is routine[398,399,400] indicating it is a reliable source of biomarkers of infection.

6.2.7 Potential health hazard if present in wastewater

Given the bacteria is likely present in urine, where an infected individual urinates on a plane or at the airport there could be a potential hazard to people collecting or processing aircraft/airport wastewater samples, or to WWTP staff. However, given that chlamydia is not known to be transmitted via aerosols or droplets, transmission via contaminated wastewater is considered unlikely. Further research is needed to confirm this.

6.3 GONORRHOEA

6.3.1 Transmission

Gonorrhoea is a bacterial infection caused by the bacterium *Neisseria gonorrhoeae*[401]. Gonorrhoea can be transmitted by sexual contact and can be passed from mother to child during childbirth[401].

6.3.2 Prevention

No vaccine currently exists for gonorrhoea, although a vaccine against the closely related *Neisseria meningitidis* which causes meningitis appears to provide some “cross-protection” against gonorrhoea[402].

6.3.3 Geographical distribution

Gonorrhoea is the second most common bacterial STI and the WHO estimate that in 2020 there were 82.4 million new gonorrhoea infections globally[403].

[398] https://www.labtests.co.nz/for-patients/preparing-for-my-test/urine-collection-for-chlamydia-or-tb-testing/ Accessed 30 August 2023
[399] https://www.wellingtonscl.co.nz/for-patients/preparing-for-your-test/chlamydia-gonorrhoea-urine/ Accessed 30 August 2023
[400] https://www.nhs.uk/conditions/chlamydia/ Accessed 30 August 2023
[401] https://www.ecdc.europa.eu/en/gonorrhoea/facts. Accessed 30 August 2023
[402] https://www.rnz.co.nz/news/world/334916/nz-research-shows-promise-for-gonorrhoea-protection Accessed 30 August 2023
[403] https://www.who.int/news/item/22-11-2021-gonorrhoea-antimicrobial-resistance-results-and-guidance-vaccine-development Accessed 30 August 2023

6.3.4 New Zealand epidemiology

In New Zealand, gonorrhoea is a notifiable disease, although like HIV, AIDS and syphilis, the identifying information of the patient or deceased person is not notified[404]. Gonorrhoea case numbers for 2014 – 2022 are shown in Figure 77. Case counts were on the rise from 2014 – 2020, peaking at 7667 cases in 2020. Reported case numbers fell in 2021 to 6458, although this may be due to COVID-19 public health measures affecting access to healthcare and testing[405], with case numbers again increasing (to 6972) in 2022.

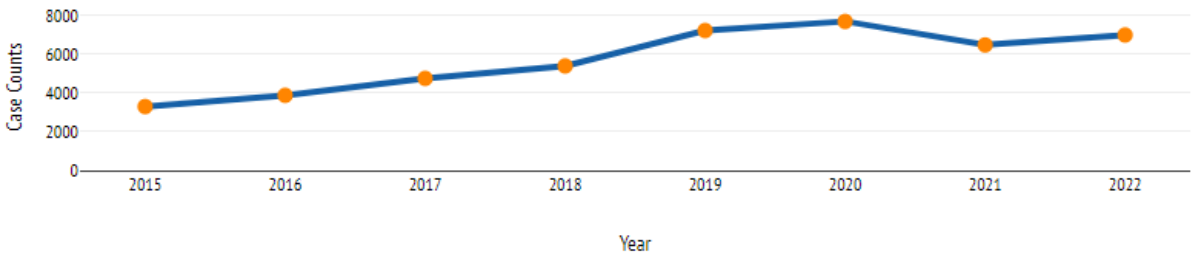

Figure 77 New Zealand national case counts for gonorrhoea 2014 – 2022

Reproduced from https://esr-cri.shinyapps.io/2022STIAnnualDashboard/. Accessed 8 April 2024

6.3.5 Symptoms

The incubation period for gonorrhoea is generally 2 – 7 days after exposure[406]. Approximately 10% of males and 50% of females infected with gonorrhoea are asymptomatic[407]. However, gonorrhoea can be spread even in the absence of symptoms[408], and people are considered potentially contagious until seven days after treatment[409]. Pregnant women can pass the infection to their baby during childbirth which may result in neonatal conjunctivitis that can cause scarring and blindness[410], and in some cases can cause meningitis and bacteraemia (bacterial infection of the bloodstream)[411].

Symptoms of gonorrhoea infection include thick yellow or green discharge from the penis or vagina, painful urination, and bleeding between periods[407]. In men, gonorrhoea can cause epididymitis (inflammation of the testicles close to where the sperm ducts are located), which if untreated can lead to infertility[412,413]. In women, untreated gonorrhoea can cause pelvic inflammatory disease, as discussed above.

[404] https://www.health.govt.nz/system/files/documents/pages/schedule-of-notifiable-diseases-updated-jun22.pdf Accessed 30 August 2023
[405] https://esr-cri.shinyapps.io/2022STIAnnualDashboard/ Accessed 8 April 2024
[406] https://www.health.vic.gov.au/infectious-diseases/gonorrhoea Accessed 30 August 2023
[407] https://www.nhs.uk/conditions/gonorrhoea/ Accessed 30 August 2023
[408] https://www.health.ny.gov/publications/3802.pdf Accessed 30 August 2023
[409] https://www.health.nsw.gov.au/Infectious/controlguideline/Pages/gonorrhoea.aspx Accessed 30 August 2023
[410] https://www3.paho.org/hq/index.php?option=com_content&view=article&id=14872:sti-gonorrhea&Itemid=0&lang=en Accessed 30 August 2023
[411] https://www.cdc.gov/conjunctivitis/newborns.html Accessed 30 August 2023
[412] https://www.cdc.gov/std/gonorrhea/stdfact-gonorrhea.htm Accessed 30 August 2023
[413] https://www.mayoclinic.org/diseases-conditions/gonorrhea/symptoms-causes/syc-20351774 Accessed 30 August 2023

6.3.6 Excretion of biomarkers of infection

Neisseria gonorrhoeae has been detected in municipal wastewater in China (Fu et al., 2022), Hong Kong (Li et al., 2015), India (Madhukar et al., 2023), Ohio, USA (Spurbeck et al., 2023) and Miami, USA (Tierney et al., 2023) using metagenomics approaches. It has also been detected in wastewater collected from various sites across the University of Miami, USA using metagenomics, including residential dormitories, the medical and marine campuses and the University hospital (Tierney et al., 2023). Urine is noted to be a suitable specimen for nucleic acid testing for gonorrhoea (Kacena et al., 1998; Ng & Martin, 2005) indicating it is a reliable source of biomarkers of infection.

6.3.7 Potential health hazard if present in wastewater

Given the bacteria is likely present in urine, where an infected individual urinates on a plane or at the airport there could be a potential hazard to people collecting or processing aircraft/airport wastewater samples, or to WWTP staff. However, given that gonorrhoea is not known to be transmitted via aerosols or droplets, transmission via contaminated wastewater is considered unlikely. Further research is needed to confirm this.

6.4 SYPHILIS

6.4.1 Transmission

Syphilis is a bacterial infection caused by the bacterium *Treponema pallidum*[414]. Syphilis can be transmitted through sexual contact, via blood transfusion or passed from a pregnant mother to her unborn foetus via the placenta[414].

6.4.2 Prevention

No vaccine currently exists for syphilis[415].

6.4.3 Geographical distribution

In 2020, an estimated 7.1 million adults (15 – 49 years) acquired syphilis globally[416].

6.4.4 New Zealand epidemiology

In New Zealand, infectious syphilis is a notifiable disease[417]. Case numbers for 2014 – 2022 are shown in Figure 78. Case counts were on the rise from 2014 – 2019, peaking at 723 cases in 2019. Reported case numbers fell in 2020 and 2021, although this may be due to COVID-19 public health measures affecting access to healthcare and testing, with a small increase observed in 2022[418].

[414] https://www.who.int/health-topics/syphilis Accessed 30 August 2023
[415] https://dermnetnz.org/topics/syphilis Accessed 30 August 2023
[416] https://www.who.int/news-room/fact-sheets/detail/syphilis Accessed 30 August 2023
[417] https://www.health.govt.nz/system/files/documents/pages/schedule-of-notifiable-diseases-updated-jun22.pdf Accessed 30 August 2023
[418] https://esr-cri.shinyapps.io/2022STIAnnualDashboard/ Accessed 8 April 2024

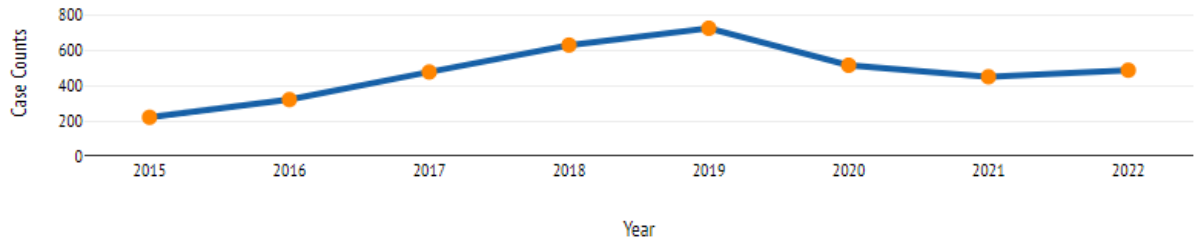

Figure 78 New Zealand national case counts for syphilis 2014 - 2022

Reproduced from https://esr-cri.shinyapps.io/2022STIAnnualDashboard/. Accessed 8 April 2024

6.4.5 Symptoms

The incubation period for syphilis is on average 21 days but can range from 10 – 90 days[419]. Most cases of syphilis are asymptomatic or display only mild symptoms. Where symptoms develop, they progress through a series of different stages over a course of weeks to years[419]. The primary stage starts with development of a chancre, or syphilitic sore, at the site where the bacteria entered the body[419]. Chancre are painless and appear round and often firm, with multiple sometimes developing[419]. These sores last for 3 – 6 weeks before healing regardless of any treatment[419]. However, if an infected person does not receive treatment during the primary stage, it will progress to the secondary stage[419]. In the secondary stage, skin rashes and/or lesions develop on the mucous membranes (e.g., mouth, vagina, anus), either while the primary chancre is healing or in the weeks after it has healed[419]. The rashes are generally non-itchy and may be very faint or similar to rashes caused by other illnesses[419]. Rough red (or reddish-brown) rashes may develop on the palms and soles of the feet[419]. Large, raised lesions (white or grey) may also develop in moist areas such as the groin, mouth and armpits[419]. Other symptoms of the secondary stage include headache, fatigue, muscle aches, sore throat, swollen lymph nodes, fever, weight loss and patchy hair loss[419]. Similar to the primary stage, these secondary stage symptoms will resolve regardless of treatment, but without treatment the disease will progress to the latent and potentially tertiary stage[419]. In the latent stage there are no obvious signs of infection, and this stage can last for many years but may progress to the rare tertiary stage anywhere from 10 – 30 years after the initial infection[419]. Tertiary syphilis may be fatal as it can affect multiple organs including the brain, heart, liver, bones, nerves, eyes, blood vessels and joints[419]. During any stage of the syphilis infection, the bacteria may invade the eyes (ocular syphilis), nervous system (neurosyphilis) or auditory and/or vestibular system (otosyphilis) [419].

