New Zealand Food Safety
Haumaru Kai Aotearoa

Annual report concerning Foodborne Diseases in New Zealand 2024

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Prepared for New Zealand Food Safety
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Cover Image: medical illustration of *Staphylococcus aureus*
Credit: Centers for Disease Control and Prevention(CDC)/ Meredith Newlove

Scientific Interpretative Summary

This Scientific Interpretative Summary is prepared by New Zealand Food Safety risk assessors to provide context to the following report for Ministry for Primary Industries risk managers and external readers.

Annual report concerning foodborne diseases in New Zealand 2024

Public Health and Forensic Science Report FW25015

Human health surveillance and its relationship to foodborne illness is essential for informing the strategic direction that New Zealand Food Safety (NZFS) takes and regulatory measures it puts in place to minimise foodborne illness in New Zealand and for overseas consumers. The annual foodborne disease reports are critical, allowing NZFS to monitor trends in foodborne illness in New Zealand by describing in consistent manner evidence from case notifications, case enquiries, outbreak investigations, and other epidemiological studies of human enteric disease.

This report is the latest in a series providing a consistent source of data annually to monitor trends in foodborne illness in New Zealand. The series can be found here.

When reading these reports, it is necessary to bear in mind that notified cases of illness represent only a subset of all the cases that occur in New Zealand each year because:

- Many sick individuals do not visit a GP or otherwise come to the attention of the health system.
- Multiple factors (e.g., change in sensitivity of testing methods, proportion of human faecal specimens being tested) affect the notification rates on top of any underlying changes to disease incidence happening in New Zealand. Some cases notified in New Zealand are due to exposure to a pathogen or toxin while they were overseas.

Since 2015, New Zealand diagnostic laboratories have made changes in enteric organism testing methods and screening criteria. For some years traditional culture-based methods for enteric bacteria and microscopy for parasites were gradually being replaced by molecular-based culture independent diagnostic testing (CIDT) methods. In 2024 all faecal specimens are now screened by CIDT for *Campylobacter* spp., *Salmonella* spp., *Shigella* spp., STEC and *Yersinia enterocolitica*.

The case numbers and rates presented in this report initially relate to the total number of notified cases for the disease in New Zealand, irrespective of the mode of transmission of the pathogen i.e. foodborne or person-to-person. Likewise, data analysis (e.g. by demographics) is based on all notified cases, not just on those attributable to foodborne transmission. Consumption of contaminated food is only one of the routes by which humans are exposed to pathogens; other routes of exposure include water ingestion, animal contact, and person-to-person contact. Among the reported diseases, only listeriosis is fully attributable to consumption of contaminated food.

Similarly to previous years, most cases of foodborne disease in New Zealand are sporadic, with limited data available on where (home, premises, or event) food was prepared or consumed. In 2024, there were 39 notified outbreaks of potentially foodborne disease reported in EpiSurv (New Zealand's national public health surveillance database), represented by 920 cases. The pathogen was identified in 26 outbreaks, with the other 13 outbreaks reported as gastroenteritis. Norovirus infection was the most commonly reported pathogen reported in outbreaks (10 outbreaks that involved 563 cases). The majority (71.8%) of reported outbreaks were predominantly associated with commercial food operators e.g. restaurant/cafe/bakery or caterers. Only 6 outbreaks (15.4%) were associated with food prepared at consumer's homes or community events. The remaining 5 outbreaks were associated with food prepared in different types of institutions, e.g. marae or hostel.

Campylobacteriosis, yersiniosis, infection caused by STEC, and salmonellosis remain the predominantly notified foodborne illnesses. Notification rates for these foodborne pathogens

are generally stable, being highest for very young children (less than 4 years of age) and for elderly people (70+ years) as with previously reported years The 2024 trends for three foodborne illnesses are further described below.

Campylobacteriosis

The reduction of human cases of foodborne campylobacteriosis by 20% from 88 to 70 per 100,000 population by the end of 2024 was a strategic priority for NZFS. During the past several years, both the total number of human campylobacteriosis cases and rates per 100,000 population have been consistently, albeit slowly, decreasing and in 2024 the domestically acquired foodborne campylobacteriosis rate reached the target. This is reported in the section entitled “Reporting against targets”.

In contrast to the number of notified cases, starting from 2021, the number and rate of hospitalised cases has been steadily increasing. The increase in hospitalised cases alongside the decrease in notified cases might be due to a range of contributing factors such as:

a) *COVID-19 pandemic impacts*: a major COVID-19 study in New Zealand found that with one in five people reported long COVID-19 symptoms after their initial infection. For these people, common foodborne infections may lead to more severe illness that required hospitalisation;

b) *delays in seeking or inability to timely get medical attention*: health of infected people deteriorates if they delay seeking medical attentions and as such require hospitalisation;

c) *increased cost of living and shortage of General Practitioners*: some people (even with mild symptoms of the disease) go straight to the hospital bypassing primary health care to avoid costs. This is supported by the observation that over 38 percent of all hospitalised in 2024 cases were discharged on the same day or the next day of admission;

d) *increases in molecular based testing methods for Campylobacter*: quicker and easier test methods can impact in-hospital testing practices. For example, increased testing of hospitalised patients can detect *Campylobacter* even when this is due to an historical infection and not the reason for the hospitalisation. This can impact hospitalisation case numbers as community patients are only likely to be tested if showing symptoms, while hospitalised patients may be tested as part of other diagnostic investigations.

It is also possible that a higher proportion of cases require hospitalisation due to increased pathogenicity of circulating strains. Additional research is needed to validate this assumption.

The higher rate of campylobacteriosis in rural areas compared with urban areas in the last 3 years suggests risk factors other than food (e.g. direct contact with farm animals or exposure to potentially contaminated water) may be assuming greater importance as a source of infection as the contamination of food, predominantly from chicken meat, is lowered.

NZFS set a strategic goal to reduce foodborne campylobacteriosis cases by 20% by the end of 2024, from 88 to 70 per 100,000 population. To maintain momentum, a new public health target proposes a further 15% reduction over 2025-2029. This goal builds on previous success and depends on developing an effective work programme and intervention. If achieved early, NZFS will review and adjust the target to sustain progress.

Yersiniosis

Since 2013, the number and the rate of yersiniosis notifications has been increasing up to 2021 when the number of notifications has stabilised on a relatively high number of about 1400 cases. In 2024 both the number and the rate of yersiniosis notifications dropped. The 2024 notification rate of 21.4 cases per 100,000 population was much lower than the previous three-year mean (26.6 cases per 100,000 population). A similar reduction has been noticed in the rate of hospitalisation.

Yersiniosis is currently the second most prevalent notifiable foodborne disease in New Zealand. As such, further focus on this pathogen is planned, with an emphasis on strengthening the scientific evidence base and improving understanding of its transmission dynamics. This work will support more targeted risk assessment and inform future food safety interventions.

Listeriosis

Listeriosis, while low in total numbers, has a very high rate of hospitalisation and is associated with fatality in frail elderly and immuno-compromised people, and foetal loss in pregnancy. In 2024 all 36 reported cases of listeriosis were hospitalised and most of them spent more than seven days in the hospital.

In contrast to the relatively high numbers of fatalities in 2022 and 2023, no deaths of adults were reported in 2024 as directly attributed to listeriosis. There was one perinatal fatality case attributed to listeriosis in a pregnant woman.

NZFS continues to carry out targeted consumer education campaigns directed specifically at elderly people and pregnant women which aims to help the most vulnerable people to protect themselves from listeriosis.

New Zealand Food Safety, PHF Science, and the National Public Health Service (Health New Zealand / Te Whatu Ora) are working together to improve reporting, analysis, and presentation of human foodborne illness surveillance and investigation data to provide better insights into the causes of - and hence the means to mitigate - foodborne illness.

PHF Science

ANNUAL REPORT CONCERNING FOODBORNE DISEASE IN NEW ZEALAND 2024

PREPARED FOR:	**New Zealand Food Safety under Project 406850 – Systematic reporting of epidemiology of potentially foodborne disease in New Zealand for year 2024**
CLIENT REPORT No:	**FW 25015**
PREPARED BY:	**Isabelle Pattis, Beverley Horn, Joanne Kingsbury, Peter Cressey, Liza Lopez**
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This report is available at www.mpi.govt.nz

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INTRODUCTION

New Zealand Food Safety (NZFS), a business unit of the Ministry for Primary Industries (MPI), leads New Zealand's food safety system, protecting the health and wellbeing of consumers locally and overseas. This includes reducing food-related risks to human health. Human health surveillance is an essential element of the monitoring and review component of the NZFS risk management framework. In addition, evidence from notifications, case enquiries, outbreak investigations and other epidemiological studies of human enteric diseases are used as sources of data for risk profiles and assessments. There is ongoing interest in foodborne disease statistics within NZFS and its stakeholders, including consumers.

This report for the calendar year 2024 is part of a series providing a consistent source of data and method of presentation to allow monitoring of foodborne illness in New Zealand.

Human health surveillance data and foodborne disease

The information in this report concerns reported cases of notifiable disease and reported outbreaks collected in EpiSurv (the national notifiable disease database; described in further detail in Appendix A, page 123). In addition to EpiSurv notified outbreaks, relevant potentially foodborne outbreaks investigated by Food Compliance Services, NZFS, are included in this report. Some notifiable illnesses may be caused by transmission of pathogens through foods,[1] but it is important to remember that most of the information in this report relates to the illness, not the mode of transmission. The information needs to be considered with two caveats:

1. Notified cases of illness and reported outbreaks represent a subset of all the cases and outbreaks that occur in New Zealand each year. Many sick individuals do not visit a GP or otherwise come to the attention of the health system. By using notification and outbreak data as indicators, we are assuming that they are epidemiologically representative of all the cases and outbreaks that occur [1].
2. Consumption of contaminated food is only one of the routes by which humans are exposed to pathogens; other routes of exposure include water ingestion, animal contact and person to person contact. There are some sources from which we can get information on the proportion of cases caused by foodborne transmission:
    - Outbreak reports: The circumstances of an outbreak (multiple cases from a single event) mean that an investigation is more likely to identify a source of exposure to the pathogen than investigation of sporadic cases.
    - Expert opinion: Based on their experience in laboratories and epidemiological investigations, as well as knowledge of factors influencing the risk, experts can provide estimates of the proportion of cases caused by foodborne transmission. Estimates for New Zealand have been developed for some foodborne diseases [2, 3], as presented in relevant report sections. These are not fixed values; future changes to the New Zealand food chain may require the values to be amended.
    - Overseas analyses and estimates: Information from countries with food supplies similar to New Zealand can be helpful, especially for illnesses where a foodborne estimate could not be developed from local studies. New Zealand estimates [2, 3] and published country-specific estimates, for the United States of America (USA) [4, 5], Canada [6], Australia [7, 8], England and Wales [9] and the Netherlands [10] are given in Table 1. In addition, a World Health Organization (WHO) project to estimate the global burden of foodborne diseases derived

[1] Note that water, other than bottled water, is not considered a food in this context.

estimates for 14 international regions [11, 12]. The estimates for New Zealand, Australia, Canada, the Netherlands and the international WHO estimates are based on expert opinion, the estimates for England and Wales are based on outbreak analysis, while the USA estimates are based on data from surveillance, risk factor studies and a literature review.

Table 1. New Zealand and overseas estimates of the food attributable proportion of selected illnesses due to microbial hazards

Hazard		Percentage foodborne (%)					
	New Zealand (2013, 2021) [2, 3]	WHO (2015)[a] [11, 12]	USA (2011, 2021) [4, 5]	Canada (2015) [6]	Australia (2005, 2014) [7, 8]	England and Wales (2002) [9]	Netherlands (2008) [10]
Bacteria							
Bacillus cereus	NE	100	100	99	100	100	90
Campylobacter spp.	75	51–76	57[b]	62	77[c]	80	42
Clostridium perfringens	NE	100	100	93	98[c]	94	91
Shiga toxin-producing *Escherichia coli* (STEC) O157:H7	20	40–60[d]	60[b]	61	56[c, d]	63	40
STEC non-O157	40	40–60[d]	50[b]	60	56[c, d]	63	42
Listeria monocytogenes	88[e]	100	99	77	98[c]	99	69
Salmonella non-typhoidal	62	46–76	66[b]	63	72[c]	92	55
Shigella spp.	NE	7–36	8[b]	26	12[c]	8	NE
Staphylococcus aureus	NE	100	100	78	100	96	87
Vibrio parahaemolyticus	91	NE	74[b]	83	71	NE	NE
Yersinia enterocolitica	75	NE	77[b]	83	84	90[f]	NE
Parasites							
Cryptosporidium parvum	NE	8–16	7[b]	11	10	6	12
Giardia lamblia	NE	11–14	10[b]	7	5	10	13
Viruses							
Hepatitis A virus	NE	29–42	42[b]	30	12[c]	11	11
Norovirus	33	12–26	19[b]	18	18[c]	NE	17
Sapovirus	NE	NE	13[b]	17	NE	0	NE

The information contained in this table spans literature over 20 years and represents the most current and up-to-date literature available for the countries specified.

The Netherlands study considered food and travel as separate transmission pathways, although a proportion of travel-associated cases will be due to consumption of contaminated food. Consequently, the Netherlands study may under-estimate the proportion of cases that are due to contaminated food (percentage foodborne). Of the other studies, the US study only considered domestically acquired cases, while the other studies did not specifically address whether cases were travel-related or domestically acquired and for these studies the percentage foodborne will include both domestically acquired and travel-related cases.

[a] The WHO study estimated proportions for 14 international regions. Figures presented here are the range of those estimates.

[b] The 2021 USA publication did not cover the full range of organisms covered in the 2011 publication. Estimates marked with a superscript are from the 2021 study, others are from the 2011 study.

[c] The 2014 Australian publication did not cover the full range of organisms covered in the 2005 publication. Estimates marked with a superscript are from the 2014 publication.

[d] Estimate was derived for total STEC.

[e] It has been estimated by expert consultation that 88% of listeriosis incidence is due to foodborne transmission [2]. However, human infections from sources other than food are unlikely and the fact that the estimate is less than 100% is likely an artefact of the expert elicitation methodology.

[f] For England and Wales the estimate refers to *Yersinia* spp., for all other countries the estimate refers to *Yersinia enterocolitica.*

NE = not estimated, no information is available on the food attributable proportion in New Zealand.

This report considers information for the 2024 calendar year. Information from the scientific literature and other sources concerning food safety in New Zealand for that year has been summarised. However, the time taken to publish scientific information is often lengthy, and additional information relevant to foodborne illness and foodborne transmission in 2024 may become available in the future.

Diseases included in this report

The diseases that have been selected for inclusion in this report are those that have:

1. The potential to be caused by foodborne transmission; and,
2. Available historical and current national data sources.

The potentially foodborne diseases included in this report are listed in Table 2. Data have been drawn from a number of sources including EpiSurv disease notification and outbreak reports, national hospitalisation records, and the New Zealand Institute for Public Health and Forensic Science (PHF Science), formerly known as Institute of Environmental Science and Research Limited (ESR), laboratory surveillance databases.

Table 2. Potentially foodborne conditions included in this report

Disease	Type	Sources[a]	Hospital diagnosis ICD-10 code[b]
Bacillus cereus intoxication	Bacterium	N, O, H	A05.4 Foodborne *Bacillus cereus* intoxication
Campylobacteriosis	Bacterium	N, O, H	A04.5 *Campylobacter* enteritis
Ciguatera poisoning	Toxin	N, O, H	T61.0 Toxic effect: Ciguatera fish poisoning
Clostridium perfringens intoxication	Bacterium	N, O, H	A05.2 Foodborne *Clostridium perfringens* [*Clostridium welchii*] intoxication
Cryptosporidiosis	Protozoan	N, O, H	A07.2 Cryptosporidiosis
Giardiasis	Protozoan	N, O, H	A07.1 Giardiasis [lambliasis]
Hepatitis A infection	Virus	N, O, H, L	B15 Acute hepatitis A
Histamine (scombroid) fish poisoning	Toxin	N, O, H	T61.1 Toxic effect: scombroid fish poisoning
Listeriosis (total and perinatal)	Bacterium	N, O, H, L	A32 Listeriosis
Norovirus infection	Virus	N, O, H, L	A08.1 Acute gastroenteropathy due to Norwalk agent
Salmonellosis	Bacterium	N, O, H, L	A02.0 *Salmonella* enteritis
Sapovirus infection	Virus	N, O, L	No specific ICD-10 code
Shigellosis	Bacterium	N, O, H, L	A03 Shigellosis
Staphylococcus aureus intoxication	Bacterium	N, O, H	A05.0 Foodborne staphylococcal intoxication
Toxic shellfish poisoning	Toxin	N, O, H	T61.2 Other fish and shellfish poisoning
Shiga toxin-producing *Escherichia coli* (STEC) infection	Bacterium	N, O, L	A04.3 Enterohaemorrhagic *Escherichia coli* infection[c]
Vibrio parahaemolyticus infection	Bacterium	N, O, H, L	A05.3 Foodborne *Vibrio parahaemolyticus* intoxication
Yersiniosis	Bacterium	N, O, H, L	A04.6 Enteritis due to *Yersinia enterocolitica*

[a] Data sources: EpiSurv notifications (N), EpiSurv outbreaks (O), Health New Zealand Te Whatu Ora hospitalisations (H), PHF Science laboratory data (L).

[b] International statistical classification of diseases and related health problems (ICD), 10th revision [13].

[c] Prior to 2023, hospitalisation data in this report was presented based on the ICD-10 code A04.3 (enterohaemorrhagic *E. coli* (EHEC) infection) diagnoses records in the Health New Zealand Te Whatu Ora NMDS database. EHEC and STEC are synonymous [14]but ICD-10 uses EHEC rather than STEC. While A04.3 is the technically correct diagnostic code for STEC infection, research in 2024 has shown that hospital admissions for STEC cases may be coded to diagnostic codes other than A04.3 [15]. Therefore, hospitalisation data for cases with STEC infection in this report is based on EpiSurv notifications rather than the NMDS database.

Notifiable diseases were selected for inclusion in this report where a significant proportion is expected to be foodborne, or the disease organism has been reported as the cause of foodborne outbreaks. Typhoid and paratyphoid fever are not included as the majority of cases acquire their infection overseas. Case definitions for diseases were obtained from the Communicable Disease Control Manual, published by Health New Zealand Te Whatu Ora [16] or the EpiSurv Case Report Form (CRF) Instructions website [17].

Cases with certain conditions (intoxications from the bacteria *Bacillus cereus*, *Clostridium perfringens,* and *Staphylococcus aureus*, ciguatera poisoning, histamine (scombroid) fish poisoning, toxic shellfish poisoning and *Vibrio parahaemolyticus,* norovirus and sapovirus infections) are notified under the heading of acute gastroenteritis.

Not all individual cases of acute gastroenteritis are notifiable, only those when: (i) the infected person is in a high-risk category (e.g. food handler, early childhood service worker, or another person with increased risk of spreading the disease), (ii) it is an infectious gastroenteritis of public health importance such as *C. perfringens* and *V. parahaemolyticus* or (iii) it is a single case of chemical or toxic food poisoning such as botulism, histamine (scombroid) poisoning or any type of toxic shellfish poisoning [16]. Summary details of acute gastroenteritis cases may be recorded in an outbreak notification if they are part of a common source outbreak (two or more cases) but may not be notified as individual cases unless one of the three conditions above apply.

It is worth noting that, although foodborne transmission is considered significant for most of the diseases included in this report, there are several illnesses (shigellosis, giardiasis, cryptosporidiosis, hepatitis A) where foodborne transmission only contributes a small proportion of the total disease burden.

This report includes both potentially foodborne notifiable diseases and the sequelae which are considered to result from preceding infections (Table 3). The two sequelae included in the report, haemolytic uraemic syndrome (HUS) and Guillain-Barré syndrome (GBS), are severe and occasionally life-threatening illnesses.

Table 3. Sequelae to potentially foodborne conditions included in the report

Disease	Source[a]	ICD-10 code[b]	Comment
Guillain-Barré syndrome (GBS)	H	G61.0 Guillain-Barré syndrome	Sequela to infection with *Campylobacter*[c]
Haemolytic uraemic syndrome (HUS)	H	D59.3 Haemolytic-uraemic syndrome	Sequela to infection with STEC[d]

[a] Data Source: Health New Zealand Te Whatu Ora hospitalisations (H).

[b] International statistical classification of diseases and related health problems, 10th revision [13].

[c] While there is evidence that GBS can be triggered by other microbial infections (e.g., cytomegalovirus, Epstein-Barr virus, *Mycoplasma pneumonia*), *Campylobacter* infection is the only recognised triggering organism that is potentially foodborne.

[d] While HUS may occasionally be triggered by other organisms, such as *Streptococcus pneumoniae*, it is predominantly a sequela to STEC infection.

Changes in laboratory testing methodology

Since 2015, New Zealand diagnostic laboratories have made changes in enteric organism testing methods and screening criteria. Traditional culture-based methods for enteric bacteria and microscopy for parasites are gradually being replaced by culture-independent diagnostic testing methods (CIDT) utilising nucleic acid amplification methods. All faecal specimens are now screened by CIDT for *Campylobacter* spp., *Salmonella* spp., *Shigella* spp., STEC and *Yersinia enterocolitica*. In some Health Districts all faecal specimens are also routinely screened for *Giardia* spp., *Cryptosporidium* spp., *Yersinia pseudotuberculosis* and/or *Vibrio parahaemolyticus.* An overview of when laboratories

servicing different Health Districts moved to CIDT detection methods and which pathogens are included in the respective CIDT panels[1] is provided in Table 63 in Appendix B.

By the end of 2023 all but one laboratory had changed to CIDT. In March 2024, the remaining laboratory, Waikato hospital, transitioned faecal specimen testing to CIDT-based methods.

Different testing related factors (e.g., change in sensitivity of methods, proportion of faecal specimens tested) may affect the notification rates on top of any underlying changes to the incidence of diseases in New Zealand. Initial analyses comparing notification trends for bacterial infections in areas where laboratories covering faecal specimens from community-based patients had changed to CIDT and areas that had not changed to CIDT suggested the change in methodology has had a significant impact on reporting rates for STEC infections, but no apparent impact for campylobacteriosis, salmonellosis, shigellosis and yersiniosis [18]. Any observed trends in changes in STEC notification rates between 2015 and 2024 must be considered in the context of changes to testing approaches. It is unclear at this stage if laboratory changes, and the increased number of screened samples have affected the notification rates for cryptosporidiosis, giardiasis and *V. parahaemolyticus* infection (Table 63 and table footnotes in Appendix B).

Changes in overseas travel

Some cases notified in New Zealand are due to people being exposed to a pathogen or toxin while overseas. The global pandemic of coronavirus disease 19 (COVID-19), caused by SARS-CoV-2, reduced the number of people entering New Zealand from overseas (Table 4).

In 2024, the number of New Zealand residents returning from absences of less than 12 months was about 97% of those recorded for the pre-COVID-19-year 2019 (Table 4). Total passenger arrivals in 2024 were 91% of the numbers observed in 2019. The effect of reduced overseas travel on New Zealand notification rates is disease-specific and is discussed in the respective sections of the report, where relevant.

Table 4. International travel and migration passenger arrivals in New Zealand, 2019 – 2024

	2019	2020	2021	2022	2023	2024
NZ resident travellers	3,101,427	681,893	142,879	1,327,126	2,683,654	2,993,720
Total passenger arrivals[a]	7,100,373	1,733,521	398,556	2,856,072	5,825,798	6,436,681

Data Source: Stats NZ, https://infoshare.stats.govt.nz/, NZ-resident traveller arrival totals (Annual - Dec), total passenger movements by travel mode (Annual-Dec) accessed 08 April 2025.

[a] Total passenger arrivals include NZ resident traveller arrivals (absence < 12 months), visitor arrivals (for a stay of < 12 months) and permanent and long-term migration arrivals.

[1] Different laboratories are using different CIDT methods, i.e. panels developed by different companies which differ in some of the target organisms.

REPORTING

Unless specifically stated, the case numbers and rates presented in this report relate to the total number of notified human cases for the disease in New Zealand and do not differentiate between mode of transmission, i.e. foodborne or person-to person. Likewise, all data analyses, e.g. by demographics, is based on all notified cases and not limited to those attributable to foodborne transmission. Furthermore, all bacterial isolates mentioned in the report are derived from human cases, unless specified otherwise.

SUMMARY OF MAIN FOODBORNE DISEASES

The incidence of the main foodborne diseases in 2024 is summarised in Table 5 below.

Table 5. Estimated proportion and incidence of the main foodborne diseases for 2024

	Total notified[a]		Estimated domestically acquired foodborne transmission[b]		
	Cases	Rate[c]	Cases	Proportion (%)[d]	Rate[c]
Campylobacteriosis	5801	108.7	3750	75	70.2
Hepatitis A	68	1.3	NE	-	-
Listeriosis	36	0.7	NE	-	-
Salmonellosis	844	15.8	288	62	5.4
STEC infection	1115	20.9	401	40[e]	7.5
Yersiniosis	1140	21.4	798	75	14.9

NE = not estimated, no information is available on the food attributable proportion in New Zealand. For listeriosis, sources other than food are unlikely [19].

[a] This table includes selected diseases which are considered the main potentially foodborne diseases in New Zealand, all of which are among the individually notifiable diseases in New Zealand [16]. Cases of disease due to other potentially foodborne organisms may be notified under their own disease name (cryptosporidiosis, giardiasis and shigellosis) or notified in the category of acute gastroenteritis if of high public health importance or if the case is in a high-risk category (food handler, early childhood service worker).

[b] For estimation of food-related cases, the proportions derived from expert consultation exclude potentially travel-related cases. The estimated proportion of potentially travel-related cases is calculated from the proportion of cases recorded as having been overseas during the incubation period for the disease out of all notifications which included an entry ('yes' or 'no') for the overseas travel question.

[c] Rate per 100,000, 2024 mid-year estimated population. At 30 June 2024, the New Zealand population was estimated to be 5,338,500.

[d] Estimated foodborne transmission proportions were derived from two expert consultations in 2013 and 2020, respectively [2, 3].

[e] The expert elicitation [3] derived separate estimates of the foodborne proportion for O157 STEC (20%) and non-O157 STEC (40%). The estimate for non-O157 STEC, the dominant set of serotypes, has been used to estimate the number of food-related cases.

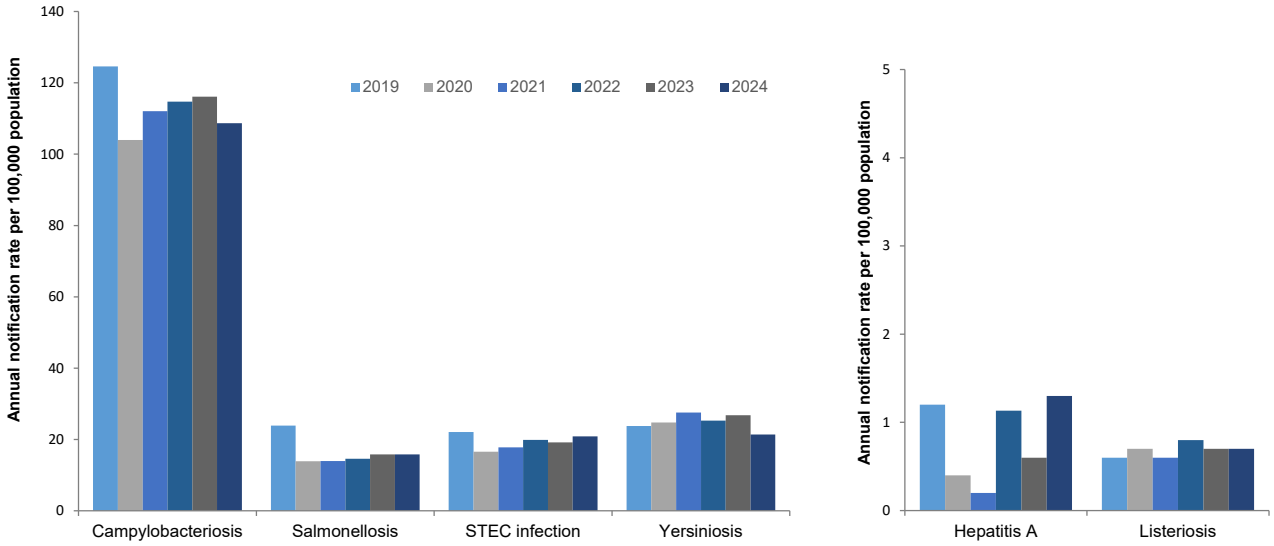
In 2024, notification rates for the main foodborne diseases showed distinct disease specific temporal patterns compared with the preceding years (Figure 1 and Appendix C, Table 64). The campylobacteriosis notification rate decreased from 116.1 cases per 100,000 population in 2023 to 108.7 cases per 100,000 population in 2024. The preceding five years showed a pronounced drop of the campylobacteriosis notification rate in 2020 followed by a steady increase up to 2023, but remaining below the 2019 rate. Notification rates for hepatitis A increased from 2023 to 2024 from 0.6 to 1.3 cases per 100,000 population. In the previous five years notification rates for hepatitis A ranged between 0.2 and 1.2 cases per 100,000 population. Listeriosis notification rates have been relatively stable over the last six years with between 0.6 and 0.8 listeriosis cases per 100,000 population. Salmonellosis notification rates were equal in 2023 and 2024 (15.8 cases per 100,000 population). Since 2019, salmonellosis notification rates have remained consistently below pre COVID-19 rates (24.2 cases per 100,000 population in 2019). STEC infection notification rates increased from 2023 to 2024 (19.2 and 20.9 cases per 100,000 population, respectively). Since 2019, STEC infection notification rates have been consistently lower than pre COVID-19 rates (22.4 cases per 100,000

population in 2019). Yersiniosis notification rates decreased from 2023 to 2024 from 26.8 to 21.4 cases per 100,000 population. The 2024 notification rate was significantly lower compared with the rates reported for the preceding five years, which ranged between 24.1 and 27.6 cases per 100,000 population (2019 and 2021, respectively).

Note that case notifications or rates in this report may differ slightly from previously reported figures due to data extraction dates and/or updates to the population denominator.

Public health and social measures introduced in 2020 and 2021 to prevent the spread of COVID-19 in New Zealand affected exposure behaviours and pathways, access to medical care and laboratory testing priorities. Thus, multiple factors had an impact on notification rates during this time. This is discussed in more detail in the *Annual Report concerning Foodborne Disease in New Zealand 2021* [18].

Figure 1. Notification rates of the main foodborne diseases, 2019–2024



Reporting against targets

Performance targets for potentially foodborne diseases are reviewed by NZFS on an annual basis. Currently, the only performance target set by NZFS is for domestically acquired foodborne campylobacteriosis.

In 2020, NZFS introduced the goal of reducing the incidence of human cases of domestically acquired foodborne campylobacteriosis by 20% from the mean rate for the years 2017–2019 of 87.7 cases per 100,000 population to 70.2 by the end of 2024[1]. The target uses the estimate of the food attributable campylobacteriosis proportion (75%) from the latest expert elicitation process (2020) [3].

Rationale

Campylobacteriosis is the most commonly notified potentially foodborne disease in New Zealand. A study commissioned by NZFS and conducted in 2018–2019 [20], provided updated information on

[1] https://www.mpi.govt.nz/dmsdocument/42766-Campylobacter-Action-Plan-2020-21 (Accessed 16th May 2023)

how New Zealanders become infected with the *Campylobacter* bacterium. The study identified that food remained the dominant pathway for exposure and infection in New Zealand, with poultry meat still being the main source of *Campylobacter* infections, especially for the urban population.

Other potentially foodborne illnesses are currently covered by core business activities within NZFS, which include close monitoring of notifications and outbreaks. Specific targets are introduced if warranted by the current situation or changing trends. NZFS continues to closely monitor sources and potential pathways that are most often associated with potentially foodborne illness in New Zealand.

Methodology, tools and reporting

Historical baseline data on the number of notified cases of the targeted potentially foodborne diseases are available from the *Notifiable Diseases in New Zealand Annual Report,* produced by PHF Science for the Ministry of Health [21].

To assess reporting against targets, the annual number of notified cases is adjusted for the estimated proportion of cases having travelled overseas during the likely incubation period. The number of (non-travel related) notified cases is also adjusted for the proportion of disease estimated to be due to foodborne transmission.

The annual incidence of campylobacteriosis is reported in terms of calendar year cases per 100,000 population (*Notifiable Diseases in New Zealand Annual Report*) [21]. This allows for demographic changes within the New Zealand population to be appropriately captured. The proportion of infections acquired overseas is estimated through data from the EpiSurv programme administered by PHF Science on behalf of the Ministry of Health.

Campylobacteriosis 2020 to 2024 performance target

The incidence of human cases of domestically acquired foodborne campylobacteriosis reduced by 20% from 87.7 to 70.2 cases per 100,000 population by the end of 2024.

Measurement

The measurement used is the annual (calendar year) rate (per 100,000 mid-year population estimate) of notified cases of human domestically acquired foodborne campylobacteriosis, with the baseline being the average foodborne rate for 2017 to 2019 (87.7 cases per 100,000 mid-year population). The 2020 data have been excluded for setting the baseline, due to COVID-19 related changes in notification rates [18].

The estimated incidence of domestically acquired foodborne campylobacteriosis in 2024 is given in Table 6.

Table 6. Estimated proportion and incidence of foodborne campylobacteriosis for 2024

	Cases	Proportion of total notified cases (%)	Rate (per 100,000, mid-year estimated population)
Total notified	5801	-	108.7
Total estimated as not related to overseas travel[a]	5000	86.2	93.7
Estimated domestically acquired foodborne transmission[b]	3750	64.7	70.2

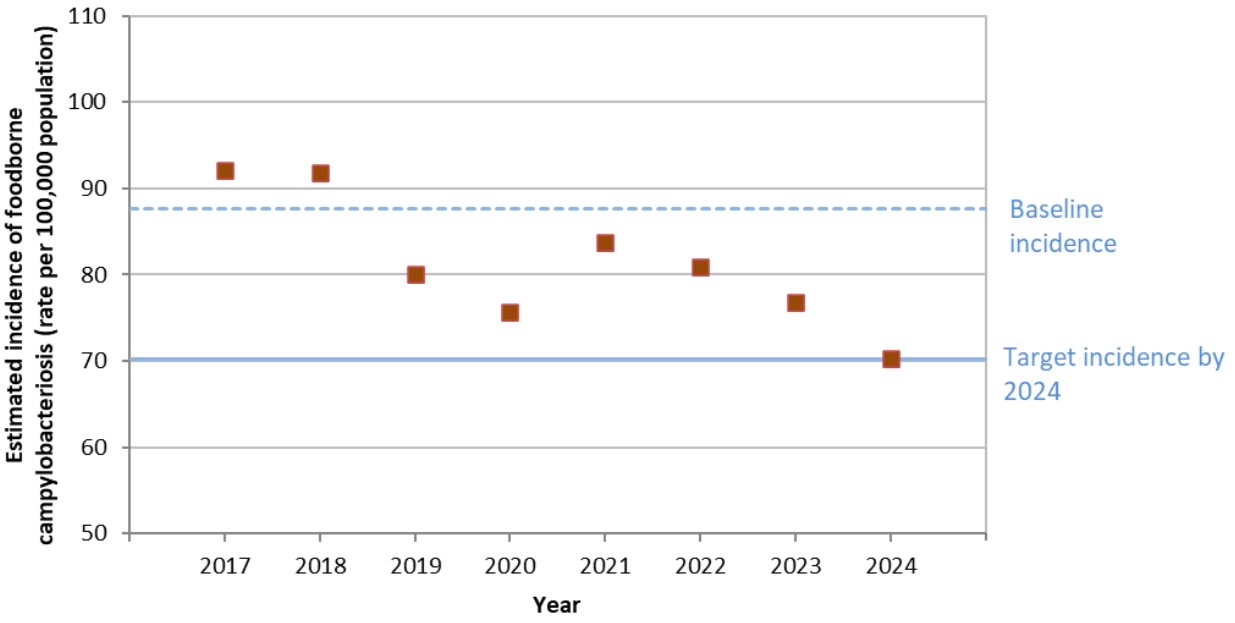
[a] The number of cases listing overseas travel as a risk factor in 2024 was 306, out of 2216 completed (“yes” or “no”) responses (13.8%). Thus, it was estimated 86.2% of all notified campylobacteriosis infections were domestically acquired.

[b] From expert consultation in 2020, 75% of domestic cases are assumed to be foodborne [3].

Presentation

The trend in the estimated domestically acquired foodborne campylobacteriosis rate compared with the 2020 to 2024 performance target (solid blue line) is shown in Figure 2. The domestically acquired foodborne campylobacteriosis rate in 2024 (70.2 per 100,000 population) equals the target value. There has been a decrease in the domestically acquired foodborne campylobacteriosis rate each year compared with the previous year since 2021.

Figure 2. Estimated incidence of domestically acquired foodborne campylobacteriosis compared with the 2020 to 2024 performance target



Reporting of incidence and severity of selected foodborne conditions

This report includes a summary of the notified incidence for each potentially foodborne condition. For conditions with sufficient numbers (approximately 100 cases or more per year), a full analysis, drawn from notification, hospitalisation, mortality, and laboratory data has been carried out. For conditions with a smaller number of cases, a more limited analysis has been performed.

These data are followed by contextual information on the foodborne proportion of the overall incidence of illness. The individual sections include the following information, where available:

- statement of estimated foodborne percentage and range provided by expert elicitation processes conducted in 2013 [2] and 2020 [3]. Note that these estimates are only available for some of the conditions included in this report.
- statement of estimated foodborne percentage and range for any specific foods provided by the same expert elicitation process.
- information on pathogen typing (principally from data generated by PHF Science's Enteric Reference Laboratory, Enteric, Food and Environmental Virology/Norovirus Reference Laboratory or Special Bacteriology Laboratory), where it is available and informative about foodborne disease.
- comments on specific food-related incidents or outbreaks of the disease that were reported to the notification system during the calendar year.
- studies informing foodborne attribution for specific conditions conducted or published during the calendar year.
- information on the prevalence of the toxin or microbial hazard in particular foods from surveys conducted during the calendar year.
- regulatory or other risk management actions in New Zealand that might be expected to affect the foodborne disease data.

Interpreting data

Data in this report may differ from those published in other reports depending on:

- the date of extraction of the data.
- the date used to aggregate data (e.g. date reported or date of onset of illness).
- filters used to extract the data, such as exclusion of records classified as 'not a case'.

The information in this report shows disease trends by age group, sex, ethnicity, and health district of the case's place of residence.

Due to low numbers of cases for some foodborne illnesses, such as listeriosis, the rates calculated in this report may be highly variable from year to year and it is necessary to interpret trends with caution.

Bacillus cereus intoxication

Case definition

Clinical description:	Gastroenteritis where either vomiting or profuse watery diarrhoea dominate.
Laboratory test for diagnosis:	Isolation of ≥10^3/gram *Bacillus cereus* from a clinical specimen or ≥10^4/gram *B. cereus* from leftover food or detection of diarrhoeal toxin in a faecal sample.
Case classification:	
Probable	A clinically compatible illness.
Confirmed	A clinically compatible illness that is laboratory confirmed, OR a clinically compatible illness and a common exposure associated with a laboratory confirmed case.

Bacillus cereus intoxication individual cases reported in 2024 by data source

During 2024, no individual cases of *B. cereus* intoxication were reported in EpiSurv.

Note that not every individual case of *B. cereus* intoxication is necessarily notifiable; only when the infected person is in a high-risk category (e.g., food handler, early childhood service worker) or the case is part of an outbreak.

The international statistical classification of diseases and related health problems (ICD-10) code A05.4 was used to extract foodborne *B. cereus* intoxication hospitalisation data from the Health New Zealand Te Whatu Ora National Minimum Dataset (NMDS). In 2024, one case was hospitalised[1] with *B. cereus* intoxication as the principal diagnosis.

It should be noted that EpiSurv and NMDS are two separate databases that are used for different purposes. Therefore, NMDS and EpiSurv hospitalisation numbers may differ for several reasons, including criteria used for notifications or diagnostic coding, i.e. a hospital discharge may be coded to an infectious cause without a case being recorded in EpiSurv and vice versa (see also Appendix A–Methods, page 123).

Outbreaks reported as caused by *Bacillus cereus*

In 2024 there was one outbreak report in EpiSurv with *B. cereus* confirmed as the causative agent (Table 7). It is important to note that a single outbreak may have multiple pathogens, settings and possible modes of transmission.

Table 7. *B. cereus* outbreak reported in EpiSurv, 2024

	Possible foodborne transmission with a suspected or confirmed source	Possible foodborne transmission but no suspected food source	Total *B. cereus* outbreaks
Outbreaks	1	0	1
Outbreak associated cases	2	0	2
Outbreak hospitalised cases	0	0	0

[1] Rate per 100,000 population not calculated when fewer than five cases reported.

A beef rib dish was the suspected but not confirmed food source for this outbreak (Table 8). Two people who had no common exposures in the month before the group meal both became ill. Four people who attended the meal and did not eat the beef rib dish were not ill.

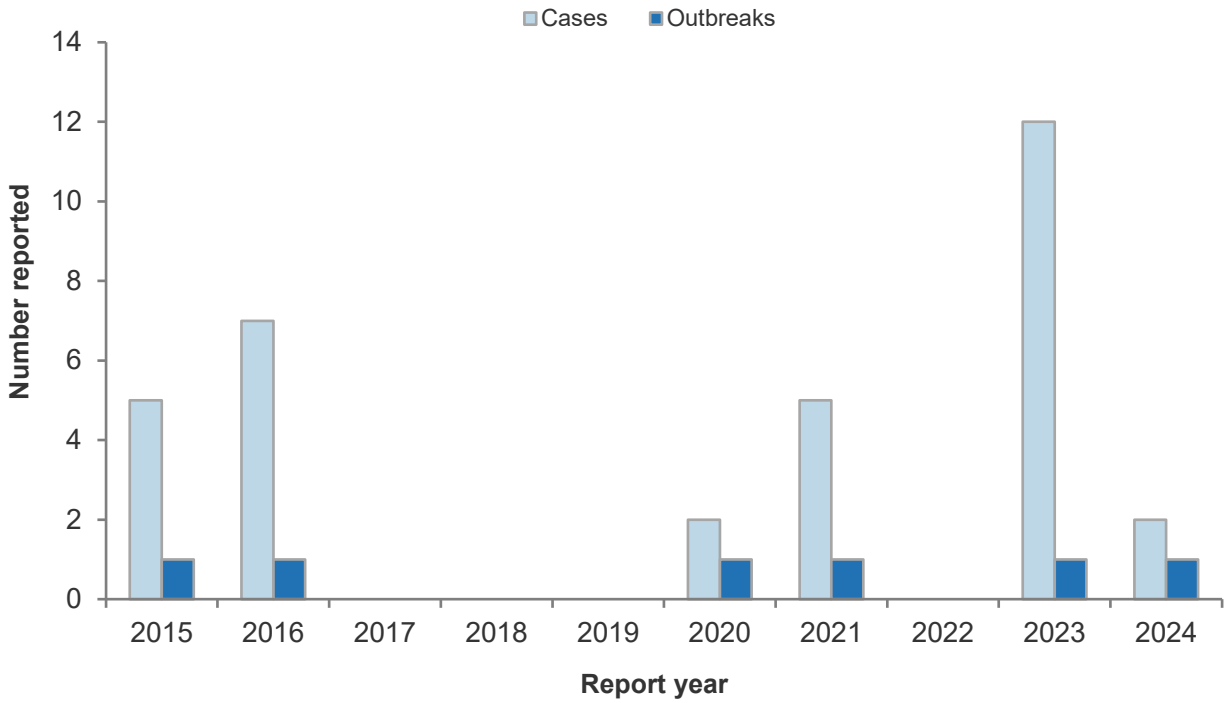
Table 8. Details of *B. cereus* outbreak reported in 2024

Health district	Report Month	Suspected source	Evidence	Setting	No. ill
Southern	July	Beef rib dish	Common meal	Restaurant/café/bakery	1C 1P

Number ill: C: Confirmed, P: Probable

Outbreaks of *B. cereus* intoxication are rare, with only six outbreaks reported in EpiSurv since 2015. The number of cases associated with individual outbreaks ranged between two and 12 cases (Figure 3).

Figure 3. *B. cereus* intoxication outbreaks with food reported as a possible mode of transmission and associated cases reported by year, 2015–2024



Note: The data in this figure comes from EpiSurv for the years up to 2021. From 2021 the plot includes foodborne outbreaks recorded in EpiSurv and any outbreaks that were referred to NZFS but were not recorded in EpiSurv as an outbreak.

Recent surveys

Nil.

Relevant New Zealand studies and publications

Nil.

Relevant regulatory developments

No *B. cereus*-specific regulatory developments.

Campylobacteriosis

Case definition

Clinical description:	An illness of variable severity with symptoms of abdominal pain, fever and watery diarrhoea, and sometimes bloody stools. Less frequently, *Campylobacter* can present as an invasive disease.
Laboratory test for diagnosis:	Isolation of *Campylobacter* spp. from a clinical specimen OR detection of *Campylobacter* nucleic acid OR detection of antigen.
Case classification:	
Probable	A clinically compatible illness that is either a contact of a confirmed case of the same disease or has had contact with the same common source – that is, is part of a common-source outbreak.
Confirmed	A clinically compatible illness that is laboratory confirmed.

Summary data

Summary data for campylobacteriosis in 2024 are given in Table 9.

Table 9. Summary of surveillance data for campylobacteriosis, 2024

Parameter	Value in 2024	Source
Number of notified cases	5801	EpiSurv
Notification rate (per 100,000)	108.7	EpiSurv
Hospitalised cases[a]	1038	NMDS
Deaths[b]	1	EpiSurv
Estimated number of cases related to travel (%)[c,d]	801 (13.8%)	EpiSurv
Estimated domestically acquired food-related cases[e]	3750	EpiSurv and expert consultation

NMDS = Health New Zealand Te Whatu Ora National Minimum Dataset of hospitalisations.

[a] Cases hospitalised may not be notified on EpiSurv.

[b] In 2024, seven cases with campylobacteriosis were recorded in EpiSurv as having died but death was attributed to campylobacteriosis for only one case. Three cases died from a cause other than campylobacteriosis and the cause of death was not recorded for the remaining three cases.

[c] Estimated number and % of cases related to travel. Of the 5801 notified cases, the overseas travel question had a 'yes' or 'no' entry for 2216 cases (38.2%); of these, 306 cases (13.8%) had travelled overseas during the incubation period and 1910 cases (86.2%) had not been overseas. The overseas travel history for the remaining 3585 cases is unknown. The estimated number of cases related to travel is given as 13.8% percent of all cases in 2024.

[d] While international travel has increased again since restrictions ceased in 2022, overseas travel in 2024 was still slightly lower compared with the pre-COVID-19 year 2019 (see section Changes in overseas travel, page 11).

[e] Estimation of food-related cases is given by (Total cases – Estimate of cases acquired overseas) x Estimate of proportion of domestically acquired cases likely to be due to foodborne transmission). The estimate of domestic proportion of campylobacteriosis cases due to foodborne transmission (75%) was derived from expert consultation [3].

Campylobacteriosis individual cases reported in 2024 by data source

During 2024, 5801 individual cases (108.7 cases per 100,000 population) of campylobacteriosis and one resulting death in the 60-69 age group were reported in EpiSurv.

The ICD-10 code A04.5 was used to extract campylobacteriosis hospitalisation data from the Health New Zealand Te Whatu Ora NMDS database. Of the 1038 hospitalised cases (19.4 hospitalised cases per 100,000 population) recorded in 2024, 874 cases were reported with campylobacteriosis as the principal diagnosis and 164 were reported with campylobacteriosis as another relevant diagnosis.

Some of the 1038 hospitalised cases were admitted to hospital more than once resulting in a total of 1104 hospital admissions. The majority of hospitalised cases (52%) spent between two and six nights in hospital, with 2.1% of hospitalised cases admitted to an intensive care unit (Appendix C, Table 69).

It should be noted that EpiSurv and NMDS are two separate databases that are used for different purposes. Therefore, NMDS and EpiSurv hospitalisation numbers may differ for several reasons, including criteria used for notifications or diagnostic coding (see also Appendix A–Methods, page 123).

Foodborne transmission

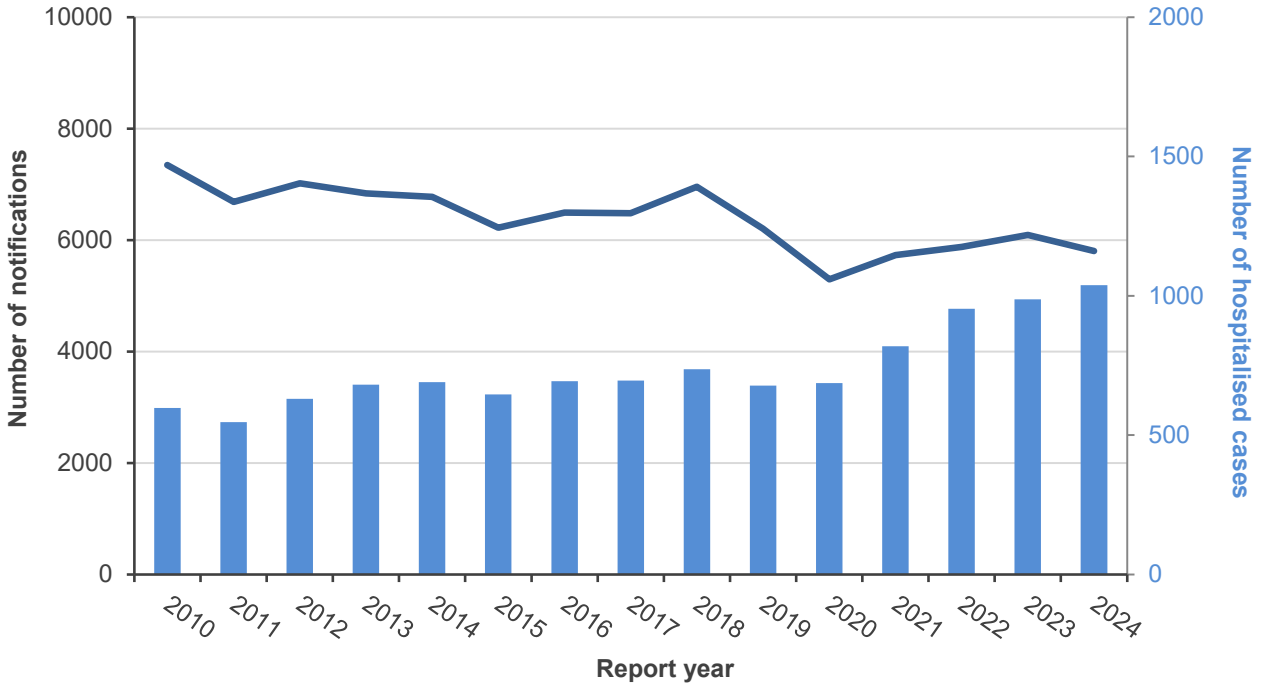
It has been estimated by expert consultation that 75% of campylobacteriosis incidence is due to foodborne transmission [3]. It was further estimated that approximately 75% of foodborne campylobacteriosis was due to transmission via poultry [2].

Annual data

Historically, the number of campylobacteriosis notifications reported had increased year-on-year up to the highest number recorded in 2006 (15,873 cases). Due to measures taken by NZFS (and its predecessors) and the poultry industry, there was a significant decrease in the number of notified cases from 2006 to 2008 [22, 23]. Between 2010 and 2019 the annual number of notifications varied between 6202 and 7346 cases. The decrease in 2020 is attributable to the national protection measures implemented in response to the COVID-19 pandemic (Figure 4 and Figure 5) [18]. Some of that decrease may have been due to a reduction in the frequency of overseas travel from 2020 (see section Changes in overseas travel, page 11) but the resultant outcome of decreased notifications was likely multifactorial [24]. In 2024, the estimated percentage of campylobacteriosis cases related to overseas travel was 13.8% (95% CI: 12.7-14.9%), compared with 14.2% (95% CI: 13.3-15.2%) in 2019 (pre-COVID-19 pandemic) and 0.3% (95% CI: 0.1-0.5%) in 2021 (year of greatest reduction in travel). In 2024, the number of notifications was slightly lower than in 2023 (5801 and 6092 notifications, respectively).

Between 2010 and 2020 the number of hospitalised cases with campylobacteriosis as a principal or other relevant diagnosis ranged between 540 to 695 cases per year. From 2021 the number and rate of hospitalised cases has been steadily increasing, with 1038 hospitalised cases in 2024. The decrease in notified cases alongside the increase in hospitalised cases (i.e., a higher proportion of cases requiring hospitalisation) may be due to a combination of different factors. A recent Health New Zealand report highlighted that in recent years, overall visits to the GP decreased while overall visits to the emergency department increased. It noted that it was increasingly difficult to access primary healthcare due to increased wait times and cost [25]. Therefore, people with less or mild symptoms may not seek healthcare and those with more severe symptoms may directly access the hospital service. The possibility of increased pathogenicity of circulating strains cannot be determined without comparison of current and more historic strains.

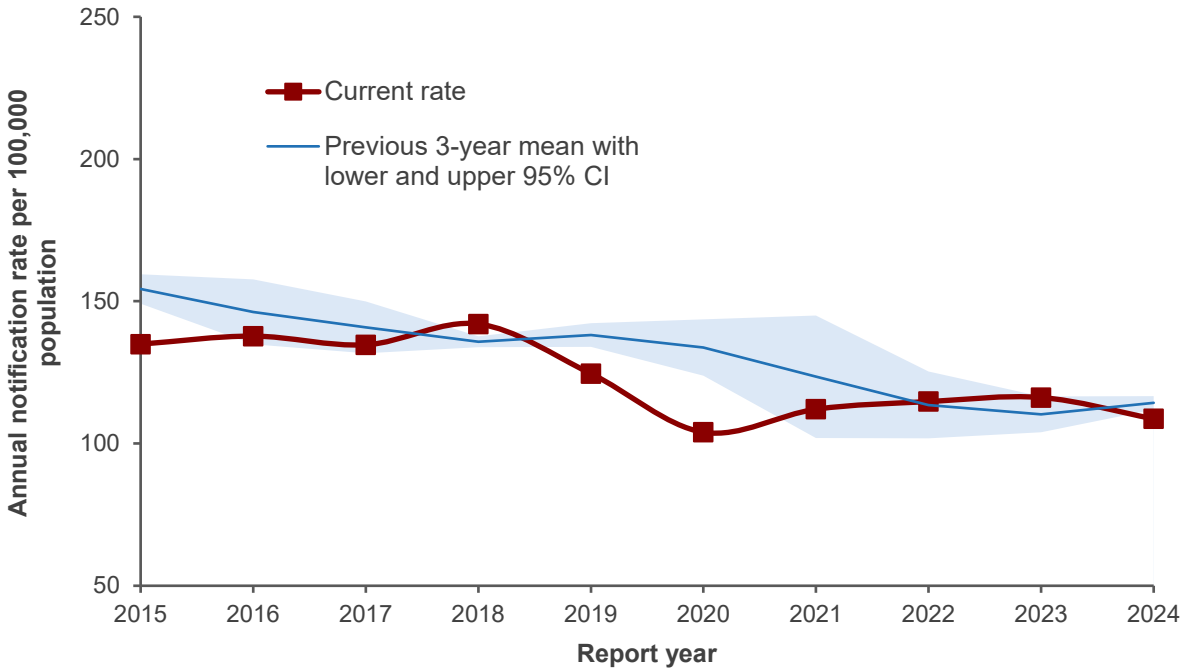
Figure 4. Campylobacteriosis EpiSurv notifications (line) and NMDS hospitalised cases (bar) by year, 2010–2024



Note: 2016 campylobacteriosis notifications have been adjusted to exclude 964 cases associated with the Hawke's Bay drinking water-related campylobacteriosis outbreak.

In 2024, the notification rate for campylobacteriosis (108.7 cases per 100,000 population) was lower (outside the 95% CI) than the previous three-year mean (114.5 cases per 100,000 population). The trend for the previous three-year mean was generally downward since 2015. In 2020, the campylobacteriosis notification rate (104.0 cases per 100,000 population) was much lower compared with the previous years, likely due to the impact of COVID-19-related health measures (Figure 5).

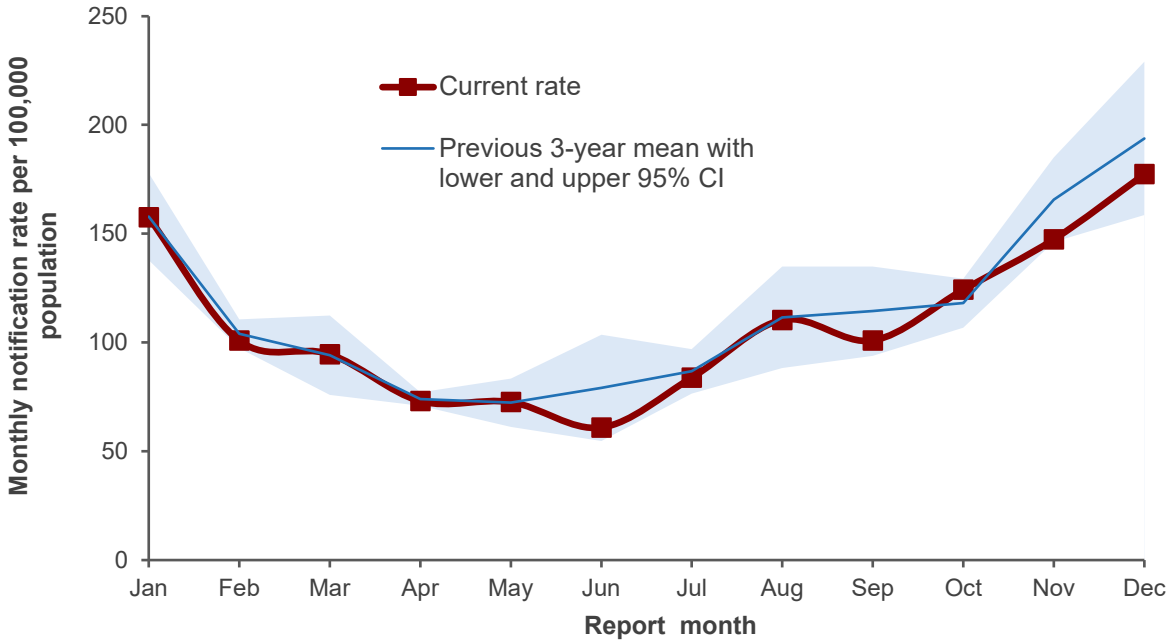
Figure 5. Campylobacteriosis notification rate by year, 2015–2024



Seasonal data

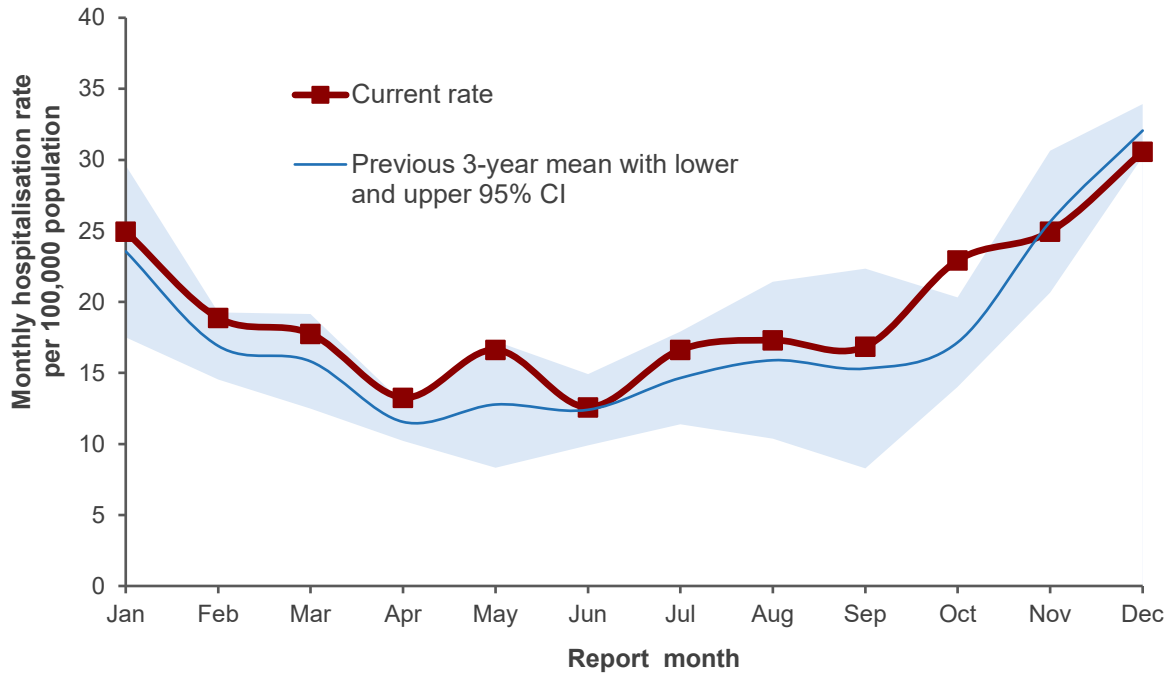
Campylobacteriosis notification rates per 100,000 population by month for 2024 are shown in Figure 6. In 2024, monthly notification rates followed a similar trend compared with previous years. The monthly number of notifications in 2024 ranged from 271 cases (June, 60.9 cases per 100,000 population) to 789 cases (December, 177.4 cases per 100,000 population).

Figure 6. Campylobacteriosis monthly notification rate (annualised), 2024



In 2024, monthly hospitalisation rates (Figure 7) followed a similar trend to monthly notification rates (Figure 6) with higher rates in spring and early to mid-summer. Monthly hospitalisation rates were comparable with previous years, except for the months April and October where the monthly rate was above the upper 95% confidence interval for the previous three-year mean. The monthly number of hospitalised cases in 2024 ranged from 56 cases (June, 12.6 cases per 100,000 population) to 136 cases (December, 30.6 cases per 100,000 population).

Figure 7. Campylobacteriosis monthly hospitalisation rate (annualised), 2024



Demographics

In 2024, the rates of notifications and hospitalised cases for campylobacteriosis were higher for males (120.8 notified cases and 21.4 hospitalised cases per 100,000 population) compared with females (96.5 notified cases and 17.5 hospitalised cases per 100,000 population) (Table 10).

Table 10. Campylobacteriosis cases by sex, 2024

Sex	EpiSurv notified cases		Hospitalised cases[a]	
	No.	Rate[b]	No.	Rate[b]
Male	3210	120.8	569	21.4
Female	2589	96.5	469	17.5
Total[c]	**5801**	**108.7**	**1038**	**19.4**

[a] Health New Zealand Te Whatu Ora NMDS data.

[b] Per 100,000 population in this sex group.

[c] Total includes cases where sex was not recorded.

The highest age-specific notification rate for campylobacteriosis in 2024 was reported for children in the 1 to 4 years age group (194.3 cases per 100,000 population, 474 cases). The highest hospitalised case rate was for the 70 years and over age group (52.9 hospitalised cases per 100,000 population, 328 cases) (Table 11). The 70+ years age group was also the age group with the longest hospital stays (Appendix C, Table 79 and the most admissions to an intensive care unit (Appendix C, Table 80).

Table 11. Campylobacteriosis cases by age group, 2024

Age group (years)	EpiSurv notified cases		Hospitalised cases[a]	
	No.	Rate[b]	No.	Rate[b]
<1	102	176.3	21	36.3
1 to 4	474	194.3	50	20.5
5 to 9	205	62.4	22	6.7
10 to 14	186	53.3	20	5.7
15 to 19	295	86.5	43	12.6
20 to 29	738	107.5	115	16.7
30 to 39	633	78.3	93	11.5
40 to 49	594	89.2	88	13.2
50 to 59	724	111.0	119	18.2
60 to 69	828	141.6	139	23.8
70+	1022	164.9	328	52.9
Total	**5801**	**108.7**	**1038**	**19.4**

[a] Health New Zealand Te Whatu Ora NMDS data.

[b] Per 100,000 population in this age group.

In 2024, the campylobacteriosis notification and hospitalised case rates were highest for the ethnic groups ‘European or Other’ (127.9 cases and 22.7 hospitalised cases per 100,000 population) and MELAA (108.1 cases and 23.2 hospitalised cases per 100,000 population) (Appendix C, Table 70 and Table 71).

Geographic distribution

The notification rates by Health District calculated per 100,000 resident population are presented in Figure 8 (see also Appendix C, Table 83). The number of notified cases by Health District are presented in Appendix C, Table 82.

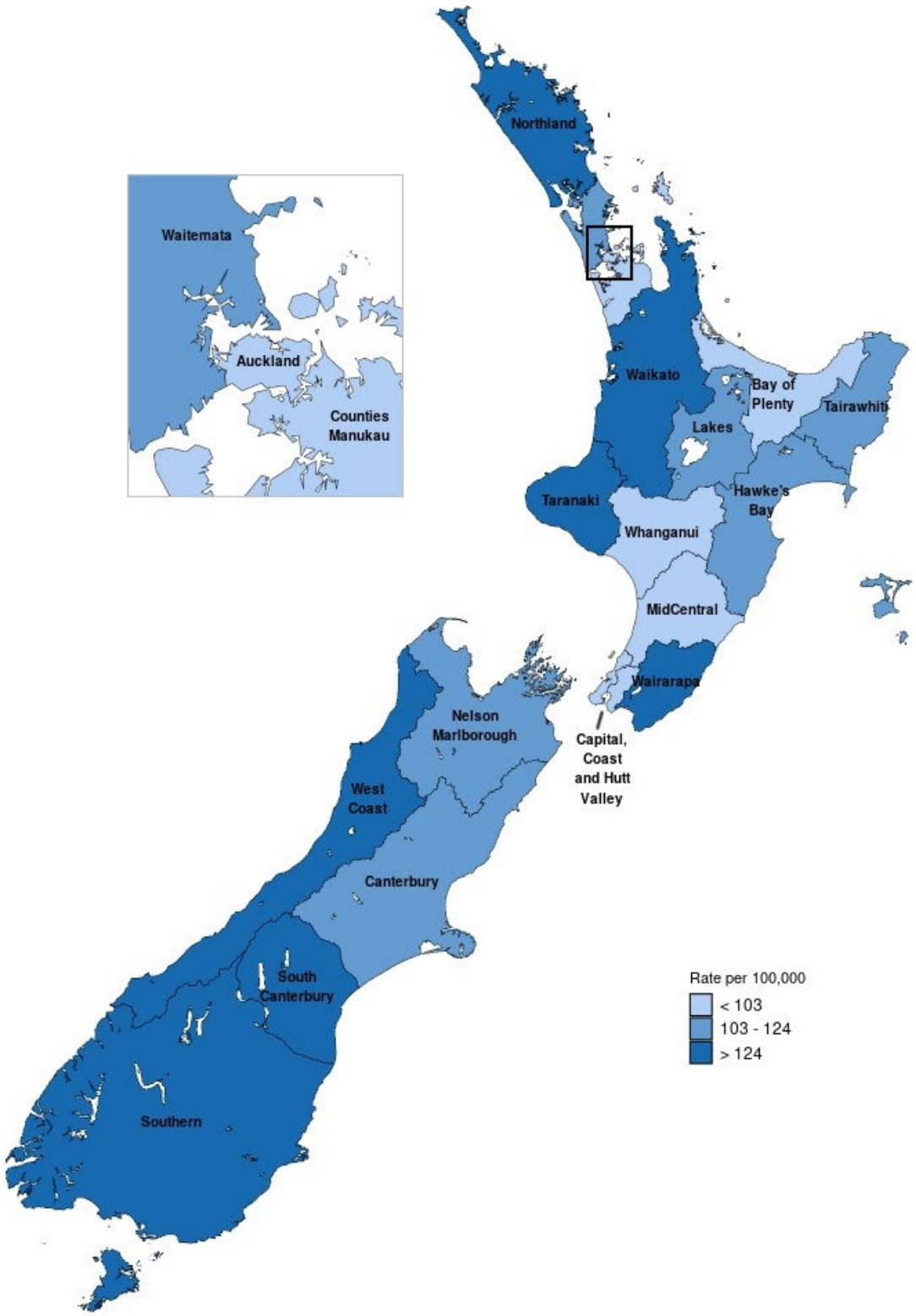
In 2024, Health District notification rates of campylobacteriosis ranged from 86.4 cases per 100,000 population (552 cases) in Counties Manukau to 180.6 cases per 100,000 population (117 cases) in South Canterbury. Taranaki Health District (174.0 cases per 100,000 population, 228 cases) had the second highest notification rate.

From 2020 to 2024, notification rates for campylobacteriosis have been variable across New Zealand with the Health Districts; South Canterbury, Wairarapa, and Taranaki consistently in the highest quartile. South Canterbury Health District has had the highest rates since 2020 ranging from 180.6 cases per 100,000 population in 2024 to 246.0 cases per 100,000 population in 2021.

Campylobacteriosis notification rates, stratified by the 2023 Urban Rural Classification [26] of the cases’ residential address and excluding cases associated with overseas travel, generally increased as the area of residence became more rural (Appendix C, Table 84). Rates of cases residing in urban areas ranged from 80.5 to 110.6 cases per 100,000 population. The highest case notification rate was for the ‘rural other’ category (192.3 cases per 100,000 population). The highest hospitalised case rate

was for the ‘rural settlement’ category (48.2 hospitalised cases per 100,000 population) but lowest for ‘rural other’ (7.2 hospitalised cases per 100,000 population) (Appendix C, Table 85).

Figure 8. Geographic distribution of campylobacteriosis notifications, 2024



Outbreaks reported as caused by *Campylobacter* spp.

In 2024, there were a total of 10 campylobacteriosis outbreak notifications in EpiSurv. One outbreak was due to an infection acquired overseas. Four outbreaks recorded food as a possible mode of transmission (Table 12). It is important to note that a single outbreak may have multiple pathogens, settings, and possible modes of transmission.

Table 12. Campylobacteriosis outbreaks reported in EpiSurv, 2024

	Possible foodborne transmission with a suspected or confirmed source	Possible foodborne transmission but no suspected food source	Total campylobacteriosis outbreaks
Outbreaks	4	0	10
Outbreak associated cases	25	0	102
Outbreak hospitalised cases	1	0	1

Table 13 contains details of the four domestic campylobacteriosis outbreaks reported in EpiSurv with food as a possible mode of transmission. In addition, three suspected outbreaks (two cases each) are included, which were referred to NZFS.

The evidence for the food source was strong for the February raw milk outbreak, where students consumed milk on farm visits. A cohort study provided evidence for consumption of unpasteurised milk as a likely source and a dose response was observed with higher consumption of milk resulting in a higher risk of illness.

For the two outbreaks related to chicken liver parfait, the food source could not be confirmed as the cause of illness. At both venues people with no prior common exposures became ill after eating chicken liver parfait. The food source for the other poultry liver outbreaks could also not be confirmed. NZFS investigations confirmed the lambs fry to be the cause of the May outbreak.

Table 13. Details of campylobacteriosis outbreaks with food reported as a possible mode of transmission, 2024

Health district	Report month	Suspected or confirmed source	Evidence	Setting	No. ill
Canterbury	February	Raw milk	Common exposure and cohort study	Student farm visits	3C 9P
Bay of Plenty	April	Chicken liver pâté	Common food	Restaurant/café/bakery	2C
Capital, Coast and Hutt Valley	May	Lambs fry	Common food	Restaurant/café/bakery	1C 1P
Canterbury	June	Chicken liver parfait	Common food/venue	Restaurant/café/bakery	1C 2P
Capital, Coast and Hutt Valley	September	Chicken liver	Common food	Restaurant/café/bakery	2C
Canterbury	September	Chicken liver parfait	Common food/venue	Restaurant/café/bakery	8C
Capital, Coast and Hutt Valley	September	Duck liver aperitif	Common food	Restaurant/café/bakery	1C 1P

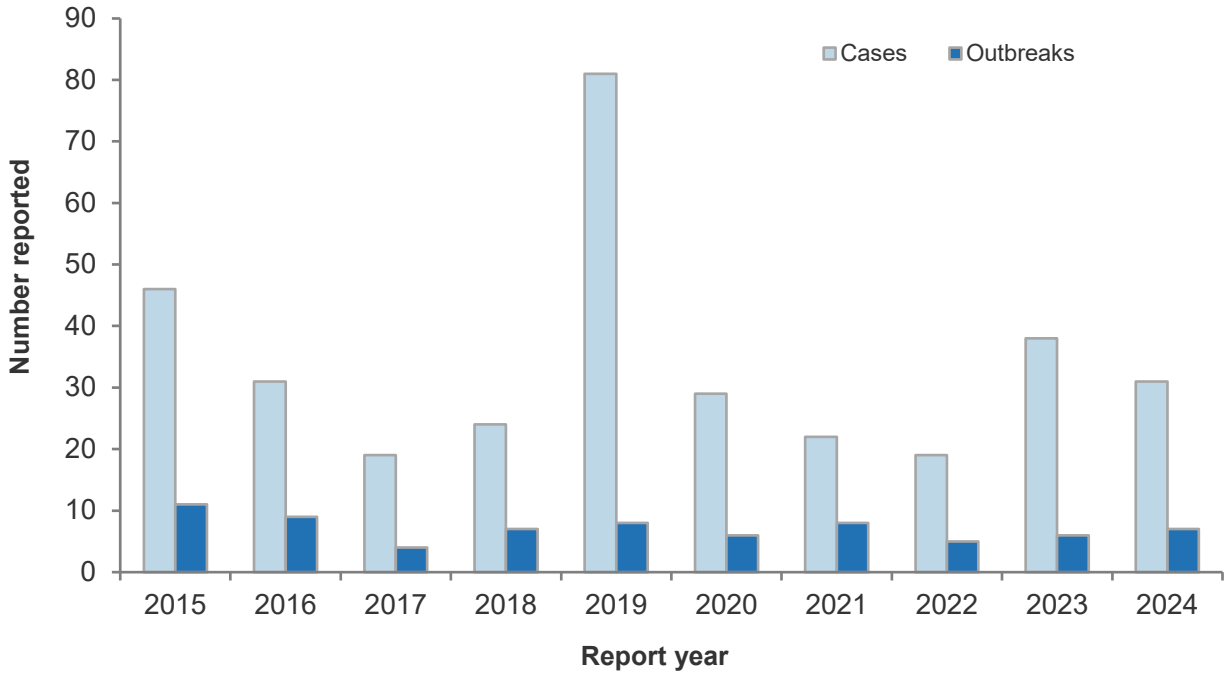
Number ill: C: confirmed, P: probable.

Note: The May outbreak and the two Capital, Coast and Hutt Valley September outbreaks were referred to NZFS for investigation but not listed as an outbreak in EpiSurv.

In 2024 NZFS also investigated a further two cases of campylobacteriosis associated with a raw milk outbreak that involved three cases in November 2023.

Between 2015 and 2024 the number of outbreaks of campylobacteriosis with food reported as a possible mode of transmission ranged from four to 11 outbreaks each year with between 19 (2017 and 2022) and 81 (2019) annual outbreak-associated cases (Figure 9)

Figure 9. Campylobacteriosis outbreaks with food reported as a possible mode of transmission and associated cases reported by year (excluding outbreaks associated with overseas travel), 2015–2024



Note: Prior to 2021, the data presented is derived from EpiSurv. From 2021 the figure includes foodborne outbreaks recorded in EpiSurv plus any outbreaks that were referred to NZFS but were not recorded in EpiSurv as an outbreak.

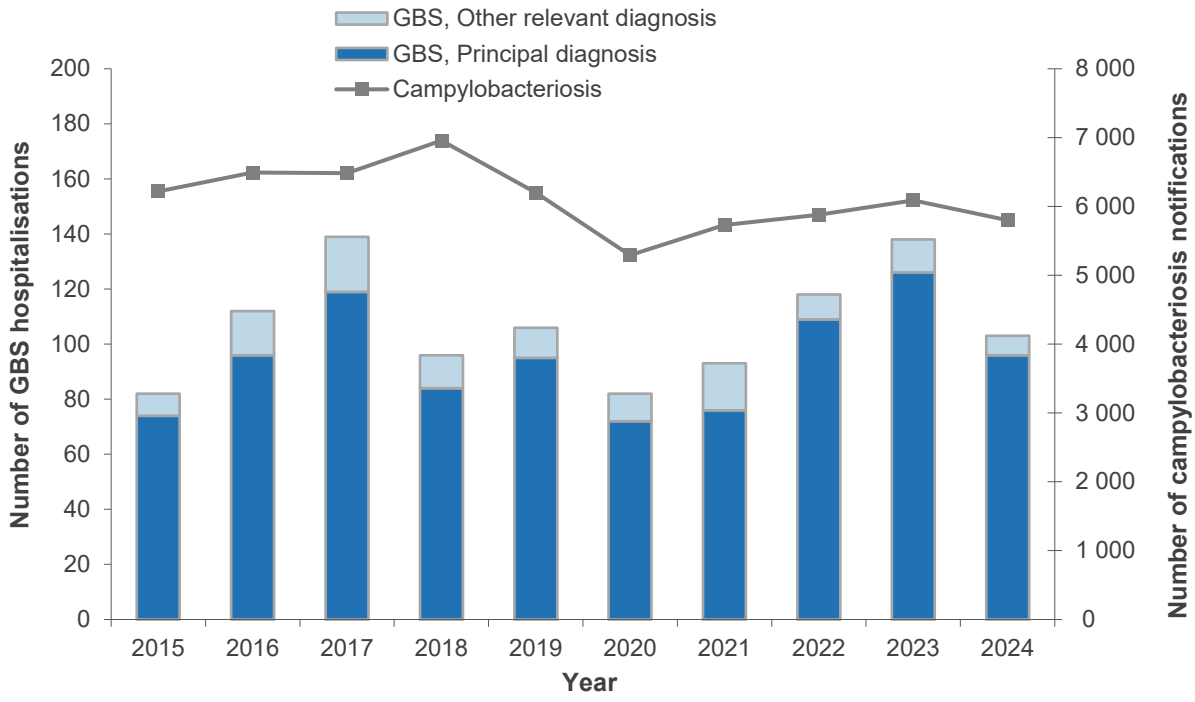
Disease sequelae - Guillain-Barré syndrome

Guillain-Barré syndrome (GBS) is a post-infectious disorder, which may be preceded by a range of respiratory or intestinal infections but is predominantly associated with *Campylobacter jejuni* infections, with approximately 30% of GBS cases having had a *C. jejuni* infection 1-3 weeks before onset of GBS [27].

The ICD-10 code G61.0 was used to extract GBS hospitalisation data from the Health New Zealand Te Whatu Ora NMDS database. Only GBS cases that were incident in 2024 were considered, rather than all cases that were hospitalised in 2024. That is, if a GBS case hospitalised in 2024 had been hospitalised with GBS in a previous year, the 2024 admission was considered to be a readmission, rather than an incident case. There were 103 incident cases recorded in 2024 (1.9 hospitalised cases per 100,000 population), 96 were reported with GBS as the principal diagnosis and 7 with GBS as another relevant diagnosis.

Between 2015 and 2024, the annual number of incident cases (any diagnosis code) for GBS ranged from 82 to 139 (Figure 10). The numbers of campylobacteriosis notifications during the same period are also included in Figure 10 for comparison. It was reported that three years after the major decrease in campylobacteriosis cases, campylobacteriosis notification had decreased by 52%, while GBS hospitalised cases had decreased by 13% [28]. This would be consistent with 20-30% of GBS cases being due to a preceding *C. jejuni* infection. The year-to-year variability in incident hospitalisation due to GBS means that any correlations during 2015-2024 would be difficult to detect.

Figure 10. Guillain-Barré syndrome incident cases, 2015–2024



In 2024, the number of incident cases due to GBS was higher for males than for females (Table 14). This is consistent with the pattern seen for GBS in most previous years, except 2016 when case numbers for males and females were almost identical. It is also consistent with the gender differences seen in notification rates for campylobacteriosis in males and females in 2024 (Table 10).

Table 14. Guillain-Barré syndrome incident cases by sex, 2024

Sex	Cases[a]	
	No.	Rate[b]
Male	58	2.2
Female	45	1.7
Total	**103**	**1.9**

[a] Health New Zealand Te Whatu Ora NMDS data.

[b] per 100,000 population.

In 2024, the highest rates of incident cases for GBS were in the 60 to 69 years age group, followed by the 70+ and 50-59 years age groups (Table 15).

Table 15. Guillain-Barré syndrome incident cases by age group, 2024

Age group (years)	Cases[a]	
	No.	Rate[b]
<1	0	-
1 to 4	3	-
5 to 9	2	-
10 to 14	3	-
15 to 19	3	-
20 to 29	10	1.5
30 to 39	14	1.7
40 to 49	9	1.4
50 to 59	20	3.1
60 to 69	20	3.4
70+	19	3.1
Total	**103**	**1.9**

[a] Health New Zealand Te Whatu Ora NMDS data.

[b] per 100,000 population (rate not calculated when fewer than five cases reported).

Recent surveys

Consumer magazine carried out a small survey of frozen, crumbed chicken products, such as nuggets, burgers and tenders (*n* = 39) [29]. *Campylobacter* was not detected in any of the samples analysed. An associated survey of 1001 New Zealanders, aged 18 years and older, found that most (51%) assessed whether products were sufficiently cooked by visual inspection of the interior of the product. A further 29% cooked products according to manufacturer's instructions.

Relevant New Zealand studies and publications

Journal papers

Antimicrobial resistance in selected bacteria from food animals in New Zealand 2018–2022 – Cornelius et al., 2024

Campylobacter isolates (*n* = 300) from poultry, collected during 2018-2019, were examined for resistance to gentamicin, streptomycin, ciprofloxacin, erythromycin, nalidixic acid and tetracycline [30]. Most *C. jejuni* isolates (81.9%) were susceptible to all tested antimicrobials. However, 16.6% of isolates were resistant to the quinolones (ciprofloxacin and nalidixic acid) and tetracycline. Most *C. coli* isolates were susceptible to all tested antimicrobials. Isolates showing resistance only showed resistance to a single antimicrobial, either streptomycin or tetracycline.

Relevant regulatory developments

No *Campylobacter*-specific regulatory developments.

Ciguatera poisoning

Case definition

Clinical description:	Gastroenteritis, possibly followed by neurologic symptoms.
Laboratory test for diagnosis:	Demonstration of ciguatoxin in implicated fish.
Case classification:	Not applicable.

Ciguatera poisoning individual cases reported in 2024 by data source

During 2024, no individual cases of ciguatera poisoning were reported in EpiSurv.

The ICD-10 code T61.0 was used to extract foodborne ciguatera poisoning hospitalisation data from the Health New Zealand Te Whatu Ora NMDS database. In 2024, four cases were hospitalised[1] with ciguatera poisoning, three of which were reported with ciguatera poisoning as the principal diagnosis and one case with ciguatera poisoning as another relevant diagnosis. One of the four hospitalised cases was hospitalised twice.

It should be noted that EpiSurv and NMDS are two separate databases that are used for different purposes. Therefore, NMDS and EpiSurv hospitalisation numbers may differ for several reasons, including criteria used for notifications or diagnostic coding, i.e. a hospital discharge may be coded to an infectious cause without a case being recorded in EpiSurv and vice versa (see also Appendix A–Methods, page 123).

Outbreaks reported as caused by ciguatera poisoning

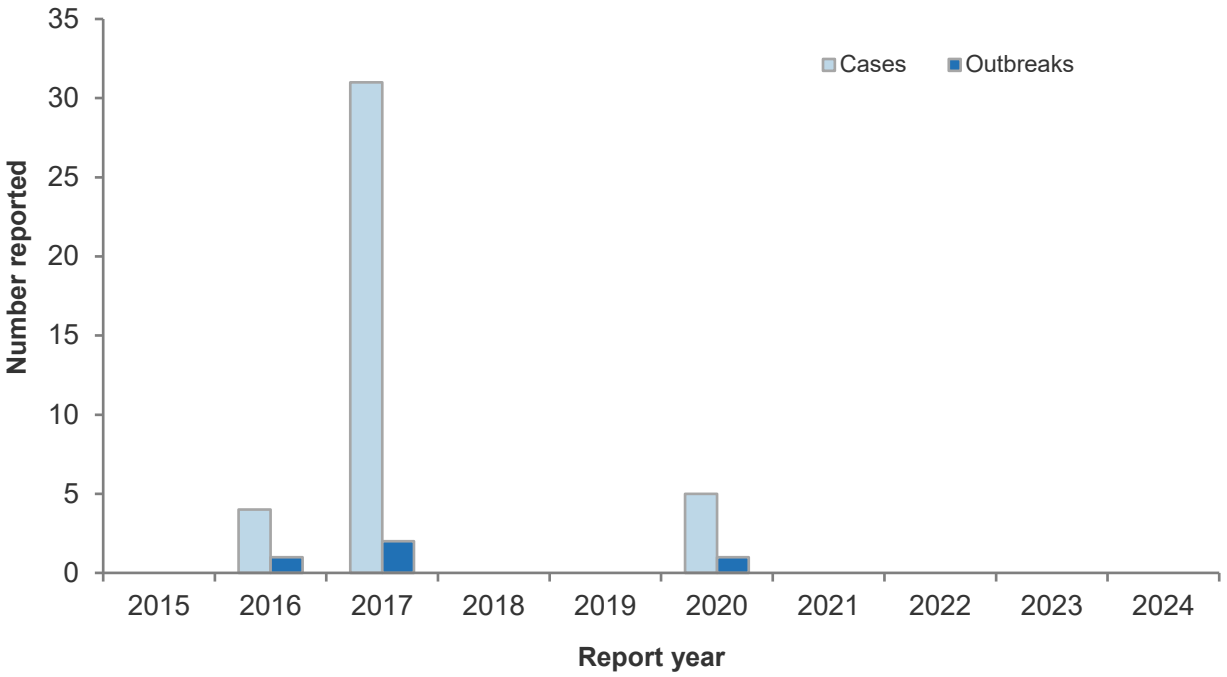
During 2024, no outbreaks of ciguatera poisoning were reported in EpiSurv.

It should be noted that all cases of ciguatera poisoning will be categorised as foodborne as consumption of contaminated seafood is the only recognised transmission route for this disease.