Syphilis is particularly dangerous during pregnancy as it increases risk of stillbirth, or death soon after birth, with infant death occurring in up to 40% of pregnancies with undiagnosed syphilis[419].

[419] https://www.cdc.gov/std/syphilis/stdfact-syphilis-detailed.htm Accessed 30 August 2023

Syphilis is not contagious during the incubation period[420], but is very contagious during the primary and secondary stages, and sometimes during the early latent period[421] and people may remain infectious for up to 2 years[422].

6.4.6 Excretion of biomarkers of infection

Treponema pallidum has been detected in municipal wastewater in China using a metagenomics approach (Fu et al., 2022). *T. pallidum* DNA has also been detected in the urine of syphilis patients, with 14.9% (31/208) of patients having detectable DNA in their urinary supernatant and 24.2% (50/207) having detectable DNA in their urinary sediment (Wang et al., 2022). A similar study found 16% (4/25) of urine samples from syphilis patients had detectable *T. pallidum* DNA in their urine (Dubourg et al., 2015). In contrast to chlamydia and gonorrhoea, urinary tests are generally not used for diagnosis of syphilis[423].

6.4.7 Potential health hazard if present in wastewater

No information relating to potential transmission of syphilis via wastewater (e.g., while sampling, processing samples in the laboratory, or at the WWTP) was identified during preparation of this report. Given that syphilis is not transmitted via aerosols or droplets, transmission via contaminated wastewater is considered unlikely. However, further research is needed to confirm this.

[420] https://dph.illinois.gov/content/dam/soi/en/web/idph/files/publications/2018-ohp-syphilis-staging-and-treatment-2018-053018.pdf Accessed 30 August 2023
[421] https://www.mayoclinic.org/diseases-conditions/syphilis/symptoms-causes/syc-20351756 Accessed 30 August 2023
[422] https://www.nzshs.org/docman/guidelines/management-of-sexual-health-conditions/syphilis/175-syphilis-patient-information/file Accessed 30 August 2023
[423] https://ashs.org.nz/faqs/test-faqs/ Accessed 30 August 2023

7. RADIOACTIVE SUBSTANCES

The aim of this chapter is to evaluate whether WBS at the border could be used to monitor for international radiation contamination events that could pose a potential health hazard to aircraft passengers on the same flight as a contaminated individual, as well as to airline/airport staff, WWTP personnel and the general public in New Zealand, due to the excretion of radioisotope by internally contaminated individuals (e.g., in urine, faeces, saliva, sweat[424]). Numerous international events have led to internal contamination of individuals with radioisotopes, including the Chernobyl reactor core meltdown, Fukushima Daiichi nuclear power plant incident following the Tohoku earthquake and tsunami, the highly publicised 2006 polonium poisoning of Mr Alexander Litvinenko (Maguire et al., 2010), and several other incidents as summarised in Table 24. After all these incidents, the extent of internal radioisotope contamination in specific exposed populations was examined by measuring the level of selected radioisotopes in urine, suggesting that WBS could potentially be a viable approach for screening arrivals en masse for internal radioisotope contamination. However, an important caveat is that many radioisotopes are also used in medical diagnostics and radiotherapy, so detections may not necessarily be due to an environmental exposure event. Another important consideration is the logistics of monitoring for the huge variety of radioisotopes which individuals could be exposed to. As such, this section will focus on the feasibility of border WBS for the main radioisotopes released during previous major nuclear incidents (e.g., Chernobyl , Fukushima) – iodine-131, caesium-134, caesium-137 (McLaughlin et al., 2012)[425], as well as polonium-210 due to its role in the 2006 poisoning incident (Maguire et al., 2010).

7.1 IODINE-131

Iodine-131 (I-131) is an artificially generated radioisotope[426] with a physical half-life of 8.1 days (time taken for the quantity of radioisotope to decay by half) and a biological half-life of 138 days (time taken for half the amount of radionuclide to be expelled from the body)[427]. Iodine-131 decays to form the stable element xenon-131 via emission of a β-particle as well as several gamma rays (Mettler & Guiberteau, 2012). It is widely used in medicine, particularly for diagnosis and treatment of thyroid cancers[428]. Thus, detection of I-131 in aircraft/airport wastewater could be due to excretion by individuals administered this radioisotope for medical reasons. Demir et al. (2013) previously assessed urinary excretion of I-131 by cancer patients and found that 99% of administered I-131 was excreted within 5 days, relatively independently of the dose (based on assessment of 48 patients who received 3,700 MBq, 18 patients who received 5,550 MBq and 17 patients who received

[424] https://www.cancerresearchuk.org/about-cancer/treatment/radiotherapy/internal/safety Accessed 31 August 2023
[425] https://nuclearsafety.gc.ca/eng/resources/health/health-effects-chernobyl-accident.cfm Accessed 31 August 2023
[426] https://doh.wa.gov/sites/default/files/legacy/Documents/Pubs/320-085_i131_fs.pdf Accessed 31 August 2023
[427] https://dec.alaska.gov/eh/radiation/half-lives-explained/ Accessed 18 September 2023
[428] https://www.cdc.gov/nceh/radiation/emergencies/isotopes/iodine.htm Accessed 31 August 2023

Table 24 Summary of selected studies assessing accidental radiation exposure via urine and faeces

Year	Event	Country	Isotopes assessed	Sample type	Reference
1954	Fallout from the 1954 Bravo nuclear test at Bikini Atoll	Marshall Islands	^{131}I, ^{90}Sr, ^{239}Pu	Urine	Harris et al. (2010); Lessard et al. (1984)
1980s	Improper storage of a tritiated water sample which evaporated into the laboratory	China	^{3}H	Urine	Li et al. (2022)
1986	Chernobyl reactor core meltdown	Assessed exposure to fallout in Japan	^{131}I	Urine	Kawamura et al. (1988)
		Assessed exposure to fallout in North-East Italy	^{137}Cs	Urine	Capra et al. (1989)
1987	Removal of radioactive Cs-137 from a teletherapy machine in an abandoned private radiotherapy institute	Brazil	^{137}Cs	Urine and faeces	IAEA (1988)
2006	Polonium poisoning incident	United Kingdom	^{210}Po	Urine	Maguire et al. (2010)
2011	Nuclear incident at Fukushima Daiichi nuclear power plant following the Tohoku earthquake and subsequent tsunami	Japan	^{131}I, ^{134}Cs, ^{137}Cs	Urine	Kamada et al. (2012)

7,400 MBq) (Figure 79). This is despite the biological half-life of I-131 being much longer[429] and is due to the "combined action of radioactive decay and biological elimination" – in what is referred to as an effective half-life[430], with the effective half-life determined by Demir et al. (2013) being 18.7 ± 1.9 h within the first 24 hours after administration and 68.1 ± 6.2 between 48 and 120 h after administration (based on external dose measured using a Geiger–Muller probe). As such, detection of medically administered I-131 in aircraft wastewater is most likely to occur where passengers are travelling within 5 days of I-131 treatment.

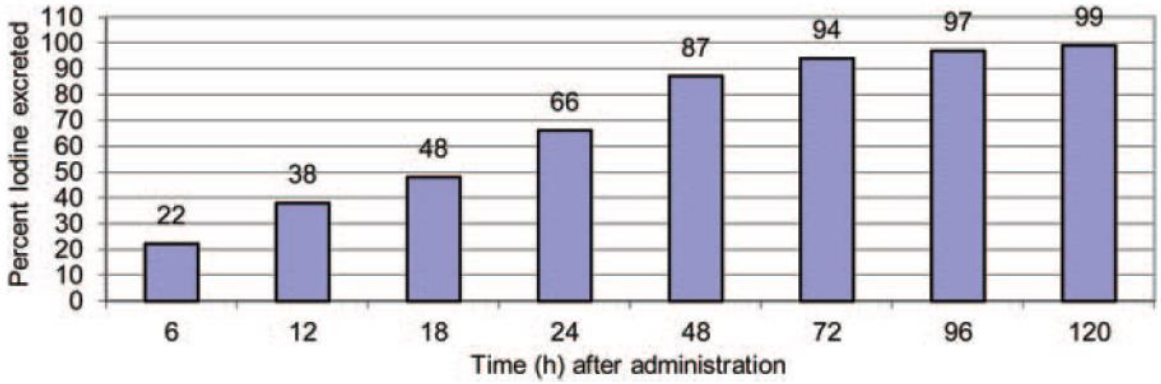

Figure 79 Excretion of iodine through the urinary tract by patients receiving radioiodine therapy

Reproduced from Demir et al. (2013).