Over the 10-year period 2015 to 2024, a total of four outbreaks of ciguatera poisoning were reported, with no more than two outbreaks reported in a single year and no outbreaks reported in the last four years (Figure 11). In 2017, the number of cases associated with one outbreak was unusually high (27 cases). The preparation setting for this 2017 outbreak was reported as an overseas manufacturer.

[1] Rate per 100,000 population not calculated when fewer than five cases reported.

Figure 11. Ciguatera poisoning outbreaks and associated cases reported by year, 2015–2024



Note: The data in this figure comes from EpiSurv for the years up to 2021. From 2021 the plot includes foodborne outbreaks recorded in EpiSurv and any outbreaks that were referred to NZFS but were not recorded in EpiSurv as an outbreak.

Recent surveys

Nil.

Relevant New Zealand studies and publications

Nil.

Relevant regulatory developments

No ciguatera-specific regulatory developments.

Clostridium perfringens intoxication

Case definition

Clinical description:	Gastroenteritis with profuse watery diarrhoea.
Laboratory test for diagnosis:	Detection of enterotoxin in faecal specimen or faecal spore count of ≥10^6/gram or isolation of ≥10^5/gram *Clostridium perfringens* in leftover food.
Case classification:	
Probable	A clinically compatible illness.
Confirmed	A clinically compatible illness that is laboratory confirmed, OR a clinically compatible illness and a common exposure associated with a laboratory confirmed case.

Clostridium perfringens intoxication cases reported in 2024 by data source

During 2024, nine individual cases of confirmed *C. perfringens* intoxication were reported in EpiSurv.

The ICD-10 code A05.2 was used to extract foodborne *C. perfringens* intoxication hospitalisation data from the Health New Zealand Te Whatu Ora NMDS database. In 2024, one case was hospitalised[1] with *C. perfringens* intoxication as another relevant diagnosis.

It should be noted that EpiSurv and NMDS are two separate databases that are used for different purposes. Therefore, NMDS and EpiSurv hospitalisation numbers may differ for several reasons, including criteria used for notifications or diagnostic coding, i.e. a hospital discharge may be coded to an infectious cause without a case being recorded in EpiSurv and vice versa (see also Appendix A–Methods, page 123).

Outbreaks reported as caused by *Clostridium perfringens*

In 2024 there were three *C. perfringens* intoxication outbreaks with a total of 180 cases and no hospitalisations reported in EpiSurv (Table 16). For all three outbreaks food was reported as a possible mode of transmission.

Table 16. *C. perfringens* outbreaks reported in EpiSurv, 2024

	Possible foodborne transmission with a suspected or confirmed source	Possible foodborne transmission but no suspected food source	Total *C. perfringens* outbreaks
Outbreaks	3	0	3
Outbreak associated cases	180	0	180
Outbreak hospitalised cases	0	0	0

Table 17 contains details of the three *C. perfringens* intoxication outbreaks with food as a possible mode of transmission. The food source for the February and December outbreaks could not be confirmed. The suspected food in the February outbreak was lamb that was partially cooked at a commercial kitchen and then reheated at the food premise.

[1] Rate per 100,000 population not calculated when fewer than five cases reported.

The large outbreak (171 cases, no hospitalisations) of *C. perfringens* intoxication reported in EpiSurv in November was associated with a meal served at a university hall. A questionnaire completed by diners provided strong evidence the outbreak was due to chicken souvlaki. No food was available for laboratory testing.

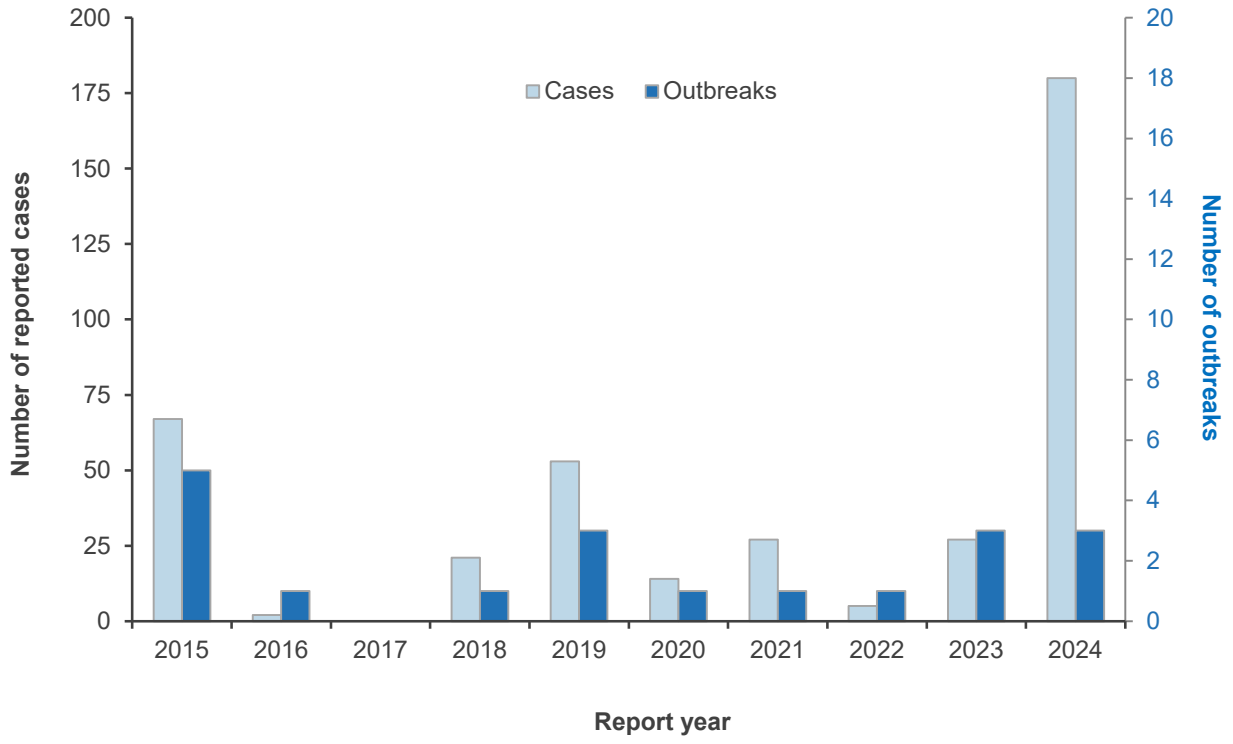
Table 17. Details of *C. perfringens* intoxication outbreaks with food reported as a possible mode of transmission, 2024

Health District	Month	Suspected source	Evidence	Setting	No. ill
Capital, Coast and Hutt Valley	February	Lamb	Common event	Restaurant	2C 3P
Canterbury	November	Chicken souvlaki	Common meal	Hostel/boarding house	6C 165P
Capital, Coast and Hutt Valley	December	Lamb tacos	Common event	Restaurant	1C 3P

Number ill: C: Confirmed, P: Probable

Over the 10-year period 2015-2024, the number of outbreaks of *C. perfringens* intoxication with food reported as a possible mode of transmission ranged from zero (2017) to five outbreaks (in 2015) (Figure 12). The number of cases associated with outbreaks of *C. perfringens* intoxication has also varied markedly over time. The highest number of cases in an outbreak of *C. perfringens* intoxication with possible transmission by food occurred in 2024 (171 cases), which is substantially more cases than observed in other outbreaks of *C. perfringens* intoxication in the last 10 years.

Figure 12. *C. perfringens* intoxication outbreaks with food reported as a possible mode of transmission and associated cases reported by year, 2015–2024



Note: The data in this figure comes from EpiSurv for the years up to 2021. From 2021 the plot includes foodborne outbreaks recorded in EpiSurv and any outbreaks that were referred to NZFS but were not recorded in EpiSurv as an outbreak.

Recent surveys

Nil.

Relevant New Zealand studies and publications

Nil.

Relevant regulatory developments

No *C. perfringens*-specific regulatory developments.

Cryptosporidiosis

Case definition

Clinical description:	An acute illness that includes symptoms of diarrhoea (may be profuse and watery) and abdominal pain. The infection may be asymptomatic but to meet the case definition the individual must have compatible symptoms.
Laboratory test for diagnosis:	Detection of *Cryptosporidium* spp. oocysts OR *Cryptosporidium* antigen OR *Cryptosporidium* nucleic acid in a faecal specimen.
Case classification:	
Probable	A clinically compatible illness that is either a contact of a confirmed case of the same disease, or has had contact with the same common source, i.e., is part of an identified common source outbreak.
Confirmed	A clinically compatible illness that is laboratory confirmed.

Summary data

Summary data for cryptosporidiosis in 2024 are given in Table 18.

Table 18. Summary of surveillance data for cryptosporidiosis, 2024

Parameter	Value in 2024	Source
Number of notified cases	1234	EpiSurv
Notification rate (per 100,000)	23.1	EpiSurv
Hospitalised cases[a]	93	NMDS
Deaths	0	EpiSurv
Estimated number of cases related to travel (%)[b,c]	166 (13.4%)	EpiSurv
Estimated domestically acquired food-related cases (%)	NE	-

NE = not estimated, no information is available on the food attributable proportion of cryptosporidiosis in New Zealand, NMDS = Health New Zealand Te Whatu Ora National Minimum Dataset of hospitalisations.

[a] Cases hospitalised may not be notified on EpiSurv.

[b] Estimated number and % of cases related to travel. Of the 1234 notified cases, the overseas travel question had a 'yes' or 'no' entry for 632 cases (51.2%); of these, 85 cases (13.4%) had travelled overseas during the incubation period and 547 cases (86.6%) had not been overseas. The overseas travel history for the remaining 602 cases is unknown. The estimated number of cases related to travel is given as 13.4% percent of all cases in 2024.

[c] While international travel has increased again since restrictions ceased in 2022, overseas travel in 2024 was still slightly lower compared with the pre-COVID-19 year 2019 (see section Changes in overseas travel, page 11).

Cryptosporidiosis individual cases reported in 2024 by data source

During 2024, 1234 individual cases (23.1 cases per 100,000 population) of cryptosporidiosis and no resulting deaths were reported in EpiSurv.

The ICD-10 code A07.2 was used to extract cryptosporidiosis hospitalisation data from the Health New Zealand Te Whatu Ora NMDS database. Of the 93 hospitalised cases (1.7 hospitalised cases per 100,000 population) recorded in 2024, 65 cases were reported with cryptosporidiosis as the principal diagnosis and 28 were reported with cryptosporidiosis as another relevant diagnosis. Some of the 93 hospitalised cases were admitted to hospital more than once resulting in a total of 107 hospital admissions.

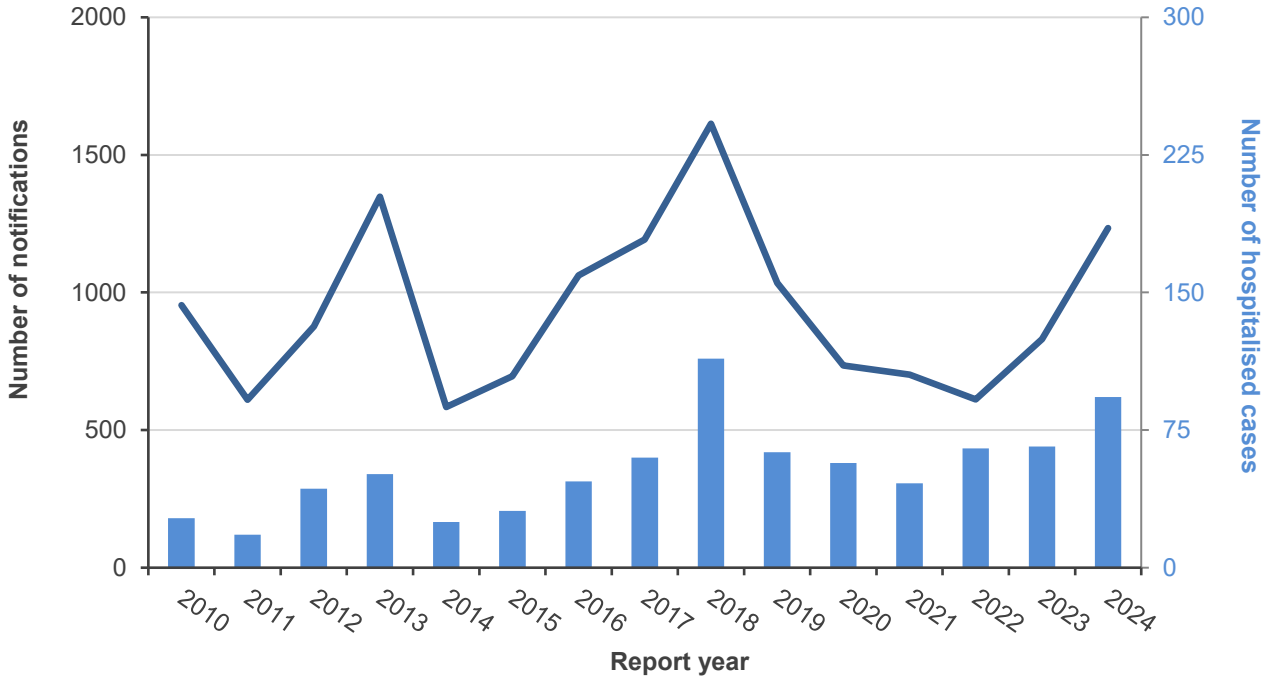
It should be noted that EpiSurv and NMDS are two separate databases that are used for different purposes. Therefore, NMDS and EpiSurv hospitalisation numbers may differ for several reasons, including criteria used for notifications or diagnostic coding (see also Appendix A–Methods, page 123).

Annual data

Over the last 15 years the number of cryptosporidiosis notifications and hospitalised cases per year has been variable (Figure 13). In 2024, the number of notifications and hospitalised cases were within the range seen in the previous 14 years. The number of hospitalised cases with cryptosporidiosis as the principal or another relevant diagnosis varied year by year and ranged between 18 (2011) and 114 (2018).

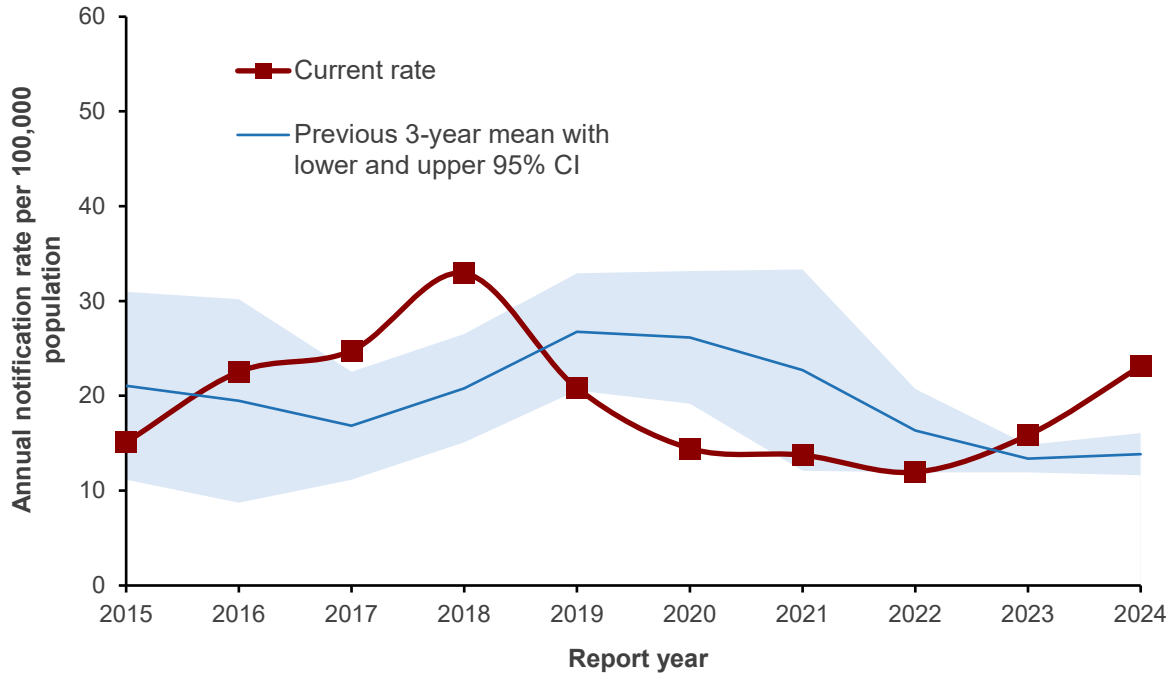
The frequency of overseas travel was lower in 2020 to 2023 and still slightly lower in 2024 compared with the pre-COVID-19 year 2019 (see section Changes in overseas travel, page 11). In 2024, the estimated percentage of cryptosporidiosis cases related to travel was 13.4% (95% CI: 11.6-15.3%), compared with 9.0% (95% CI: 7.4-10.6%) in 2019 (pre-COVID-19 pandemic) and 0.0% (95% CI: 0.0-<0.6%) in 2021 (year of greatest reduction in travel).

Figure 13. Cryptosporidiosis EpiSurv notifications (line) and NMDS hospitalised cases (bar) by year, 2010–2024



In 2024, the notification rate for cryptosporidiosis (23.1 cases per 100,000 population) was higher than the previous three-year mean (13.9 cases per 100,000 population) (Figure 14).

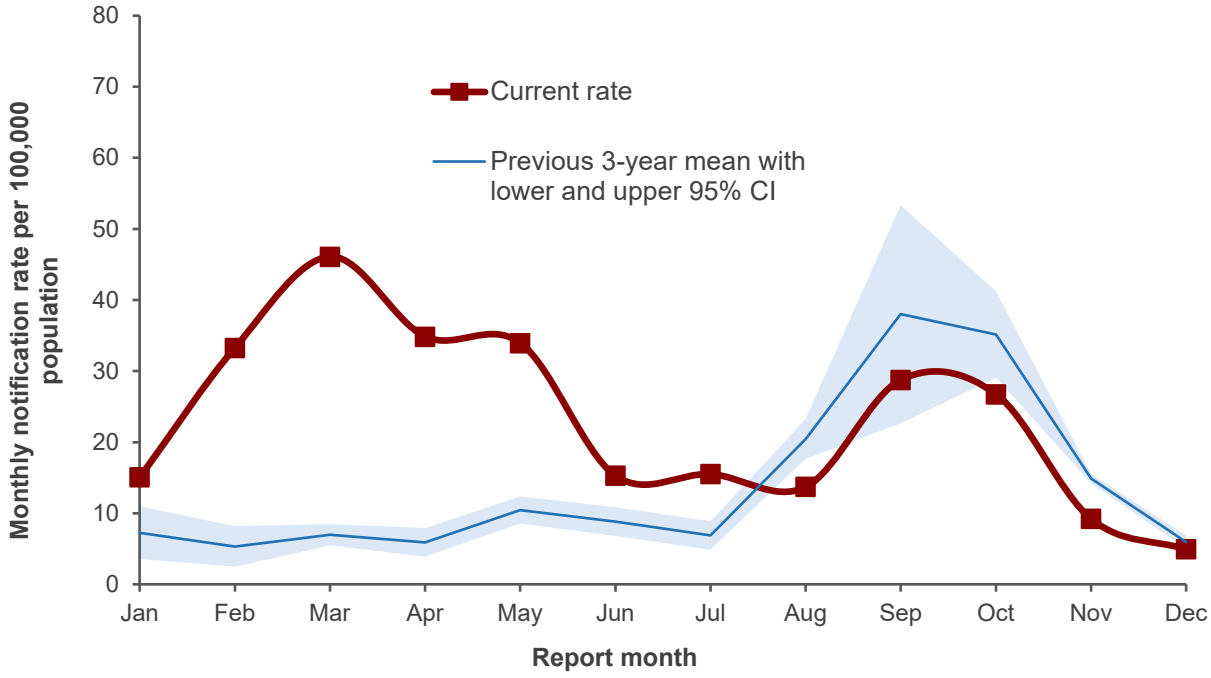
Figure 14. Cryptosporidiosis notification rate by year, 2015–2024



Seasonal data

Cryptosporidiosis notification rates per 100,000 population by month for 2024 are shown in Figure 15. In 2024, monthly notification rates showed two pronounced peaks with the expected seasonal peak in spring and higher-than-normal rates from February to May which is partially due to 5 distinct outbreaks. There were no outbreaks reported from January to July in 2023. The monthly number of notifications in 2024 ranged from 22 notifications (December, 5.0 cases per 100,000 population) to 205 notifications (March, 46.1 cases per 100,000 population).

Figure 15. Cryptosporidiosis monthly notification rate (annualised), 2024



Demographics

In 2024, the rates of notifications and hospitalised cases for cryptosporidiosis were higher for females (25.1 notified cases and 1.9 hospitalised cases per 100,000 population) compared with males (21.0 notified cases and 1.6 hospitalised cases per 100,000 population) (Table 19).

Table 19. Cryptosporidiosis cases by sex, 2024

Sex	EpiSurv notified cases		Hospitalised cases[a]	
	No.	Rate[b]	No.	Rate[b]
Male	559	21.0	42	1.6
Female	674	25.1	51	1.9
Total[c]	**1234**	**23.1**	**93**	**1.7**

[a] Health New Zealand Te Whatu Ora NMDS data.

[b] Per 100,000 population.

[c] Total includes one case where sex was not recorded.

In 2024, the highest cryptosporidiosis age-specific notification and hospitalisation rate was reported for the 1 to 4 years age group (98.8 notified cases and 7.8 hospitalised cases per 100,000 population). The lowest rates of notified cases were for the over 50 years age groups (Table 20).

Table 20. Cryptosporidiosis cases by age group, 2024

Age group (years)	EpiSurv notified cases		Hospitalised cases[a]	
	No.	Rate[b]	No.	Rate[b]
<1	24	41.5	2	-
1 to 4	241	98.8	19	7.8
5 to 9	138	42.0	11	3.3
10 to 14	59	16.9	5	1.4
15 to 19	50	14.7	6	1.8
20 to 29	165	24.0	17	2.5
30 to 39	283	35.0	12	1.5
40 to 49	121	18.2	8	1.2
50 to 59	59	9.0	5	0.8
60 to 69	64	10.9	3	-
70+	30	4.8	5	0.8
Total	**1234**	**23.1**	**93**	**1.7**

[a] Health New Zealand Te Whatu Ora NMDS data.

[b] Per 100,000 population in this age group (rate not calculated when fewer than five cases reported).

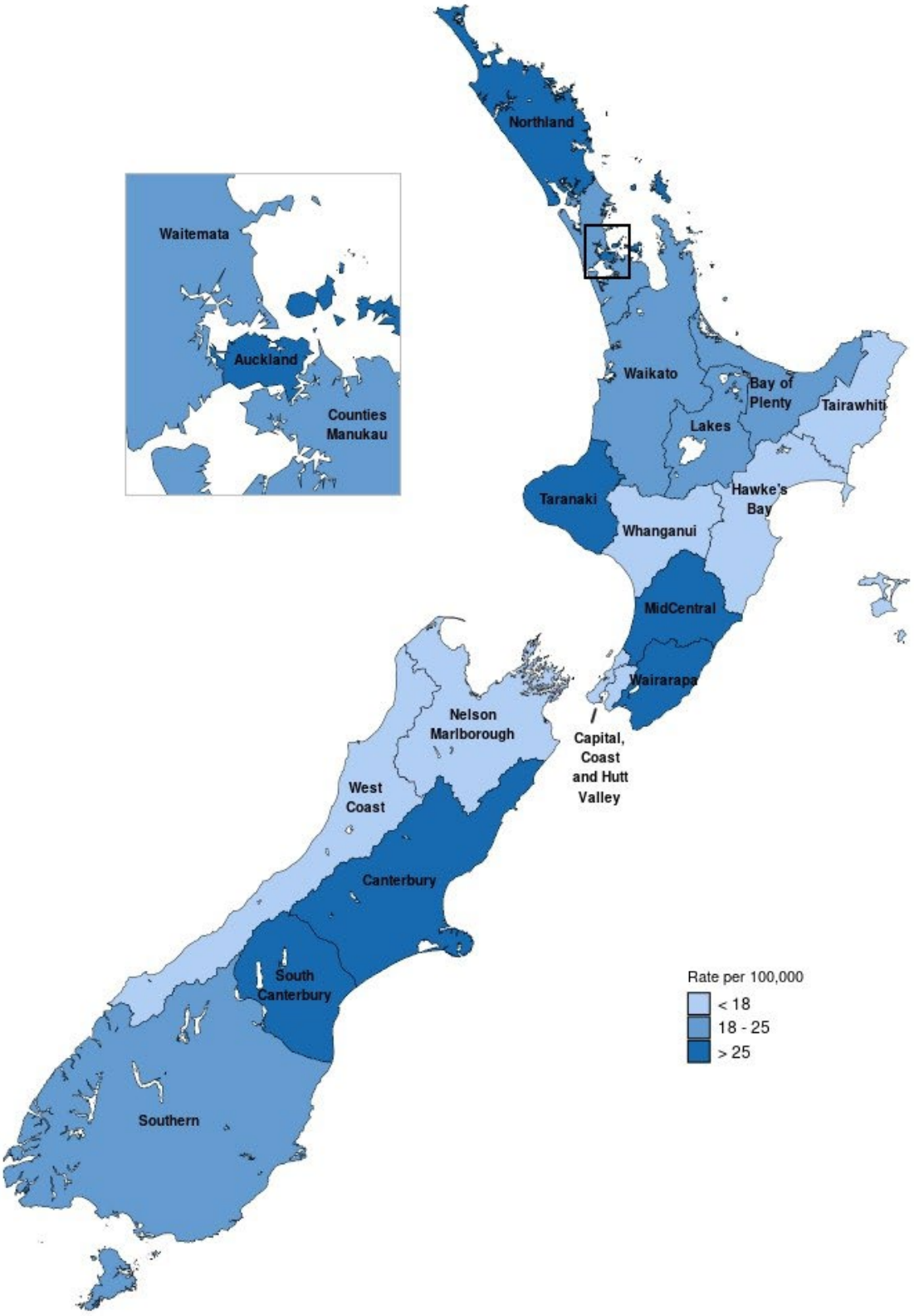
Geographic distribution

The notification rates by Health District calculated per 100,000 resident population are presented in Figure 16.

In 2024, the Health District notification rates of cryptosporidiosis ranged from 10.7 cases per 100,000 population in Nelson Marlborough (18 cases) to 52.5 cases per 100,000 population (34 cases) in South Canterbury. South Canterbury, Canterbury (34.7 cases per 100,000 population, 218 cases), MidCentral (34.4 cases per 100,000 population, 67 cases) and Taranaki (30.5 cases per 100,000 population, 40 cases) Health Districts had the highest notification rates.

Historically, notification rates for cryptosporidiosis have been variable across New Zealand with the Health Districts Taranaki and South Canterbury consistently in the highest quartile of notification rates since 2020 and 2021, respectively.

Figure 16. Geographic distribution of cryptosporidiosis notifications, 2024

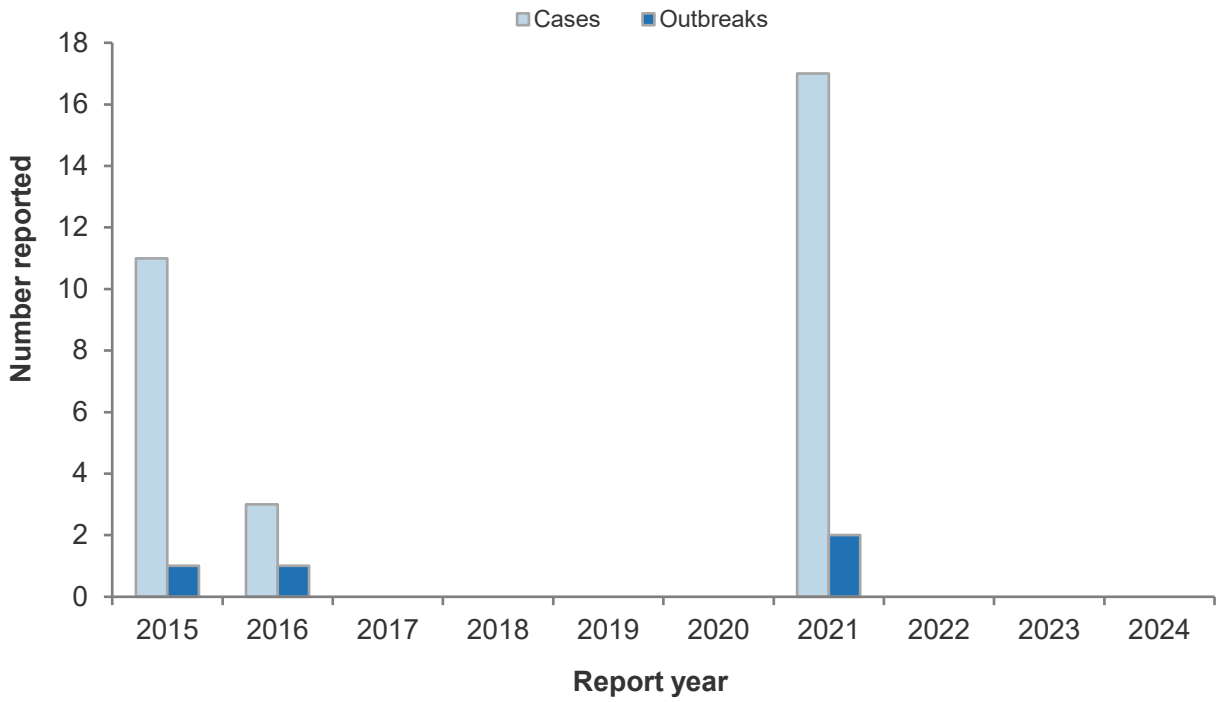


Outbreaks reported as caused by *Cryptosporidium* spp.

In 2024, there were 13 cryptosporidiosis outbreaks with 176 associated cases reported in EpiSurv. None of these outbreaks reported overseas travel or food as a possible mode of transmission. It is important to note that a single outbreak may have multiple pathogens, settings, and possible modes of transmission.

Between 2015 and 2024 there have been a total of four outbreaks of potentially foodborne cryptosporidiosis (Figure 17), one in 2015 and 2016 and two in 2021. The annual number of cases associated with outbreaks ranged between three and 17.

Figure 17. Cryptosporidiosis outbreaks with food reported as a possible mode of transmission and associated cases (excluding travel associated outbreaks) reported by year, 2015–2024



Note: The data in this figure comes from EpiSurv for the years up to 2021. From 2021 the plot includes foodborne outbreaks recorded in EpiSurv and any outbreaks that were referred to NZFS but were not recorded in EpiSurv as an outbreak.

Recent surveys

Nil.

Relevant New Zealand studies and publications

Nil.

Relevant regulatory developments

No *Cryptosporidium*-specific regulatory developments.

Giardiasis

Case definition

Clinical description:	An illness characterised by diarrhoea, abdominal cramps, bloating, flatulence, nausea, weight loss and malabsorption. The infection may be asymptomatic.
Laboratory test for diagnosis:	Detection of *Giardia* cysts or trophozoites OR *Giardia* antigen OR *Giardia* nucleic acid in an appropriate gastrointestinal clinical specimen.
Case classification:	
Probable	A clinically compatible illness that is either a contact of a confirmed case of the same disease or has had contact with the same common source – that is, is part of a common-source outbreak.
Confirmed	A clinically compatible illness that is laboratory confirmed.

Summary data

Summary data for giardiasis in 2024 are given in Table 21.

Table 21. Summary of surveillance data for giardiasis, 2024

Parameter	Value in 2024	Source
Number of notified cases	844	EpiSurv
Notification rate (per 100,000)	15.8	EpiSurv
Hospitalised cases[a]	51	NMDS
Deaths	0	EpiSurv
Estimated number of cases related to travel (%)[b,c]	215 (25.5%)	EpiSurv
Estimated domestically acquired food-related cases	NE	-

NE = not estimated, no information is available on the food attributable proportion of giardiasis in New Zealand, NMDS = Health New Zealand Te Whatu Ora National Minimum Dataset of hospitalisations.

[a] Cases hospitalised may not be notified on EpiSurv.

[b] Estimated number and % of cases related to travel. Of the 844 notified cases, the overseas travel question had a 'yes' or 'no' entry for 423 cases (50.1%); of these, 108 cases (25.5%) had travelled overseas during the incubation period and 315 cases (74.5%) had not been overseas. The overseas travel history for the remaining 421 cases is unknown. The estimated number of cases related to travel is given as 25.5% percent of all cases in 2024.

[c] While international travel has increased again since restrictions ceased in 2022, overseas travel in 2024 was still slightly lower compared with the pre-COVID-19 year 2019 (see section Changes in overseas travel, page 11).

Giardiasis individual cases reported in 2024 by data source

During 2024, 844 individual cases (15.8 cases per 100,000 population) of giardiasis and no resulting deaths were reported in EpiSurv.

The ICD-10 code A07.1 was used to extract giardiasis hospitalisation data from the Health New Zealand Te Whatu Ora NMDS database. Of the 51 hospitalised cases (1.0 hospitalised cases per 100,000 population) recorded in 2024, 31 cases were reported with giardiasis as the principal diagnosis and 20 were reported with giardiasis as another relevant diagnosis. Three of the 51 hospitalised cases were admitted to hospital twice resulting in a total of 54 hospital admissions.

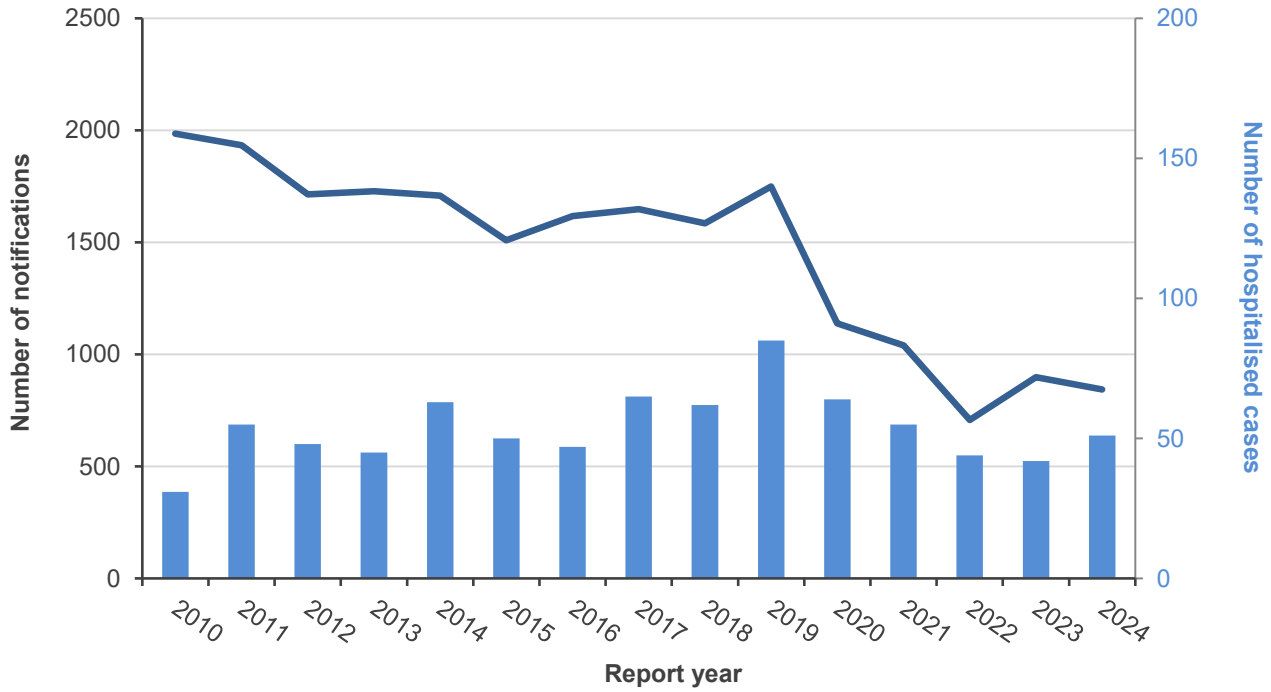
It should be noted that EpiSurv and NMDS are two separate databases that are used for different purposes. Therefore, NMDS and EpiSurv hospitalisation numbers may differ for several reasons, including criteria used for notifications or diagnostic coding (see also Appendix A–Methods, page 123).

Annual data

From 2010 to 2019, the number of giardiasis notifications reported each year ranged from 1510 (2015) to 1985 (2010) (Figure 18). There was a pronounced drop in notifications in 2020 and notifications remained below 2019 case numbers in the following years. The numbers of hospitalised cases have not dropped to the same extent as the notified cases following 2019.

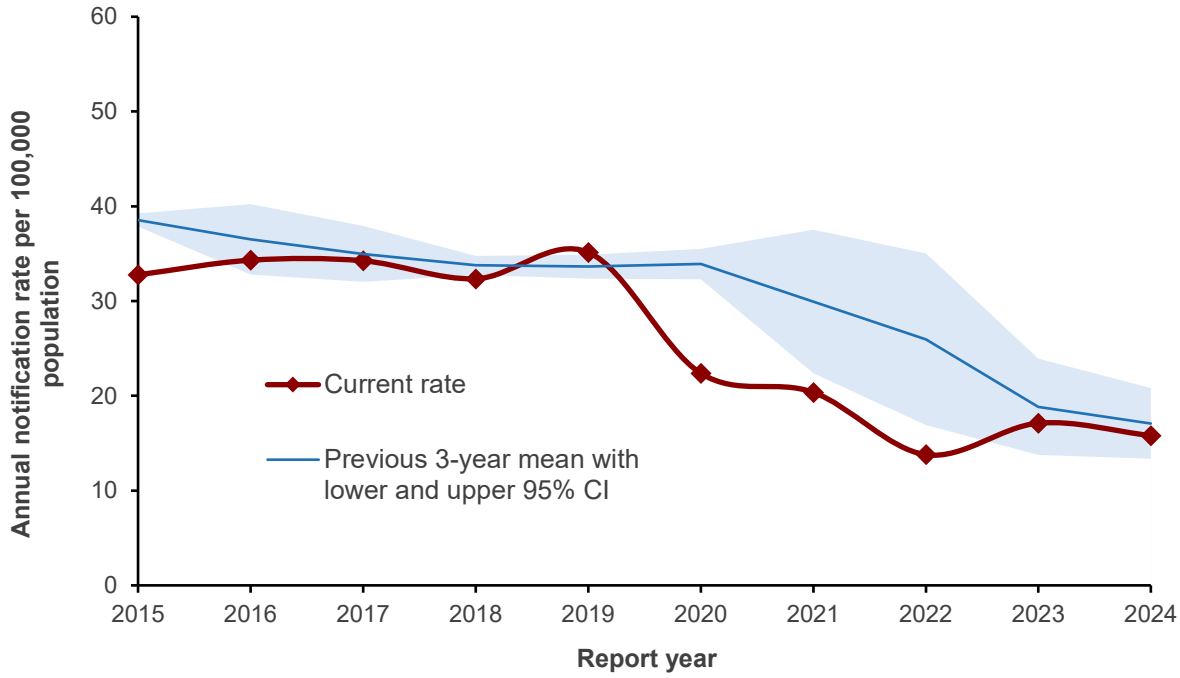
The frequency of overseas travel was lower in 2020 to 2023 compared with the pre COVID-19 year 2019 (see section Changes in overseas travel, page 11) and was still slightly lower in 2024. This is reflected in the notifications; in 2024, the estimated percentage of giardiasis cases related to travel was 25.5% (95% CI: 22.6-28.5%), compared with 18.9% (95% CI: 17.2-20.5%) in 2019 (pre-COVID-19 pandemic) and 1.1% (95% CI: 0.5-1.6%) in 2021 (year of greatest reduction in travel).

Figure 18. Giardiasis EpiSurv notifications (line) and NMDS hospitalised cases (bar) by year, 2010–2024



In 2024, the notification rate for giardiasis (15.8 cases per 100,000 population) was similar to the previous three-year mean (17.1 cases per 100,000 population) (Figure 19). The drop in notification rates from 2020 to 2022 can be attributed to the COVID-19 pandemic [18].

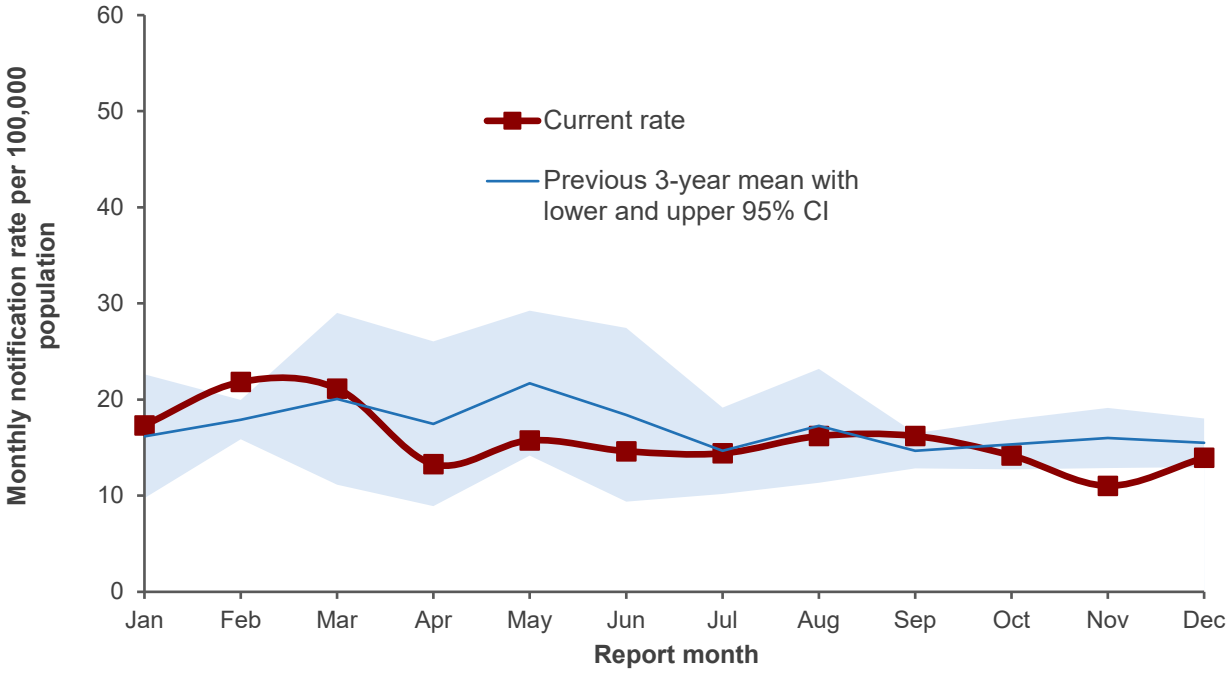
Figure 19. Giardiasis notification rate by year, 2015–2024



Seasonal data

Giardiasis notification rates per 100,000 population by month for 2024 are shown in Figure 20. For most of the year, the monthly notification rates were similar to the mean of the previous three years, apart from two months where rates lay outside the 95% confidence interval. The monthly number of notifications in 2024 ranged from 49 cases (November, 11.0 cases per 100,000 population) to 97 cases (February, 21.8 cases per 100,000 population).

Figure 20. Giardiasis monthly notification rate (annualised), 2024



Demographics

In 2024, the rate of notifications for giardiasis was higher for males (16.9 cases per 100,000 population) compared with females (14.8 cases per 100,000 population). However, the rate of hospitalised cases was higher for females (1.1 hospitalised cases per 100,000 population) compared with males (0.8 hospitalised cases per 100,000 population) (Table 22).