Iodine-131 has been detected in urine from residents of the Marshall Islands who were exposed to radioactive fallout from the Bravo nuclear test at Bikini Atoll in March 1954 (Harris et al., 2010). It has also been detected in urine from Japanese individuals exposed to nuclear fallout from the Chernobyl reactor core meltdown (Kawamura et al., 1988) and the nuclear incident at the Fukushima Daiichi nuclear power plant following the Tohoku earthquake and subsequent tsunami (Kamada et al., 2012).

On 3 May 1986, radioactive fallout from the 26 April Chernobyl reactor core meltdown was detected in Ibaraki Prefecture on Honshu Island, Japan (Kawamura et al., 1988). Urine samples from 15 individuals living in this region collected between 4 – 29 May were screened for the presence of I-131 to assess radioisotope exposure (Kawamura et al., 1988). Concentrations ranged from < 0.2 – 7.6 Bq/L and likely correlated with consumption of leafy vegetables contaminated with radioactive fallout (Kawamura et al., 1988).

On 11 March 2011, a magnitude 9.0 earthquake struck 130 km off the coast of Japan, triggering a 15-metre tsunami which disabled the power supply and cooling to three nuclear reactors at the Fukushima Daiichi nuclear power plant, leading to meltdown of these reactors[431]. To assess radiation exposure by residents of two towns situated close to the

[429] https://dec.alaska.gov/eh/radiation/half-lives-explained/ Accessed 18 September 2023
[430] https://www.nrc.gov/reading-rm/basic-ref/glossary/effective-half-life.html Accessed 18 September 2023
[431] https://world-nuclear.org/information-library/safety-and-security/safety-of-plants/fukushima-daiichi-accident.aspx Accessed 18 September 2023

nuclear power plant (~ 37 km away), urine samples were collected from 15 individuals 54 and 78 – 85 days after the nuclear incident (Kamada et al., 2012). The level of I-131 detected ranged from < 0.33 Bq/L (the limit of detection) to 1.80 ± 0.50 Bq/L at day 54, and was not detectable in samples taken between days 78 - 85 (Kamada et al., 2012).

Although high levels of I-131 have been discharged to the environment in previous nuclear incidents (~1,760 PBq from Chernobyl) (McLaughlin et al., 2012; Steinhauser et al., 2014), given its relatively short half-life, it is only likely to be present in the environment (and therefore potentially present in urine of internally contaminated individuals) in the first two months after a contamination event (Drozdovitch, 2021).

Detection of I-131 in aircraft wastewater, could potentially provide an indication of a relatively recent contamination event. However, it is important to note that I-131 is known to adhere to surfaces, and given the high amounts excreted after medical administration this could potentially cause contamination of the aircraft wastewater collection system which would influence subsequent sampled for long periods. As such, this isotope is less ideal for monitoring using WBS.

7.2 CAESIUM-134

Caesium-134 has a physical half-life of 2 years and a biological half-life of 70 days[432]. Caesium-134 decays to form either xenon-134 or barium-134 (both of which are stable) via β and ɣ emission (Andersen, 2016). No evidence suggesting Cs-134 is used in medicine was identified during preparation of this report.

Caesium-134 has been detected in urine from residents living near the Fukushima Daiichi nuclear power plant following the 2011 nuclear reactor meltdown caused by the Tohoku earthquake and subsequent tsunami (Kamada et al., 2012). As noted above for I-131, urine samples were collected from 15 individuals living close to Fukushima 54 and 78 – 85 days after the nuclear incident (Kamada et al., 2012). The level of Cs-134 detected ranged from 0.32 ± 0.32 – 9.14 ± 0.93 Bq/L at day 54, and 0.24 ± 0.51 – 9.44 ± 0.64 Bq/L between days 78 - 85 (Kamada et al., 2012).

Given the majority of Cs-134 discharged to the environment by past nuclear incidents will have already decayed given its physical half-life of only 2 years, detection of Cs-134 in aircraft wastewater could be indicative of a relatively recent international radiation contamination event, which could pose a potential risk to other passengers, airline/airport staff, WWTP personnel and the general public due to excretion of radioisotope by the internally contaminated individuals.

7.3 CAESIUM-137

Caesium-137 has a physical half-life of 30 years and a biological half-life of 70 days[432]. It decays to form barium-137m via emission of β particles[433]. Barium-137m is short-lived and

[432] https://dec.alaska.gov/eh/radiation/half-lives-explained/ Accessed 18 September 2023
[433] https://semspub.epa.gov/work/HQ/176309.pdf Accessed 18 September 2023

decays to a stable form of barium via emission of ɣ radiation[434]. It has been noted by the CDC that "small quantities of Cs-137 can be found in the environment from nuclear weapons tests that occurred in the 1950s and 1960s and from nuclear reactor accidents, such as the Chernobyl power plant accident in 1986, which distributed Cs-137 to many countries in Europe"[435]. As such, "people are exposed to some Cs-137 every day" [435].

The level of urinary Cs-137 has been assessed following three radioactive incidents – radioactive fallout from the Chernobyl reactor core meltdown in the Pordenone region of North-Eastern Italy in 1986 (Capra et al., 1989), the nuclear incident at the Fukushima Daiichi nuclear reactor in 2011 (Kamada et al., 2012), and a radiological incident involving an abandoned teletherapy machine in Goiânia, Brazil in 1987 (IAEA, 1988).

The radioactive cloud from the 26 April 1986 Chernobyl reactor core meltdown arrived in Italy 4 days later, on 30 April (Capra et al., 1989). To assess internal contamination of residents living in North-Eastern Italy, urinary Cs-137 concentrations were measured for 198 residents of the Pordenone area for five months in 1987 (~ 10 samples every 10 days between July and December 1987) (Capra et al., 1989). Caesium-137 was chosen as the authors noted that urinary I-131 was no longer detectable 2 months after the incident and Cs-134 displayed greater uncertainty than Cs-137 (Capra et al., 1989). Levels of Cs-137 in the assessed urine samples ranged from 6 ± 1 – 21 ± 6 Bq/d for females (average 12 ± 6 Bq/d) and 8 ± 3 – 22 ± 11 Bq/d for males (average 15 ± 9 Bq/d) (Capra et al., 1989).

Caesium-137 has been detected in urine from residents living near the Fukushima Daiichi nuclear power plant following the 2011 nuclear reactor meltdown after the Tohoku earthquake and tsunami (Kamada et al., 2012). As noted for I-131, urine samples were collected from 15 individuals living near Fukushima 54 and 78 – 85 days after the incident (Kamada et al., 2012). The level of Cs-137 detected ranged from 0.13 ± 0.38 – 7.17 ± 1.20 Bq/L at day 54, and 0.45 ± 0.29 – 7.18 ± 0.71 Bq/L between days 78 - 85 (Kamada et al., 2012).

On 13 September 1987, two residents of the city of Goiânia, Brazil removed the rotating assembly from a teletherapy machine containing radioactive Cs-137 from an abandoned private radiotherapy institute (IGR, Institute Goiano de Radioterapia), resulting in their exposure to the radioisotope (IAEA, 1988). Over a period of a few days, one of the individuals proceeded to remove some of the radioactive source from its housing, resulting in contamination of his residence (IAEA, 1988). The rotating assembly was then sold to a junkyard and due to the blue light emanating from the radioactive source various people came to view it, and fragments of the radioactive source were distributed to several people, some of whom even applied it to their skin like glitter (IAEA, 1988). Some of the dismantled assembly was also sold to another junkyard (IAEA, 1988). After numerous people became sick, the incident was discovered on September 28 (IAEA, 1988). Over 200 people were found to be externally contaminated, and there were four deaths attributed to the incident (IAEA, 1988). To assess internal contamination, the concentration of Cs-137 in urine and faeces was measured, with >4,000 samples from 80 people analysed between October 1987 and January 1988 (IAEA, 1988).

[434] https://semspub.epa.gov/work/HQ/176309.pdf Accessed 18 September 2023
[435] https://www.cdc.gov/nceh/radiation/emergencies/isotopes/cesium.htm Accessed 18 September 2023

Given there is already Cs-137 in the environment from past environmental contamination events[436], it is expected that some background level of Cs-137 will likely be detectable in aircraft wastewater. However, were a new contamination event to take place, internally exposed individuals would likely be excreting much higher amounts which would result in a higher detection level in aircraft wastewater. Although Cs-137 is used in medical devices for cancer treatment, including brachytherapy[437] where a sealed radioactive implant is placed inside the body in or near a tumour[438], there is no evidence to suggest isotope is released from the implant or is excreted in urine and/or faeces. As such, it is unlikely that an increase in the level detected in aircraft wastewater would be due to a passenger having undergone medical treatment.

7.4 POLONIUM-210

Polonium-210 (Po-210) is a naturally occurring radioisotope with a physical half-life of ~140 days, biological half-life of ~50 days and effective half-life of ~40 days[439]. Polonium-210 is found naturally in soil at very low concentrations and is taken up by some plants and can become concentrated when those plants are smoked (e.g., tobacco) or consumed[440]. As such, there is generally a low level of background exposure to Po-210 present in the environment, with normal background urinary concentrations estimated to range from 5 – 15 mBq for a 24-hr urine sample (Maguire et al., 2010).

Polonium-210 has been detected in urine from several individuals likely contaminated during a poisoning incident in the United Kingdom. On 23 November 2006, Mr Alexander Litvinenko died in a London hospital from alleged Po-210 poisoning (Maguire et al., 2010). There were several locations identified as being potentially contaminated with Po-210 as a result of this incident, including hotels, restaurants, offices, bars and hospitals (Maguire et al., 2010). Over 1,000 residents of the United Kingdom were identified as having been at potentially contaminated locations, and 753 had their urine tested for Po-210 (Maguire et al., 2010). Of these 753 people, 139 had Po-210 levels above 30 mBq in a 24-hour sample, suggestive of likely internal contamination associated with the incident (Maguire et al., 2010). “Very low traces” of Po-210 were also found on two British Airways aircraft[441].

No information suggesting Po-210 is used in medical diagnostics or therapies was identified during preparation of this report. Given Po-210 is present in the environment at low levels[440], detection in aircraft wastewater may not necessarily be indicative of an international contamination event. However, if levels are monitored frequently, an increase in the level detected above “background” levels would likely be suggestive of the presence of an internally exposed individual, or individuals, on the associated flight.

[436] https://www.cdc.gov/nceh/radiation/emergencies/isotopes/cesium.htm Accessed 18 September 2023
[437] https://kskcancercenter.com/treatments_hdr_prostate Accessed 18 September 2023
[438] https://www.cancer.org/cancer/managing-cancer/treatment-types/radiation/internal-radiation-therapy-brachytherapy.html Accessed 18 September 2023
[439] https://www.cdc.gov/nceh/radiation/fallon/polonium_factsheet.pdf Accessed 31 August 2023
[440] https://www.cdc.gov/nceh/radiation/polonium-210.htm Accessed 20 September 2023
[441] https://www.theguardian.com/business/2006/nov/30/theairlineindustry.britishairways1 Accessed 13 June 2023

8. SUMMARY

Wastewater-based surveillance (WBS) is a useful tool for non-invasively screening arrivals at the New Zealand border en masse for a range of different biological and non-biological contaminants. A previous report prepared for the Ministry of Health assessed the logistics of conducting WBS at New Zealand's international airports, including sampling directly from inbound international aircraft and from airport wastewater networks. This current report extends this assessment by evaluating a wide range of different contaminants for their suitability for WBS.

Contaminants chosen for evaluation reflect both contaminants of international concern, as highlighted by the World Health Organization (WHO) and United States Centers for Disease Control and Prevention (CDC), and interests of the Ministry of Health.

Selected groups of contaminants included 14 vector-borne diseases (9 viral, 3 bacterial, 2 parasites), four viral haemorrhagic fevers, 12 vaccine preventable diseases (8 viral, 4 bacterial), four sexually transmitted diseases (1 viral, 3 bacterial), 9 other high-risk diseases (5 viral, 3 bacterial, 1 yeast), and 4 radiological contaminants. Table 25 summarises key information across the pathogenic diseases which impact on their suitability for WBS.

For biological contaminants, analysis included symptoms of infection, and whether asymptomatic infections have been reported; how the contaminant is spread, including whether person-to-person transmission is known; global distribution of the contaminant; prevalence of case notifications in New Zealand; whether biomarkers of infection are excreted in urine and/or faeces; any previous WBS studies; and whether the infectious agent has been isolated from urine and/or faeces and therefore may pose a potential health hazard to anyone exposed to wastewater containing this contaminant (e.g., sample collectors, laboratory staff, wastewater treatment plant personnel).

For only four of these diseases are 100% of cases symptomatic (ie no asymptomatic cases). Furthermore, for some of these diseases, asymptomatic yet infectious cases are common. Many of the diseases in this report are rare in New Zealand, and diagnosis of a symptomatic case may thus be delayed due to the inexperience of New Zealand clinicians with recognising signs and/or diagnosing the disease.

Climate change will increase the potential risks from vector-borne diseases in particular. While some of the vectors do exist in New Zealand, environmental monitoring for other vectors and the diseases they harbour should be an important surveillance tool.

There needs to be clearly understood and planned responses to the detection of these diseases or contaminants in wastewater. A starting point could be increased environmental surveillance, including municipal wastewater where appropriate, to understand the prevalence of any disease in Aotearoa. In addition, targeted communications with medical professionals, in terms of heightened awareness of diseases and how to recognise them, could be useful. Increasing public awareness, in terms of actions that could be taken by those affected or potentially at risk, may also be useful. Availability of treatments or vaccines therefore become important considerations.

The viral haemorrhagic fevers and other high-risk diseases are particular targets for bioterrorism. Incidents internationally may trigger panic or a need to standup rapid monitoring. Wastewater could be a particularly useful tool to assure the public and officials of the absence of disease due to its ability to screen large pools of individuals in a single sample. An incident within New Zealand could also potentially occur (for example deliberate release/spread of a contaminant by radical individuals), whereby wastewater could be useful to indicate the spread of any disease within New Zealand.

Many of these infectious organisms have been detected in wastewater (Table 26) using targeted PCR, metagenomics, microarrays, microfluidic chips or culture-based methods. This report has not evaluated the methodology for detection of each contaminant, although for most of these quantitative PCR or droplet digital PCR would be the most practical option.

This report also explored the potential of wastewater-based analysis for detection of radioactive substances. Given the huge variety of radioisotopes individuals may be exposed to precluding evaluation of all possibilities, this report focused on the main radioisotopes released during previous major nuclear incidents – iodine-131, caesium-134 and caesium-137; and polonium-210 due to its role in a high-profile poisoning incident in 2006.

The aim of this report was not to compare the merits of different surveillance methods for the various contaminants, or indeed to ascertain whether WBS is the best surveillance choice for a given contaminant, but rather to determine whether WBS may be suitable for a given contaminant based on the aforementioned characteristics.

Information identified in this report can be used to support the future development of a framework for guiding WBS at the border, which it is anticipated can be used to guide decision making in response to international outbreaks or contamination events involving not only the evaluated contaminants, but also other contaminants, including new/emerging contaminants, based on similarity to those assessed in this report.

9. GLOSSARY

Amastigote	Nonmotile, parasitic form in the life cycle of some protozoans (especially genus *Leishmania*) that usually develops in the cells of vertebrate hosts
Bacteraemia	Presence of bacteria in the blood
Biological half-life	Time taken for half the amount of radionuclide to be expelled from the body
Cirrhosis	Widespread disruption of normal liver structure by fibrosis and the formation of regenerative nodules that is caused by chronic progressive conditions affecting the liver
Effective half-life	Combined action of radioactive decay and biological elimination
Encephalitis	Inflammation of the brain that is caused especially by infection with a virus (such as herpes simplex or West Nile virus), or less commonly by bacterial or fungal infection or autoimmune reaction
Encephalomyelitis	Concurrent inflammation of the brain and spinal cord
Eschar	Dead tissue shed/cast off from the surface of the skin
Febrile	Marked or caused by fever; feverish
Macule	A patch of skin that is altered in colour but usually not elevated
Maculopapular	Combining the characteristics of macules and papules
Malaise	An indefinite feeling of debility or lack of health often indicative of or accompanying the onset of an illness
Meningitis	A disease marked by inflammation of the meninges that is either a relatively mild illness caused by a virus, or a more severe usually life-threatening illness caused by a bacterium
Meningoencephalitis	Inflammation of the brain and meninges
Metagenomics	The study of the structure and function of entire nucleotide sequences isolated and analyzed from all the organisms (typically microbes) in a bulk sample
Microcephaly	A condition of abnormal smallness of the circumference of the head that is present at birth or develops within the first few years of life
Myalgia	Pain in one or more muscles
Natural Foci	Combination of pathogen populations and the host/vectors that support their existence
Parotitis	Inflammation of the parotid glands

PCR (Polymerase Chain Reaction)

An *in vitro* technique for rapidly synthesizing large quantities of a given DNA segment to facilitate detection

Physical half-life Time taken for the quantity of radioisotope to decay by half

Perimyocarditis (Also myopericarditis)

Inflammation of both the myocardium and pericardium

Retrovirus Any of a family (*Retroviridae*) of single-stranded RNA viruses that produce reverse transcriptase by means of which DNA is produced using their RNA as a template and incorporated into the genome of infected cells

Septicaemia Invasion of the bloodstream by pathogenic agents and especially bacteria along with their toxins from a localized infection (as of the lungs or skin) that is accompanied by acute systemic illness

WWTP Wastewater treatment plant – the point at which municipal wastewater (sewage) is collected and treated (disinfected).

Zoonosis An infection or disease that is transmissible from animals to humans under natural conditions

Table 25 Summary of data for assessed biological contaminants.

Disease category	Pathogen type	Disease	Classification (family, genus)	Asymptomatic cases?	Transmitted person-to-person	Global distribution	Notified in New Zealand	Biomarker excretion urine/faeces	Detected in Wastewater	Infectious agent detected in urine/faeces
Vector-borne diseases	Virus	Dengue	*Flaviviridae, Flavivirus*	Yes (40-80%)	No	Tropics and subtropics, >100 countries	Yes; 222 in 2019	Yes	No	No
		Yellow fever	*Flaviviridae, Flavivirus*	Yes (majority)	No	Africa, Central and South America	Never	Yes	No	Yes
		Zika	*Flaviviridae, Flavivirus*	Yes (majority)	Yes	Americas, Africa, Asia	Yes; 7 in 2019	Yes	No	Yes
		Japanese encephalitis	*Flaviviridae, Flavivirus*	Yes (majority)	No	Asia, Oceania (incl. Australia)	Never	Yes	No	Yes
		West Nile fever	*Flaviviridae, Flavivirus*	Yes (approx. 80%)	No	Europe, Africa, Middle East, North America, west Asia, Australia	Never	Yes	No	Yes
		Rift Valley fever	*Bunyaviridae, Phlebovirus*	Yes (majority)	No	Africa, Middle East	Never	Yes	No	Yes
		Crimean-Congo Haemorrhagic fever	*Bunyaviridae, Nairovirus*	Yes (approx. 80%)	Yes	Africa, Asia, Balkans, Middle East	Never	Yes	No	No
		Chikungunya	*Togaviridae, Alphavirus*	Yes (3-28%)	No	Africa, Asia, Americas	Yes; 11 in 2019	Yes	Yes	No
		Ross River virus	*Togaviridae, Alphavirus*	Yes	No	Australia, Papua New Guinea	Yes; 5 in 2019	No info	No	No