Table 22. Giardiasis cases by sex, 2024

Sex	EpiSurv notified cases		Hospitalised cases[a]	
	No.	Rate[b]	No.	Rate[b]
Male	448	16.9	21	0.8
Female	396	14.8	30	1.1
Total	**844**	**15.8**	**51**	**1.0**

[a] Health New Zealand Te Whatu Ora NMDS data.

[b] Per 100,000 population.

In 2024, the highest age-specific notification rate was for the 1 to 4 years age group (48.4 notified cases per 100,000 population) (Table 23). The highest hospitalised case rate was also reported for the 1 to 4 years age group (4.5 hospitalised cases per 100,000 population).

Table 23. Giardiasis cases by age group, 2024

Age group (years)	EpiSurv notified cases		Hospitalised cases[a]	
	No.	Rate[b]	No.	Rate[b]
<1	8	13.8	1	-
1 to 4	118	48.4	11	4.5
5 to 9	38	11.6	5	1.5
10 to 14	18	5.2	0	-
15 to 19	13	3.8	0	-
20 to 29	117	17.0	6	0.9
30 to 39	173	21.4	6	0.7
40 to 49	110	16.5	5	0.8
50 to 59	100	15.3	4	-
60 to 69	96	16.4	3	-
70+	53	8.6	10	1.6
Total	**844**	**15.8**	**51**	**1.0**

[a] Health New Zealand Te Whatu Ora NMDS data.

[b] Per 100,000 population in this age group (rate not calculated when fewer than five cases reported).

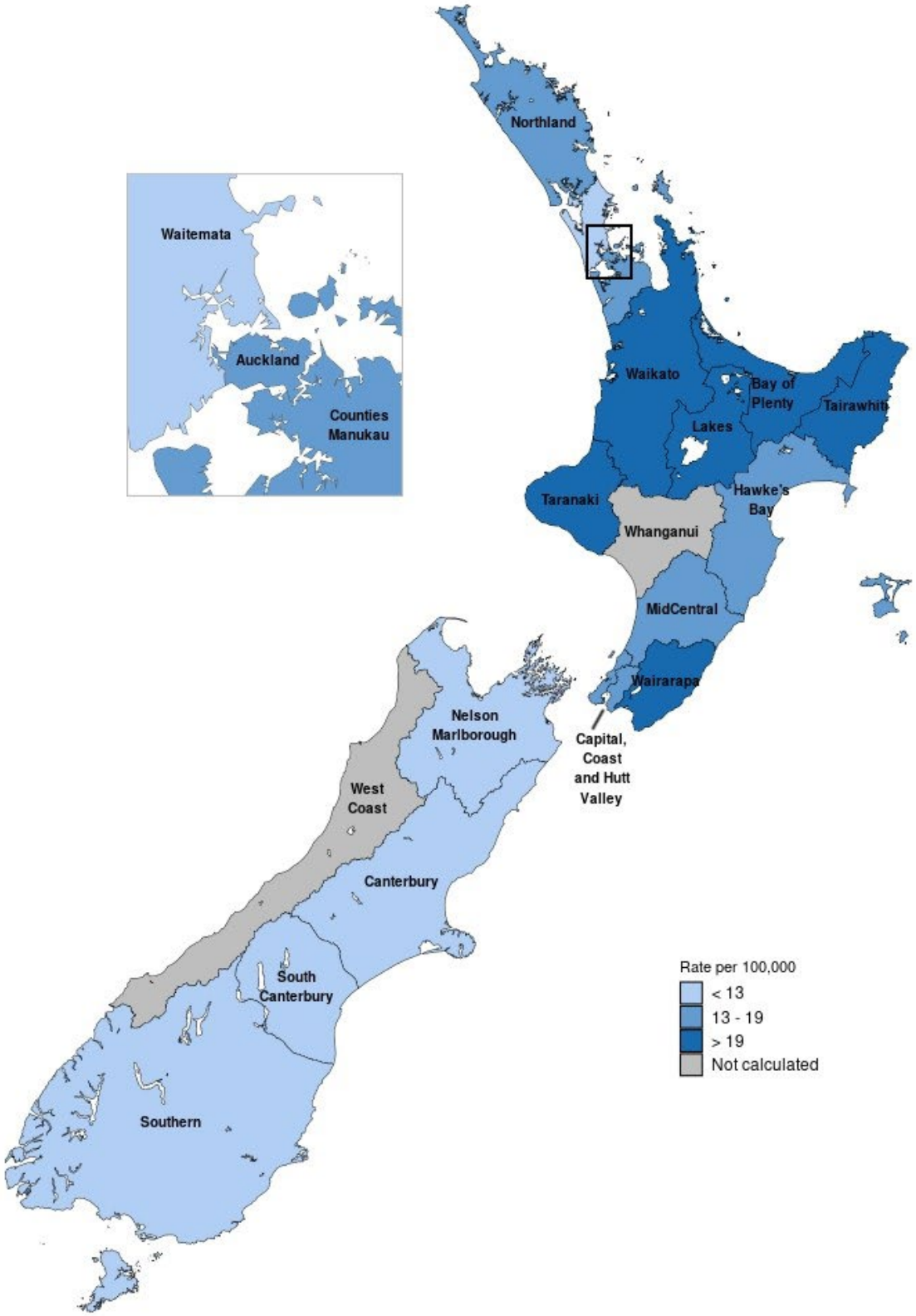
Geographic distribution

The notification rates by Health District calculated per 100,000 resident population are presented in Figure 21. The rate has not been calculated for Health Districts with fewer than five cases (grey shading): West Coast (four cases) and Whanganui (four cases).

In 2024, the Health District notification rates for giardiasis ranged from 8.9 cases per 100,000 population (15 cases) in Nelson Marlborough to 30.5 cases per 100,000 population (40 cases) in Taranaki. The Health Districts Taranaki, Lakes (29.9 cases per 100,000 population, 36 cases) and Bay of Plenty (29.2 cases per 100,000 population, 82 cases) had the highest notification rates.

From 2020 to 2024, notification rates for giardiasis have been variable across New Zealand with Tairāwhiti Health District consistently in the highest quartile.

Figure 21. Geographic distribution of giardiasis notifications, 2024

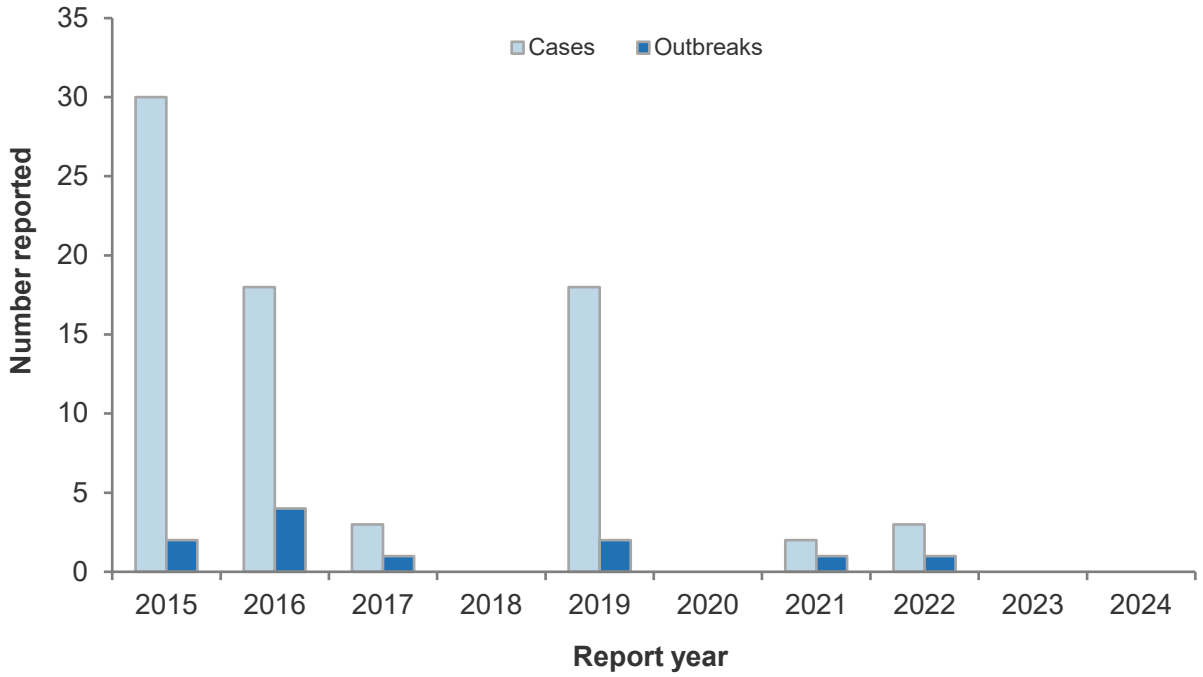


Outbreaks reported as caused by *Giardia* spp.

In 2024, there were five giardiasis outbreaks reported in EpiSurv with 48 associated cases and no hospitalised cases. None of the outbreaks reported overseas travel or food as a possible mode of transmission. The outbreaks were all associated with early childhood centres or people changing nappies of infected babies.

Over the 10-year period from 2015 to 2024, between zero and four giardiasis outbreaks with food reported as a possible mode of transmission were notified each year with between zero and 30 annual outbreak-associated cases (Figure 22).

Figure 22. Giardiasis outbreaks with food reported as a possible mode of transmission and associated cases (excluding travel associated outbreaks) reported by year, 2015–2024



Note: The data in this figure comes from EpiSurv for the years up to 2021. From 2021 the plot includes foodborne outbreaks recorded in EpiSurv and any outbreaks that were referred to NZFS but were not recorded in EpiSurv as an outbreak.

Recent surveys

Nil.

Relevant New Zealand studies and publications

Nil.

Relevant regulatory developments

No *Giardia*-specific regulatory developments.

Hepatitis A

Case definition

Clinical description:	Following a prodrome of fever, malaise, anorexia, nausea or abdominal discomfort, there is jaundice and sometimes an enlarged tender liver. Elevated serum aminotransferase levels may indicate infection. Children are often asymptomatic and occasionally present with atypical symptoms, including diarrhoea, cough, coryza or arthralgia. Jaundice is very unusual in children younger than 4 years, and 90% of cases in the 4–6 years age group are anicteric.
Laboratory test for diagnosis:	Positive hepatitis A virus-specific IgM in serum OR seroconversion between paired sera tested in the same laboratory (in the absence of recent vaccination) OR detection of hepatitis A virus nucleic acid.
Case classification:	
Probable	A clinically compatible illness that is epidemiologically linked to a confirmed case.
Confirmed	A clinically compatible illness that is laboratory confirmed.

Summary data

Summary data for hepatitis A in 2024 are given in Table 24.

Table 24. Summary of surveillance data for hepatitis A, 2024

Parameter	Value in 2024	Source
Number of notified cases	68	EpiSurv
Notification rate (per 100,000)	1.3	EpiSurv
Hospitalised cases[a]	51	NMDS
Deaths	0	EpiSurv
Estimated number of cases related to travel (%)[b,c]	42 (61.2%)	EpiSurv
Estimated domestically acquired food-related cases	NE	-

NE = not estimated, no information is available on the food attributable proportion of hepatitis A in New Zealand,

NMDS = Health New Zealand Te Whatu Ora National Minimum Dataset of hospitalisations.

[a] Hospitalisations with acute hepatitis A as the principal diagnosis. Another 31 cases were hospitalised with acute hepatitis A as another relevant diagnosis. Cases hospitalised may not be notified on EpiSurv.

[b] Estimated number and % of cases related to travel. Of the 68 notified cases, the overseas travel question had a 'yes' or 'no' entry for 67 cases (98.5%); of these, 41 cases (61.2%) had travelled overseas during the incubation period and 26 cases (38.8%) had not been overseas. The overseas travel history for the remaining case is unknown. The estimated number of cases related to travel is given as 61.2% percent of all cases in 2024.

[c] While international travel has increased again since restrictions ceased in 2022, overseas travel in 2024 was still slightly lower compared with the pre-COVID-19 year 2019 (see section Changes in overseas travel, page 11).

Hepatitis A individual cases reported in 2024 by data source

During 2024, 68 individual cases (1.3 notified cases per 100,000 population) of hepatitis A and no resulting deaths were reported in EpiSurv. Hospitalisation rates are usually high for hepatitis A; 71.6% of notified cases were recorded as hospitalised in EpiSurv in 2024.

The ICD-10 code B15 was used to extract acute hepatitis A hospitalisation data from the Health New Zealand Te Whatu Ora NMDS database. There were 82 hospitalised cases (1.5 hospitalised cases per 100,000 population) recorded in the NMDS in 2024; 51 cases were reported with acute hepatitis A as the principal diagnosis and 31 cases with acute hepatitis A as another relevant diagnosis. Five of

the 82 hospitalised cases were admitted to hospital twice resulting in a total of 87 hospital admissions. The largest proportion of hospitalised cases (49%) did not stay in hospital over night or spent one night in hospital, with none of the hospitalised cases admitted to an intensive care unit (Appendix C, Table 69).

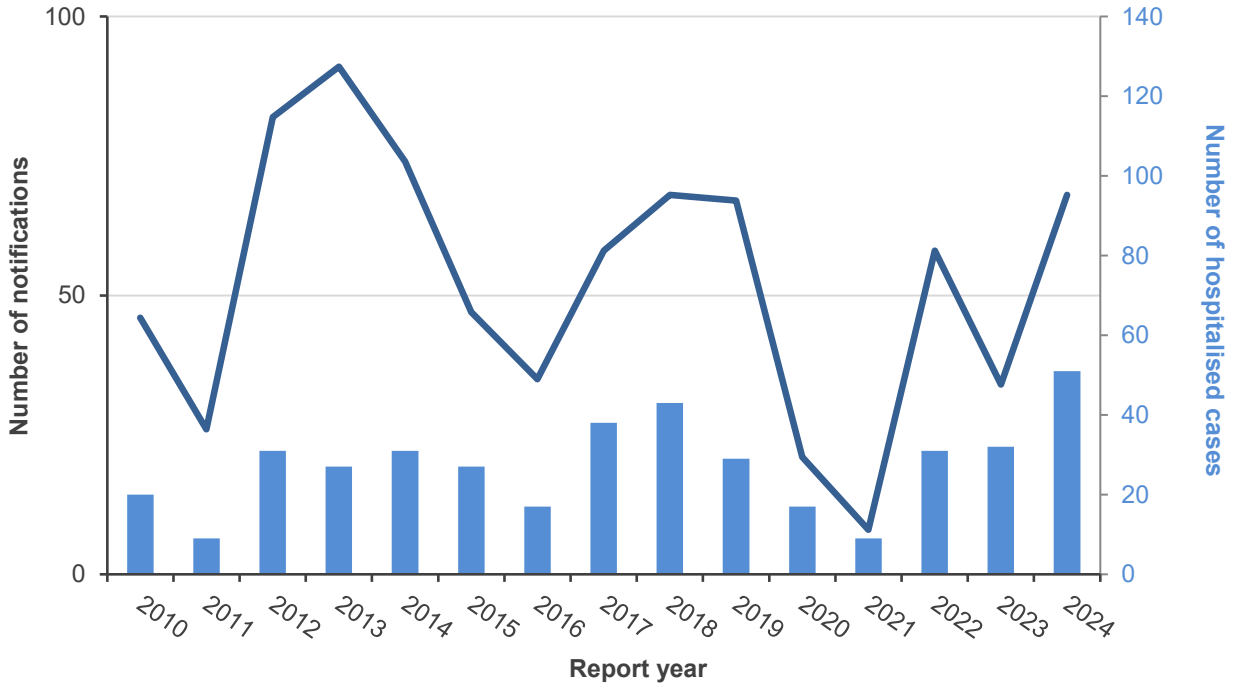
It should be noted that EpiSurv and NMDS are two separate databases that are used for different purposes. Therefore, NMDS and EpiSurv hospitalisation numbers may differ for several reasons, including criteria used for notifications or diagnostic coding (see also Appendix A–Methods, page 123).

Annual data

Between 2010 and 2019, the annual number of notifications ranged between 26 (2011) to 91 (2013) (Figure 23), followed by lower numbers in 2020 and 2021 (22 and eight notifications, respectively). In 2022, 35 of the notified cases were related to a national hepatitis A outbreak linked to frozen berries. The number of hospitalised cases with hepatitis A as the principal diagnosis largely followed the trend of the annual notifications and ranged between nine (2011 and 2021) and 51 (2024).

The frequency of overseas travel was lower in 2020 to 2023 compared with the pre COVID-19 year 2019 (see section Changes in overseas travel, page 11) and was still slightly lower in 2024. In 2024, the estimated percentage of hepatitis A cases related to travel was about 61%, similar to the pre COVID-19 year 2019 (~58%). In 2021 (year of greatest reduction in travel) two out of eight reported cases reported overseas travel as a risk factor.[1]

Figure 23. Hepatitis A EpiSurv notifications (line) and NMDS hospitalised cases (bar) by year, 2010–2024



Note: Hospitalised cases include only cases with hepatitis A as the principal diagnosis.

[1] Case numbers are too small to calculate confidence intervals.

Due to the small number of notifications per year, plots of case notification rates by year and month are not presented for hepatitis A.

Demographics

In 2024, the rate of notifications for hepatitis A was the same for males and females (1.3 cases per 100,000 population). The rate of hospitalised cases was similar for males (1.0 hospitalised cases per 100,000 population) and females (0.9 hospitalised cases per 100,000 population) (Table 25).

Table 25. Hepatitis A cases by sex, 2024

Sex	EpiSurv notified cases		Hospitalised cases[a]	
	No.	Rate[b]	No.	Rate[b]
Male	34	1.3	27	1.0
Female	34	1.3	24	0.9
Total	**68**	**1.3**	**51**	**1.0**

[a] Health New Zealand Te Whatu NMDS data for hospitalised cases with hepatitis A as the principal diagnosis.
[b] Per 100,000 population.

In 2024, the highest age-specific notification rates were for the 1 to 4, 5 to 9 and 20 to 29 years age groups (2.5, 2.4 and 2.5 cases per 100,000 population, respectively) (Table 26). The highest hospitalised case rates were reported for the 5 to 9 and 20 to 29 years age groups (1.8 and 1.9 hospitalised cases per 100,000 population, respectively).

Table 26. Hepatitis A cases by age group, 2024

Age group (years)	EpiSurv notified cases		Hospitalised cases[a]	
	No.	Rate[b]	No.	Rate[b]
<1	0	-	0	-
1 to 4	6	2.5	2	-
5 to 9	8	2.4	6	1.8
10 to 14	6	1.7	5	1.4
15 to 19	5	1.5	4	-
20 to 29	17	2.5	13	1.9
30 to 39	11	1.4	10	1.2
40 to 49	8	1.2	8	1.2
50 to 59	1	-	1	-
60 to 69	3	-	2	-
70+	3	-	0	-
Total	**68**	**1.3**	**51**	**1.0**

[a] Health New Zealand Te Whatu Ora NMDS data for hospitalised cases with hepatitis A as the principal diagnosis.
[b] Per 100,000 population in this age group (rate not calculated when fewer than five cases reported).

In 2024, the hepatitis A notification and hospitalised case rates were highest for the ethnic groups ‘MELAA’ (7.7 cases and 10.3 hospitalised cases per 100,000 population) and Asian (4.4 cases and 3.9 hospitalised cases per 100,000 population) (Appendix C, Table 70 and Table 71).

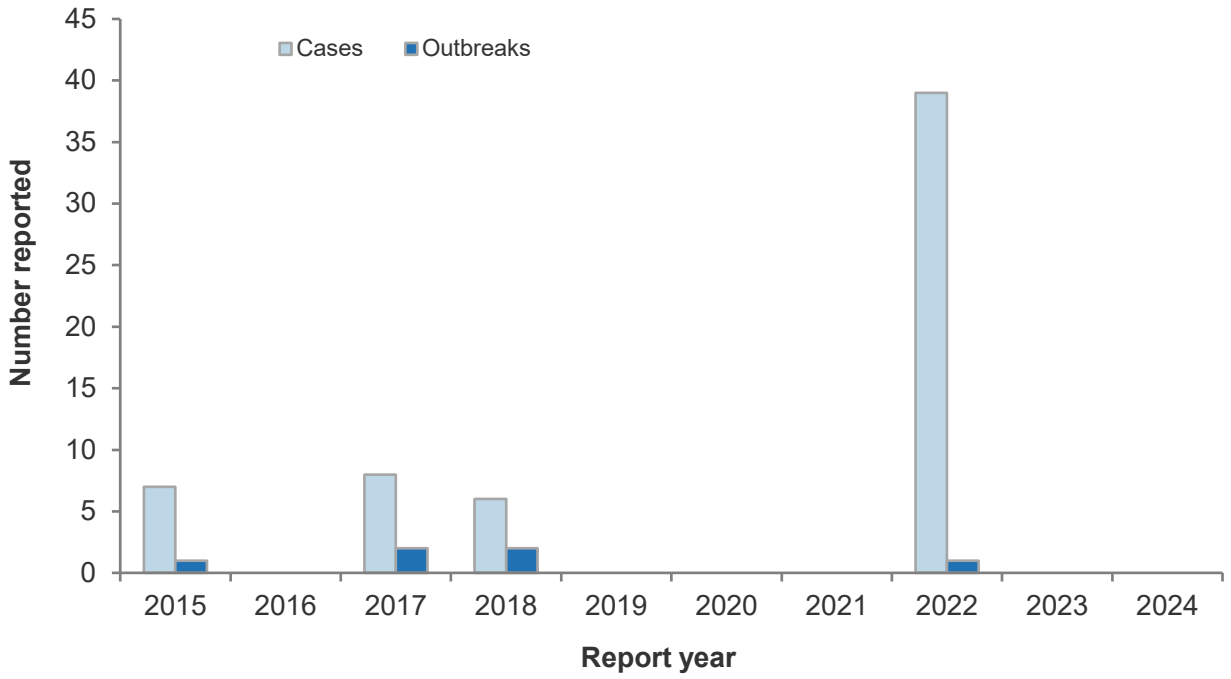
Outbreaks reported as caused by hepatitis A virus

In 2024, three hepatitis A outbreaks were reported in EpiSurv (16 cases and four hospitalisation). The cases from two of these outbreaks were infected overseas. The other outbreak was identified as due to person-to-person transmission with a known case. No outbreaks were identified as potentially foodborne.

In addition to the outbreaks reported in EpiSurv, NZFS investigated two groups of hepatitis A cases. One group of six cases was associated with a childcare centre, with one case isolate genomically linked to the 2022/23 frozen berry outbreak. There was no evidence for frozen berries as the source of this 2024 outbreak. The other group of eight cases in the upper North Island was associated with hepatitis A strains endemic in Fiji. No food sources were identified as the cause of these two outbreaks.

Over the 10-year period from 2015 to 2024, there were six potentially foodborne domestic outbreaks with a total of 60 associated cases (Figure 24). The largest outbreak of 39 cases was reported between June 2022 and April 2023. The 30 primary cases were suspected to be infected from frozen berries and nine cases were likely due to secondary transmission.

Figure 24. Hepatitis A outbreaks with food reported as a possible mode of transmission and associated cases (excluding outbreaks associated with overseas travel) reported by year, 2015–2024



Note: The data in this figure comes from EpiSurv for the years up to 2021. From 2021 the plot includes foodborne outbreaks recorded in EpiSurv and any outbreaks that were referred to NZFS but were not recorded in EpiSurv as an outbreak.

Hepatitis A virus genotypes commonly reported

In 2024, faecal and/or serum/plasma specimens from 58 hepatitis A cases were submitted to PHF Science's Enteric, Environmental and Food Virology Laboratory for hepatitis A virus typing (Table 27). This compares to specimens from 57 and 27 hepatitis A cases in 2022 and 2023, respectively. The data include cases not associated with foodborne transmission.

Table 27. Hepatitis A virus types/subtypes identified in case specimens, 2020–2024

Type/subtype	2020	2021	2022	2023	2024
IA	10	2	35	8	22
IIA	0	0	0	1	0
IIIA	4	2	19	16	32
IB	2	0	2	2	4
Unable to genotype	0	0	1	0	0
Total	**16**	**4**	**57**	**27**	**58**

Hepatitis A virus subgenotypes IA, IIIA, and IB were identified in cases in 2024, with IIIA the most commonly identified subgenotype. While IA was the most commonly identified subgenotype between 2020 and 2022, in 2022, these were mainly related to outbreaks associated with frozen berries. Since COVID-19 travel restrictions were relaxed in early 2022, an increase in travel-associated hepatitis A cases has been observed.

Recent surveys

Nil.

Relevant New Zealand studies and publications

Nil.

Relevant regulatory developments

MPI consulted on and amended *Food Notice: Requirements for Registered Food Importers and Imported Food for Sale* [31]. Specifically, the amended requirements include a transition from the current requirements for imported frozen berries (Option A) to a new set of requirements (Option B). Option B requires the overseas manufacturer to have a food safety management system that includes "a HACCP plan, which identifies significant hazards, including norovirus and hepatitis A virus, and their controls".

Histamine (scombroid) fish poisoning

Case definition

Clinical description:	Tingling and burning sensation around mouth, facial flushing, sweating, nausea and vomiting, headache, palpitations, dizziness, and rash.
Laboratory test for diagnosis:	Detection of histamine levels ≥ 50 milligram/100gram fish muscle.
Case classification:	Not applicable.

Histamine (scombroid) fish poisoning cases reported in 2024 by data source

During 2024, four individual cases with histamine (scombroid) fish poisoning were reported in EpiSurv.

The ICD-10 code T61.1 was used to extract histamine (scombroid) fish poisoning hospitalisation data from the Health New Zealand Te Whatu Ora NMDS database. All eight hospitalised cases (0.1 hospitalised cases per 100,000 population) recorded in 2024, were reported with histamine (scombroid) fish poisoning as the principal diagnosis.

It should be noted that EpiSurv and NMDS are two separate databases that are used for different purposes. Therefore, NMDS and EpiSurv hospitalisation numbers may differ for several reasons, including criteria used for notifications or diagnostic coding, i.e. a hospital discharge may be coded to an infectious cause without a case being recorded in EpiSurv and vice versa (see also Appendix A–Methods, page 123).

Outbreaks reported as caused by histamine (scombroid) fish poisoning

In 2024, three histamine (scombroid) fish poisoning outbreaks were reported in EpiSurv (Table 28).

Table 28. Histamine fish poisoning outbreaks reported in EpiSurv, 2024

	Possible foodborne transmission with a suspected or confirmed source	Possible foodborne transmission but no suspected food source	Total histamine fish poisoning outbreaks
Outbreaks	3	0	3
Outbreak associated cases	10	0	10
Outbreak hospitalised cases	1	0	1

Table 29 gives details of the histamine fish poisoning outbreaks. The evidence for the December outbreak being due to histamine fish poisoning was weak. The cases had atypical symptoms and the histamine levels in fish caught at the same time as the consumed fish were below levels usually associated with symptoms.

For the two February outbreaks, fish supplied to two Auckland restaurants by the same supplier was suspected to be the causative agent. Following the outbreak the supplier made improvements to temperature and shelf-life controls.

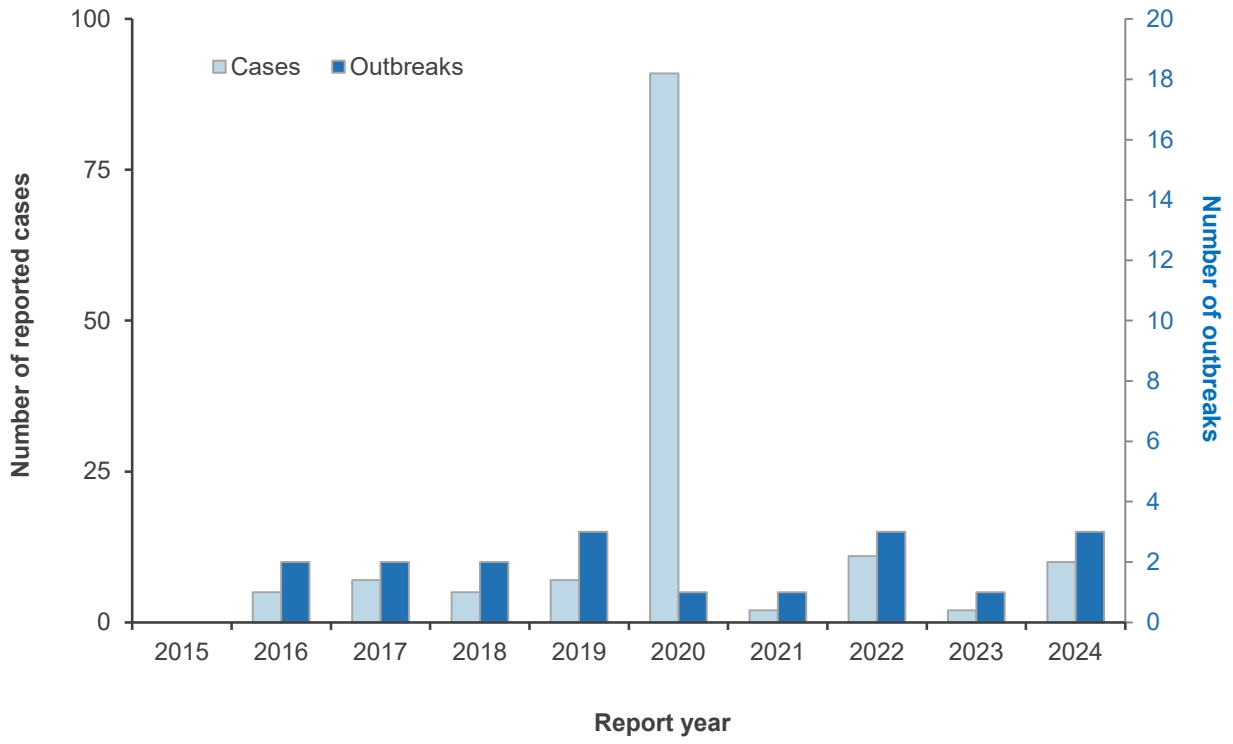
Table 29. Details of histamine (scombroid) fish poisoning, 2024

Health district	Month	Suspected source	Evidence	Setting	No. ill
Auckland	February	Battered kahawai fish	Common food	Restaurant	1C 3P
Auckland	February	Torched kahawai and mussels	Common food	Restaurant	2C 1P
Southern	December	Locally harvested kahawai fish	Common food	Home	3P

Number ill: C: confirmed, P: probable.

Over the 10-year period 2015 and 2024, the annual number of histamine (scombroid) fish poisoning outbreaks reported each year ranged from one to three, except for 2015 when no outbreaks were reported (Figure 25). The highest total number of cases associated with an outbreak over the 10-year period was reported in 2020 (91 cases) due to an outbreak related to a meal ingredient delivery service.

Figure 25. Histamine (scombroid) fish poisoning outbreaks and associated cases reported by year, 2015–2024



Note: The data in this figure comes from EpiSurv for the years up to 2021. From 2021 the plot includes foodborne outbreaks recorded in EpiSurv and outbreaks that were referred to NZFS but were not recorded in EpiSurv as an outbreak.

Recent surveys

Nil.

Relevant New Zealand studies and publications

Nil.

Relevant regulatory developments

No histamine-specific regulatory developments.

Listeriosis

Case definition

Clinical description:	Listeriosis most commonly presents with diarrhoea, often associated with fever, myalgia and vomiting. Bacteraemia most often occurs in pregnant women (usually in the third trimester), the elderly and immunosuppressed. In pregnant women, the foetus may become infected, sometimes leading to miscarriage, stillbirth, premature delivery, new-born septicaemia or meningitis. The elderly and immunosuppressed may present with septicaemia, meningitis or pyogenic foci of infection.
Laboratory test for diagnosis:	Isolation of *Listeria monocytogenes* OR detection of *L. monocytogenes* nucleic acid from a normally sterile site, including the foetal gastrointestinal tract.
Case classification:	
Probable	Not applicable.
Confirmed	A clinically compatible illness that is laboratory confirmed.

Cases can be further classified, if appropriate, as follows:

Perinatal	Cases are classified as pregnancy-associated if illness occurs in a pregnant woman, foetus, or infant aged ≤ 28 days old; for these cases it is the pregnant woman or mother who is notified as the case but information regarding the foetus or infant should be included on the case form

Summary data

Summary data for listeriosis in 2024 are given in Table 30.

Table 30. Summary of surveillance data for listeriosis, 2024

Parameter	Value in 2024	Source
Number of notified cases[a]	36	EpiSurv
Notification rate (per 100,000)	0.7	EpiSurv
Hospitalised cases[b]	36	EpiSurv
Deaths[c]	1	EpiSurv
Number of potentially travel-related cases[d,e]	5	EpiSurv
Estimated domestically acquired food-related cases	Sources other than food are unlikely	

NMDS = Health New Zealand Te Whatu Ora National Minimum Dataset of hospitalisations.

[a] Includes non-perinatal (31) and perinatal cases (5).

[b] All cases were recorded as hospitalised in EpiSurv. The NMDS database (code A32) recorded 33 hospitalised cases of listeriosis. As the case definition requires that *Listeria monocytogenes* must be isolated from a normally sterile site for a case to be confirmed, it would be expected that all confirmed cases would be hospitalised and therefore the EpiSurv data is a more accurate representation.

[c] One perinatal death from listeriosis occurred in 2024. There were four non-perinatal deaths of listeriosis cases recorded in EpiSurv. One case (60-69 age group) died from a cause other than listeriosis. The cause of death was not recorded for the three other non-perinatal listeriosis cases (70+ age group) who died.

[d] Number of notified cases reporting overseas travel as risk factor. 30 cases had not travelled overseas during the incubation period and for the remaining case travel history is unknown. While international travel has increased again since restrictions ceased in 2022, overseas travel in 2024 was still slightly lower compared with the pre-COVID-19 year 2019 (see section Changes in overseas travel, page 11). The incubation period for listeriosis is variable, with the median incubation period estimated to be three weeks. Outbreak cases have occurred 3–70 days following exposure to a contaminated food product. [16].

[e] Due to the low number of cases no travel-related estimate is provided for listeriosis.

Listeriosis individual cases reported in 2024 by data source

During 2024, 36 individual cases (0.7 per 100,000 population) of listeriosis (31 non-perinatal related cases and five perinatal cases) were reported in EpiSurv. One perinatal death from listeriosis was recorded in 2024. Furthermore, there were four non-perinatal deaths of listeriosis cases recorded in EpiSurv. One case (60-69 age group) died from a cause other than listeriosis. The cause of death was not recorded for the three other non-perinatal listeriosis cases (70+ age group) who died.

Hospitalisation rates are usually very high for listeriosis with all 36 notified cases recorded as hospitalised (100%) in EpiSurv. The NMDS database recorded 33 hospitalised cases of listeriosis. As the case definition requires that *Listeria monocytogenes* must be isolated from a normally sterile site for a case to be confirmed, it would be expected that all confirmed cases would be hospitalised. Although discrepant from the EpiSurv data, the NMDS data holds information on duration of stay information and has been used for that purpose. The majority of hospitalised cases (63.6%) spent more than six nights in hospital, with 12.1% of hospitalised cases admitted to an intensive care unit (Appendix C, Table 69). Note the severity information (nights in hospital and admission to ICU) is based on the 33 hospitalised cases associated with code A32 in the NMDS database.

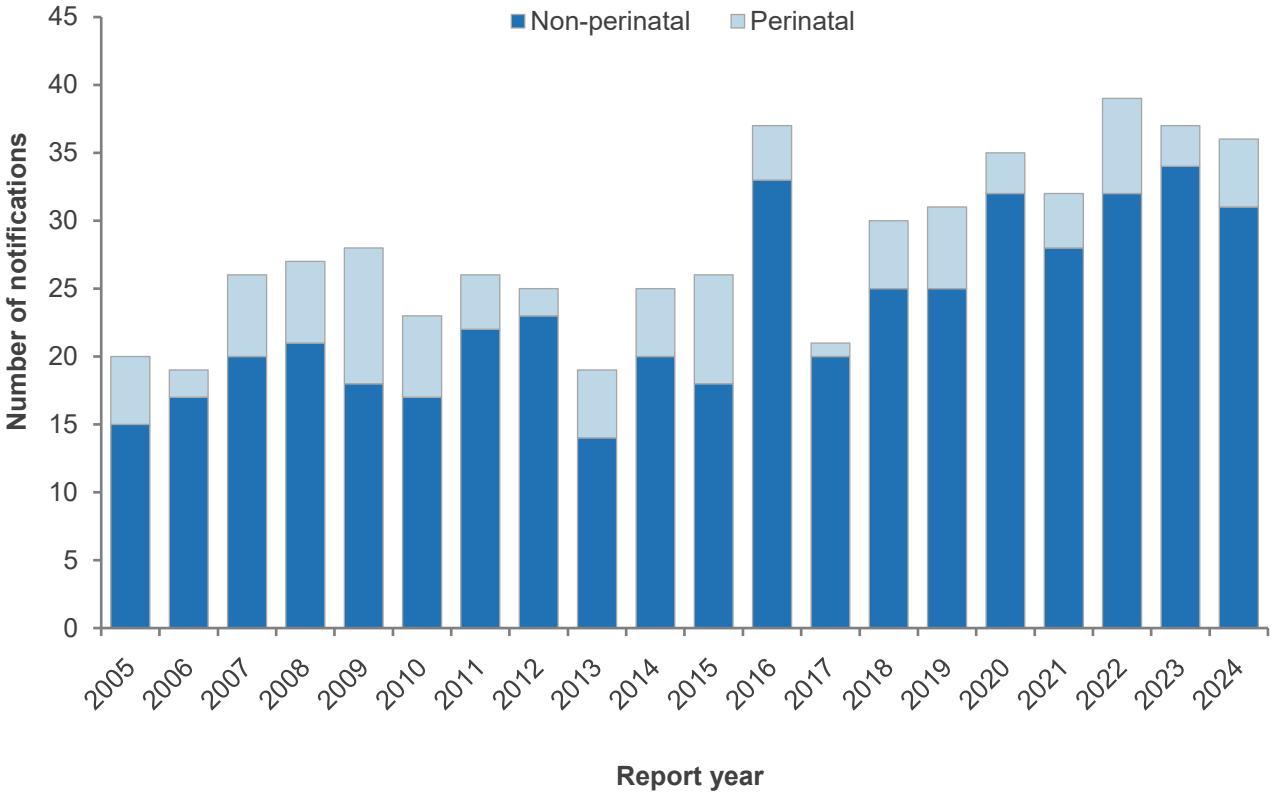
Foodborne transmission

It has been estimated by expert consultation that 87.8% of listeriosis incidence is due to foodborne transmission [2]. However, human infections from sources other than food are unlikely and the fact that the estimate is less than 100% is likely an artefact of the expert elicitation methodology. It was further estimated that approximately 55% of foodborne listeriosis was due to transmission via ready-to-eat meat.

Annual data

Between 2005 and 2024, the annual number of listeriosis notifications has fluctuated between 19 (2006 and 2013) and 39 (2022) (Figure 26). Overall, the notification rate has been relatively stable for the past 20 years at around 0.6 or 0.7 per 100,000 population. In 2024, overseas travel was recorded as a risk factor for five of the notified cases.

Figure 26. Listeriosis EpiSurv non-perinatal and perinatal notifications by year, 2005–2024



Demographics

In 2024, notification and hospitalised case rates for listeriosis were higher for females (0.9 notified cases and 0.9 hospitalised cases per 100,000 population) than for males (0.5 notified cases and 0.5 hospitalised cases per 100,000 population) (Table 31). It should be noted that notification case details for perinatal cases are those for the mother, so the female cases include the five perinatal cases.

Table 31. Listeriosis cases by sex, 2024

Sex	EpiSurv notified cases		Recorded as hospitalised in EpiSurv	
	No.	Rate[a]	No.	Rate[a]
Male	13	0.5	13	0.5
Female	23	0.9	23	0.9
Total	**36**	**0.7**	**36**	**0.7**

[a] Per 100,000 population in this sex group.

In 2024, notification and hospitalised case rates for listeriosis were highest in the 70+ years age group (2.9 notified cases and 2.9 hospitalised cases per 100,000 population) (Table 32). The 70+ years age group was also the age group with the longest hospital stays (four cases were hospitalised for 2 to 6 days and 13 cases for 7+ days) (Appendix C, Table 79).

Table 32. Listeriosis cases by age group, 2024

Age group (years)	EpiSurv notified cases		Recorded as hospitalised in EpiSurv	
	No.[a]	Rate[b]	No.	Rate[b]
<1	0	-	0	-
1 to 4	1	-	1	-
5 to 9	0	-	0	-
10 to 14	1	-	1	-
15 to 19	1	-	1	-
20 to 29	3	-	3	-
30 to 39	2	-	2	-
40 to 49	0	-	0	-
50 to 59	5	0.8	5	0.8
60 to 69	5	0.9	5	0.9
70+	18	2.9	18	2.9
Total	**36**	**0.7**	**36**	**0.7**

[a] For perinatal cases the age reported is the mother's age (one in the 15–19 age group, two in the 20–29 and two in the 30–39 age groups).

[b] Per 100,000 population in this age group (rate not calculated when fewer than five cases reported).

In 2024, the listeriosis notification and hospitalised case rates were highest for the ethnic group 'Māori' (1.0 cases and 1.0 hospitalised cases per 100,000 population) (Appendix C, Table 70 and Table 71).

Outbreaks reported as caused by *Listeria* spp.

In 2024, no listeriosis outbreaks were reported in EpiSurv.

Since 2006 there have been four listeriosis outbreaks reported. There was an outbreak with two associated cases in 2009, an outbreak with six associated cases in 2012, one outbreak associated with ready-to-eat meats with four associated cases in 2021 and one outbreak with home consumption of supermarket bought product and two associated cases in 2022. It is important to note that a single outbreak may have multiple pathogens, modes of transmission, settings where exposure occurred, or settings where preparation of food was conducted.

Listeria monocytogenes types commonly reported

PHF Science's Special Bacteriology Laboratory reported receiving 34 human isolates of *L. monocytogenes* during 2024. Table 33 shows the number of isolates and percentage of *L. monocytogenes* serotypes reported by the Special Bacteriology Laboratory at PHF Science between 2020 and 2024. The annual number of isolates identified to be serotype O4 or serotype O1/2 has been in the range of 12 to 24 isolates and 11 to 18 isolates, respectively, over the 5-year period. The most common sequence types since 2020 were ST1 (56 cases in total) and ST4 (15 cases in total).