Disease category	Pathogen type	Disease	Classification (family, genus)	Asymptomatic cases reported?	Transmitted person-to-person	Global distribution	Notified in New Zealand	Biomarker excretion urine/faeces	Detected using WBS	Infectious agent detected in urine/faeces
Vector-borne diseases	Bacteria	Plague	*Enterobacteriaceae, Yersinia*	No	Yes	All continents except Oceania	Yes, last case 1911	No info	Yes	No
		Epidemic typhus	*Rickettsiaceae, Rickettsia*	No info	No	Potentially worldwide	No cases since at least 1997	No	Yes	No
		Scrub typhus	*Rickettsiaceae, Orientia*	Yes	No	South and East Asia, Pacific Rim	Yes; none in 2019	No	No	No
		Murine typhus	*Rickettsiaceae, Ricketssia*	Yes	No	Worldwide	Yes; 3 in 2019	No	No	No
		Tularaemia	*Francisellaceae, Francisella*	Yes	No	Northern hemisphere, Australia	No info	No info	Yes	No
	Parasite	Malaria	*Plasmodiidae, Plasmodium*	Yes	No	Africa, Middle East, Central and South America, Asia	Yes; 27 in 2019	Yes	Yes*	No
		Leishmaniasis	*Trypanosomatidae, Leishmania*	Yes (20-60%)	Yes (some species)	Africa, Middle East, Central and South America, Europe	No info	Yes	No	Yes

Disease category	Pathogen type	Disease	Classification (family, genus)	Asymptomatic cases reported?	Transmitted person-to-person	Global distribution	Notified in New Zealand	Biomarker excretion urine/faeces	Detected using WBS	Infectious agent detected in urine/faeces
Viral haemorrhagic fevers	Virus	Lassa fever	*Arenaviridae, Mammarenavirus*	Yes (approx. 80%)	Yes	West Africa	Never	Yes	No	Yes
		Ebola	*Filoviridae, Ebolavirus*	Yes	Yes	Africa	Never	Yes	Yes^	Yes
		Marburg virus	*Filoviridae, Marburgvirus*	No	Yes	Sub-Saharan Africa	Never	Yes[#]	No	No
		Hantavirus	*Bunyavirus, Hantavirus*	Yes	No	Americas (HPS); Europe and Asia (HFRS)	Never	Yes	No	Yes
Other high-risk diseases	Virus	Smallpox	*Poxviridae, Orthopoxvirus*	No	Yes	Eradicated	Eradicated	No info	No	Yes
		Monkeypox	*Poxviridae, Orthopoxvirus*	Yes	Yes	Africa; 2022/23 outbreak in non-endemic countries	Yes, 41 cases as of June 2023	Yes	Yes	No
		Nipah virus	*Paramyxoviridae, Henipavirus*	Yes	Yes	Bangladesh, India, Malaysia, Singapore, Philippines	Never	Yes	No	Yes
		Hendra virus	*Paramyxoviridae, Henipavirus*	No info	No	Australia	Never	No info	No	No
		MERS	*Coronaviridae, Betacoronavirus*	Yes	Yes	Middle East	Never	Yes	No	No

Disease category	Pathogen type	Disease	Classification (family, genus)	Asymptomatic cases reported?	Transmitted person-to-person	Global distribution	Notified in New Zealand	Biomarker excretion urine/faeces	Detected using WBS	Infectious agent detected in urine/faeces
Other high-risk diseases	Bacteria	Anthrax	*Bacillaceae, Bacillus*	Yes (gastrointestinal form)	No	Almost worldwide	Yes, last case in 1940	No info	Yes	Yes
		Tuberculosis	*Mycobacteriaceae, Mycobacterium*	Yes	Yes	Worldwide	Yes; 317 in 2019	Yes	Yes	Yes
		Leprosy	*Mycobacteriaceae, Mycobacterium*	Yes[+]	Yes (prolonged contact)	Most common in Africa, Asia, South and Central America	Yes; 6 in 2019	Yes	No	Yes
	Yeast	Candida auris	*Metschnikowiaceae, Candida*	Yes	Yes	Almost worldwide	Yes, single imported case	Yes[@]	Yes	Yes
Vaccine-preventable diseases	Virus	Measles	*Paramyxoviridae, Morbillivirus*	No	Yes	Worldwide	Yes; 2,190 in 2019	Yes	Yes	Yes
		Mumps	*Paramyxoviridae, Paramyxovirus*	Yes (at least 30%)	Yes	Worldwide	Yes; 264 in 2019	Yes	Yes	Yes
		Rubella	*Matonaviridae, Rubivirus*	Yes (25-50%)	Yes	Worldwide	Yes; 2 in 2019	Yes	Yes	Yes
		Hepatitis A	*Picornaviridae, Hepatovirus*	Yes	Yes	Worldwide	Yes; 58 in 2019	Yes	Yes	Yes
		Hepatitis B	*Hepadnaviridae, Orthohepadnavirus*	Yes	Yes	Worldwide	Yes; 28 in 2019	Yes	Yes	No
		Hepatitis C	*Flaviviridae, Hepacivirus*	Yes	Yes	Worldwide	Yes; 24 in 2019	Yes	Yes	Yes
		Hepatitis D	Unknown, *Deltavirus*	Yes (majority)	Yes	Worldwide	Yes; 6 in 2019	No info	Yes	No
		Hepatitis E	*Hepeviridae, Orthohepevirus*	Yes	No (faecal-oral)	Worldwide	Yes; 3 in 2019	Yes	Yes	Yes

Disease category	Pathogen type	Disease	Classification (family, genus)	Asymptomatic cases reported?	Transmitted person-to-person	Global distribution	Notified in New Zealand	Biomarker excretion urine/faeces	Detected using WBS	Infectious agent detected in urine/faeces
Vaccine-preventable diseases	Bacteria	Pneumococcal disease	*Streptococcaceae, Streptococcus*	Yes	Yes	Worldwide	Yes; 495 in 2019	Yes	Yes	Yes
		HIB	*Pasteurellaceae, Haemophilus*	Yes	Yes	Worldwide	Yes; 2 in 2019	No info	Yes	Yes
		Diphtheria	*Corynebacteriaceae, Corynebacterium*	Yes	Yes	Worldwide	Yes; 1 in 2019	No info	Yes	No
		Pertussis	*Alcaligenaceae, Bordetella*	Yes	Yes	Worldwide	Yes; 1,206 in 2016	No info	Yes	No
Sexually-transmitted infections	Virus	HIV	*Retroviridae, Lentivirus*	Yes~	Yes	Worldwide	Yes; 135 new cases in 2022	Yes	Yes	No
	Bacteria	Chlamydia	*Chlamydieceae, Chlamydia*	Yes (majority)	Yes	Worldwide	Yes; >32,000 in 2019	Yes	Yes	No
		Gonorrhoea	*Neisseriaceae, Neisseria*	Yes (approx. 10% of males, 50% of females)	Yes	Worldwide	Yes; 7,200 in 2019	No info	Yes	No
		Syphilis	*Spirochaetaceae, Treponema*	Yes (majority)	Yes	Worldwide	Yes; 723 in 2019	Yes	Yes	No

**Plasmodium* detected but unclear if it is a species which causes malaria in humans; ^single hit to Ebola virus from metagenomic analysis of wastewater in Uganda but not confirmed by PCR; [#]virus detected in urine using immunofluorescence; [+]incubation period may be up to 20 years or more; [@]bacterial isolation not DNA biomarkers; ~asymptomatic phase can last for several years before symptoms develop.

APPENDIX

Table 26 Summary of pathogens detected by wastewater-based surveillance

Family	Name	Disease	Countries	Techniques	References
Viruses					
Adenoviridae	Adenovirus (multiple types)		Australia, Egypt, France, Kenya, Norway, Singapore, Sweden, Uganda, United States, Wales (UK)	Targeted PCR, microarray	Allayeh et al. (2022); Aw and Gin (2010); Bisseux et al. (2018); Elmahdy et al. (2019); Farkas et al. (2018); Grøndahl-Rosado et al. (2014); Hellmér et al. (2014); Kiulia et al. (2010); Lun et al. (2019); McCall et al. (2020); O'Brien et al. (2017); Prevost et al. (2015); Wang et al. (2020); Wong et al. (2013)
Astroviridae	Astrovirus (multiple genotypes)		China, France, India, Kenya, Singapore, Sweden, Uganda, United States	Targeted PCR, metagenomics, microarray	Aw and Gin (2010); Hellmér et al. (2014); Kiulia et al. (2010); O'Brien et al. (2017); Prevost et al. (2015); Stockdale et al. (2023); Wang et al. (2020); Wong et al. (2013);

Family	Name	Disease	Countries	Techniques	References
					Zhou et al. (2016); Zhou et al. (2014)
Caliciviridae	Norovirus (multiple strains)		Austria, Brazil, China, France, India, Italy, Japan, Kenya, Norway, Singapore, South Africa, Sweden, Tunisia, United States, Wales (UK)	Targeted PCR, targeted NGS, microfluidic chip, microarray, metagenomics	Aw and Gin (2010); Bisseux et al. (2018); Farkas et al. (2018); Fioretti et al. (2018); Fu et al. (2022); Fumian et al. (2019); Grøndahl-Rosado et al. (2014); Hassine-Zaafrane et al. (2014); Hellmér et al. (2014); Kazama et al. (2016); Kazama et al. (2017); Kiulia et al. (2010); La Rosa et al. (2010); Mabasa et al. (2018); Markt et al. (2023); McCall et al. (2020); Prevost et al. (2015); Stockdale et al. (2023); Tao et al. (2015); Wang et al. (2020); Wong et al. (2013)
	Sapovirus		Brazil, China, India, Kenya, Sweden, United Kingdom, United States	Targeted PCR, microarray, microfluidic chip, metagenomics	Farkas et al. (2018); Fioretti et al. (2016); Fu et al. (2022); Kiulia et al. (2010); McCall et al. (2020); Stockdale et al.

Family	Name	Disease	Countries	Techniques	References
					(2023); Wang et al. (2020); Wong et al. (2013)
Circoviridae	Circovirus		Uganda	Metagenomics	O'Brien et al. (2017)
	Torque teno virus		Uganda	Metagenomics	O'Brien et al. (2017)
Coronaviridae	Coronavirus (multiple types)		China	Targeted PCR, microfluidic chip	Fu et al. (2022)
	Seasonal coronaviruses		United States	Targeted PCR	Boehm et al. (2023)
	Torovirus		United States	Targeted PCR	Wong et al. (2013)
Deltaviridae	Hepatitis D		China	Microfluidic chip	Fu et al. (2022)
Filoviridae	Ebola virus		Uganda	Metagenomics	O'Brien et al. (2017)
Flaviviridae	Cacipacore virus		Uganda	Metagenomics	O'Brien et al. (2017)
	Hepatitis C		India, United States	Metagenomics	McCall et al. (2020); Stockdale et al. (2023)
Hepadnaviridae	Hepatitis B		China	Targeted PCR, microfluidic chip	Fu et al. (2022)
Hepeviridae	Hepatitis E		Argentina, China, France, Germany, Israel, Italy, Sweden, United States	Targeted PCR, metagenomics, microarray, microfluidic chip	Alfonsi et al. (2018); Beyer et al. (2020); Bisseux et al. (2018); Fantilli et al. (2023); Fu et al. (2022); Hellmér et al. (2014); Iaconelli et al. (2020); Ram et al. (2016); Wang et al. (2020); Wassaf et al. (2014); Wong et al. (2013)

Family	Name	Disease	Countries	Techniques	References
Herpesviridae	Kaposi sarcoma herpesvirus (herpesvirus 8)		United States	Targeted PCR	McCall et al. (2020)
	Roseola (herpesvirus 6)		United States	Targeted PCR	McCall et al. (2020)
Orthomyxoviridae	Influenza A		Austria, China, India, United States	Targeted PCR, microfluidic chip, metagenomics	Boehm et al. (2023); Fu et al. (2022); Markt et al. (2023); Stockdale et al. (2023); Wolfe, Duong, Bakker, et al. (2022); Wolken et al. (2023)
	Influenza B		China, United States	Targeted PCR, microfluidic chip	Boehm et al. (2023); Fu et al. (2022)
Papillomaviridae	Human papillomavirus	HPV	Uganda	Metagenomics	O'Brien et al. (2017)
Paramyxovirus	Measles	Measles	India, Netherlands, United Kingdom	Targeted PCR, metagenomics	Benschop et al. (2017); Kasprzyk-Hordern et al. (2023); Stockdale et al. (2023)
	Parainfluenza viruses		China, United States	Targeted PCR, microfluidic chip	Boehm et al. (2023); Fu et al. (2022)
Parvoviridae	Human bocavirus		Egypt	Targeted PCR	Shaheen et al. (2019)
Picobirnaviridae	Picobirnavirus		Uganda	Metagenomics	O'Brien et al. (2017)
Picornaviridae	Aichi virus		Egypt, France, India, Sweden	Targeted PCR, metagenomics	Hellmér et al. (2014); Prevost et al. (2015); Shaheen et al. (2019); Stockdale et al. (2023); Wang et al. (2020)
	Cosavirus		France	Targeted PCR	Prevost et al. (2015)

Family	Name	Disease	Countries	Techniques	References
	Coxsackievirus 16	Hand, foot and mouth disease	China	Targeted PCR, microfluidic chip	Fu et al. (2022)
	Encephalomyocarditis virus		India	Metagenomics	Stockdale et al. (2023)
	Enteroviruses (multiple serotypes)		China, France, Italy, Singapore, Sweden, Uganda, United States	Targeted PCR, microarray, microfluidic chip	Aw and Gin (2010); Bisseux et al. (2018); Fu et al. (2022); O'Brien et al. (2017); Pellegrinelli et al. (2019); Prevost et al. (2015); Wang et al. (2020); Wong et al. (2013)
	Hepatitis A		Argentina, China, France, Italy, Kenya, Singapore, Sweden, Tunisia, Uganda, United States	Targeted PCR, microfluidic chip	Aw and Gin (2010); Béji-Hamza et al. (2014); Bisseux et al. (2018); Fantilli et al. (2023); Fu et al. (2022); (Gharbi-Khelifi et al., 2007); Hellmér et al. (2014); Kiulia et al. (2010); La Rosa et al. (2014); McCall et al. (2020); O'Brien et al. (2017); Pellegrinelli et al. (2019); Wang et al. (2020); Yanez et al. (2014)
	Parechovirus (multiple types)		France, Japan, Netherlands,	Targeted PCR	Abe et al. (2016); Bisseux et al. (2018);

Family	Name	Disease	Countries	Techniques	References
			Scotland (UK), Sweden		Harvala et al. (2014); Lodder et al. (2013); Wang et al. (2020)
	Poliovirus	Polio	Israel	Targeted PCR	Weil et al. (2023)
	Rhinovirus		China, United States	Targeted PCR, microfluidic chip	Boehm et al. (2023); Fu et al. (2022)
	Salivirus		France, India	Targeted PCR, metagenomics	Prevost et al. (2015); Stockdale et al. (2023)
	Saffold virus		India, Italy	Targeted PCR, metagenomics	Bonanno Ferraro et al. (2020); Stockdale et al. (2023)
Pneumoviridae	Respiratory syncytial virus (RSV) A and B		United States	Targeted PCR	Boehm et al. (2023)
	Metapneumovirus		United States	Targeted PCR	Boehm et al. (2023)
Polyomaviridae	Polyomaviruses (multiple types)		Argentina, United States, Wales (UK)	Targeted PCR, microarray	Farkas et al. (2018); Torres et al. (2016); Wong et al. (2013)
Poxviridae	Monkeypox		France, Italy, Netherlands, Poland, United States	Targeted PCR	de Jonge et al. (2022); Gazecka et al. (2023); La Rosa et al. (2023); Sharkey et al. (2023); Sherchan et al. (2023); Wolfe, Duong, Hughes, et al. (2022); Wurtzer et al. (2022)
	Tanapox		China, Uganda	Targeted PCR, metagenomics	Fu et al. (2022); O'Brien et al. (2017)
Reoviridae	Rotavirus		Argentina, Brazil, China, France,	Targeted PCR, metagenomics	Barril et al. (2015); Bisseux et al. (2018);

Family	Name	Disease	Countries	Techniques	References
			India, Japan, Kenya, Iran, Italy, Nigeria, Sweden, Tunisia, Uganda, United States		Fumian et al. (2011); Hassine-Zaafrane et al. (2015); Hellmér et al. (2014); Kargar et al. (2013); Kiulia et al. (2010); Kumazaki and Usuku (2015); Li et al. (2011); Motayo et al. (2016); O'Brien et al. (2017); Prevost et al. (2015); Ruggeri et al. (2015); Stockdale et al. (2023); Wang et al. (2020); Wong et al. (2013)
Retroviridae	Human immunodeficiency virus	HIV	United States	Targeted PCR	Terwilliger et al. (2022)
Rhabdoviridae	Rabies virus	Rabies	India	Metagenomics	Stockdale et al. (2023)
Rubulaviridae	Mumps virus	Mumps	China	Targeted PCR, microfluidic chip	Fu et al. (2022)
Togaviridae	Chikungunya	Chikungunya	India	Metagenomics	Stockdale et al. (2023)
Unclassified	Jingmen tick virus		India	Metagenomics	Stockdale et al. (2023)
	Husavirus		India	Metagenomics	Stockdale et al. (2023)
Bacteria					
Family	**Name**	**Disease**	**Countries detected**	**Techniques**	**References**
Acidaminococcaceae	*Acidaminococcus fermentans*		Hong Kong	Metagenomics	Li et al. (2015)

Family	Name	Disease	Countries	Techniques	References
Actinomycetaceae	*Actinomyces graevenitzii*	Actinomycosis	United States	NGS panel	Spurbeck et al. (2023)
	Actinomyces odontolyticus		Hong Kong	Metagenomics	Li et al. (2015)
Aerococcaceae	*Abiotrophia defectiva*		Hong Kong	Metagenomics	Li et al. (2015)
	Aerococcus viridans		Hong Kong	Metagenomics	Li et al. (2015)
Aeromonadaceae	*Aeromonas caviae*		China, United States	Metagenomics, NGS panel	Fu et al. (2022); Spurbeck et al. (2023)
	Aeromonas enteropelogenes		China	Metagenomics	Fu et al. (2022)
	Aeromonas hydrophila		China, Hong Kong, United States	Metagenomics, NGS panel	Fu et al. (2022); Li et al. (2015); Spurbeck et al. (2023)
	Aeromonas media		China	Metagenomics	Fu et al. (2022)
	Aeromonas salmonicida		China	Metagenomics	Fu et al. (2022)
	Aeromonas sobria		United States	NGS panel	Spurbeck et al. (2023)
	Aeromonas veronii		China, United States	Metagenomics, NGS panel	Fu et al. (2022); Spurbeck et al. (2023)
Alcaligenaceae	*Bordetella pertussis*	Whooping cough	China, United States	Metagenomics	Fu et al. (2022); Spurbeck et al. (2023); Tierney et al. (2023)
Bacillaceae	*Bacillus anthracis*	Anthrax	Hong Kong, United States	Metagenomics	Li et al. (2015); Spurbeck et al. (2023)
	Bacillus cereus		Hong Kong, China	Metagenomics	Fu et al. (2022); Li et al. (2015)
	Bacillus pumilus		Hong Kong	Metagenomics	Li et al. (2015)
	Bacillus subtilis		Hong Kong	Metagenomics	Li et al. (2015)
	Bacillus thuringiensis		Hong Kong	Metagenomics	Li et al. (2015)