Table 33. *L. monocytogenes* serotypes and sequence types of case isolates, 2020–2024

Serotype / Sequence type (ST)	2020	2021	2022	2023	2024
Serotype O1/2	**13**	**11**	**15**	**18**	**18**
ST120	1	1	1	0	2
ST14	0	0	0	3	1
ST155	1	2	0	1	0
ST18	1	0	0	0	0
ST204	0	1	1	0	0
ST224	2	0	1	1	1
ST26	1	0	1	1	0
ST2994	0	1	0	0	0
ST3	0	1	0	1	0
ST307	1	0	0	0	0
ST321	4	1	1	1	1
ST324	0	0	3	1	0
ST37	0	0	0	2	3
ST378	0	0	0	1	0
ST394	0	0	0	2	0
ST391	0	0	0	0	1
ST399	0	0	0	1	0
ST424	0	0	1	0	0
ST451	0	1	2	1	6
ST489	1	0	0	0	0
ST59	0	1	1	1	1
ST649	0	0	0	0	1
ST9	1	2	0	0	0
ST91	0	0	3	0	0
Undefined	0	0	0	1	1
Serotype O4	**18**	**21**	**24**	**16**	**12**
ST1	10	11	16	12	7
ST1262	0	0	0	1	0
ST194	0	0	1	0	0
ST2	1	3	1	0	1
ST299	0	0	0	1	0
ST4	5	4	3	2	1
ST455	2	2	1	0	1
ST6	0	0	1	0	2
ST707	0	1	0	0	0
Undefined	0	0	1	0	0
Non-serotypeable	**0**	**0**	**0**	**1**	**4**
ST1	0	0	0	0	3
ST26	0	0	0	1	0
ST299	0	0	0	0	1
Total	**31**	**32**	**39**	**35**	**34**

Recent surveys

Nil.

Relevant New Zealand studies and publications

Nil.

Relevant regulatory developments

No *L. monocytogenes*-specific regulatory developments.

Norovirus infection

Case definition

Clinical description:	Gastroenteritis usually lasting 12–60 hours.
Laboratory test for diagnosis:	Detection of norovirus in faecal or vomit specimen or leftover food (currently there is a limited range of foods able to be tested for norovirus).
Case classification:	
Probable	A clinically compatible illness.
Confirmed	A clinically compatible illness that is laboratory confirmed, OR a clinically compatible illness and a common exposure associated with a laboratory confirmed case.

Norovirus infection individual cases reported in 2024 by data source

During 2024, 32 individual cases of norovirus infection were reported in EpiSurv, of which 15 were reported associated to outbreaks. No deaths of norovirus cases were reported in EpiSurv. For three cases infection with enteropathogenic *E. coli* was also recorded, with one of those cases also testing positive for adenovirus.

It should be noted that not every individual case of norovirus infection is notifiable; only those when the infected person is in a high-risk category (e.g. food handler, early childhood service worker) or the case is part of an outbreak. Outbreaks of norovirus infection are reported separately and involve large numbers of cases.

The ICD-10 code A08.1 was used to extract norovirus infection hospitalisation data from the Health New Zealand Te Whatu Ora NMDS database. Of the 845 hospitalised cases (15.8 hospitalised cases per 100,000 population) recorded in 2024, 427 cases were reported with norovirus infection as the principal diagnosis and 418 were reported with norovirus infection as another relevant diagnosis. Of the 845 hospitalised cases, 181 were less than five years old and 317 were in the 70+ years age group. Some of the 845 hospitalised cases were admitted to hospital more than once resulting in a total of 916 hospital admissions.

It should be noted that EpiSurv and NMDS are two separate databases that are used for different purposes. Therefore, NMDS and EpiSurv hospitalisation numbers may differ for several reasons, including criteria used for notifications or diagnostic coding, i.e. a hospital discharge may be coded to an infectious cause without a case being recorded in EpiSurv and vice versa (see also Appendix A–Methods, page 123).

Foodborne transmission

It has been estimated by expert consultation that 32.7% (95th percentile credible interval: 10.0% to 66.4%) of norovirus infections are due to foodborne transmission [2]. It was further estimated that approximately 24% of foodborne norovirus infections were due to consumption of seafood.

Outbreaks reported as caused by norovirus

In 2024, there were 181 outbreaks due to norovirus infection recorded in EpiSurv. No outbreaks were associated with overseas travel. Ten of these outbreaks reported food or a food handler as one of the possible modes of transmission (Table 34). There were two hospitalised cases reported for these potentially foodborne norovirus infection outbreaks. It is important to note that a single outbreak may have multiple pathogens, modes of transmission, settings where exposure occurred, or settings where preparation of food was conducted.

Table 34. Norovirus infection outbreaks reported in EpiSurv, 2024

	Possible foodborne transmission with a suspected or confirmed source	Possible foodborne transmission but no suspected food source	Total norovirus infection outbreaks
Outbreaks	1	9	181
Outbreak associated cases	49	514	4684
Outbreak hospitalised cases	0	2	42

Table 35 contains details of the 10 norovirus infection outbreaks with food reported as a possible mode of transmission in 2024. The evidence for a food source was strong for an outbreak which occurred in Auckland in August which was attributed to commercial oysters sold to food service outlets. Unrelated cases had eaten the oysters from four different food service outlets. This outbreak resulted in a product recall.

The evidence for foodborne transmission was weak for the other nine outbreaks, and person-to-person transmission is likely to be a risk factor. In two outbreaks, a sick food handler was identified as a possible source of the outbreak.

Table 35. Details of norovirus infection outbreaks with food or food handling reported as a possible mode of transmission, 2024

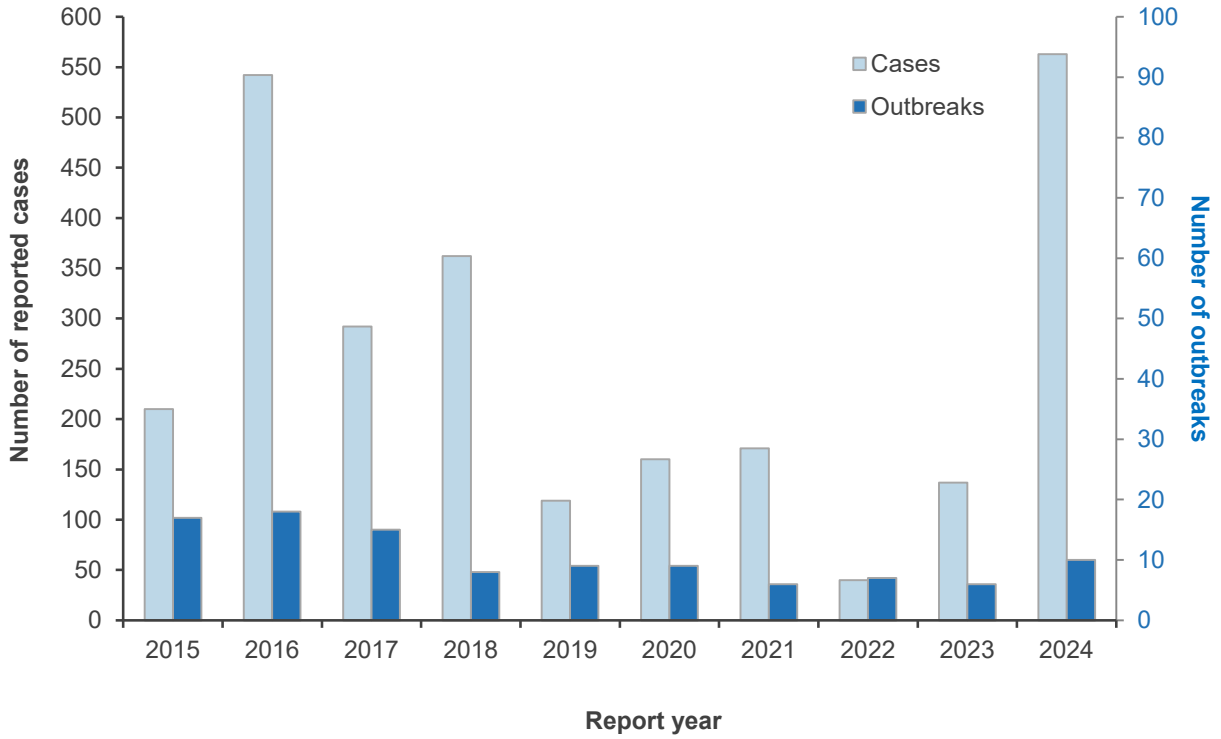
Health district	Month	Suspected source	Evidence	Setting	Number Ill	Norovirus genotype
MidCentral	February	Food and/or Person to Person	Common site	Educational	3C 267P	GII.1[P33]
Capital, Coast and Hutt Valley	March	Unknown	Common source	Food service (eat in and takeaway)	5C	GII.2[P2]
Waikato	March	Unknown	Common event	Community	1C 58P	GII.7[P7]
Wairarapa	May	Unknown	Common site	Educational	5C 82P	GII – not genotyped
Canterbury	May	Customer vomited in restaurant	Common event	Restaurant	1C 10P	GII.4 Sydney[P16]
Southern	May	Food handler	Common meal	Restaurant	2C 4P	GII.17[P17]
MidCentral	July	Unknown	Family group	Home	2C 4P	GII.17[P17]
Auckland	August	Commercial oysters	Common food	Multiple restaurants	4C 45P	GII.17[P17]
Hawke's Bay	October	Food handler	Common event	Restaurant	1C 7P	GII.17[P17]
Waikato	December	Unknown	Common event	Catered function	4C 58P	GII.17[P17]

Number ill: C: confirmed, P: probable.

During investigation of suspected foodborne illness outbreaks by PHF Science's Public Health Laboratory and the Enteric, Food and Environmental Virology/Norovirus Reference Laboratory (NRL), faecal specimens relating to ten outbreaks (Table 35) were received for norovirus testing/typing. Norovirus was detected in faecal samples from those outbreaks. The outbreaks were associated with GII.1[P33] (x1), GII.2[P2] (x1), GII.4 Sydney[P16] (x1), GII.7[P7] (x1), GII.17[P17] (x5), and one genogroup II (GII) norovirus that could not be genotyped.

Over the 10-year period 2015 to 2024, the annual number of norovirus infection outbreaks with food reported as a possible mode of transmission reported each year ranged from six (2021) to 18 (2016) (Figure 27). The total number of cases associated with these outbreaks each year ranged from 40 (2022) to 563 cases (2024).

Figure 27. Norovirus infection outbreaks with food reported as a possible mode of transmission and associated cases reported by year, 2015–2024



Note: The data in this figure comes from EpiSurv for the years up to 2021. From 2021 the plot includes foodborne outbreaks recorded in EpiSurv and any outbreaks that were referred to NZFS but were not recorded in EpiSurv as an outbreak.

Norovirus types commonly reported

Norovirus genotyping data from the NRL are shown in Table 36. The data relate to outbreaks rather than individual cases and contain all outbreaks, including those which are not associated with foodborne transmission. The number of norovirus outbreaks reported to the NRL differs from the number recorded in EpiSurv. Not all specimens from the norovirus outbreaks reported in EpiSurv are sent to PHF Science for genotyping and not all gastroenteritis outbreaks caused by norovirus are reported as norovirus outbreaks in EpiSurv.

In 2024, PHF Science typed the outbreak-associated norovirus for 114 outbreaks, of which 10 were food associated. Norovirus genogroup II (GII) was identified in 100/114 (87.7%) outbreaks. In the previous four years (2020-2023), GII was also the predominant norovirus genogroup, identified from between 73.0% (2023) and 91.3% (2022) of outbreaks.

The norovirus genotype was determined for 112 of the 114 (98.2%) norovirus outbreaks. GII.4 Sydney[P16] was the most common (42/112, 37.5% of outbreaks) genotype identified.

Table 36. Norovirus genotypes identified in outbreak-related cases, 2020–2024

Norovirus genotypes	2020	2021	2022	2023	2024
Genogroup I	**33**	**22**	**10**	**49**	**12**
GI untyped	2	2	0	1	0
GI.1[P1]	0	0	0	1	3
GI.2[P2]	0	0	5	3	0
GI.3[P3]	5	0	0	8	2
GI.3[P13]	8	14	2	0	4
GI.4[P4]	0	0	1	1	1
GI.5[P4]	14	1	0	0	0
GI.5[P5]	0	0	2	25	0
GI.5[P12]	1	0	0	0	0
GI.6[P11]	3	5	0	8	1
GI.7[P7]	0	0	0	2	1
Genogroup II	**125**	**75**	**126**	**135**	**100**
GII.2[P16]	93	35	5	4	1
GII.3[P12]	5	0	11	13	9
GII.4 Sydney[P16][a]	6	0	18	82	42
GII.4 Sydney[P31][a]	0	34	28	5	1
GII.4 Sydney[P4 New Orleans][a]	1	0	0	0	0
GII.6[P7]	3	2	54	1	5
GII.7[P7]	2	0	1	15	8
GII.8[P8]	1	0	0	2	1
GII.14[P7]	1	0	0	0	0
GII.17[P17]	6	2	2	8	24
Other[b]	7	2	7	5	9
Mixed GI and GII	**2**	**0**	**1**	**1**	**0**
Genogroup GIX[c]	**1**	**0**	**1**	**0**	**2**
Total outbreaks[d]	**161**	**97**	**138**	**185**	**114**

[a] GII.4 variants.

[b] 'Other' includes GII untyped, Mixed GII types, GII.1[P33], GII.2[P16], GII.3[P16], GII.3[P21], GII.3[P30], GII.12[P16], GII.13[P16], GII.13[P21].

[c] The capsid genotype GII.15 was reclassified as (human) GIX genogroup in 2019 (typed as GIX.1[P.15].

[d] The number of norovirus outbreaks reported to the NRL differs from the number recorded in EpiSurv. Not all specimens from the norovirus outbreaks reported in EpiSurv are sent to PHF Science for genotyping and not all gastroenteritis outbreaks caused by norovirus are reported as norovirus outbreaks in EpiSurv.

Recent surveys

Nil.

Relevant New Zealand studies and publications

Journal papers

Study of shellfish growing area during normal harvesting periods and following wastewater overflows in an urban estuary with complex hydrography – Campos et al., 2024

A study, carried out in Otago Harbour, tracked the impact of municipal wastewater overflow events on viral contamination of shellfish (little neck clams, *Austrovenus stutchburyi*) from two commercial growing areas in the harbour [32]. Norovirus (genogroups I and II) were not detected in any of the 218 shellfish samples tested. Samples included 136 baseline samples and 82 samples taken during emergency closures due to overflow events. There was some evidence of increased concentrations of indicator viruses (crAssphage and pepper mild mottle virus) in shellfish samples taken during emergency closures.

Relevant regulatory developments

MPI consulted on and amended *Food Notice: Requirements for Registered Food Importers and Imported Food for Sale* [31]. Specifically, the amended requirements include a transition from the current requirements for imported frozen berries (Option A) to a new set of requirements (Option B). Option B requires the overseas manufacturer to have a food safety management system that includes “a HACCP plan, which identifies significant hazards, including norovirus and hepatitis A virus, and their controls”.

Salmonellosis

Case definition

Clinical description:	Salmonellosis presents as gastroenteritis, with abdominal pains, diarrhoea (occasionally bloody), fever, nausea and vomiting. Asymptomatic infections may occur, and symptoms are not necessary to meet the case definition.
Laboratory test for diagnosis:	Isolation of *Salmonella* species OR detection of *Salmonella* nucleic acid from a clinical specimen.
Case classification:	
Probable	A clinically compatible illness that is either a contact of a confirmed case of the same disease or has had contact with the same common source – that is, is part of a common-source outbreak.
Confirmed	Meets the clinical description (that includes asymptomatic cases) and is laboratory confirmed.

Summary data

Summary data for salmonellosis in 2024 are given in Table 37. Note that in the following sections the term *Salmonella* refers to non-typhoidal serotypes of *Salmonella enterica*. Since the end of 2017, this has included *Salmonella enterica* subspecies *enterica* serotype Paratyphi B var. Java, which is typically associated with gastroenteritis.

Table 37. Summary of surveillance data for salmonellosis, 2024

Parameter	Value in 2024	Source
Number of notified cases	844	EpiSurv
Notification rate (per 100,000)	15.8	EpiSurv
Hospitalised cases[a]	213	NMDS
Deaths[b]	0	EpiSurv
Estimated number of cases related to travel (%)[c,d]	380 (45.0%)	EpiSurv
Estimated domestically acquired food-related cases[e]	288	Expert consultation and EpiSurv

NMDS = Health New Zealand Te Whatu Ora National Minimum Dataset of hospitalisations.

[a] Cases hospitalised may not be notified on EpiSurv.

[b] Of the three deaths of salmonellosis cases recorded in EpiSurv in 2024, none were recorded as due to salmonellosis. Two cases died from a cause other than salmonellosis and the cause of death was not recorded for the other case.

[c] Estimated number and % of cases related to travel. Of the 844 notified cases, the overseas travel question had a 'yes' or 'no' entry for 729 cases (86.4%); of these, 328 cases (45.0%) had travelled overseas during the incubation period and 401 cases (55.0%) had not been overseas. The overseas travel history for the remaining 115 cases is unknown. The estimated number of cases related to travel is given as 45.0% percent of all cases in 2024.

[d] While international travel has increased again since restrictions ceased in 2022, overseas travel in 2024 was still slightly lower compared with the pre-COVID-19 year 2019 (see section Changes in overseas travel, page 11).

[e] Estimation of food-related cases is given by *(Total cases – Estimate of cases acquired overseas) x Estimate of proportion of domestically acquired cases likely to be due to foodborne transmission*. The estimate of domestic proportion of salmonellosis cases due to foodborne transmission (62.1%) was derived from expert consultation [2].

Salmonellosis individual cases reported in 2024 by data source

During 2024, 844 individual cases (15.8 per 100,000 population) of salmonellosis were reported in EpiSurv. Two salmonellosis cases were recorded in EpiSurv as having died from a cause other than salmonellosis and one salmonellosis case was recorded as having died from an unknown cause.

The ICD-10 code A02.0 (*Salmonella* enteritis) was used to extract salmonellosis hospitalisation data from the Health New Zealand Te Whatu Ora NMDS database. Of the 213 hospitalised cases (4.0 hospitalised cases per 100,000 population) recorded in 2024, 172 cases were reported with salmonellosis as the principal diagnosis and 41 were reported with salmonellosis as another relevant diagnosis. Ten of the 213 hospitalised cases were admitted to hospital twice resulting in a total of 223 hospital admissions. The majority of hospitalised cases (53%) spent between two and six nights in hospital, with 1.9% of hospitalised cases admitted to an intensive care unit (Appendix C, Table 69).

It should be noted that EpiSurv and NMDS are two separate databases that are used for different purposes. Therefore, NMDS and EpiSurv hospitalisation numbers may differ for several reasons, including criteria used for notifications or diagnostic coding (see also Appendix A–Methods, page 123).

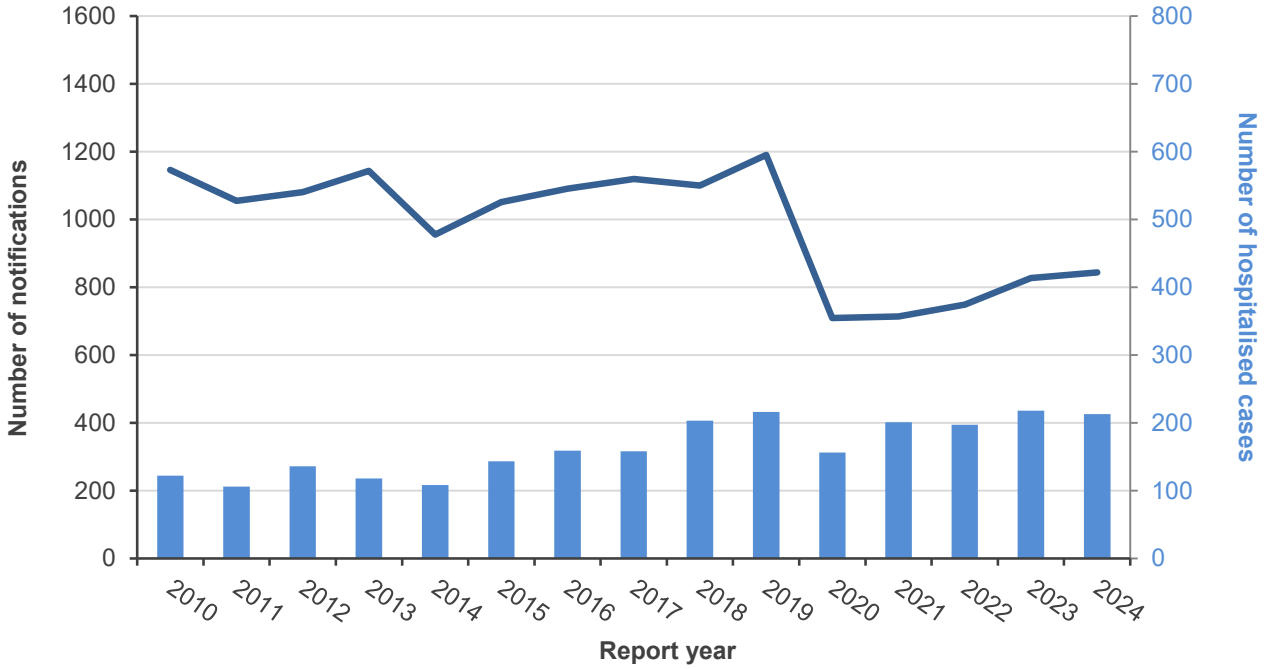
Foodborne transmission

It has been estimated by expert consultation that 62.1% (95th percentile credible interval: 35.2% to 86.4%) of salmonellosis incidence is due to foodborne transmission. It was further estimated that approximately 19% of foodborne salmonellosis was due to transmission via poultry [2].

Annual data

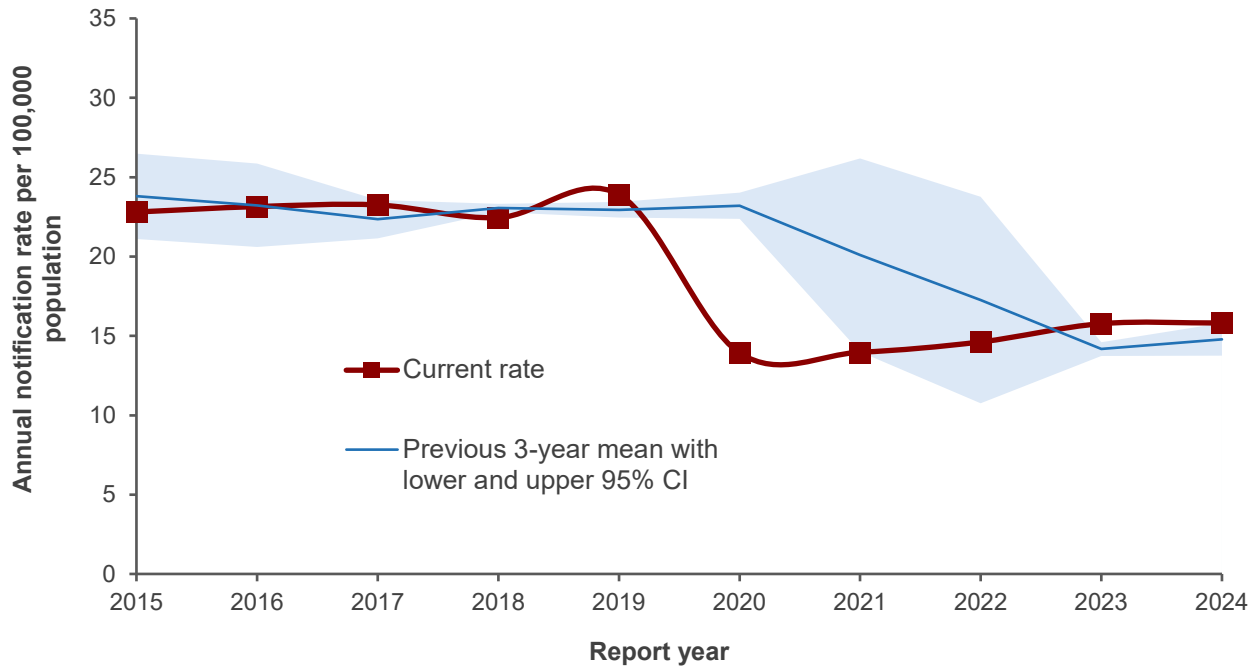
Between 2010 and 2019 the number of salmonellosis notifications per year ranged between 955 (2014) and 1188 (2019) (Figure 28), with associated notification rates between 21.1 and 23.9 cases of salmonellosis per 100,000 population per year (Figure 29). The low numbers of notifications for the years 2020 to 2022 can be attributed to the impact of the COVID-19 public health response [18] and the reduction in overseas travel (see section Changes in overseas travel, page 11). The frequency of overseas travel remained lower in 2024 compared with the pre COVID-19 year 2019. In 2024, the estimated percentage of salmonellosis cases related to travel was 45.0% (95% CI: 43.7-46.3%), compared with 34.4% (95% CI: 33.3-35.6%) in 2019 (pre-COVID-19 pandemic) and 0.0% (95% CI: 0.0-<0.2%) in 2021 (year of greatest reduction in travel).The number of hospital admissions with salmonellosis as a principal or other relevant diagnosis varied slightly year by year but did not show the same pronounced reduction in the years 2020 to 2024 as the number of annual notifications (Figure 28). The decrease in notified cases alongside the generally consistent number of hospitalised cases (i.e., a higher proportion of cases requiring hospitalisation) may be due to a combination of different factors, including increasingly difficult access to primary healthcare (increased wait time for GP visits and costs as barriers to seeking medical attention) [25], some underreporting (fewer people with mild symptoms seeking health care and providing a sample) or increased number of cases with types of greater pathogenicity.

Figure 28. Salmonellosis EpiSurv notifications (line) and NMDS hospitalised cases (bar) by year, 2010–2024



The notification rate in 2024 (15.8 cases per 100,000 population) was slightly higher than the previous three-year mean (14.8 cases per 100,000 population) (Figure 29).

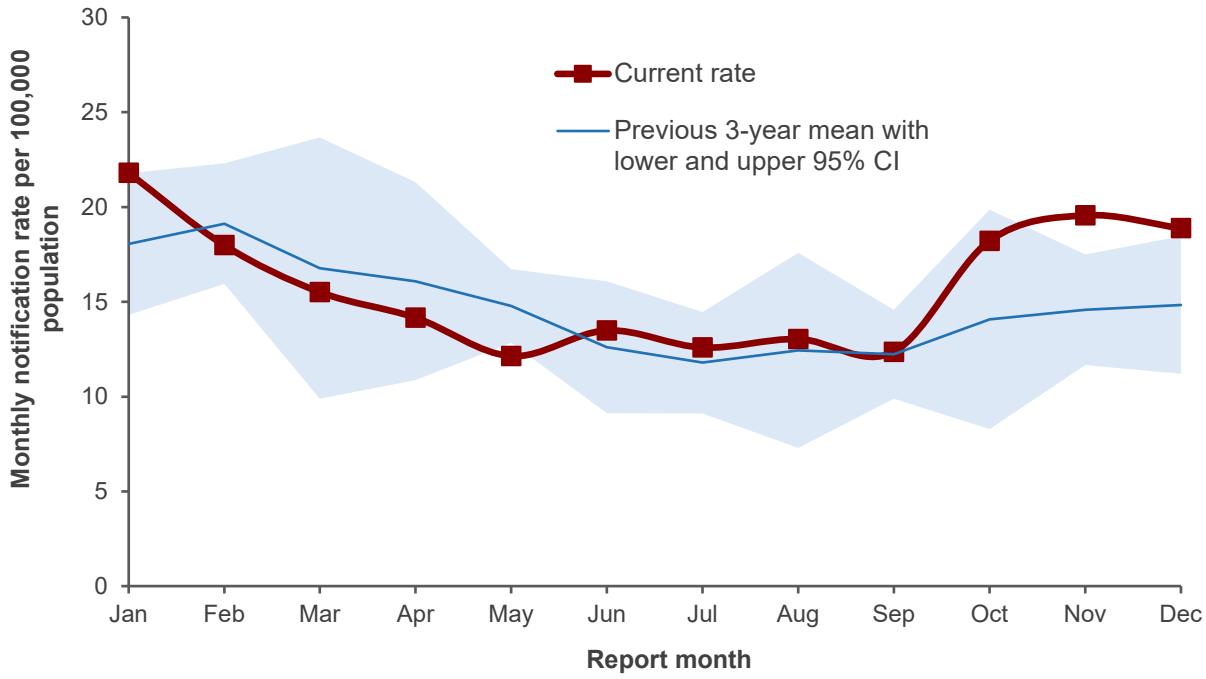
Figure 29. Salmonellosis notification rate by year, 2015–2024



Seasonal data

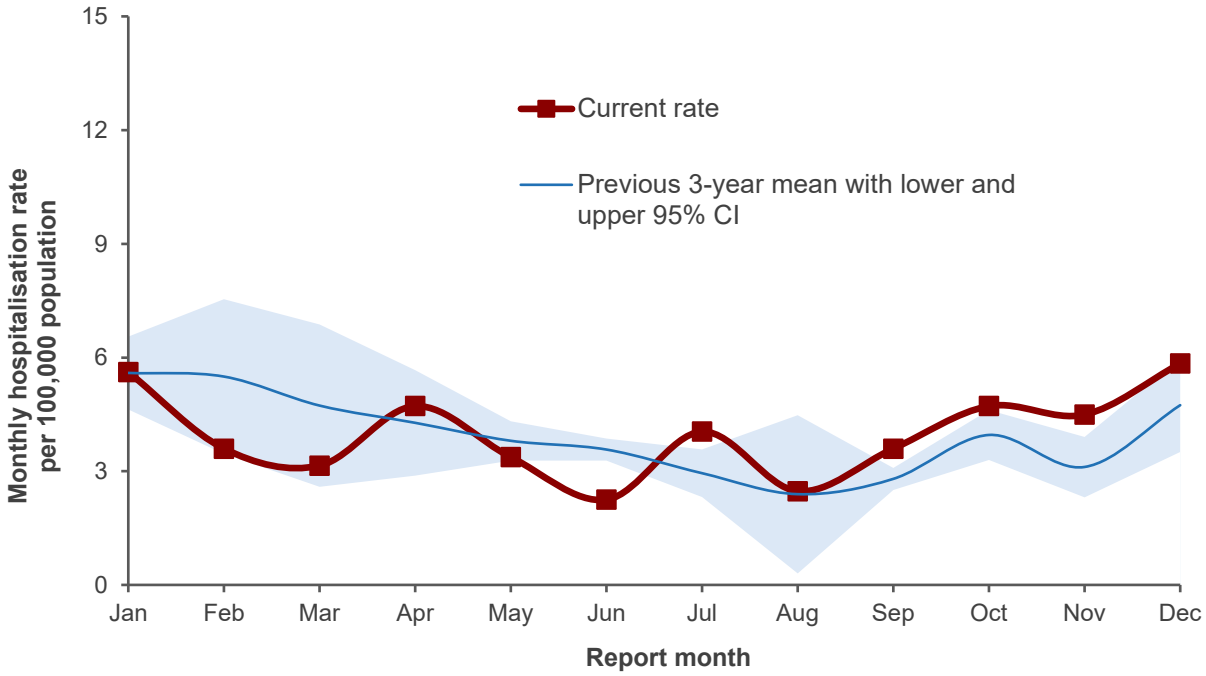
Salmonellosis case notification rates per 100,000 population by month for 2024 are shown in Figure 30. For most of the year, the monthly notification rates were similar to the mean of the previous three years. The monthly number of notifications in 2024 ranged from 54 cases (May, 12.1 cases per 100,000 population) to 97 cases (January, 21.8 cases per 100,000 population).

Figure 30. Salmonellosis monthly notification rate (annualised), 2024



In 2024, monthly hospitalisation rates varied over the year (Figure 31) with the highest rates in the summer months, similar to the previous three years. The monthly number of hospitalised cases in 2024 ranged from 10 cases (June, 2.3 cases per 100,000 population) to 26 cases (December, 5.8 cases per 100,000 population).

Figure 31. Salmonellosis monthly hospitalisation rate (annualised), 2024



Demographics

In 2024, the notification rate was similar for males (15.7 cases per 100,000 population, 418 cases) and females (15.8 cases per 100,000 population, 425 cases). The rate of hospitalised cases was the same for males and females (4.0 hospitalised cases per 100,000 population) (Table 38).

Table 38. Salmonellosis cases by sex, 2024

Sex	EpiSurv notified cases		Hospitalised cases[a]	
	No.	Rate[b]	No.	Rate[b]
Male	418	15.7	106	4.0
Female	425	15.8	107	4.0
Total[c]	**844**	**15.8**	**213**	**4.0**

[a] Health New Zealand Te Whatu Ora NMDS data.

[b] Per 100,000 population.

[c] Total includes one case where sex was not recorded.

In 2024, notification and hospital admission rates of salmonellosis were highest for children in the <1 years age group (79.5 cases and 15.6 hospitalised cases per 100,000 population) (Table 39). The 70+ years age group had the longest hospital stays (30 cases admitted for two or more nights) (Appendix C, Table 79).

Table 39. Salmonellosis cases by age group, 2024

Age group (years)	EpiSurv notified cases		Hospitalised cases[a]	
	No.	Rate[b]	No.	Rate[b]
< 1	46	79.5	9	15.6
1 to 4	82	33.6	21	8.6
5 to 9	42	12.8	13	4.0
10 to 14	28	8.0	5	1.4
15 to 19	25	7.3	3	-
20 to 29	95	13.8	22	3.2
30 to 39	95	11.7	19	2.3
40 to 49	103	15.5	25	3.8
50 to 59	124	19.0	32	4.9
60 to 69	114	19.5	28	4.8
70+	90	14.5	36	5.8
Total[c]	**844**	**15.8**	**213**	**4.0**

[a] Health New Zealand Te Whatu Ora NMDS data.

[b] Per 100,000 population in this age group (rate not calculated when fewer than five cases reported).

In 2024, the salmonellosis notification and hospitalised case rates were highest for the ethnic group 'Pacific peoples' (17.8 cases and 9.4 hospitalised cases per 100,000 population) (Appendix C, Table 70 and Table 71). The 'European or Other' ethnic group had the second highest notification rate (16.4 cases per 100,000 population), but lowest hospitalised case rate (3.3 hospitalised cases per 100,000 population).

Geographic distribution

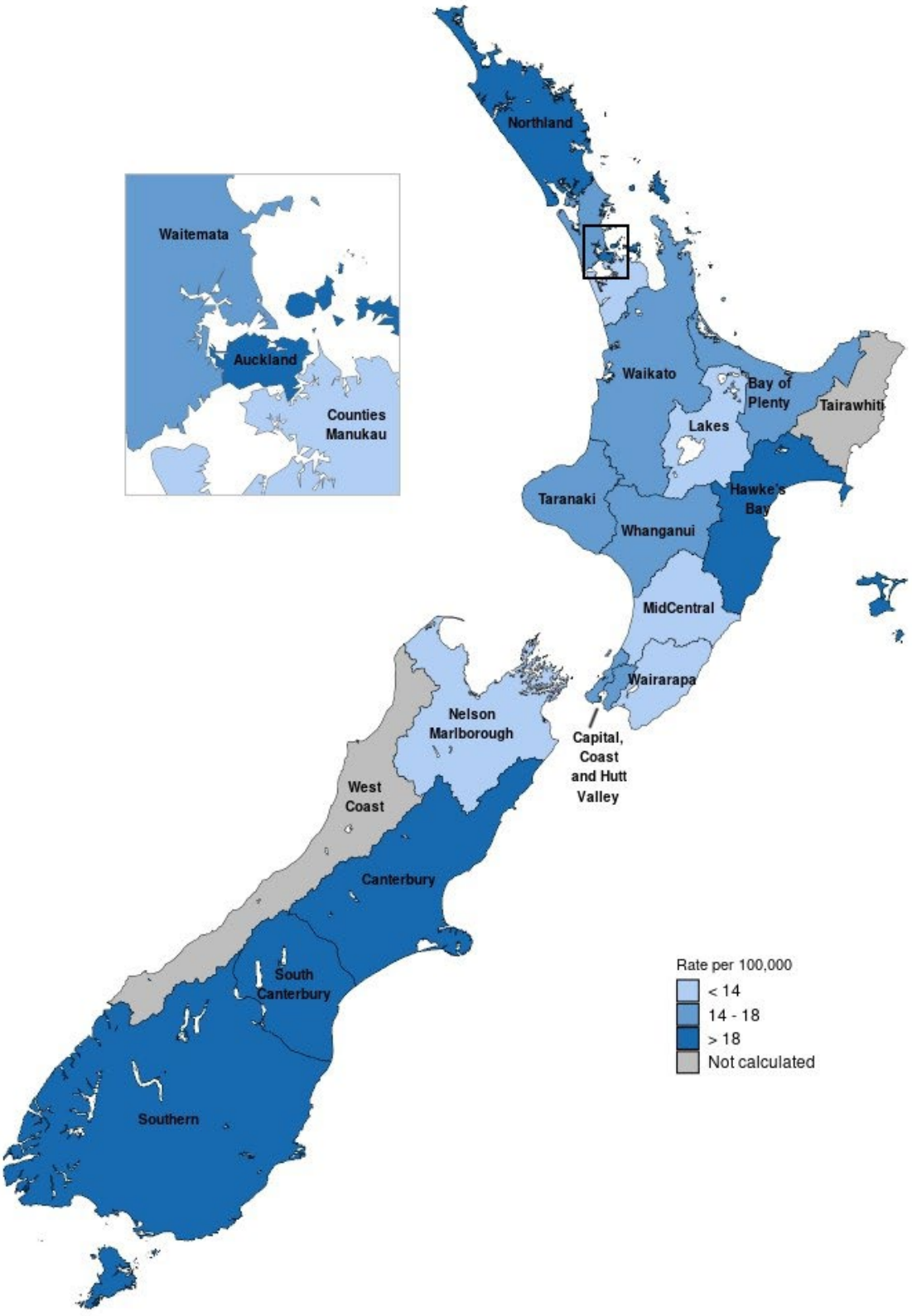
The notification rates by Health District calculated per 100,000 resident population are presented in Figure 32 (see also Appendix C, Table 83). The number of notified cases by Health District are presented in Appendix C, Table 82.

In 2024, the Health District notification rates of salmonellosis ranged from 9.3 per 100,000 population in MidCentral (18 cases) to 27.8 cases per 100,000 population (18 cases) in South Canterbury. The Health Districts Southern (77 cases), Hawke's Bay (36 cases), Canterbury (120 cases) and Auckland (93 cases) had the next highest notification rates (18.2 to 21.1 cases per 100,000 population).

From 2020 to 2024, the regions from the lower half of the South Island including South Canterbury, Southern and Canterbury Health Districts have had rates in the highest quartile of notification rates.

Salmonellosis notification rates, stratified by 2023 Urban Rural Classification [26] of the cases' residential address and excluding cases associated with overseas travel, were lower for urban area categories compared with rural categories (Appendix C, Table 84). Case notification rates for urban categories ranged from 7.1 to 11 cases per 100,000 population, while rates for rural categories were 11.9 cases per 100,000 population for 'rural settlement' and 15.5 cases per 100,000 population for 'rural other'. Hospitalised case rates were the highest for the 'rural settlement' category (8.8 hospitalised cases per 100,000 population) but the lowest for 'rural other' (1.8 hospitalised cases per 100,000 population) (Appendix C, Table 85).

Figure 32. Geographic distribution of salmonellosis notifications, 2024



Outbreaks reported as caused by *Salmonella*

In 2024, there were nine salmonellosis outbreaks notified in EpiSurv (Table 40). The cases from two outbreaks were reported as infected overseas (total of eight cases). Of the remaining seven outbreaks two were reported as potentially foodborne.

It is important to note that a single outbreak may have multiple pathogens, modes of transmission, settings where exposure occurred, or settings where preparation of food was conducted.

Table 40. Salmonellosis outbreaks reported in EpiSurv, 2024

	Possible foodborne transmission with a suspected or confirmed source	Possible foodborne transmission but no suspected food source	Total salmonellosis outbreaks
Outbreaks	0	2	9
Outbreak associated cases	0	36	56
Outbreak hospitalised cases	0	11	11

In March, PHF Science identified a genomic cluster of 21 cases, which were linked to two school camps at the same venue and time period plus other cases that were not associated with the camps. While this suggests a potential foodborne source, no specific food source was identified. The second potentially foodborne outbreak in EpiSurv was related to a community sporting event in December, but no specific food was identified (Table 41).

In addition to the EpiSurv outbreaks recorded as potentially foodborne, there was an outbreak of three cases in EpiSurv which NZFS investigated. WGS of two case isolates matched those from an earlier poultry-associated outbreak. Although cases had consumed an egg-based dish, food could not be confirmed as the cause of illness (Table 41).

NZFS also investigated two groups of gastroenteritis cases (three and four cases) who had consumed imported sesame seeds that where part of a product recall due to the potential presence of *Salmonella*. In both investigations *Salmonella* or a food source could not be confirmed as the cause of illness.

Table 41. Details of the suspected salmonellosis outbreaks with food reported as a possible mode of transmission, 2024

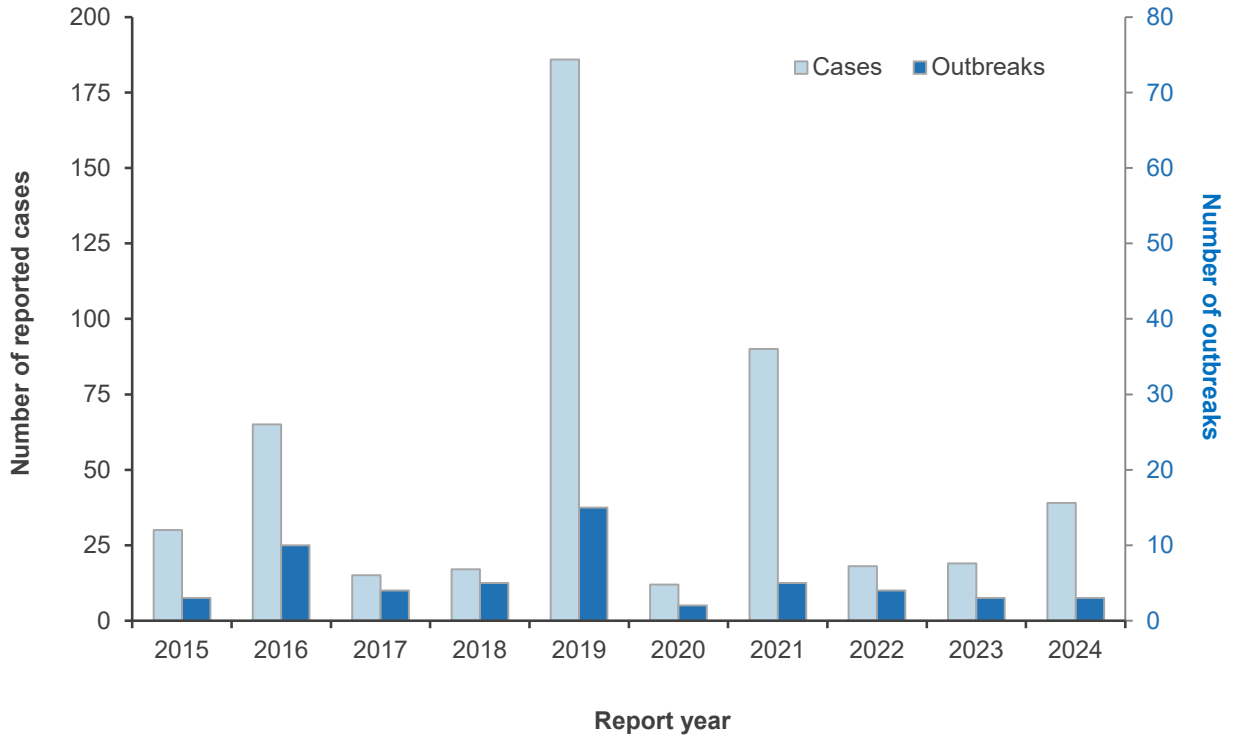
Health district	Month	Suspected source	Evidence	Setting	No. ill
Canterbury and Southern	March	Unknown	WGS cluster	Camp, Home	21C
Auckland	March	Eggs used in meat patties	Common food, WGS type previously associated with poultry	Farm	2C 1P
Auckland	December	Unknown	Common event	Community event	7C 8P

Number ill: C: confirmed, P: probable.