Family	Name	Disease	Countries	Techniques	References
Bacteroidaceae	*Bacteroides caccae*		Hong Kong	Metagenomics	Li et al. (2015)
	Bacteroides eggerthii		Hong Kong	Metagenomics	Li et al. (2015)
	Bacteroides fragilis		Hong Kong, United States	Metagenomics, NGS panel	Li et al. (2015); Spurbeck et al. (2023)
	Bacteroides ovatus		Hong Kong	Metagenomics	Li et al. (2015)
	Bacteroides pectinophilus		Hong Kong	Metagenomics	Li et al. (2015)
	Bacteroides stercoris		Hong Kong	Metagenomics	Li et al. (2015)
	Bacteroides thetaiotaomicron		Hong Kong	Metagenomics	Li et al. (2015)
	Bacteroides uniformis		Hong Kong	Metagenomics	Li et al. (2015)
	Bacteroides vulgatus		Hong Kong	Metagenomics	Li et al. (2015)
Bartonellaceae	*Bartonella quintana*	Trench fever	United States	Metagenomics	Tierney et al. (2023)
Bifidobacteriaceae	*Bifidobacterium dentium*		Hong Kong	Metagenomics	Li et al. (2015)
	Gardnerella vaginalis		Hong Kong	Metagenomics	Li et al. (2015)
Brucellaceae	*Brucella abortus*	Brucellosis	China, United States	Metagenomics	Fu et al. (2022); Spurbeck et al. (2023)
	Brucella suis	Brucellosis	United States	Metagenomics	Spurbeck et al. (2023)
	Ochrobactrum anthropi		Hong Kong, United States	Metagenomics, NGS panel	Li et al. (2015); Spurbeck et al. (2023)
Burkholderiaceae	*Burkholderia cepacia*		United States	NGS panel	Spurbeck et al. (2023)
	Burkholderia mallei	Glanders disease	United States	Metagenomics	Spurbeck et al. (2023); Tierney et al. (2023)
	Burkholderia pseudomallei	Melioidosis	United States	Metagenomics	Spurbeck et al. (2023)
Campylobacteraceae	*Campylobacter concisus*		China	Metagenomics	Fu et al. (2022)

Family	Name	Disease	Countries	Techniques	References
	Campylobacter jejuni		China, United States	Metagenomics	Fu et al. (2022); Tierney et al. (2023)
Chlamydiaceae	*Chlamydia trachomatis*	Chlamydia	United States	Targeted PCR	Chin Quee (2023); Tierney et al. (2023)
Clostridiaceae	*Clostridium botulinum*	Botulism	United States	Metagenomics	Spurbeck et al. (2023)
	Clostridium chauvoei		United States	Metagenomics	Tierney et al. (2023)
	Clostridium difficile		Hong Kong	Metagenomics	Li et al. (2015)
	Clostridium perfringens		Hong Kong	Metagenomics	Li et al. (2015)
	Clostridium tetani	Tetanus	United States	Metagenomics	Spurbeck et al. (2023)
Comamonadaceae	*Comamonas testosteroni*		Hong Kong	Metagenomics	Li et al. (2015)
	Delftia acidovorans		United States	NGS panel	Spurbeck et al. (2023)
Coriobacteriaceae	*Collinsella aerofaciens*		Hong Kong	Metagenomics	Li et al. (2015)
	Eggerthella lenta		Hong Kong	Metagenomics	Li et al. (2015)
Corynebacteriaceae	*Corynebacterium diphtheriae*	Diphtheria	United States	Metagenomics	Spurbeck et al. (2023); Tierney et al. (2023)
Coxiellaceae	*Coxiella burnetii*	Q fever	United States	Metagenomics	Spurbeck et al. (2023)
Desulfovibrionaceae	*Bilophila wadsworthia*		Hong Kong	Metagenomics	Li et al. (2015)
Enterobacteriaceae	*Arcobacter butzleri*		Hong Kong	Metagenomics	Li et al. (2015)
	Citrobacter freundii		United States	NGS panel	Spurbeck et al. (2023)
	Citrobacter koseri		Hong Kong	Metagenomics	Li et al. (2015)
	Cronobacter sakazakii		United States	NGS panel	Spurbeck et al. (2023)
	Enterobacter cancerogenus		Hong Kong	Metagenomics	Li et al. (2015)
	Enterobacter cloacae		United States	NGS panel	Spurbeck et al. (2023)

Family	Name	Disease	Countries	Techniques	References
	Escherichia coli		China, Hong Kong, Sweden, United States	Targeted PCR, NGS panel, metagenomics, bacterial isolation	Fu et al. (2022); Hutinel et al. (2019); Li et al. (2015); Spurbeck et al. (2023); Tierney et al. (2023); Yang et al. (2014)
	Klebsiella aerogenes		United States	NGS panel	Spurbeck et al. (2023)
	Klebsiella oxytoca		China, United States	Metagenomics, NGS panel	Fu et al. (2022); Spurbeck et al. (2023)
	Klebsiella pneumoniae		China, Hong Kong, United States	Metagenomics, NGS panel	Fu et al. (2022); Li et al. (2015); Spurbeck et al. (2023)
	Klebsiella quasipneumoniae		United States	NGS panel	Spurbeck et al. (2023)
	Klebsiella variicola		United States	NGS panel	Spurbeck et al. (2023)
	Leclercia adecarboxylata		United States	NGS panel	Spurbeck et al. (2023)
	Pantoea agglomerans		United States	NGS panel	Spurbeck et al. (2023)
	Raoultella ornithinolytica		United States	NGS panel	Spurbeck et al. (2023)
	Salmonella enterica	Salmonellosis	China, United States	Targeted PCR, Metagenomics, NGS	Diemert and Yan (2019); Fu et al. (2022); Spurbeck et al. (2023); Vincent et al. (2007); Yan et al. (2018)
	Serratia marcescens		United States	NGS panel	Spurbeck et al. (2023)
	Shigella boydii		Hong Kong	Metagenomics	Li et al. (2015)
	Shigella dysenteriae		Hong Kong	Metagenomics	Li et al. (2015)

Family	Name	Disease	Countries	Techniques	References
	Shigella flexneri		China, Hong Kong	Metagenomics	Fu et al. (2022); Li et al. (2015)
	Shigella sonnei		China, Hong Kong, United States	Metagenomics	Fu et al. (2022); Li et al. (2015); Tierney et al. (2023)
	Yersinia enterocolitica		China, United States	NGS panel, metagenomics	Fu et al. (2022); Spurbeck et al. (2023)
	Yersinia pestis	Plague	United States	Metagenomics	Spurbeck et al. (2023)
	Yersinia pseudotuberculosis		China	Metagenomics	Fu et al. (2022)
	Yersinia ruckeri		United States	Metagenomics	Tierney et al. (2023)
Enterococcaceae	*Enterococcus casseliflavis*		Hong Kong, South Africa	Metagenomics, Targeted PCR	Adegoke et al. (2022); Li et al. (2015)
	Enterococcus cecorum		South Africa	Targeted PCR	Adegoke et al. (2022)
	Enterococcus durans		South Africa	Targeted PCR	Adegoke et al. (2022)
	Enterococcus faecalis		Hong Kong, South Africa, United States	Metagenomics, targeted PCR, NGS panel	Adegoke et al. (2022); Li et al. (2015); Spurbeck et al. (2023)
	Enterococcus faecium		Hong Kong, South Africa, United States	Targeted PCR, NGS panel, metagenomics	Adegoke et al. (2022); Li et al. (2015); Spurbeck et al. (2023); Tierney et al. (2023)
	Enterococcus gallinarum		Hong Kong	Metagenomics	Li et al. (2015)
	Enterococcus hirae		South Africa	Targeted PCR	Adegoke et al. (2022)
Eubacteriaceae	*Eubacterium limosum*		Hong Kong	Metagenomics	Li et al. (2015)
	Eubacterium rectale		Hong Kong	Metagenomics	Li et al. (2015)
Francisellaceae	*Francisella tularensis*	Tularemia	United States	Metagenomics	Spurbeck et al. (2023); Tierney et al. (2023)

Family	Name	Disease	Countries	Techniques	References
Fusobacteriaceae	*Fusobacterium mortiferum*		Hong Kong	Metagenomics	Li et al. (2015)
	Fusobacterium nucleatum		Hong Kong	Metagenomics	Li et al. (2015)
	Fusobacterium ulcerans		Hong Kong	Metagenomics	Li et al. (2015)
	Fusobacterium varium		Hong Kong	Metagenomics	Li et al. (2015)
Gordoniaceae	*Gordonia bronchialis*		Hong Kong, United States	Metagenomics, NGS panel	Li et al. (2015); Spurbeck et al. (2023)
Helicobacteraceae	*Helicobacter pylori*		United States	Metagenomics	Tierney et al. (2023)
Lactobacillaceae	*Pediococcus acidilactici*		United States	NGS panel	Spurbeck et al. (2023)
Legionellaceae	*Legionella pneumophila*	Legionnaire's disease	China, United States	Metagenomics	Fu et al. (2022); Spurbeck et al. (2023); Tierney et al. (2023)
Leptospiraceae	*Leptospira interrogans*	Leptospirosis	United States	Metagenomics	Tierney et al. (2023)
	Leptospira wolffii		China	Metagenomics	Fu et al. (2022)
Leptotrichiaceae	*Sebaldella termitidis*		Hong Kong	Metagenomics	Li et al. (2015)
Listeriaceae	*Listeria monocytogenes*	Listeriosis	United States	Metagenomics	Spurbeck et al. (2023)
Micrococcaceae	*Rothia dentocariosa*		Hong Kong	Metagenomics	Li et al. (2015)
	Rothia mucilaginosa		United States	NGS panel	Spurbeck et al. (2023)
Moraxellaceae	*Moraxella osloensis*		United States	NGS panel	Spurbeck et al. (2023)
	Actinobacter baumannii		China, Hong Kong, United States	Metagenomics, NGS panel	Fu et al. (2022); Li et al. (2015); Spurbeck et al. (2023)
	Actinobacter calcoaceticus		China	Metagenomics	Fu et al. (2022)