WGS: Whole genome sequencing

Over the 10-year period 2015 to 2024, the annual number of salmonellosis outbreaks with food reported as a possible mode of transmission ranged from two (2020) to 15 (2019) (Figure 33). The annual number of cases associated with the outbreaks over the same period ranged between 12 (2020) and 186 (2019).

Figure 33. Salmonellosis outbreaks with food reported as a possible mode of transmission and associated cases (excluding outbreaks associated with overseas travel) reported by year, 2015–2024



Note: The data in this figure comes from EpiSurv for the years up to 2021. From 2021 the plot includes foodborne outbreaks recorded in EpiSurv and any outbreaks that were referred to NZFS but were not recorded in EpiSurv as an outbreak.

Salmonella types commonly reported

Human isolates

In 2024, isolates from 753 notified cases with non-typhoidal *Salmonella* infections were typed by the PHF Science Enteric Reference Laboratory (Table 42). *S.* Typhimurium (238 cases) and *S.* Enteritidis (95 cases) were the most common serotypes identified. Other serotypes commonly reported were *S.* Paratyphi B var. Java (59 cases), monophasic *S.* Typhimurium (31 cases), *S.* Saintpaul (30 cases), *S.* Chester (28 cases) and *S.* Bovismorbificans (24 cases).

Table 42. Annual number of case notifications with different *Salmonella* serotypes, 2020–2024

Serotype[a]	2020	2021	2022	2023	2024	Count of cases with overseas travel history (%), 2024[b]	Count of cases with unknown travel history (%), 2024[c]
S. Typhimurium	329	310	348	237	238	41 (19)	24 (11)
S. Enteritidis	70	131	73	92	95	45 (49)	3 (3)
S. Agona	4	4	9	18	10	7 (70)	0
S. Anatum	3	0	3	6	6	4 (67)	0
S. Bareilly	1	1	5	6	7	3 (50)	1 (14)
S. Bovismorbificans	60	50	43	24	24	1 (8)	11 (46)
S. Braenderup	0	2	4	4	5	3 (100)	2 (40)
S. Brandenburg	36	39	20	24	12	1 (13)	4 (33)
S. Chester	1	2	2	15	28	20 (83)	4 (14)
S. Corvallis	0	0	1	3	6	5 (100)	1 (17)
S. Give	5	2	8	2	3	0	0
S. Hvittingfoss	1	6	3	5	10	5 (56)	1 (10)
S. Infantis	7	9	5	8	5	2 (50)	1 (20)
S. Javiana	2	1	8	9	8	8 (100)	0
S. Kentucky	0	1	0	2	6	5 (100)	1 (17)
S. Mississippi	17	7	14	19	11	0	2 (18)
S. Newport	3	1	2	14	13	6 (60)	3 (23)
S. Paratyphi B var. Java	8	3	3	20	59	48 (89)	5 (8)
Monophasic *S.* Paratyphi B var. Java	1	0	2	8	14	9 (75)	2 (14)
S. Pensacola	1	8	6	5	6	1 (25)	2 (33)
S. Saintpaul	26	29	21	26	30	9 (35)	4 (13)
S. Stanley	11	9	18	27	18	14 (88)	2 (11)
S. Thompson	11	10	11	12	11	1 (13)	3 (27)
Monophasic *S.* Typhimurium	1	2	1	15	31	12 (48)	6 (19)
S. Virchow	3	0	9	5	12	9 (82)	1 (8)
S. Weltevreden	11	3	6	25	17	8 (50)	1 (6)
Other[d]	37	33	55	88	70	33 (56)	11 (16)
Untyped[e]	63	54	72	121	91	29 (41)	20 (22)
Total Cases	**709**	**714**	**750**	**827[f]**	**844[f]**		

[a] Excludes *S.* Typhi and *S.* Paratyphi (except *S.* Paratyphi B var. Java which is typically associated with gastroenteritis). Table lists the serotypes which had five or more associated cases in 2024 or had more than 10 cases in the previous three years combined.

[b] Percentage refers to the number of cases that answered "yes" for overseas travel during the incubation period out of the total number of cases for which travel information was recorded. However, even if a person has travelled within the incubation period, it does not necessarily imply the infection has been acquired in the respective country. Incubation periods for salmonellosis typically range between 6-72 hours [33], for atypical cases incubation periods of up to 16 days have been reported.

[c] Percentage refers to the number of cases with unknown travel history during the incubation period out of the total number of cases.

[d] Serotypes were able to be determined, but there were four or fewer associated notified cases in 2024 and less than 10 cases in the previous three years combined.

[e] Viable isolate not received for typing by the Enteric Reference Laboratory.

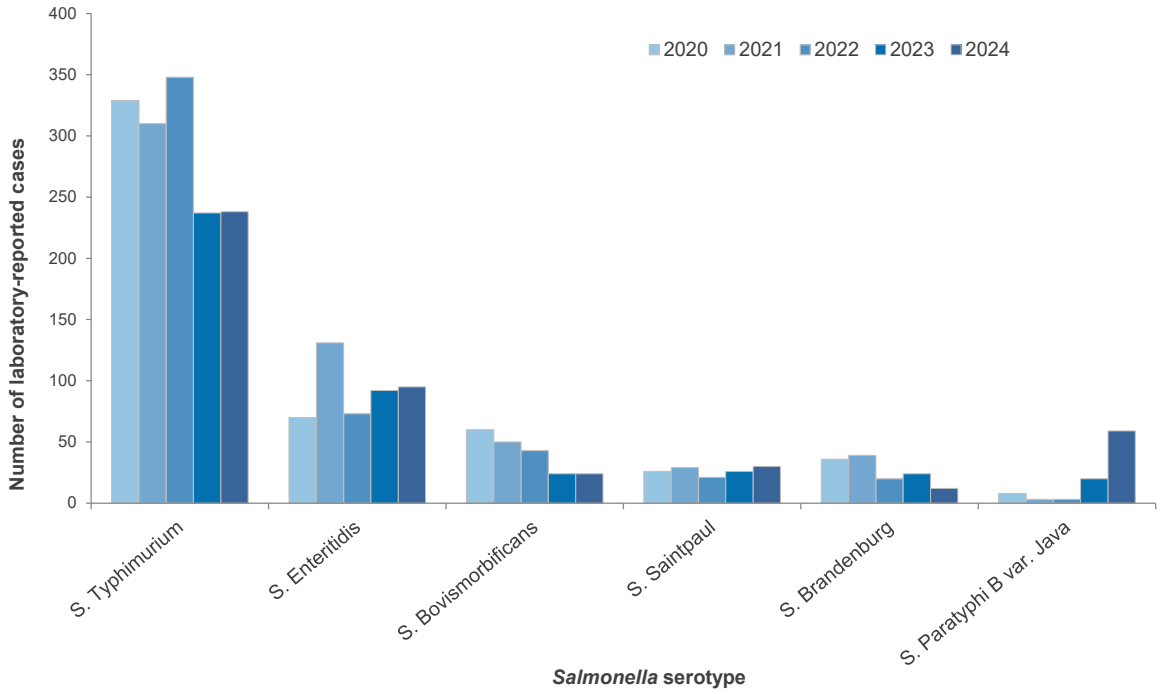
[f] One case in 2023 and two cases in 2024 had a mixed infection, i.e., an individual case was represented by two *Salmonella* serotypes.

EpiSurv records for 2024 indicate that 40% of cases infected with *S*. Typhimurium and 32% of cases infected with *S*. Enteritidis were recorded as hospitalised. For serotypes where at least five cases were reported in 2024, the highest hospitalisation rates were for cases infected with *S*. Bareilly (71%), *S*. Pensacola (50%), *S*. Weltevreden (47%) and *S*. Newport (46%), with hospitalisation status reported for all of these (100%). In contrast, cases infected with the commonly reported serotypes *S*. Saintpaul and *S*. Chester were less often hospitalised (10% and 11%, with hospitalisation status reported for 93% and 89% of these cases, respectively).

Figure 34 shows the annual trend for selected *Salmonella* serotypes from 2020 to 2024. For the types shown, there is within-type variation year to year. *S*. Typhimurium was the most prevalent serotype isolated from notified cases.

There was a drop in *S*. Enteritidis cases in 2020 likely due to COVID-19 overseas travel restrictions. In 2019, overseas travel was reported as a risk factor for 40% of *S*. Enteritidis cases and 10% of *S*. Typhimurium cases. While travel restrictions continued in 2021, there were two domestically acquired *S*. Enteritidis outbreaks (74 cases) in 2021 accounting for the increase in *S*. Enteritidis cases compared with 2020. Of the 95 *S*. Enteritidis cases in 2024, 49% had recorded overseas travel.

Figure 34. Number of laboratory-reported case related isolates for selected *Salmonella* serotypes by year, 2020–2024



Non-human isolates

A total of 638 non-human *Salmonella* isolates were serotyped by the Enteric Reference Laboratory during 2024 (Table 43). *S.* Typhimurium (282 isolates) was the most common serotype in non-human samples in 2024. The next most common serotypes were *S*. Bovismorbificans (119 isolates), *S*. Brandenburg (58 isolates) and *S*. Give (43 isolates). In 2021 and 2022, there was a shift in the proportion of types of non-human serotypes, with more *S*. Enteritidis being recorded than in previous years. This increase was related to intensive testing of poultry samples following an outbreak of human *S*. Enteritidis infections. Some caution should be exercised with respect to trends in non-human isolate typing data as the basis for sample selection may differ from year to year.

Table 43. *Salmonella* serotypes from non-human sources, 2020–2024

Serotype[a]	2020	2021	2022	2023	2024	Major sources, 2024
S. Typhimurium	**336**	**330**	**248**	**190**	**282**	Avian (5), bovine (212), canine (13), cervine (1), equine (4), feline (7), ovine (5), environmental (3), feed (15), food[d] (2), not specified (3), poultry environmental (4), poultry feed (5), poultry miscellaneous[e] (3)
S. Enteritidis	**5**	**188[b]**	**101[b,c]**	**29**	**16[c]**	Bovine (3), environmental (1), poultry environmental (5), poultry miscellaneous[e] (7)
Other serotypes	**492**	**497**	**436**	**407**	**340**	-
S. Agona	9	7	30	14	9	Bovine (3), canine (5), food[d] (1)
S. Bovismorbificans	247	127	100	114	119	Avian (2), bovine (103), canine (1), feline (2), ovine (4), reptile (1), environmental (3), food[d] (2), not specified (1)
S. Brandenburg	91	89	23	39	58	Bovine (41), canine (3), ovine (4), feed (1), food[d] (8), not specified (1)
S. Emek	4	12	9	16	7	Bovine (6), food[d] (1)
S. Give	78	88	102	57	43	Bovine (37), canine (2), food[d] (3), poultry environmental (1)
S. Hindmarsh	8	23	17	62	33	Bovine (4), ovine (28), food[d] (1)
S. Infantis	3	17	14	7	3	Bovine (2), canine (1)
S. Livingstone	0	1	24	17	6	Canine (6)
S. Mbandaka	7	39	19	9	11	Canine (1), environmental (3), food[d] (1), meat/bone meal (5), not specified (1)
S. Saintpaul	8	9	15	15	9	Avian (3), bovine (2), canine (2), equine (1), feline (1)
S. Senftenberg	2	7	19	5	5	Food[e] (1), poultry environmental (3), poultry miscellaneous[e] (1)
S. Thompson	1	46	4	8	1	Canine (1)
Other or unknown serotypes	33	32	59	36	36	-
Total	**833**	**1015**	**785**	**626**	**638**	-

[a] The table lists the serotypes which had five or more associated isolations from non-human sources in 2024, or more than 10 isolations in the previous three years combined.

[b] The 2021 and 2022 increase in *S.* Enteritidis is related to extensive testing for *S.* Enteritidis in the poultry environment following an outbreak of human *S.* Enteritidis infections in 2021.

[c] 74 of the 101 *S.* Enteritidis isolates from 2022 and 10 of the 16 *S.* Enteritidis isolates from 2024 were typed by a different laboratory.

[d] Includes animal carcasses from meat works.

[e] Including product.

Recent surveys

Are frozen, crumbed chicken products safe to eat? – Castles, 2024

Consumer magazine carried out a small survey of frozen, crumbed chicken products, such as nuggets, burgers and tenders (n = 39) [29]. Salmonella was not detected in any of the samples analysed. An associated survey of 1001 New Zealanders, aged 18 years and older, found that most (51%) assessed whether products were sufficiently cooked by visual inspection of the interior of the product. A further 29% cooked products according to manufacturers' instructions.

Relevant New Zealand studies and publications

Reports

Risk profile update: Salmonella (non-typhoidal) in and on eggs – Kingsbury et al., 2024

The Risk Profile sought to answer four specific Risk Management Questions (RMQs), with a focus on information that has become available since the 2016 update was produced [34]:

RMQ1: Considering the detection of *Salmonella* Enteritidis in chicken hatcheries/day-one chicken suppliers in 2021, how has the public health risk from *Salmonella* in or on eggs changed since the 2016 Risk Profile update?

Detection of the *S*. Enteritidis DT8, ST11 strain SE_2019_C_01 in layer flocks has the potential to increase the risk to the New Zealand layer industry and to consumers of eggs. The potential for transovarian transmission of *S*. Enteritidis to eggs via the breeder flocks at the apex of the supply chain could result in widespread dissemination through the layer poultry supply chain. Colonisation of layer flocks poses a greater risk for consumers because egg contents are more likely to be contaminated via transovarian transmission by *S*. Enteritidis than by other *Salmonella* serotypes. There is some evidence that this strain poses a greater risk to human health than other *Salmonella* serotypes because of a higher hospitalisation rate. There is also a risk to international trade in hatching and table eggs. The residual level of risk will be determined by the efficacy of the new control measures implemented to detect flock colonisation, eliminate colonised flocks, and control dissemination of *S*. Enteritidis. Although this strain has the potential to increase the risk to consumers of eggs, the absence of reported cases of infection with the outbreak strain since February 2023 suggests that risk management procedures have been effective at controlling the risk. The risk associated with non-Enteritidis *Salmonella* serotypes in and on eggs does not appear to have changed since the 2016 Risk Profile.

RMQ2: What interventions are available to manage the risk from *Salmonella* in and on eggs and what is known about their effectiveness?

The most effective overall strategy to control *Salmonella* in and on eggs is by applying multiple interventions throughout the egg production chain to control colonisation of layer chickens and prevent contamination of the farm environment. Environmental management includes controlling the food and water supply, biosecurity and pest management, and ensuring effective cleaning regimes are in place. Vaccination is widely practiced on New Zealand layer farms, and can reduce, but not prevent, flock colonisation, shedding, and contamination of eggs. Adding prebiotics, probiotics, bacteriophages, organic acids or phytochemicals to feed for hens has been shown to provide some protection against *Salmonella*. Post-harvest control measures may include egg washing/sanitising or UV treatment of eggs, which can reduce *Salmonella* numbers on egg surfaces. Pasteurisation or fully cooking eggs inactivates *Salmonella* in egg contents. Other effective hazard mitigation behaviours for consumers include discarding eggs that are dirty, cracked or past their best before date, and washing hands and surfaces following contact with raw eggs. Refrigerating eggs post-lay will control the growth of any *Salmonella* that might be present in the egg contents.

RMQ3: What information is available to advise industry regarding shelf life and storage conditions for eggs in relation to the risk from *Salmonella*?

The current shelf life for New Zealand eggs is 35 days (shown as a best before date) regardless of storage temperature. *Salmonella* present on clean eggshells will not grow and will die faster at warmer storage temperatures (for example, room temperature compared with refrigeration). However, warmer temperatures promote faster breakdown of the vitelline membrane and more rapid growth of any *Salmonella* present in egg yolk, whereas *Salmonella* will not grow at refrigeration temperatures. New Zealand shelf life considerations were guided by the very low likelihood that *Salmonella* would be

present in egg contents, but the risk for contamination of egg contents is higher for *S*. Enteritidis because it is potentially transovarian. Current data suggest that the risk management interventions are effectively mitigating *S*. Enteritidis in New Zealand layer flocks. However, a reconsideration of shelf life guidelines would be important if the strain were to re-emerge and become endemic in New Zealand layer flocks.

RMQ4: What is the best way to gather information on the prevalence of *Salmonella* in New Zealand eggs?

The best approach to gather information on the prevalence of *Salmonella* on New Zealand eggs is by environmental sampling of dust and faeces in layer sheds. Testing egg contact surfaces at packhouses can also indicate that contamination of egg surfaces is occurring. The newly implemented testing programme for *S*. Enteritidis in New Zealand breeder, layer and broiler flocks and hatcheries has been designed to maximise the likelihood of *S*. Enteritidis detection if it is present in flocks. The testing programme appears as rigorous as that conducted in the European Union with respect to sampling frequency, timing, and sensitivity of sample types. However, the testing does not cover the risk of egg contamination from other *Salmonella* serotypes. Testing regulatory framework samples for total *Salmonella* prevalence and targeting other serotypes of higher concern such as *S*. Typhimurium in addition to *S*. Enteritidis, would provide valuable information on the risk of all *Salmonella* serotypes to New Zealand eggs.

Journal papers

Antimicrobial resistance in selected bacteria from food animals in New Zealand 2018–2022 – Cornelius et al., 2024

Salmonella isolates (*n* = 8) from very young calves, collected during 2020, were examined for resistance to apramycin, gentamicin, streptomycin, cefotaxime, ceftazidime, cefoxitin, ciprofloxacin, ampicillin, amoxicillin/clavulanic acid, colistin, sulfamethoxazole, trimethoprim and tetracycline [30]. All isolates were susceptible to all tested antimicrobials.

New Zealand microbiological risk ranking of imported fruits and vegetables – Perchec-Merien and Esguerra, 2024

A multi-criteria scoring and ranking approach was used to rank microbial risks associated with fruits and vegetables imported into New Zealand [35]. *Salmonella* spp. were assessed to be in the highest risk category (1-5, with 5 being the highest) for other leafy greens, melons and other cucurbits. Additionally, *Salmonella* spp. were in risk category 4 for 10 other categories of fruit or vegetables.

Relevant regulatory developments

No *Salmonella*-specific regulatory developments.

Sapovirus infection

Case definition

Clinical description:	Gastroenteritis usually lasting 2–6 days.
Laboratory test for diagnosis:	Detection of sapovirus in faecal or vomit specimen or leftover food (currently there is a limited range of foods able to be tested for sapovirus).
Case classification:	
Probable	A clinically compatible illness.
Confirmed	A clinically compatible illness that is laboratory confirmed, OR a clinically compatible illness and a common exposure associated with a laboratory confirmed case.

Sapovirus infection individual cases reported in 2024 by data source

During 2024, one individual case of sapovirus infection was reported in EpiSurv. The case was not reported as hospitalised in EpiSurv. Note that not every individual case of sapovirus infection is necessarily notifiable; only those when the infected person is in a high-risk category (e.g. food handler, early childhood service worker) or the case is part of an outbreak.

There is no ICD-10 code specifically for diagnosis of sapovirus infection in the Health New Zealand Te Whatu Ora NMDS database. Thus, hospitalisation data for sapovirus infection from the NMDS cannot be reported.

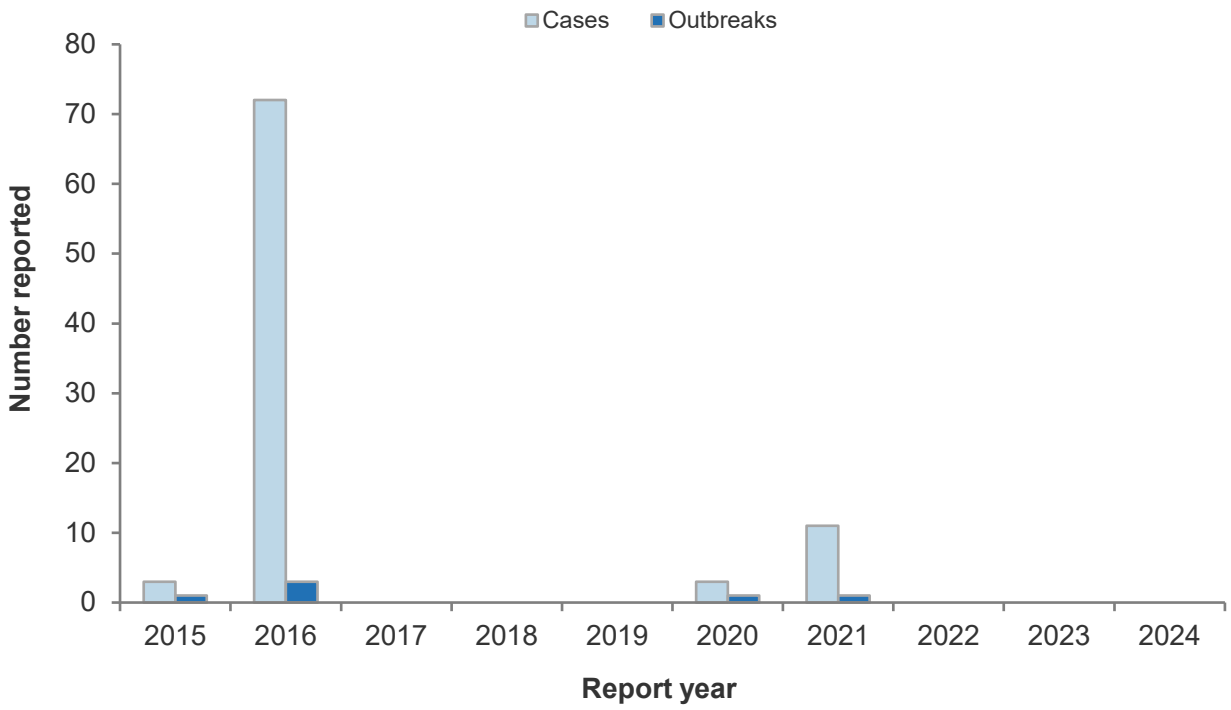
Outbreaks reported as caused by sapovirus

In 2024, there were 13 sapovirus infection outbreaks with 205 associated cases and two hospitalised cases notified in EpiSurv. None were reported as potentially foodborne.

It is important to note that a single outbreak may have multiple pathogens, modes of transmission, settings where exposure occurred, or settings where preparation of food was conducted.

In the last 10 years, with the exception of 2016, there have been three years with a single potentially foodborne sapovirus outbreak recorded, with between three and 11 cases being associated with an outbreak. In 2016, there was a total of 72 cases from three outbreaks (Figure 35). The largest outbreak in 2016 consisted of 65 cases at a hotel, with strong evidence of either person-to-person transmission or indirect contact via eating leafy greens or fruit salad at the hotel.

Figure 35. Sapovirus infection outbreaks reported with food reported as a possible mode of transmission and associated cases reported by year, 2015–2024



Recent surveys

Nil.

Relevant New Zealand studies and publications

Nil.

Relevant regulatory developments

No sapovirus-specific regulatory developments.

Shigellosis

Case definition

Clinical description:	Acute diarrhoea with fever, abdominal cramps, blood or mucus in the stools.
Laboratory test for diagnosis:	Requires isolation of any *Shigella* spp. from a stool sample or rectal swab and confirmation of genus. Nucleic acid testing may be used for screening only.
Case classification:	
Probable	A clinically compatible illness that is either a contact of a confirmed case or has had contact with the same common source i.e., is part of an identified common source outbreak.
Confirmed	A clinically compatible illness that is laboratory confirmed.

Summary data

Summary data for shigellosis in 2024 are given in Table 44.

Table 44. Summary of surveillance data for shigellosis, 2024

Parameter	Value in 2024	Source
Number of notified cases	157	EpiSurv
Notification rate (per 100,000)	2.9	EpiSurv
Hospitalised cases[a]	106	NMDS
Deaths	0	EpiSurv
Estimated number of cases related to travel[b,c]	105 (66.7%)	EpiSurv
Estimated domestically acquired food-related cases (%)	NE	-

NE = not estimated, no information is available on the food attributable proportion of shigellosis in New Zealand,
NMDS = Health New Zealand Te Whatu Ora National Minimum Dataset of hospitalisations.

[a] Cases hospitalised may not be notified on EpiSurv.

[b] Estimated number and % of cases related to travel. Of the 157 notified cases, the overseas travel question had a 'yes' or 'no' entry for 153 cases (97.5%); of these, 102 cases (66.7%) had travelled overseas during the incubation period and 51 cases (33.3%) had not been overseas. The overseas travel history for the remaining four cases is unknown. The estimated number of cases related to travel is given as 66.7% percent of all cases in 2024.

[c] While international travel has increased again since restrictions ceased in 2022, overseas travel in 2024 was still slightly lower compared with the pre-COVID-19 year 2019 (see section Changes in overseas travel, page 11).

Shigellosis individual cases reported in 2024 by data source

In 2024, 157 individual cases (2.9 per 100,000 population) of shigellosis and no resulting deaths were reported in EpiSurv.

The ICD-10 code A03 was used to extract shigellosis hospitalisation data from the Health New Zealand Te Whatu Ora NMDS database. Of the 106 hospitalised cases (2.0 hospitalised cases per 100,000 population) recorded in 2024, 54 were reported with shigellosis as the principal diagnosis and 52 with shigellosis as another relevant diagnosis. Two of the 106 hospitalised cases were admitted to hospital twice resulting in a total of 108 hospital admissions.

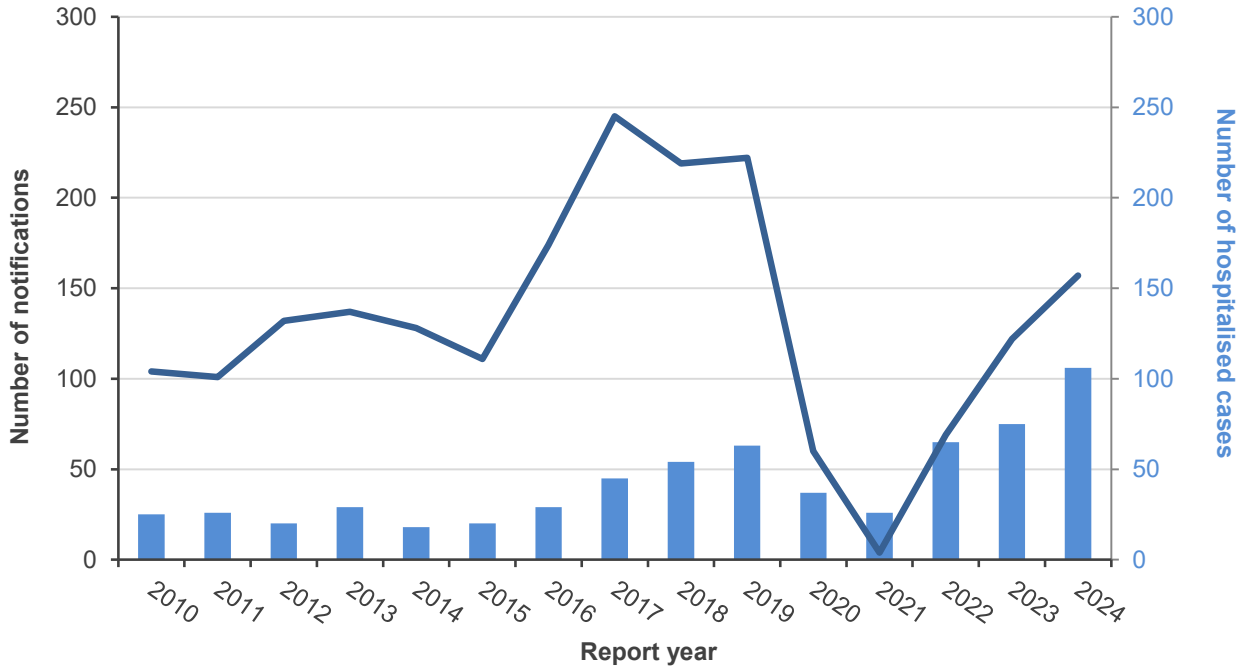
It should be noted that EpiSurv and NMDS are two separate databases that are used for different purposes. Therefore, NMDS and EpiSurv hospitalisation numbers may differ for several reasons, including criteria used for notifications or diagnostic coding (see also Appendix A–Methods, page 123).

Annual data

Between 2010 and 2015 the number of shigellosis notifications was in the range of 101 to 137 cases per year. From 2016 to 2019 there was an increase in notifications and the notification rate per 100,000 population, followed by much lower numbers in the years 2020 and 2022 (Figure 36 and Figure 37), attributed to the reduced frequency of overseas travel compared with pre COVID-19 years (see section Changes in overseas travel, page 11). In 2024, the estimated percentage of shigellosis cases related to travel was 66.7% (95% CI: 65.5-67.9%), compared with 60.6% (95% CI: 58.1-63.1%) in 2019 (pre-COVID-19 pandemic) and 0.0% (95% CI: 0.0-0.0%) in 2021 (year of greatest reduction in travel).

The number of hospital admissions with shigellosis as a principal or other relevant diagnosis varied year by year, following a similar pattern to the number of annual notifications. The number of hospital admissions in 2024 was much higher than observed in previous years.

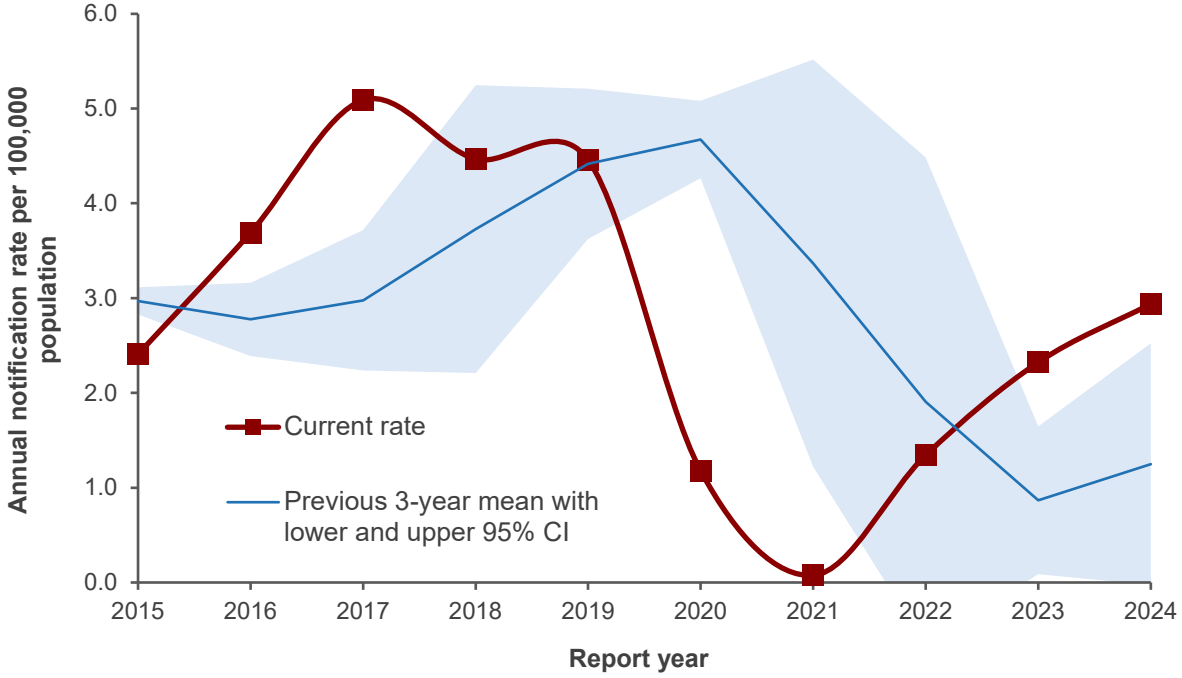
Figure 36. Shigellosis EpiSurv notifications (line) and NMDS hospitalised cases (bar) by year, 2010–2024



Note: The EpiSurv and NMDS databases are separate systems, and discrepancies in reported case numbers may arise due to differences in case classification and reporting practices. For more detail see also Appendix A–Methods, page 123.

The drop in shigellosis notification rates in 2020 and 2021 can be attributed to the COVID-19 pandemic and the corresponding travel restrictions. Increasing rates since 2022 are due to re-opening of borders and increasing international travel. The notification rate in 2024 (2.9 cases per 100,000 population) was higher than the previous three-year mean (1.3 cases per 100,000 population) (Figure 37).

Figure 37. Shigellosis notification rate by year, 2015–2024



Demographics

In 2024, notification rates were higher for males than females (3.5 compared with 2.3 cases per 100,0000 population). The rate of hospitalised cases was higher for females than males (2.2 compared with 1.8 hospitalised cases per 100,000 population) (Table 45).

Table 45. Shigellosis cases by sex, 2024

Sex	EpiSurv notified cases		Hospitalised cases[a]	
	No.	Rate[b]	No.	Rate[b]
Male	94	3.5	47	1.8
Female	63	2.3	59	2.2
Total	**157**	**2.9**	**106**	**2.0**

[a] Health New Zealand Te Whatu Ora NMDS data.

[b] Per 100,000 population in this group.

In 2024, shigellosis notification rates were highest for the 1 to 4 years age group (8.6 cases per 100,000 population) and 30 to 39 age group (4.5 cases per 100,000) (Table 46). Hospitalised case rates were highest for the 1 to 4 years and 70+ years age group (4.1 and 4.2 hospitalised cases per 100,000 population).

Table 46. Shigellosis cases by age group, 2024

Age group (years)	EpiSurv notified cases		Hospitalised cases[a]	
	No.	Rate[b]	No.	Rate[b]
<1	2	-	2	-
1 to 4	21	8.6	10	4.1
5 to 9	5	1.5	8	2.4
10 to 14	3	-	1	-
15 to 19	6	1.8	3	-
20 to 29	25	3.6	10	1.5
30 to 39	36	4.5	10	1.2
40 to 49	17	2.6	13	2.0
50 to 59	20	3.1	14	2.1
60 to 69	16	2.7	9	1.5
70+	6	1.0	26	4.2
Total	**157**	**2.9**	**106**	**2.0**

[a] Health New Zealand Te Whatu Ora NMDS data.

[b] Per 100,000 population in this age group (rate not calculated when fewer than five cases reported).

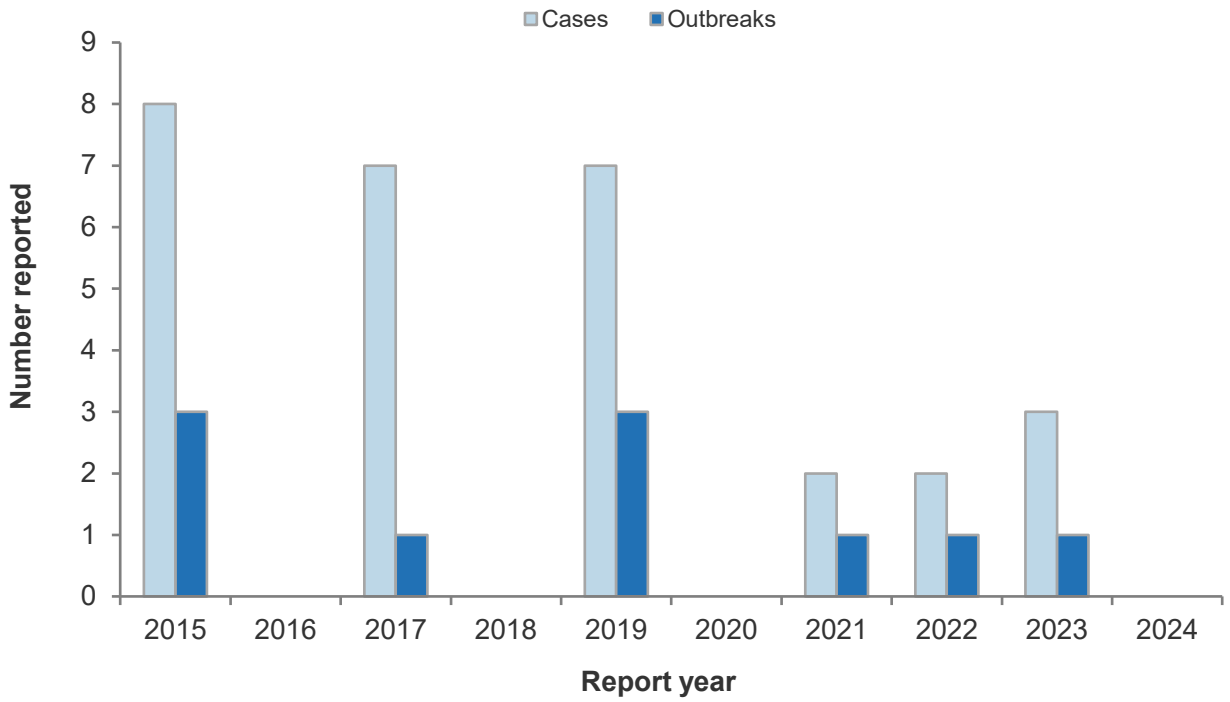
Outbreaks reported as caused by *Shigella* spp.

In 2024, there were six shigellosis outbreaks reported in EpiSurv (20 cases and one hospitalisation). Four outbreaks had strong evidence of cases becoming infected while overseas. The two remaining outbreaks were household outbreaks attributed to person-to-person transmission.

It is important to note that an outbreak may have multiple pathogens, modes of transmission, settings where exposure occurred, or settings where preparation of food was conducted.

Over the 10-year period 2015–2024, the annual number of shigellosis outbreaks with food reported as a possible mode of transmission has ranged between one and three outbreaks in each of the six years outbreaks were reported. Outbreaks ranged in size from two to eight cases (Figure 38).

Figure 38. Shigellosis outbreaks with food reported as a possible mode of transmission and associated cases reported by year (excluding outbreaks associated with overseas travel), 2015–2024



Note: The data in this figure comes from EpiSurv for the years up to 2021. From 2021 the plot includes foodborne outbreaks recorded in EpiSurv and any outbreaks that were referred to NZFS but were not recorded in EpiSurv as an outbreak.

Shigella species commonly reported

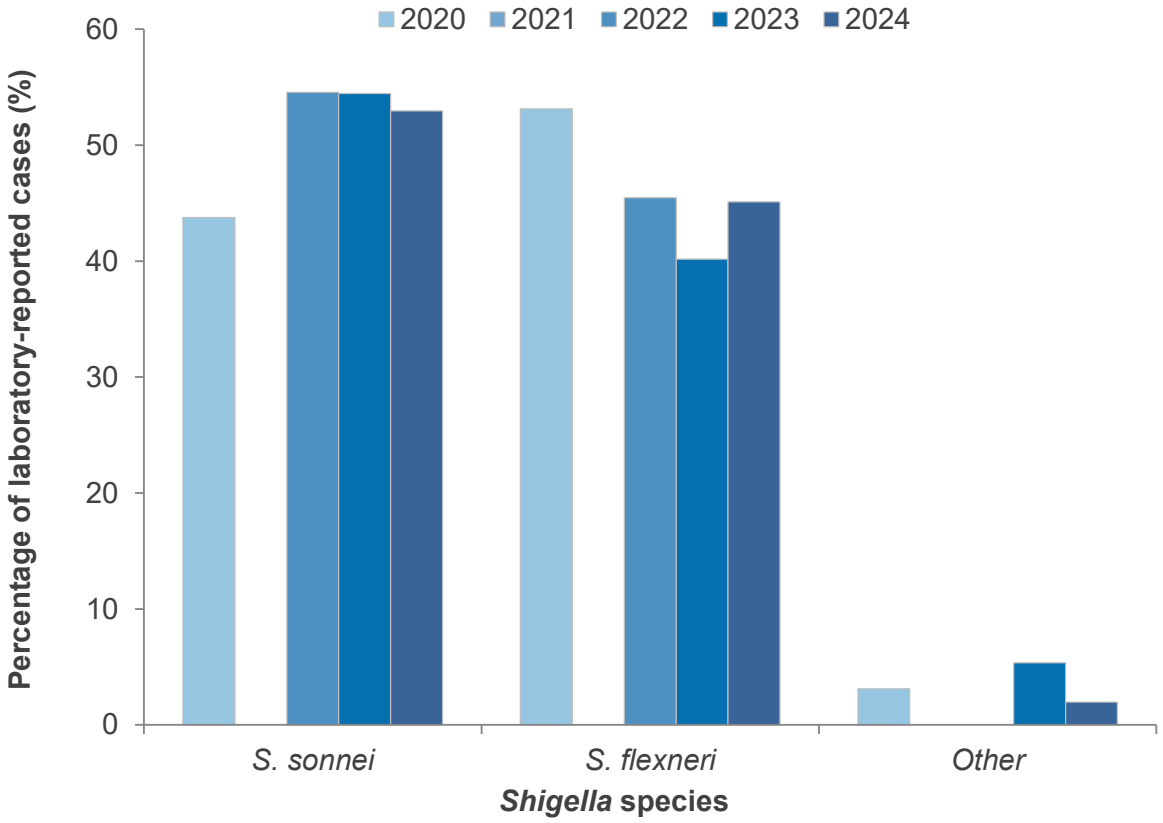
In 2024, isolates from 153 out of the 157 notified cases infected with *Shigella* spp. (97%) were typed by the Enteric Reference Laboratory at PHF Science. *S. sonnei* was isolated most frequently (81 cases) followed by *S. flexneri* (69 cases), which is similar in relative proportions to 2023 (Table 47, Figure 39).

Table 47. *Shigella* species and subtypes for notified cases of shigellosis, 2020–2024

Species[a]	2020	2021	2022	2023	2024
S. sonnei	**28**	**0**	**30**	**61**	**81**
biotype a	9	0	16	9	-
biotype f	2	0	2	2	-
biotype g	17	0	12	31	-
ST152	-	-	-	19	81
S. flexneri	**34**	**2**	**25**	**45**	**69**
1a	4	0	0	0	-
1b	2	0	2	4	-
1c	2	1	4	2	-
2a	12	0	5	17	-
2b	5	0	1	5	-
3a	1	0	2	4	-
3b	2	0	1	1	-
4av	0	0	3	1	-
4b	1	0	0	0	-
6 biotype Boyd 88	1	0	4	1	-
X	1	1	0	0	-
Y	1	0	2	0	-
untyped	2	0	1	0	-
ST145	-	-	-	-	9
ST245	-	-	-	10	48
ST628	-	-	-	-	2
ST1024	-	-	-	-	2
ST1025	-	-	-	-	6
ST1513	-	-	-	-	2
S. boydii	**2**	**1**	**0**	**4**	**3**
ST145	-	-	-	-	1
ST243	-	-	-	-	2
S. dysenteriae	**0**	**0**	**0**	**2**	**0**
Total	**64**	**3**	**55**	**112**	**153**

[a] Prior to late 2023, serotypes and biotypes of *S. flexneri* and *S. sonnei* were reported, respectively. During 2023, biotyping and serotyping were discontinued and PHF Science moved to whole genome sequencing (WGS) of *Shigella* isolates. A seven gene multi locus sequence type (ST) using the Achtman scheme for *Shigella* and *E. coli* [36] is now reported. The serotype and biotype cannot be reliably predicted based on the WGS data, and historic data do not reliably translate to the ST. To date, all *S. sonnei* are ST152 or very closely related STs.

Figure 39. Percentage of notified shigellosis cases by species by year, 2020-2024



Note: Percentage not calculated or displayed for 2021 as only 3 cases typed for the year.

Recent surveys

Nil.

Relevant New Zealand studies and publications

Nil.

Relevant regulatory developments

No *Shigella*-specific regulatory developments.

Staphylococcus aureus intoxication

Case definition

Clinical description:	Gastroenteritis with sudden onset of severe nausea and vomiting.
Laboratory test for diagnosis:	Detection of enterotoxin in faecal or vomit specimen or in leftover food or isolation of ≥10^3/gram coagulase-positive *S. aureus* from faecal or vomit specimen or ≥10^5/gram from leftover food.
Case classification:	
Probable	A clinically compatible illness.
Confirmed	A clinically compatible illness that is laboratory confirmed, OR a clinically compatible illness and a common exposure associated with a laboratory confirmed case.

Staphylococcus aureus intoxication individual cases reported in 2024 by data source

In 2024, no individual cases of *S. aureus* intoxication were reported in EpiSurv. Note that not every individual case of *S. aureus* intoxication is necessarily notifiable; only those when the infected person is in a high-risk category (e.g., food handler, early childhood service worker) or the case is part of an outbreak.

The ICD-10 code A05.0 was used to extract foodborne staphylococcal intoxication hospitalisation data from the Health New Zealand Te Whatu Ora NMDS database. All five hospitalised cases (0.1 hospitalised cases per 100,000 population) recorded in 2024 were reported with *S. aureus* intoxication as the principal diagnosis.

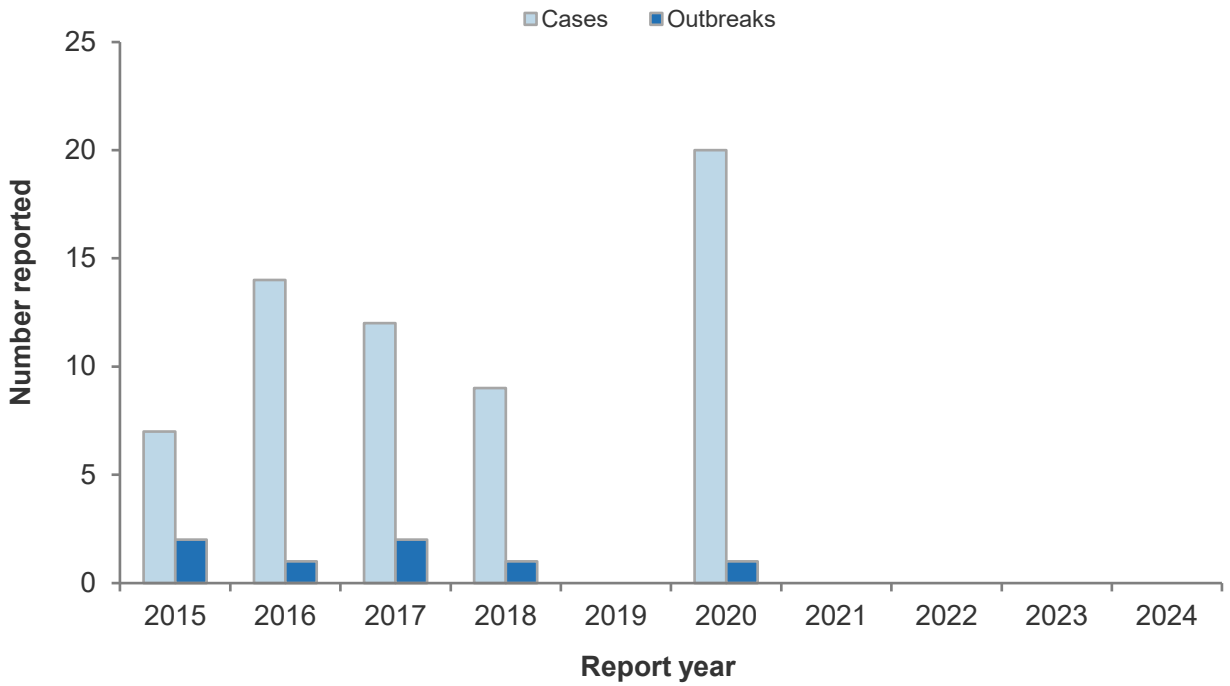
It should be noted that EpiSurv and NMDS are two separate databases that are used for different purposes. Therefore, NMDS and EpiSurv hospitalisation numbers may differ for several reasons, including criteria used for notifications or diagnostic coding, i.e. a hospital discharge may be coded to an infectious cause without a case being recorded in EpiSurv and vice versa (see also Appendix A–Methods, page 123).

Outbreaks reported as caused by *Staphylococcus aureus*

During 2024, there were no outbreaks attributed to *S. aureus* intoxication.

Over the 10-year period 2015 to 2024, the annual number of *S. aureus* intoxication outbreaks with food reported as a possible mode of transmission ranged from zero to two, with between seven and 20 associated cases in years when outbreaks were reported (Figure 40). No outbreaks have been reported in the last four years.

Figure 40. *S. aureus* intoxication outbreaks with food reported as a possible mode of transmission and associated cases reported by year, 2015–2024



Note: The data in this figure comes from EpiSurv for the years up to 2021. From 2021 the plot includes foodborne outbreaks recorded in EpiSurv and any outbreaks that were referred to NZFS but were not recorded in EpiSurv as an outbreak.

Recent surveys

Nil.

Relevant New Zealand studies and publications

Journal papers

Zoonotic transmission of asymptomatic carriage Staphylococcus aureus *on dairy farms in Canterbury, New Zealand – Straub et al., 2024*

Nasal swabs were taken from healthy humans and cattle on three dairy farms and a near-by primary school and whole genome sequencing carried out on 96 *S. aureus* isolates (44 human, 52 cattle) [37]. Fourteen potential transmission clusters were identified by single nucleotide polymorphism (SNP) analysis, with seven involving only bovine isolates (bovine to bovine transmission), six involving only human isolates (human to human transmission) and one involving human and bovine isolates (zoonotic transmission). Bovine to bovine transmission was restricted to within farm events. It was not possible to confirm whether the direction of the potential zoonotic transmission – bovine to human or human to bovine.

Relevant regulatory developments

No *S. aureus*-specific regulatory developments.

STEC infection

Case definition

Clinical description:	An acute onset diarrhoeal illness (with or without blood or mucus in stool) OR any case with Haemolytic Uraemic Syndrome (HUS) or Thrombotic Thrombocytopenic Purpura (TTP) with or without a history of an acute onset diarrhoeal illness. In the absence of HUS/TTP, asymptomatic infection or presentations with milder bowel symptoms (e.g., occasional loose stools) and/or non-diarrhoeal abdominal symptoms do not meet the case definition.
Laboratory test for diagnosis:	Isolation of Shiga toxin-producing *Escherichia coli* OR detection of the genes (*stx1* and/or *stx2*) associated with the production of Shiga toxin in *E. coli.* Isolates producing Shiga toxin 2 (*stx2*) are more likely to cause serious human disease than isolates producing Shiga toxin 1 (*stx1*) or both toxins together.
Case classification:	
Probable	A clinically compatible illness that is either epidemiologically linked to a confirmed case or has had contact with the same common source as a confirmed case, i.e., is part of a common-source outbreak.
Confirmed	A clinically compatible illness that is laboratory confirmed.

Summary data

Summary data for STEC[1] infection in 2024 are given in Table 48.

Table 48. Summary of surveillance data for STEC infection, 2024

Parameter	Value in 2024	Source
Number of notified cases	1115	EpiSurv
Notification rate (per 100,000)	20.9	EpiSurv
Hospitalised cases[a]	291	EpiSurv
Deaths[b]	0	EpiSurv
Estimated number of cases related to travel [c,d]	112 (10.0%)	EpiSurv
Estimated domestically acquired food-related cases[e]	401	Expert consultation and EpiSurv

[a] Cases recorded as admitted to hospital in EpiSurv. Up to the year 2022, hospitalisations were reported according to the NMDS number of hospital admissions with the A04.3 diagnostic code, not hospitalised cases as per notification in EpiSurv. The values were lower than reported here using EpiSurv data. A new 2024 study [15] has shown that ICD-10 code A04.3 does not capture all the cases hospitalised due to STEC infection.

[b] There were six deaths of STEC infection cases recorded in EpiSurv in 2024. All six cases died from a cause other than STEC infection.

[c] Estimated number and % of cases related to travel. Of the 1115 notified cases, the overseas travel question had a 'yes' or 'no' entry for 858 cases (77.0%); of these, 86 cases (10.0%) had travelled overseas during the incubation period and 772 cases (90.0%) had not been overseas. The overseas travel history for the remaining 257 cases is unknown. The estimated number of cases related to travel is given as 10.0% percent of all cases in 2024.

[d] While international travel has increased again since restrictions ceased in 2022, overseas travel in 2024 was still slightly lower compared with the pre-COVID-19 year 2019 (see section Changes in overseas travel, page 11).

[e] Estimation of food-related cases is given by (*Total cases – Estimate of cases acquired overseas*) x *Estimate of proportion of domestically acquired cases likely to be due to foodborne transmission*. The estimate of domestic proportion of STEC infection cases due to foodborne transmission (40%) was derived from expert elicitation [3].

Note: The expert elicitation derived separate estimates of the foodborne proportion for O157 STEC (20%) and non-O157 STEC (40%). The estimate for non-O157 STEC, the dominant set of serotypes, has been used to estimate the number of food-related cases.

[1] Note: Shiga toxin-producing *E. coli* (STEC) may also be referred to as verotoxin-producing or verocytotoxigenic *E. coli* (VTEC) or enterohaemorrhagic *E. coli* (EHEC). STEC is now the preferred term and will be used throughout this document.

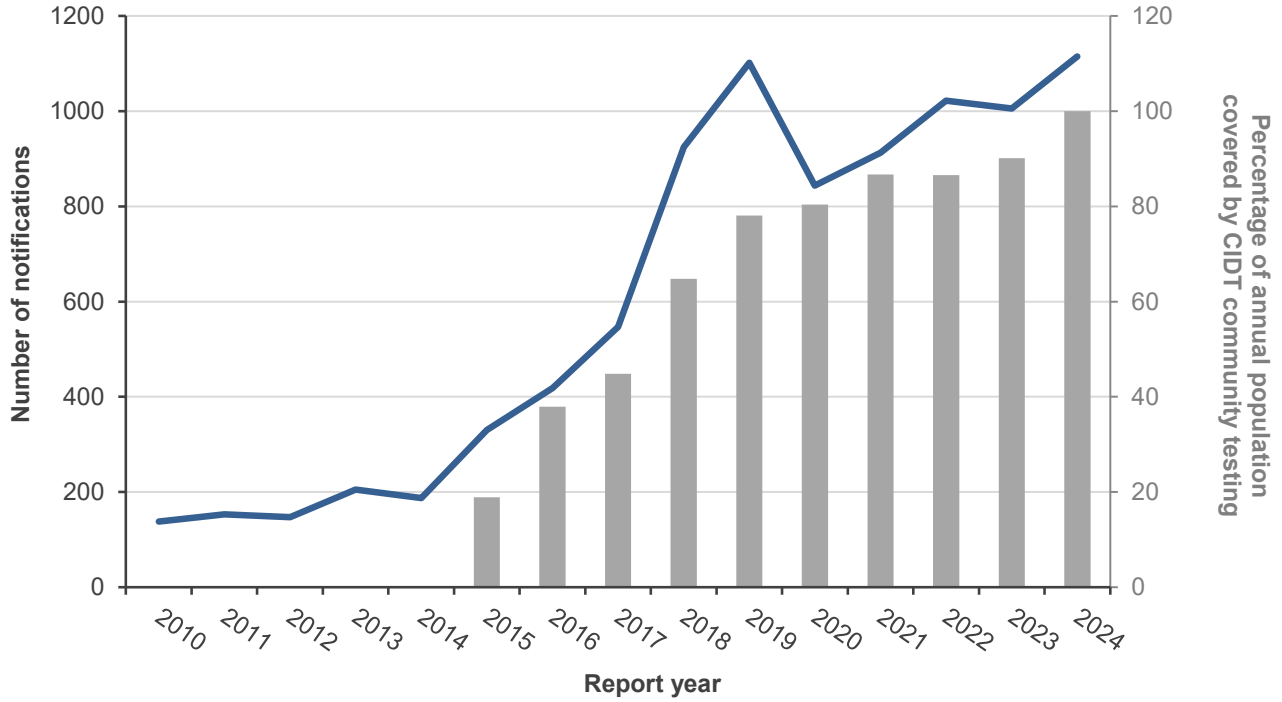
Changes to laboratory methods

Since 2015, laboratories across New Zealand have gradually changed the methodology for testing faecal specimens (Appendix B, page 128). As of October 2023, faecal specimens from community-based patients in all Health Districts are screened by CIDT for a range of pathogens, including STEC.

Prior to the changes in methodology, only specimens from patients meeting certain epidemiological or clinical criteria (e.g., aged less than 5 years, presence of haemolytic uraemic syndrome (HUS), or bloody diarrhoea) were tested for STEC infection, particularly O157. With CIDT testing, all faecal samples are screened for all STEC serotypes, approximately doubling the number of samples tested (Michael Addidle, PHF Science, personal communication). This increase in the number of faecal samples tested for STEC resulted in many more cases being diagnosed with a non-O157 infection. Serotyped non-O157 case isolates are now just over three-fold higher than O157 case isolates. Where STEC is detected by screening CIDT, cultures are referred to the Enteric Reference Laboratory at PHF Science to isolate STEC for serotyping. In 2024, isolates were recovered for 57% of notified cases.

Between 2015 and 2019, the annual increases in STEC infection notifications correspond to the increase in the population being tested by CIDT (Appendix B page 130) (Figure 41). The increased sensitivity of CIDT to detect non-O157 STEC serotypes (Table 54) and the increased number of samples routinely tested for STEC appears to have caused the majority of the increase in STEC notifications [38]. Areas and time periods that have not used CIDT or increased screening for STEC, show no increase in notification rates for STEC [18].

Figure 41. STEC infection EpiSurv notifications (line) and proportion of the NZ population covered by community CIDT (bar) by year, 2010–2024



Note: In 2023, faecal specimens from community-based patients in the West Coast Health District (June 2023) and the Canterbury and South Canterbury Health Districts (October 2023), respectively, changed to CIDT. Therefore, the percentage of the annual population covered by CIDT was adjusted for the months of the year when community samples were covered by CIDT, e.g. 3 months for the Canterbury and South Canterbury population, resulting in 90.2% of the annual population covered by CIDT for the year 2023. Therefore, neither change impacted the expected summer peak of case notifications in 2023 but did so in 2024.

STEC individual cases reported in 2024 by data source

During 2024, 1115 individual cases (20.9 cases per 100,000 population) of STEC were reported in EpiSurv.

Prior to 2023, hospitalisation data was presented based on the ICD-10 code A04.3 (enterohaemorrhagic *E. coli* (EHEC) infection) diagnoses records in the Health New Zealand Te Whatu Ora NMDS database. EHEC and STEC are synonymous [14], but ICD-10 uses EHEC rather than STEC. While A04.3 is the technically correct diagnostic code for STEC infection, research in 2024 has shown that hospital admissions for STEC cases may be coded to diagnostic codes other than A04.3 [15]. Therefore, this section of the report includes hospital information from EpiSurv rather than the NMDS database.

The EpiSurv field indicating if a case was hospitalised was completed for 1032 cases (92.6%). Of these 1032 cases, 291 were reported as being hospitalised (5.5 hospitalised cases per 100,000 population).

The largest proportion of hospitalised cases (46%) spent between two and six nights in hospital, with 13.2% of hospitalised cases admitted to an intensive care unit (Appendix C, Table 69). Note the severity information (nights in hospital and admission to ICU) is based on the 68 hospitalised cases associated with code A04.3 in the NMDS database.

Foodborne transmission

It has been estimated by expert consultation that 20% of O157 STEC and 40% of non-O157 STEC incidence is due to foodborne transmission [3].

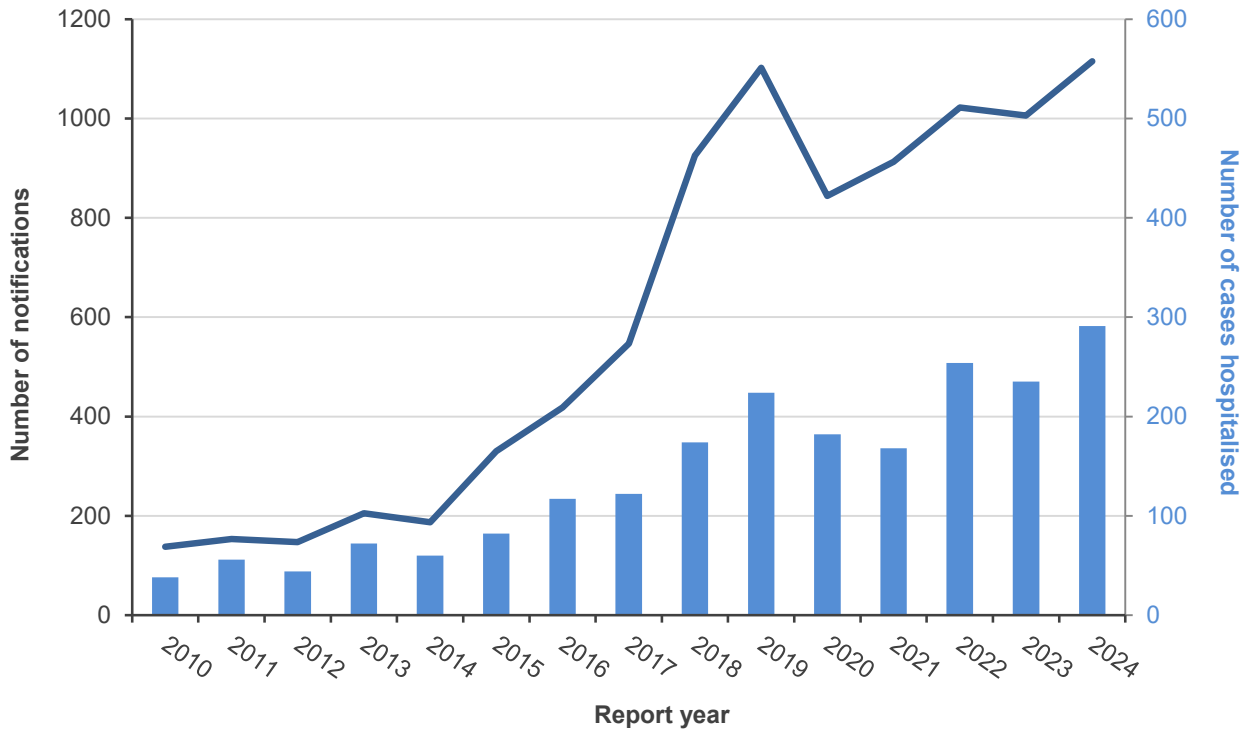
Annual data

Until 2014, the number of STEC notifications was below 210 cases per year. From 2015 there was a steady increase in notifications until 2019 which corresponded to the increase in population being tested by CIDT (Figure 41). A small drop in case numbers in 2020 and 2021 was followed by increasing case numbers (Figure 42). The decrease in 2020 and 2021 compared with 2019 data is related to the reduction in reported cases during months with COVID-19 Alert Level restrictions [18].

Since 2018, the number of hospitalised cases recorded in EpiSurv was consistently higher than prior to 2018 (Figure 42). Of the 291 hospitalisations recorded in EpiSurv in 2024, 24% were identified with the O157:H7 serotype, 13% with the O26:H11 serotype, and 24% with other serotypes. The remaining 38% of cases did not have isolates that could be typed. Before the introduction of CIDT, non-O157 cases hospitalised with gastrointestinal infection symptoms may not have been diagnosed with an STEC infection.

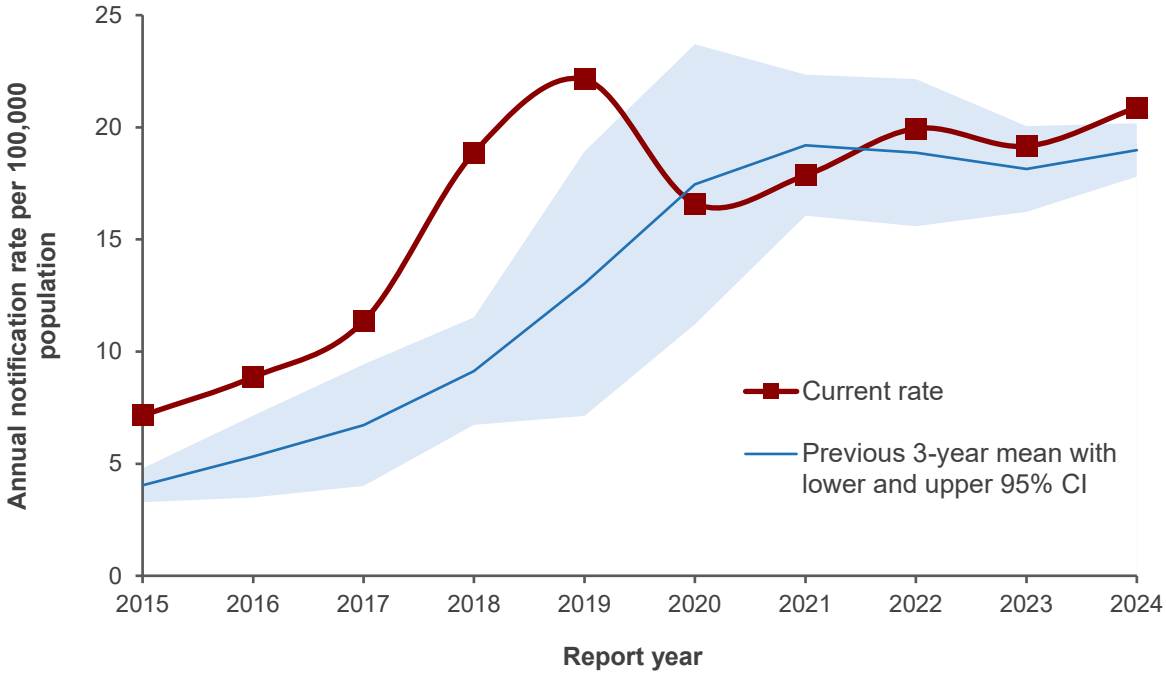
The frequency of overseas travel was lower in 2020 to 2023 to the pre COVID-19 year 2019 (see section Changes in overseas travel, page 11) and was still slightly lower in 2024. In 2024, the estimated percentage of STEC infection cases related to travel was 10.0% (95% CI: 9.1-11.0%), compared with 11.6% (95% CI: 10.9-12.3%) in 2019 (pre-COVID-19 pandemic) and 0.3% (95% CI: <0.1-0.5%) in 2021 (year of greatest reduction in travel).

Figure 42. STEC infection EpiSurv notifications (line) and EpiSurv hospitalised cases (bar) by year, 2010–2024



Prior to 2015, notification rates for STEC infection were generally below five notifications per 100,000 population. Since 2015, rates increased every year until 2019 (22.1 cases per 100,000 population), followed by a drop attributed to the COVID-19 pandemic. The 2024 notification rate was 20.9 cases per 100,000 population, higher than the previous three-year mean (19.0 cases per 100,000 population) (Figure 43).

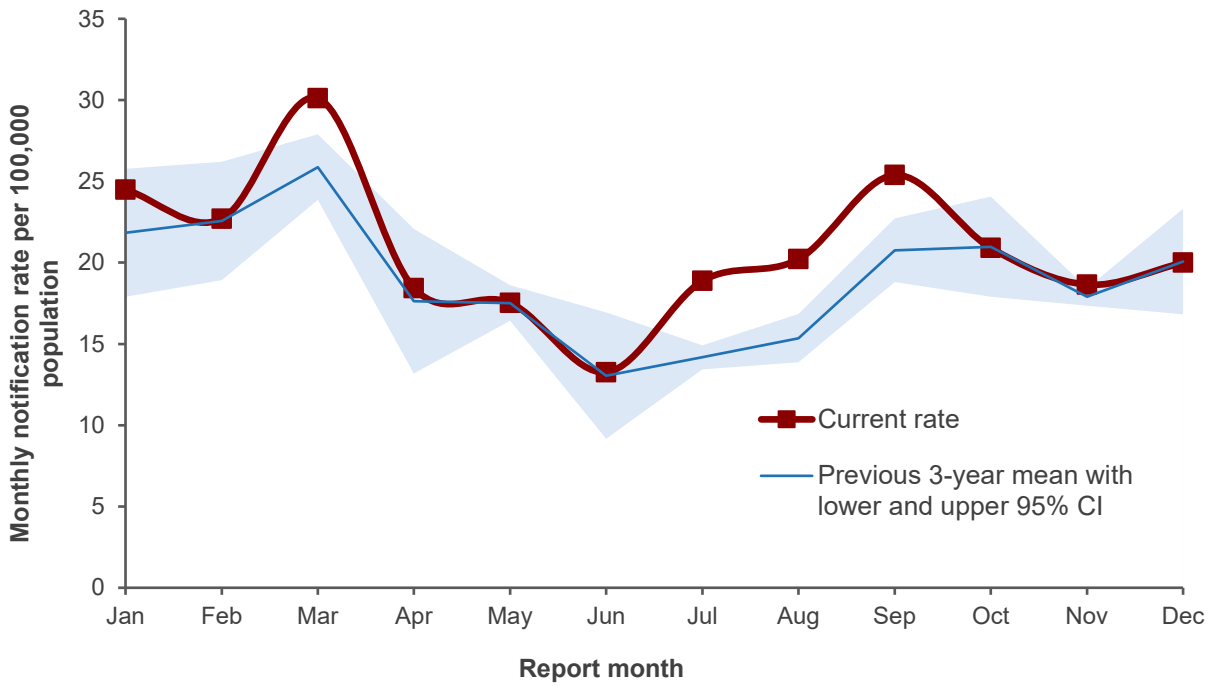
Figure 43. STEC infection notification rate by year, 2015–2024



Seasonal data

STEC infection notification rates per 100,000 population by month for 2024 are shown in Figure 44. For most of the year, the monthly notification rates were similar to the mean of the previous three years, apart from four months where rates were higher. The monthly number of notifications in 2024 ranged from 59 notifications in June (13.3 cases per 100,000 population) to 134 notifications in March (30.1 cases per 100,000 population).

Figure 44. STEC infection monthly notification rate (annualised), 2024



In the last five years, the monthly numbers of cases recorded as hospitalised in EpiSurv varied over the year (Table 49), with fewer hospitalised cases during the winter months.

Table 49. STEC infection monthly EpiSurv cases recording hospitalisation, 2020-2024

Month	Hospital admissions recorded in EpiSurv				
	2020	2021	2022	2023	2024
January	21	18	26	36	35
February	22	21	19	21	25
March	25	26	33	26	45
April	9	14	30	14	22
May	9	9	17	23	14
June	3	14	12	14	16
July	11	9	20	14	12
August	15	12	23	11	27
September	17	7	19	21	25
October	21	13	17	24	24
November	11	12	17	19	19
December	19	13	21	12	27
Total	**183**	**168**	**254**	**235**	**291**

Demographics

In 2024, notification rates and hospitalised case rates were higher for females (21.8 cases and 5.6 hospitalised cases per 100,000 population) than for males (19.9 cases and 5.3 hospitalised cases per 100,000 population) (Table 50).

Table 50. STEC cases by sex, 2024

Sex	EpiSurv notified cases		Recorded as hospitalised in EpiSurv	
	No.	Rate[a]	No.	Rate[a]
Male	529	19.9	141	5.3
Female	585	21.8	150	5.6
Total[b]	**1115**	**20.9**	**291**	**5.5**

[a] Per 100,000 population in this group.

[b] Total includes one case where sex was not recorded.

In 2024, the STEC infection notification rate was highest for the <1 year age group followed by the 1 to 4 years age group (69.1 cases and 66.8 cases per 100,000 population, respectively). The hospitalised case rate was highest for the 1 to 4 years, <1 year and 70+ years age groups (19.3, 17.3 and 13.4 EpiSurv hospitalised cases per 100,000 population) (Table 51). Based on NMDS database records, the 70+ years age group had the longest hospital stays (19 cases that were admitted for two or more nights) (Appendix C, Table 79).

Table 51. STEC cases by age group, 2024

Age group (years)	EpiSurv notified cases		Recorded as hospitalised in EpiSurv	
	No.	Rate[a]	No.	Rate[a]
<1	40	69.1	10	17.3
1 to 4	163	66.8	47	19.3
5 to 9	51	15.5	19	5.8
10 to 14	38	10.9	7	2.0
15 to 19	47	13.8	6	1.8
20 to 29	100	14.6	24	3.5
30 to 39	82	10.1	16	2.0
40 to 49	84	12.6	12	1.8
50 to 59	120	18.4	32	4.9
60 to 69	145	24.8	35	6.0
70+	245	39.5	83	13.4
Total	**1115**	**20.9**	**291**	**5.5**

[a] Per 100,000 population in this age group.

In 2024, the STEC infection notification case rates were highest for the ethnic groups ‘European or Other’ (26.5 cases per 100,000 population) and ‘MELAA’ (24.4 cases per 100,000 population) (Appendix C, Table 70). STEC hospitalised case rates were highest for the ethnic groups ‘European or Other’ (6.5 hospitalised cases per 100,000 population) and Māori (5.2 hospitalised cases per 100,000 population) (Appendix C, Table 71).

Geographic distribution

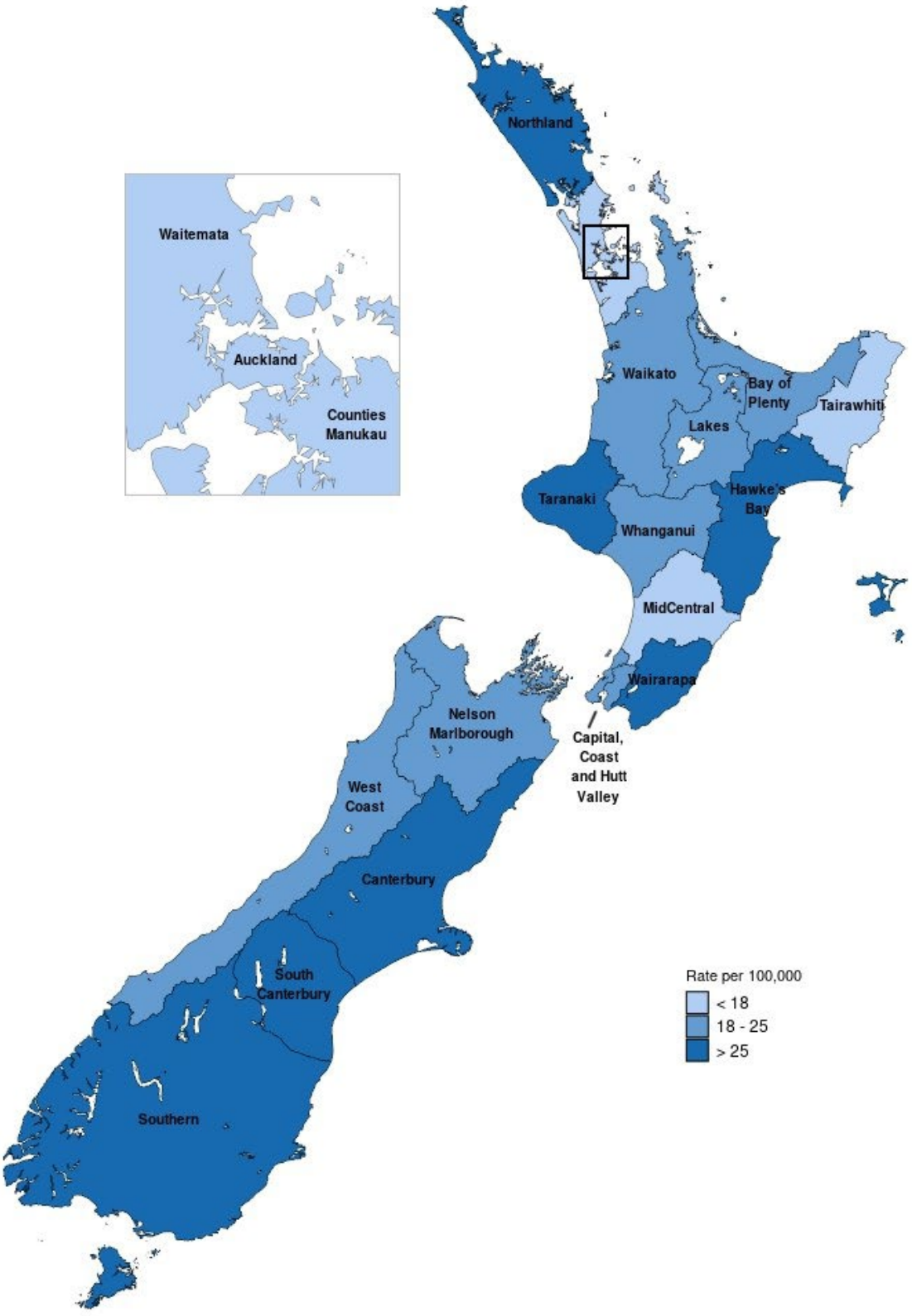
The notification rates by Health District calculated per 100,000 resident population are presented in Figure 45 (see also Appendix C, Table 83). The number of notified cases by Health District are presented in Appendix C, Table 82.

In 2024, the Health District notification rates of STEC infection ranged from 7.0 per 100,000 population in Auckland (36 cases) to 75.6 per 100,000 population (49 cases) in South Canterbury. The Health Districts South Canterbury, Wairarapa (44.2 per 100,000 population), Southern (43.0 per 100,000 population), Taranaki (42.7 per 100,000 population) and Northland (36.6 per 100,000 population) had the highest notification rates.

For the last four years, notification rates for STEC infection have been highest in Northland, Taranaki, Wairarapa, South Canterbury and Southern Health Districts. Note, the changes in laboratory methods in different parts of the country at different times most likely affected reporting rates (see also Changes to laboratory methods, page 92 and Appendix B, page 128).

STEC notification rates, stratified by 2023 Urban Rural Classification [26] of the cases' residential address and excluding cases associated with overseas travel, generally increased with decreasing urbanisation (Appendix C, Table 84). The exception was 'rural settlement' which had lower notification rates than 'medium urban' and 'small urban' areas. Notification rates were the lowest for 'major urban area' (9.8 cases per 100,000 population) and highest for 'rural other' (49 cases per 100,000 population). Hospitalised case rates were also the highest for 'rural other' areas (12.3 hospitalised cases per 100,000 population) (Appendix C, Table 85).

Figure 45. Geographic distribution of STEC infection notifications, 2024



Outbreaks reported as caused by STEC

In 2024 there were nine outbreaks of STEC infection notified in EpiSurv (Table 52). The cases from two outbreaks (6 cases) were infected while overseas. One of the outbreaks was listed as potentially due to a food source.

Table 52. STEC infection outbreaks reported in EpiSurv, 2024

	Possible foodborne transmission with a suspected or confirmed source	Possible foodborne transmission but no suspected food source	Total STEC infection outbreaks
Outbreaks	1	0	9
Outbreak associated cases	5	0	35
Outbreak hospitalised cases	0	0	2

Details of the outbreak suspected due to a food source is provided in Table 53. This outbreak was suspected to be due to biltong. The outbreak was referred to NZFS who identified inadequate control processes relating to the product that led to a consumer level product recall. However, NZFS was unable to confirm if the outbreak was due to the biltong product.

It is important to note that an outbreak may have multiple pathogens, modes of transmission, settings where exposure occurred, or settings where preparation of food was conducted.

Table 53. Details of the suspected STEC infection outbreak with food reported as a possible mode of transmission, 2024

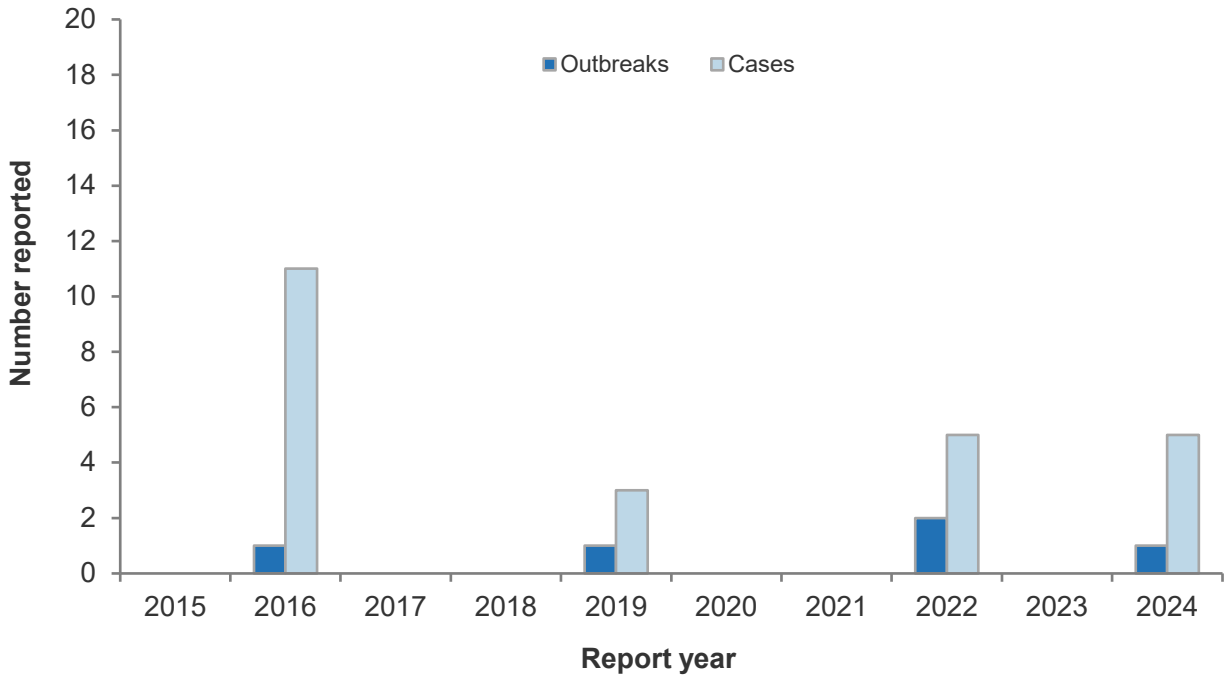
Health district	Month	Suspected source	Evidence	Setting	No. ill
South Canterbury	August	Biltong	Common food	Retail food	2C 3P

Number ill: C: confirmed, P: probable.

Over the 10-year period 2015 to 2024 and excluding cases being exposed to STEC infection overseas, the annual number of STEC outbreaks with food reported as a possible mode of transmission ranged from zero to two per year, with no outbreaks with food reported as a possible mode of transmission reported for six of the ten years (Figure 46). The total annual number of cases associated with potentially foodborne outbreaks has ranged from three to eleven cases.

In 2017 there was an outbreak on a cruise ship (157 cases), but no specific food was recorded as a suspected source for the outbreak. The cruise ship outbreak is not included in Figure 46 as it is classed as an overseas outbreak.

Figure 46. STEC infection outbreaks with food reported as a possible mode of transmission and associated cases (excluding outbreaks associated with overseas travel) reported by year, 2015–2024



Note: The data in this figure comes from EpiSurv for the years up to 2021. From 2021 the plot includes foodborne outbreaks recorded in EpiSurv and any outbreaks that were referred to NZFS but were not recorded in EpiSurv as an outbreak.

STEC types reported for notified cases

Isolates from 632 notified cases infected with STEC were typed by the PHF Science Enteric Reference Laboratory in 2024. A single STEC serotype was confirmed from 625 cases and in seven cases two different STEC serotypes were isolated and typed. Of the 639 typed isolates, 151 (24%) were identified as STEC O157:H7 and 488 (76%) as non-O157:H7 STEC (Table 54). As in the previous four years, the most frequently typed non-O157:H7 STEC serotypes were O26:H11 (132 isolates, 21% of typed isolates) and O128:H2 (68 isolates, 11% of typed isolates).

Table 54. Annual number of EpiSurv case notifications with different STEC serotypes, 2020–2024

Serotype	2020	2021	2022	2023	2024
O157:H7 [a]	**167**	**183**	**259**	**134**	**151**
Non-O157	**388**	**444**	**448**	**482**	**488**
O26:H11	112	127	105	114	132
O38:H26	27	22	35	30	27
O84:H2	10	7	9	9	8
O88:H8	8	9	8	8	4
O91:H14	10	25	18	26	42
O103:H2	9	17	10	15	20
O103:H25	7	5	10	3	7
O112:H9	3	6	6	7	5
O117:H7	4	1	0	8	8
O123:H10	8	3	7	16	13
O128:H2	62	62	65	68	68
O146:H21	17	24	30	23	31
O146:H28	4	3	2	4	5
O153:H2	6	8	5	11	6
O174:H8	9	11	15	7	8
O176:H4	14	14	20	19	13
O177:H25	2	4	4	4	7
Other types[b]	63	76	77	106	84
Cases without typing information	**291**	**291**	**328**	**403**	**483**

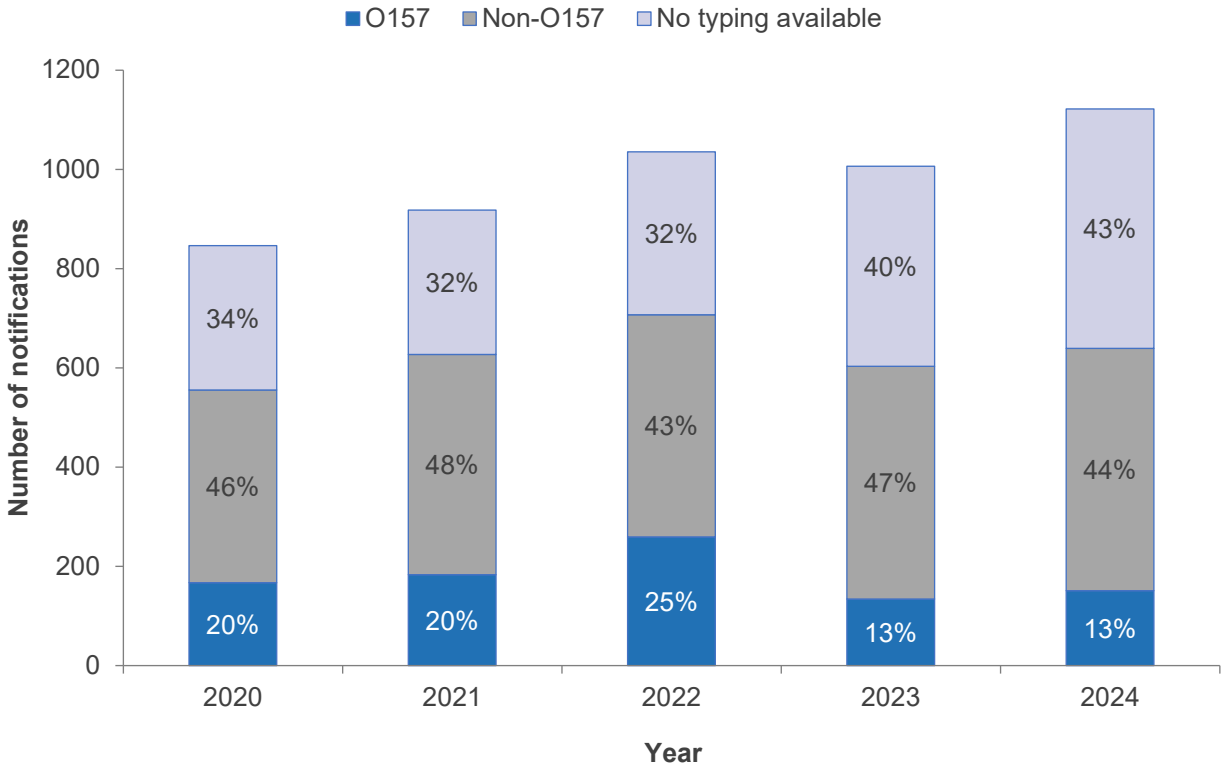
[a] Whole genome sequencing of human O157:H7 isolates from 2021 to 2024 revealed a wide diversity of genotypes present, with most of the isolates genomically distinct from each other (> 5 SNP differences).