Family	Name	Disease	Countries	Techniques	References
	Actinobacter haemolyticus		China, Hong Kong	Metagenomics	Fu et al. (2022); Li et al. (2015)
	Actinobacter johnsonii		China, Hong Kong	Metagenomics	Fu et al. (2022); Li et al. (2015)
	Actinobacter junii		China, Hong Kong	Metagenomics	Fu et al. (2022); Li et al. (2015)
	Acinetobacter lwoffii		Hong Kong, United States	Metagenomics, NGS panel	Li et al. (2015); Spurbeck et al. (2023)
	Acinetobacter pittii		China, United States	Metagenomics, NGS panel	Fu et al. (2022); Spurbeck et al. (2023)
	Acinetobacter radioresistens		Hong Kong	Metagenomics	Li et al. (2015)
Morganellaceae	*Morganella morganii*		United States	NGS panel	Spurbeck et al. (2023)
Mycobacteriaceae	*Mycobacterium africanum*	Tuberculosis	South Africa	Targeted PCR	Mtetwa et al. (2022a)
	Mycobacterium avium	MAC lung disease	Hong Kong, United States	Metagenomics, NGS panel	Li et al. (2015); Spurbeck et al. (2023)
	Mycobacterium fortuitum		United States	NGS panel	Spurbeck et al. (2023)
	Mycobacterium gordonae		United States	NGS panel	Spurbeck et al. (2023)
	Mycobacterium marinum		Hong Kong	Metagenomics	Li et al. (2015)
	Mycobacterium smegmatis		Hong Kong	Metagenomics	Li et al. (2015)
	Mycobacterium tuberculosis	Tuberculosis	China, South Africa, United States	Targeted PCR, metagenomics	Fu et al. (2022); Mtetwa et al. (2022a); Spurbeck et al. (2023)
	Mycobacterium simiae		United States	NGS panel	Spurbeck et al. (2023)

Family	Name	Disease	Countries	Techniques	References
	Mycobacterium ulcerans	Buruli ulcer	Hong Kong, United States	Metagenomics	Li et al. (2015); Tierney et al. (2023)
	Mycobacteroides chelonae		United States	NGS panel	Spurbeck et al. (2023)
Mycoplasmataceae	*Ureaplasma urealyticum*		United States	Metagenomics	Tierney et al. (2023)
Neisseriaceae	*Eikenella corrodens*		Hong Kong	Metagenomics	Li et al. (2015)
	Neisseria elongata		Hong Kong	Metagenomics	Li et al. (2015)
	Neisseria flavescens		Hong Kong	Metagenomics	Li et al. (2015)
	Neisseria gonorrhoeae	Gonorrhea	China, Hong Kong, United States	Metagenomics	Fu et al. (2022); Li et al. (2015); Spurbeck et al. (2023); Tierney et al. (2023)
	Neisseria meningitidis	Meningococcal disease	China, Hong Kong, United States	Metagenomics	Fu et al. (2022); Li et al. (2015); Spurbeck et al. (2023); Tierney et al. (2023)
	Neisseria mucosa		Hong Kong	Metagenomics	Li et al. (2015)
	Neisseria sicca		Hong Kong	Metagenomics	Li et al. (2015)
	Neisseria subflava		Hong Kong	Metagenomics	Li et al. (2015)
Nocardiaceae	*Rhodococcus erythropolis*		Hong Kong	Metagenomics	Li et al. (2015)
Pasteurellaceae	*Haemophilus influenzae*		United States	Metagenomics	Spurbeck et al. (2023); Tierney et al. (2023)
	Haemophilus parainfluenzae		Hong Kong, United States	Metagenomics, NGS panel	Li et al. (2015); Spurbeck et al. (2023)
	Mannheimia haemolytica		Hong Kong	Metagenomics	Li et al. (2015)

Family	Name	Disease	Countries	Techniques	References
Peptostreptococcaceae	*Finegoldia magna*		Hong Kong, United States	Metagenomics, NGS panel	Li et al. (2015); Spurbeck et al. (2023)
Prevotellaceae	*Prevotella buccae*		United States	NGS panel	Spurbeck et al. (2023)
Propionibacteriaceae	*Propionibacterium acnes*		Hong Kong	Metagenomics	Li et al. (2015)
Pseudomonadaceae	*Pseudomonas aeruginosa*		United States	Metagenomics, NGS panel	Spurbeck et al. (2023); Tierney et al. (2023)
	Pseudomonas fluorescens		Hong Kong, United States	Metagenomics, NGS panel	Li et al. (2015); Spurbeck et al. (2023)
	Pseudomonas stutzeri		Hong Kong, United States	Metagenomics, NGS panel	Li et al. (2015); Spurbeck et al. (2023)
Rickettsiaceae	*Rickettsia prowazekii*	Epidemic typhus	United States	Metagenomics	Spurbeck et al. (2023)
Selenomonadaceae	*Megamonas hypermegale*		Hong Kong	Metagenomics	Li et al. (2015)
Shewanellaceae	*Shewanella putrefaciens*		United States	NGS panel	Spurbeck et al. (2023)
Spirochaetaceae	*Treponema pallidum*	Syphilis	China	Metagenomics	Fu et al. (2022)
Staphylococcaceae	*Staphylococcus aureus*		China, Hong Kong, United States	Metagenomics	Fu et al. (2022); Li et al. (2015); Spurbeck et al. (2023)
	Staphylococcus saprophyticus		Hong Kong	Metagenomics	Li et al. (2015)
Streptococcaceae	*Streptococcus agalactiae*		Hong Kong, United States	Metagenomics	Li et al. (2015); Spurbeck et al. (2023)
	Streptococcus anginosus		Hong Kong, United States	Metagenomics, NGS panel	Li et al. (2015); Spurbeck et al. (2023)
	Streptococcus bovis		Hong Kong	Metagenomics	Li et al. (2015)
	Streptococcus gordonii		Hong Kong	Metagenomics	Li et al. (2015)
	Streptococcus mitis		Hong Kong	Metagenomics	Li et al. (2015)

Family	Name	Disease	Countries	Techniques	References
	Streptococcus mutans		Hong Kong	Metagenomics	Li et al. (2015)
	Streptococcus pneumoniae	Pneumococcal disease	China, United States	Metagenomics	Fu et al. (2022); Spurbeck et al. (2023)
	Streptococcus pyogenes	Strep throat; impetigo	United States	Metagenomics	Spurbeck et al. (2023)
	Streptococcus salivarius		Hong Kong	Metagenomics	Li et al. (2015)
	Streptococcus suis		China, Hong Kong	Metagenomics	Fu et al. (2022); Li et al. (2015)
Sutterellaceae	*Sutterella wadsworthensis*		Hong Kong	Metagenomics	Li et al. (2015)
Veillonellaceae	*Veillonella atypica*		Hong Kong	Metagenomics	Li et al. (2015)
	Veillonella dispar		Hong Kong	Metagenomics	Li et al. (2015)
	Veillonella parvula		Hong Kong, United States	Metagenomics, NGS panel	Li et al. (2015); Spurbeck et al. (2023)
Vibrionaceae	*Vibrio alginolyticus*		China, United States	Metagenomics	Fu et al. (2022); Spurbeck et al. (2023); Tierney et al. (2023)
	Vibrio chloreae	Cholera	China, Hong Kong, United States	Metagenomics	Fu et al. (2022); Li et al. (2015); Spurbeck et al. (2023)
	Vibrio furnissii		Hong Kong	Metagenomics	Li et al. (2015)
	Vibrio harveyi		China	Metagenomics	Fu et al. (2022)
	Vibrio mimicus		Hong Kong	Metagenomics	Li et al. (2015)
	Vibrio parahaemolyticus		China, Hong Kong, United States	Metagenomics	Fu et al. (2022); Li et al. (2015); Spurbeck et al. (2023); Tierney et al. (2023)

Family	Name	Disease	Countries	Techniques	References
	Vibrio vulnificus		Hong Kong, United States	Metagenomics	Li et al. (2015); Spurbeck et al. (2023); Tierney et al. (2023)
Xanthomonadaceae	*Stenotrophomonas maltophilia*		Hong Kong, United States	Metagenomics, NGS panel	Li et al. (2015); Spurbeck et al. (2023)
Fungi					
Saccharomycetaceae	*Candida auris*		United States	qPCR, culture-based detection	Barber et al. (2023)
Trichocomaceae	*Aspergillus versicolor*		United States	NGS panel	Rossi et al. (2023); Spurbeck et al. (2023)
Parasites					
Family	**Name**	**Disease**	**Countries detected**	**Techniques**	**References**
Cryptosporidiidae	*Cryptosporidium* (*parvum*- and *muris*-like)		Canada	Immunofluorescence	Heitman et al. (2002)
	Cryptosporidium baileyi		Brazil	Targeted PCR	Martins et al. (2019)
	Cryptosporidium hominis		Brazil	Targeted PCR	Martins et al. (2019)
	Cryptosporidium muris		Brazil, Canada	Targeted PCR	Martins et al. (2019)
	Cryptosporidium parvum	Cryptosporidiosis	Brazil, United States	Targeted PCR, metagenomics	Martins et al. (2019); Spurbeck et al. (2023)
	Cryptosporidium suis		Brazil	Targeted PCR	Martins et al. (2019)
Hexamitidae	*Giardia*		Brazil, Germany	Targeted PCR, immunofluorescence	Ajonina et al. (2013); Martins et al. (2019)
	Giardia duodenalis		Canada	Immunofluorescence	Heitman et al. (2002)
Plasmodiidae	*Plasmodium*		United States	Metagenomics	Spurbeck et al. (2023)
Sarcocystidae	*Toxoplasma gondii*	Toxoplasmosis	China	Targeted PCR	Lass et al. (2022)

Family	Name	Disease	Countries	Techniques	References
Trichinellidae	*Trichinella*	Trichinosis	United States	Metagenomics	Spurbeck et al. (2023)

Non-exhaustive summary of WBS studies for infectious diseases. Does not include SARS-CoV-2. NGS panel refers to the Illumina Respiratory Pathogen Infectious Disease/AMR Enrichment Panel Kit[442].

[442] https://www.illumina.com/products/by-type/sequencing-kits/library-prep-kits/respiratory-pathogen-id-panel.html Accessed 14 June 2023

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