[b] Other isolates with identifiable non-O157 serotypes, not listed in table. Full list available in Appendix C, Table 93.

Note: Seven cases have been identified with two serotypes in 2024 by the PHF Science Enteric Reference Laboratory. The sum of the blue rows will not equal the number of notifications in a year.

For 483 (43%) of the 1115 STEC notifications, no typing information was available (Figure 47) due to ERL not receiving culture samples from diagnostic laboratories or due to the culture no longer being viable.

Figure 47. STEC O157 and non-O157 associated notifications by year, 2020–2024



Investigation of the 2024 EpiSurv-recorded hospitalisation status for the three most commonly identified serotypes found that STEC O157:H7 infected cases were most frequently reported to have been hospitalised (46% of O157:H7 cases hospitalised, 5% no hospital information recorded). The proportion of cases hospitalised was lower for STEC O26:H11 (29% cases hospitalised, 3% no hospital information recorded) and STEC O128:H2 (12% cases hospitalised, 9% no hospital information recorded).

Other *E. coli* pathotypes reported in 2024 for individual notified gastroenteritis cases and gastroenteritis outbreaks

Strains of *E. coli* that cause gastroenteritis are subdivided into pathotypes and include, in addition to STEC and others, enterotoxigenic *E. coli* (ETEC) and enteropathogenic *E. coli* (EPEC). Clinical symptoms often include watery diarrhoea, abdominal pain and vomiting, with ETEC infection being the leading cause of travellers' diarrhoea.

During 2024, 136 individual cases of ETEC infection and 10 individual cases of EPEC infection were reported in EpiSurv. These ETEC cases were from health districts covered by laboratories using a CIDT panel which can identify ETEC infection. These laboratories cover about 16% of the New Zealand population. Currently, no further culture, isolation and typing is undertaken.

The EpiSurv field indicating if a case was hospitalised was completed for 132 ETEC infection cases (97%). Of these 132 cases, four were reported as being hospitalised. The EpiSurv field indicating if a case was hospitalised was completed for all 10 cases with EPEC infection. Of the 10 cases, two were reported as being hospitalised.

Note that not every individual case of ETEC or EPEC infection is necessarily notifiable; only when the infected person is in a high-risk category (e.g., food handler, early childhood service worker).

In 2024, there were two ETEC outbreaks reported in EpiSurv from Waikato Health District with food reported as a possible mode of transmission. The first outbreak of nine cases was at a family event with home-made food. The second outbreak of 17 cases was based at a prison with undercooked beef

or chicken as possible sources. Contamination of food preparation areas by wild birds was also identified as a possible risk factor. For both outbreaks, the evidence of a food source was weak.

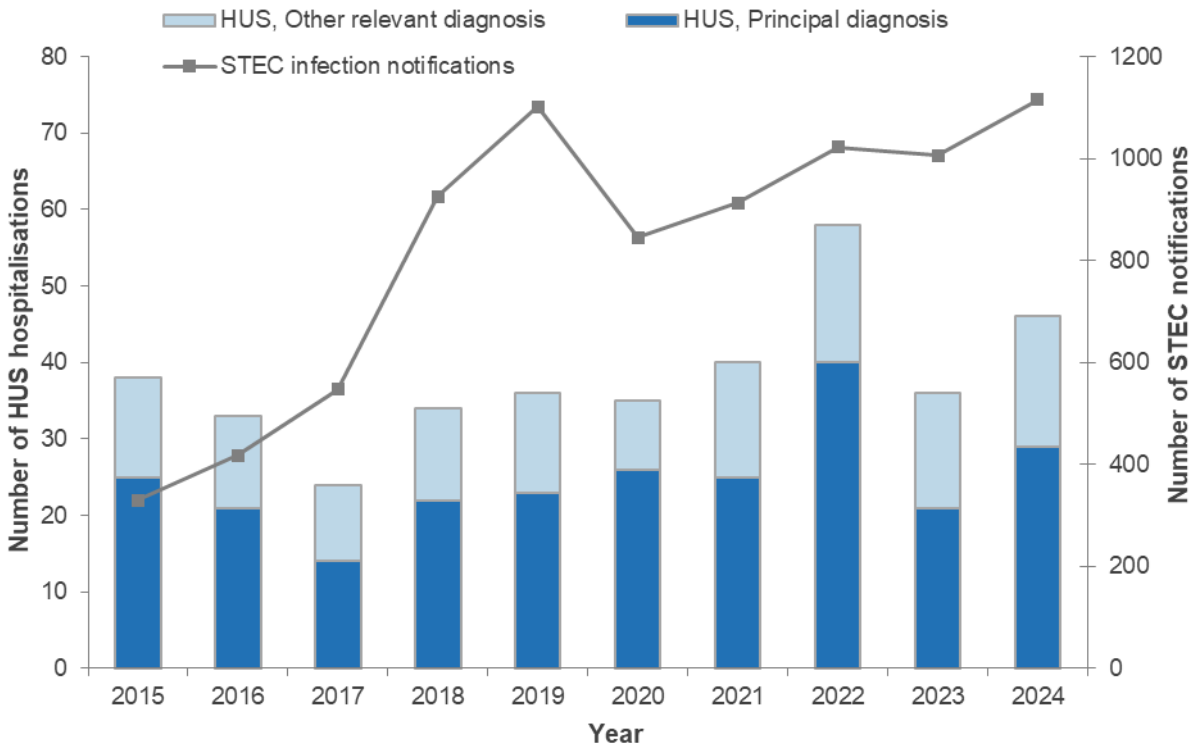
Disease sequelae – haemolytic uraemic syndrome (HUS)

HUS is a serious sequela that may result from an STEC infection. HUS is commonly preceded by an STEC infection [39, 40]. While it has previously been reported that two-thirds of HUS cases are associated with STEC O157:H7 infections [41], a more recent European publication reported that STEC O26:H11 was most frequently associated with HUS cases [42]. A review of New Zealand STEC-related HUS cases during the period 2016-2023 found that 65% were associated with STEC O157:H7 and 28% with STEC O26:H11. The majority of these cases were associated with the *stx2a* toxin subtype [15]. In 2024, 22 STEC cases notified in EpiSurv were reported to have developed HUS. The associated serotypes were O26:H11 (11), O157:H7 (5), O177:H25 (1), while for five cases the serotype was not reported.

The ICD-10 code D59.3 was used to extract HUS hospitalisation data from the Health New Zealand NMDS database. Only HUS cases that were incident in the 2024 year were considered, rather than all cases that were hospitalised in that year. That is, if an HUS case hospitalised in 2024 had been hospitalised with HUS in a previous year, the 2024 admission was considered as a re-admission, rather than an incident case. Of the 46 incident cases recorded in 2024 (0.9 per 100,000 population), 29 were reported with HUS as the principal diagnosis and 17 with HUS as another relevant diagnosis. It should be noted that the number of incident HUS cases reported through the NMDS is always greater than the number of STEC cases identified as having developed HUS reported in EpiSurv. This may be an artefact of the reporting systems but the reported recent increase in cases of *Streptococcus pneumoniae* associated HUS in young children will also contribute to the difference between HUS cases in the NMDS and HUS cases in EpiSurv [43].

Between 2015 and 2024, the number of incident cases (any diagnosis code) of HUS each year ranged from 24 to 58 (Figure 48). In 2024, the number of incident cases (46) was above the mean for the 10-year period 2015 – 2024 (38). STEC case notifications have increased steadily over this period. However annual numbers of incident HUS cases have remained largely similar over the last decade, with the exception of the 2022 year.

Figure 48. Haemolytic uraemic syndrome (HUS) incident cases reported in the NMDS, 2015–2024



In 2024, the number of female cases hospitalised due to HUS was greater than the number of male cases (Table 55). This is the predominant pattern seen in the last 10 years.

Table 55. Haemolytic uraemic syndrome incident cases by sex, 2024

Sex	Cases[a]	
	No.	Rate[b]
Male	17	0.6
Female	29	0.9
Total	**46**	**1.1**

[a] Health New Zealand Te Whatu Ora NMDS data.

[b] Per 100,000 population in group.

In 2024, the highest age-specific rates of incident cases due to HUS were for children in the <1 and 1 to 4 years age groups (Table 56).

Table 56. Haemolytic uraemic syndrome incident cases by age group, 2024

Age group (years)	Cases [a]	
	No.	Rate[b]
<1	4	6.9
1 to 4	23	9.4
5 to 9	8	2.4
10 to 14	1	-
15 to 19	1	-
20 to 29	2	-
30 to 39	1	-
40 to 49	-	-
50 to 59	1	-
60 to 69	1	-
70+	4	-
Total	**46**	**0.9**

[a] Health New Zealand Te Whatu Ora NMDS data.

[b] Per 100,000 population in age group (rate not calculated when fewer than five cases reported).

Recent surveys

Nil.

Relevant New Zealand studies and publications

Reports

Data for Top 7 Shiga toxin-producing Escherichia coli *isolated from adult beef and whole genome sequencing of E. coli O157 isolates from bovine and veal 2023 – Wright et al., 2024*

The PHF Science Enteric Reference Laboratory tested a total of 201 PCR screen-positive enrichment broths submitted by six laboratories from meat samples collected during the 2023 calendar year. Of the 201 screen positive samples, 189 required confirmatory testing for Top 6 STEC (serogroups O26, O45, O103, O111, O121, O145) and 29 required confirmatory testing for STEC O157.

Nineteen enrichment broths (9.5%) were confirmed culture positive for a Top 7 STEC serotype with two different STEC serogroups observed: O26 (n = 8); and O157 (n = 11). This overall confirmation rate of 9% from all samples received for confirmatory testing is slightly less than previous years.

Of the 189 sample broths re-screened for Top 6 STEC serogroups, 161 (85%) yielded a positive multiplex real-time polymerase chain reaction (RT-PCR) result for one or more of the Top 6 serogroups tested. Following isolation procedures, 153 (81%) failed to yield colonies that fulfilled the criteria for Top 6 STEC confirmation (biochemically reacting as an *E. coli* and serogroup confirmed by titration; and positive for *eae* and *stx*1 and/or *stx*2 by PCR). Of the 29 broths received for STEC O157 testing, 11 yielded isolates that fulfilled the United States Department of Agriculture (USDA) criteria for STEC O157.

Additionally, 67 primary laboratory screen-positive bobby veal broths were received of which New Zealand Food Safety requested seven samples be defrosted and cultured for STEC O157. Five of

these samples had been confirmed by NeoSeek™ as STEC O157 positive, one was reported as non-STEC O157 by NeoSeek™, and one screen-negative sample was mistakenly included. Four of these broths yielded viable STEC O157 colonies following culture isolation attempts.

Fifteen STEC O157 isolates (from four bobby veal and 11 bovine trim samples) underwent whole genome sequencing (WGS). The sequenced genomes were analysed using PHF Science's GNReporter, core genome multi-locus sequencing typing (cgMLST) and single nucleotide polymorphism (SNP) cluster analysis pipelines. All but one STEC O157 isolate were identified as sequence type (ST) 11. The other was ST10084. None of the STEC O157 bovine isolates obtained for 2023 were genetically closely related to each other (fewer than 5-SNP differences). However, one STEC O157 isolate from a bovine trim sample was observed to be genetically closely related (fewer than 5-SNP differences) with a 2023 human clinical isolate (collection dates for the two isolates differed by 10 months). Two 2023 STEC O157 from bovine isolates were genetically closely related (within 5-SNP differences) to two separate historic human clinical cases.

A review of New Zealand human clinical STEC strains isolated from 2016-2022 demonstrated that New Zealand clinical strains do not fit the USA "Top 7" STEC model, with many other serotypes, some of which are *eae* negative, being isolated from clinical cases. As the New Zealand STEC genomic database grows, so too does our understanding of clinical STEC epidemiology in New Zealand but additional source data are necessary to improve our knowledge of transmission pathways. A recent MPI STEC attribution project (see next item), coupled with a proposed STEC case control study, are intended to assist in elucidation of infection pathways.

Attribution and characterisation of New Zealand domestic Shiga toxin-producing Escherichia coli infections – Horn et al., 2024

New Zealand has one of the highest reported rates of STEC infections among developed countries, but very few reported outbreaks. This project aimed to (1) improve the understanding of key transmission pathways of human STEC infections in New Zealand, including an estimate of the proportion attributable to food, and (2) identify and prioritise food sources associated with STEC infection cases [15].

Across the period 1 January 2016 to 30 June 2023 the most prevalent serotypes confirmed in human cases were O157:H7, O26:H11, O128:H2, O38:H26, and O146:H21. The *eae* gene was absent in some isolates associated with all disease presentations (36%) and some isolates from HUS cases (7%), supporting current thinking that e*ae* negative STEC cause illness and should not be discounted as being non-pathogenic. Most genomic clusters comprised 5 or fewer cases (95% of the 177 SNP-clusters, 83% of 273 cgMLST-clusters), suggesting that STEC infection is predominately sporadic with few cases being exposed to common events or sources.

The EpiSurv data allowed estimation of the proportion of cases attributable to becoming infected either overseas (10 to 14% of cases), from person-to-person transmission (2 to 9% of cases) or due to rural type activities (estimate 53 to 66% of cases). The remaining proportion of cases were considered to be due to an 'other' transmission pathways group. The 'other' group will include STEC infection cases who became ill from foodborne pathways (consumption or handling), contact with pets or raw pet food, other recreational outdoor activities and any unknown risk factors. The proportion of cases attributable to these 'other' risk factors represents an upper bound for the proportion attributable to foodborne pathways. The best estimate of the current percentage of all cases infected via 'other' transmission pathways is 18 to 31% of cases. If we exclude cases associated with overseas travel, but include all other transmission pathways, then the percentage of domestically acquired STEC infection due to "other" pathways is 22 to 36%.

Relevant regulatory developments

No STEC-specific regulatory developments.

Toxic shellfish poisoning

Case definition

Due to the diverse nature of toxins that may cause toxic shellfish poisoning, no consistent clinical description is provided for this condition. Depending on the toxin involved, toxic shellfish poisoning may result in various combinations of gastrointestinal, neurosensory, neurocerebellar/neuromotor, general neurological and other symptoms.

Suspected:

Amnesic shellfish poisoning (ASP): Vomiting or diarrhoea or abdominal cramps occurring within 24 hours of consuming shellfish AND no other probable cause identified by microbiological examination of faecal specimen from the case or microbiological testing of leftover food AND/OR one or more of the neurological symptoms from group C (see below) occurring within 48 hours of consuming shellfish.

Diarrhoeic shellfish poisoning (DSP): Vomiting or diarrhoea occurring within 24 hours of consuming shellfish AND no other probable cause identified by microbiological examination of faecal specimen from the case or microbiological testing of leftover food.

Neurologic shellfish poisoning (NSP): Two or more of the neurological symptoms from groups A and B (see below) occurring within 24 hours of consuming shellfish.

Paralytic shellfish poisoning (PSP): Paraesthesia occurring within 12 hours of consuming shellfish AND one of the neurological symptoms from group B (see below).

Toxic shellfish poisoning type unspecified (TSP): Vomiting or diarrhoea occurring within 24 hours of consuming shellfish AND no other probable cause identified by microbiological examination of faecal specimen from the case or microbiological testing of leftover food OR any of the neurological symptoms from groups A and B (see below) occurring within 24 hours of consuming shellfish OR one or more of the neurological signs/symptoms from group C (see below) occurring within 48 hours of consuming shellfish.

Clinical symptoms for assigning classification

Group A
- paraesthesia - i.e. numbness or tingling around the mouth, face or extremities
- alteration of temperature sensation

Group B
- weakness such as trouble rising from seat or bed
- difficulty swallowing
- difficulty breathing
- paralysis
- clumsiness
- unsteady walking
- dizziness/vertigo
- slurred/unclear speech
- double vision

Group C
- confusion
- memory loss
- disorientation
- seizure
- coma

Probable:

Meets case definition for suspect case AND detection of relevant biotoxin at or above the regulatory limit in shellfish obtained from near or same site (not leftovers) within seven days of collection of shellfish consumed by case. Current levels are as follows:

ASP: 20 mg domoic acid/kg shellfish

DSP: 0.16 mg of okadaic acid equivalent/kg shellfish

NSP: 0.8 mg brevetoxin-2 equivalent/kg shellfish

PSP: 0.8 mg saxitoxin dihydrochloride equivalent/kg shellfish

Confirmed:
Meets case definition for suspect case AND detection of PSP biotoxin in leftover shellfish at a level resulting in the case consuming a dose likely to cause illness. Current dose levels are as follows:

ASP: 0.05 mg/kg body weight
NSP: 0.3 MU/kg body weight
DSP: ingestion of 48 µg or 12 MU (MU = mouse units)
PSP: 10 MU/kg body weight (≅ 2µg/kg body weight)

Toxic shellfish poisoning cases reported in 2024 by data source

During 2024, one individual case of paralytic shellfish poisoning was reported in EpiSurv.

The ICD-10 code T61.2 was used to extract hospitalisation data for 'other fish and shellfish poisoning' from the Health New Zealand Te Whatu Ora NMDS database. All five hospitalised cases (0.1 hospitalised cases per 100,000 population) recorded in 2024 were reported with 'other fish and shellfish poisoning' as the principal diagnosis. Note that this ICD-10 code includes shellfish and other fish.

It should be noted that EpiSurv and NMDS are two separate databases that are used for different purposes. Therefore, NMDS and EpiSurv hospitalisation numbers may differ for several reasons, including criteria used for notifications or diagnostic coding, i.e. a hospital discharge may be coded to an infectious cause without a case being recorded in EpiSurv and vice versa (see also Appendix A–Methods, page 123).

Outbreaks reported as caused by toxic shellfish poisoning

In 2024, no toxic shellfish poisoning outbreaks were reported in EpiSurv. There have been no confirmed outbreaks of toxic shellfish poisoning in the last 10 years. The last outbreaks were in 2014 (one outbreak, 13 cases) and 2012 (one outbreak, 29 cases).

It should be noted that all cases of toxic shellfish poisoning will be categorised as foodborne as consumption of contaminated seafood is the only recognised transmission route for this disease.

Recent surveys

Nil.

Relevant New Zealand studies and publications

Nil.

Relevant regulatory developments

During 2024, MPI consulted on amendments to the *Animal Products Notice: Regulated Control Scheme – Bivalve Molluscan Shellfish for Human Consumption* (BMS notice) and the *Animal Products Notice: Recognised Laboratories* (Lab Notice) [44]. The amendments included moving and enhancing the requirements for laboratories undertaking testing for the purpose of the BMS Regulated Control Scheme from the BMS Notice to the Lab Notice. The evidence and documentation required when seeking a reduction in biotoxin testing frequencies, as part of the marine biotoxin management plans, were also strengthened. The amendments came into force in December 2024.

Vibrio parahaemolyticus infection

Case definition

Clinical description:	Gastroenteritis with watery diarrhoea and abdominal cramps.
Laboratory test for diagnosis:	Isolation of *Vibrio parahaemolyticus* from a faecal specimen.
Case classification:	
Probable	A clinically compatible illness.
Confirmed	A clinically compatible illness that is laboratory confirmed, OR a clinically compatible illness and a common exposure associated with a laboratory confirmed case.

Vibrio parahaemolyticus infection individual cases reported in 2024 by data source

During 2024, 29 individual cases (0.5 per 100,000 population) of *V. parahaemolyticus* infection were reported in EpiSurv.

The ICD-10 code A05.3 was used to extract foodborne *V. parahaemolyticus* infection hospitalisation data from the Health New Zealand Te Whatu Ora NMDS database. All three hospitalised cases[1] recorded in 2024 were reported with *V. parahaemolyticus* infection as the principal diagnosis.

It should be noted that EpiSurv and NMDS are two separate databases that are used for different purposes. Therefore, NMDS and EpiSurv hospitalisation numbers may differ for several reasons, including criteria used for notifications or diagnostic coding NMDS and EpiSurv hospitalisation numbers may differ for several reasons, including criteria used for notifications or diagnostic coding (see also Appendix A–Methods, page 123).

Seasonal data

The number of cases of *V. parahaemolyticus* infection notified in EpiSurv by reporting month are summarised in Table 57. Generally, notifications show no pronounced seasonal trends over multiple years.

[1] Rate per 100,000 population not calculated when fewer than five cases reported.

Table 57. *V. parahaemolyticus* infection monthly notified cases, 2020–2024

Month	*V. parahaemolyticus* infection cases notified in EpiSurv				
	2020	2021	2022	2023	2024
January	4	3	28[a]	5	6
February	5	3	8[a]	2	3
March	4	20[b]	5[a]	5	6
April	0	4	4[a]	1	0
May	0	0	4[a]	2	3
June	12[b]	3	3	1	1
July	4	0	1	0	1
August	0	0	1	0	0
September	0	2	1	2	2
October	2	2	0	0	6
November	1	7[a]	2	3	1
December	1	7[a]	2	1	0
Total	**33**	**51**	**59**	**22**	**29**

[a] Period of elevated case numbers across the country in 2021 and 2022, which have been reported as a single outbreak in EpiSurv [45].

[b] Elevated case numbers correspond to known outbreaks due to *V. parahaemolyticus* infection.

Foodborne transmission

It has been estimated by expert consultation that 90.6% (95th percentile credible interval: 56.9% to 99.9%) of *V. parahaemolyticus* infections are due to foodborne transmission [2]. It was further estimated that approximately 94% of foodborne *V. parahaemolyticus* infections were due to consumption of seafood.

Outbreaks reported as caused by *Vibrio parahaemolyticus*

In 2024, no outbreaks of *V. parahaemolyticus* infection were reported in EpiSurv. In the last 10 years there were three years with common source potentially foodborne *V. parahaemolyticus* outbreaks recorded (2019, 2020 and 2021), with between two and 24 outbreak-associated cases per year.

In addition to EpiSurv records, one suspected *Vibrio* and norovirus outbreak of two cases in the Auckland Public Health District was referred to NZFS. Sashimi was the suspected source, but the food or food premise was unable to be confirmed as the source of illness.

Vibrio parahaemolyticus sequence types commonly reported

From 2019 onwards, the PHF Science Enteric Reference Laboratory, in consultation with MPI, has performed whole genome sequencing on a selection of clinical *V. parahaemolyticus* isolates, predominantly those that were positive for the virulence markers *tdh* and *trh* (Table 58). From 2024, WGS has been conducted and reported for all *Vibrio* spp. isolates. The most frequently isolated sequence type in 2024 was ST3. ST50 was the most frequently isolated sequence type from 2020 to 2023.

Table 58. *V. parahaemolyticus* 7-gene multi locus sequence types (ST) of case isolates, 2020–2024

Sequence type	2020	2021	2022	2023	2024
ST3	0	0	7	3	5
ST8	0	0	1	3	1
ST36	2	2	0	1	1
ST50	24	24	37	6	1
ST55	0	1	1	1	0
ST69	0	0	2	0	0
ST199	0	5	1	2	0
ST607	0	0	0	1	2
ST1165	0	0	0	2	1
ST2549	0	4	1	1	1
ST2631	0	0	0	0	2
ST2904	0	0	1	1	0
Other STs isolated once[a]	0	0	5	6	14
No typing information	**18**	**0**	**1**	**1**	**1**
Total	**44**	**36**	**57**	**28**	**29**

[a]Table lists the STs which had at least two associated cases for the years 2020-2024 combined.

Recent surveys

Nil.

Relevant New Zealand studies and publications

Journal papers

Detection of non-pathogenic and pathogenic populations of *Vibrio parahaemolyticus* in various samples by the conventional, quantitative and droplet digital PCRs – Vidovic et al., 2024

Three polymerase chain reaction (PCR) assays (conventional, qPCR and droplet digital PCR) were compared for their ability to detect non-pathogenic and pathogenic populations of *Vibrio parahaemolyticus* in shellfish [46]. The methods were then applied to 480 greenshell mussel (*Perna canaliculus*) samples (80 per month) collected during January 2022, June-August 2022, and January-February 2023. Prevalence of *V. parahaemolyticus* was significantly lower in the winter months than the summer months. The ddPCR method was the most sensitive method overall, detecting *V. parahaemolyticus* DNA in 37.5% of samples from June 2022 and 77.9% of samples from January 2022. Most of the samples positive for *V. parahaemolyticus* were also positive for the *V. parahaemolyticus* virulence factor (*tdh*).

Relevant regulatory developments

During 2024, MPI consulted on amendments to the *Animal Products Notice: Regulated Control Scheme – Bivalve Molluscan Shellfish for Human Consumption* (BMS Notice) and the *Animal Products Notice: Recognised Laboratories* (Lab Notice) [44]. The amendments included moving and enhancing the requirements for laboratories undertaking testing for the purpose of the BMS Regulated Control Scheme from the BMS Notice to the Lab Notice. The amendments came into force in December 2024.

Yersiniosis

Case definition

Clinical description:	In children under five years old, *Yersinia enterocolitica* infection typically causes diarrhoea, vomiting, fever and occasionally abdominal pain. In contrast, older children and adults are more likely to experience abdominal pain as the prominent symptom. Bacteraemia and sepsis may occur in immunocompromised individuals. *Y. pseudotuberculosis* is more likely to cause mesenteric adenitis and septicaemia than *Y. enterocolitica*.
Laboratory test for diagnosis:	Isolation of *Y. enterocolitica* or *Y. pseudotuberculosis* from blood or faeces OR detection of *Yersinia* spp. nucleic acid from faeces.
Case classification:	
Probable	A clinically compatible illness that is epidemiologically linked to a confirmed case or has had contact with the same common source – that is, is part of a common-source outbreak.
Confirmed	A clinically compatible illness that is laboratory confirmed.

Summary data

Summary data for yersiniosis in 2024 are given in Table 59.

Table 59. Summary of surveillance data for yersiniosis, 2024

Parameter	Value in 2024	Source
Number of notified cases	1140	EpiSurv
Notification rate (per 100,000)	21.4	EpiSurv
Hospitalised cases[a]	165	NMDS
Deaths[b]	0	EpiSurv
Estimated number of cases related to travel (%)[c,d]	76 (6.7%)	EpiSurv
Estimated domestically acquired food-related cases[e]	798	Expert consultation and EpiSurv

NMDS = Health New Zealand Te Whatu Ora National Minimum Dataset of hospitalisations.

[a] Cases hospitalised may not be notified on EpiSurv.

[b] There were five deaths of yersiniosis cases was recorded in EpiSurv in 2024, but none were recorded as due to yersiniosis. Three cases died from a cause other than yersinosis and the cause of death was not recorded for the other two cases.

[c] Estimated number and % of cases related to travel. Of the 1140 notified cases, the overseas travel question had a 'yes' or 'no' entry for 568 cases (49.8%); of these, 38 cases (6.7%) had travelled overseas during the incubation period and 530 cases (93.3%) had not been overseas. The overseas travel history for the remaining 572 cases is unknown. The estimated number of cases related to travel is given as 6.7% percent of all cases in 2024.

[d] While international travel has increased again since restrictions ceased in 2022, overseas travel in 2024 was still slightly lower compared with the pre-COVID-19 year 2019 (see section Changes in overseas travel, page 11).

[e] Estimation of food-related cases is given by (*Total cases – Estimate of cases acquired overseas*) x *Estimate of proportion of domestically acquired cases likely to be due to foodborne transmission*. The estimate of domestic proportion of yersiniosis cases due to foodborne transmission (75%) was derived from expert consultation [3].

Yersiniosis individual cases reported in 2024 by data source

During 2024, 1140 individual cases (21.4 per 100,000 population) of yersiniosis were reported in EpiSurv. Five cases were recorded in EpiSurv as having died, but none of these identified yersinosis as the cause of death.

The ICD-10 code A04.6 was used to extract yersiniosis (enteritis due to *Y. enterocolitica)* hospitalisation data from the Health New Zealand Te Whatu Ora NMDS database. Of the 165 hospitalised cases (3.1 hospitalised cases per 100,000 population) recorded in 2024, 84 cases were reported with yersiniosis as the principal diagnosis and 81 were reported with yersiniosis as another relevant diagnosis. Some of the 165 hospitalised cases were admitted to hospital more than once resulting in a total of 182 hospital admissions. The largest proportion of hospitalised cases (47.3%) spent between two and six nights in hospital, with 4.9% of hospitalised cases admitted to an intensive care unit (Appendix C, Table 69).

It should be noted that EpiSurv and NMDS are two separate databases that are used for different purposes. Therefore, NMDS and EpiSurv hospitalisation numbers may differ for several reasons, including criteria used for notifications or diagnostic coding (see also Appendix A–Methods, page 123).

Foodborne transmission

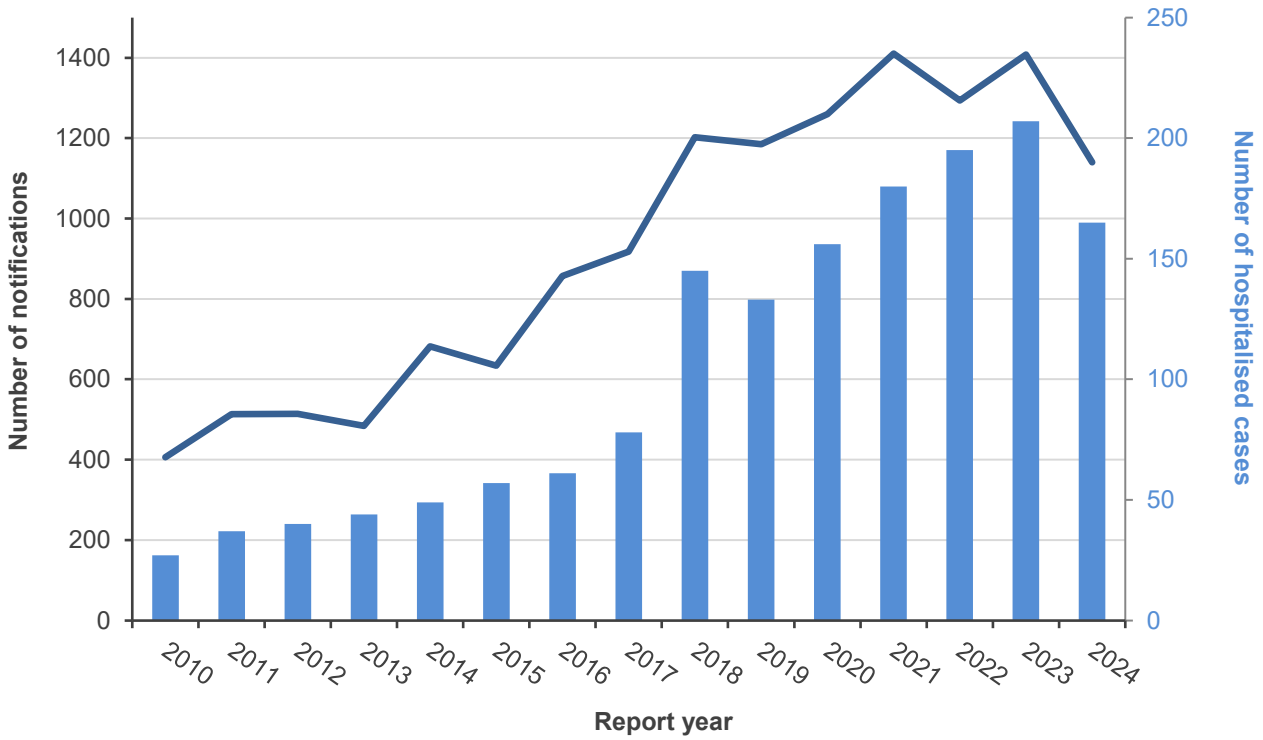
It has been estimated by expert consultation that 75% of yersiniosis incidence is due to foodborne transmission [3]. It was further estimated that approximately 71% of foodborne transmission was due to transmission via pork [2].

Annual data

Between 2010 and 2013 the annual number of yersiniosis notifications reported ranged between 406 and 514. Since 2013, the number and the rate of yersiniosis notifications has been increasing with the highest numbers reported in 2021 (1410 cases) and 2023 (1408 cases), followed by a drop in 2024 (1140 cases) (Figure 49 and Figure 50). The number of hospitalised cases with yersiniosis as the principal or other relevant diagnosis generally followed the same trend as the number of reported cases.

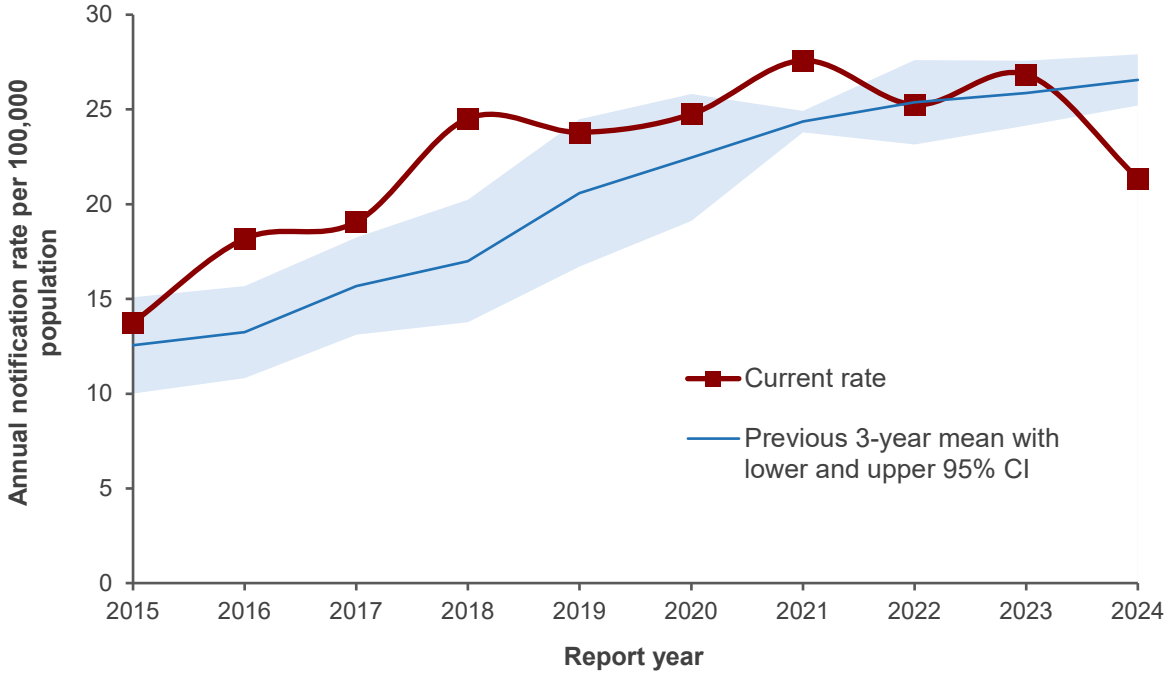
The frequency of overseas travel was lower in 2020 to 2023 and still slightly lower in 2024 compared with the pre-COVID-19 year 2019 (see section Changes in overseas travel, page 11). In 2024, the estimated percentage of yersiniosis cases related to travel was 6.7% (95% CI: 5.2-8.1%), compared with 9.3% (95% CI: 7.7-10.8%) in 2019 (pre-COVID-19 pandemic) and 0.3% (95% CI: <0.1-0.6%) in 2021 (year of greatest reduction in travel).

Figure 49. Yersiniosis EpiSurv notifications (line) and NMDS hospitalised cases (bar) by year, 2010–2024



The yersiniosis annual notification rate has been generally increasing from 2015 to 2023 (Figure 50). The 2024 notification rate of 21.4 cases per 100,000 population was much lower than the previous three-year mean (26.6 cases per 100,000 population).

Figure 50. Yersiniosis notification rate by year, 2015–2024

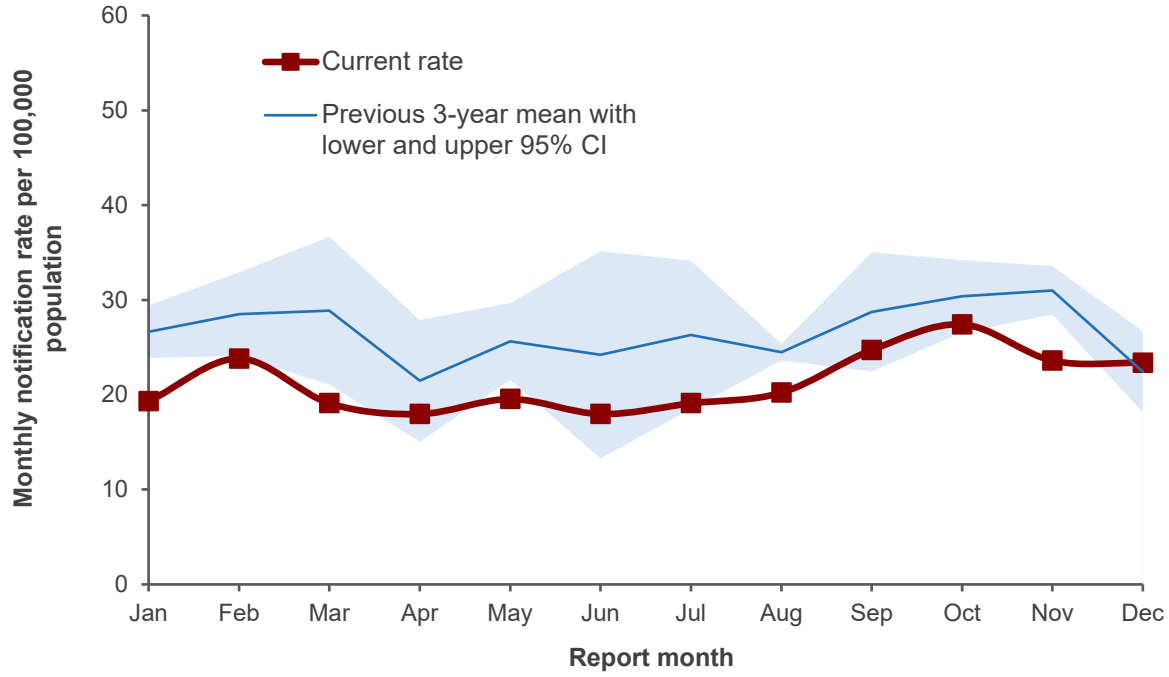


Seasonal data

Yersiniosis notification rates per 100,000 population by month for 2024 are shown in Figure 51. In 2024 the monthly notification rates were consistently lower compared with the mean of the previous

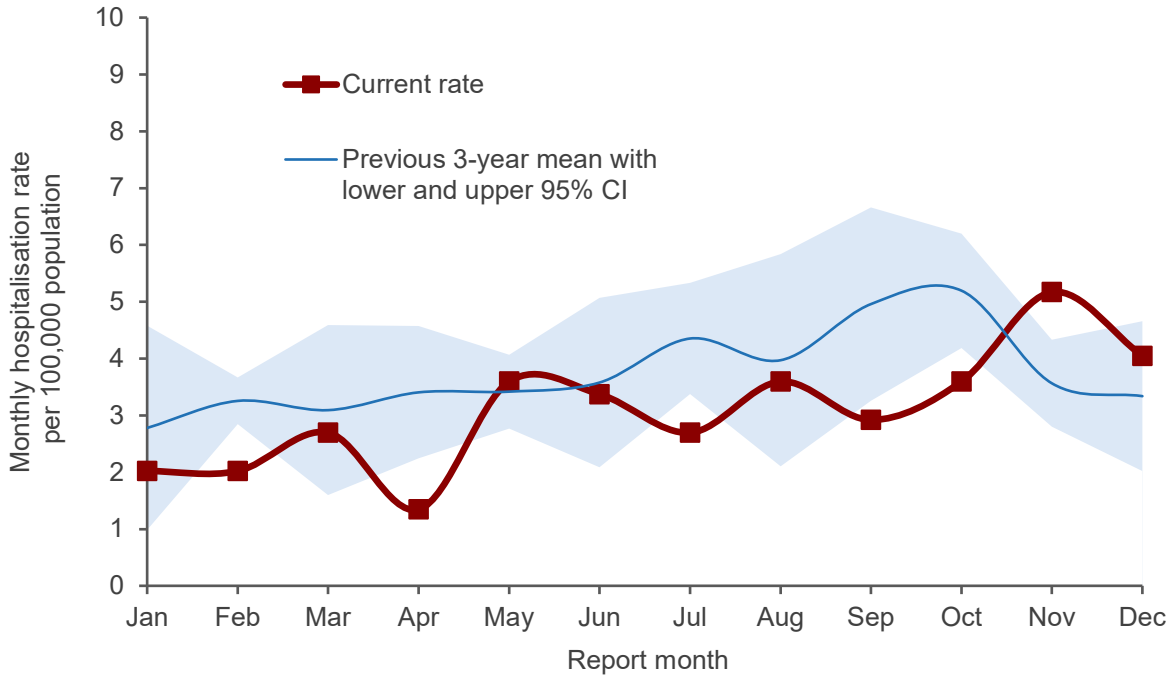
three years, albeit only marginally for some months. The monthly number of notifications in 2024 ranged from 80 notifications (April and June, 18.0 cases per 100,000 population) to 122 notifications (October, 27.4 cases per 100,000 population).

Figure 51. Yersiniosis monthly notification rate (annualised), 2024



In 2024, the monthly hospitalisation rates varied over the year with no clear seasonal pattern (Figure 52). The monthly number of hospitalised cases in 2024 ranged from six cases (April, 1.4 cases per 100,000 population) to 23 cases (November, 5.2 cases per 100,000 population).

Figure 52. Yersiniosis monthly hospitalisation rate (annualised), 2024



Demographics

In 2024, the yersiniosis notification and hospitalised case rates were higher for females (22.8 cases and 3.7 hospitalised cases per 100,000 population) than males (19.8 cases and 2.5 hospitalised cases per 100,000 population) (Table 60).

Table 60. Yersiniosis cases by sex, 2024

Sex	EpiSurv notified cases		Hospitalised cases[a]	
	No.	Rate[b]	No.	Rate[b]
Male	527	19.8	66	2.5
Female	611	22.8	99	3.7
Total[c]	**1140**	**21.4**	**165**	**3.1**

[a] Health New Zealand Te Whatu Ora NMDS data.
[b] Per 100,000 population in this sex group.
[c] Total includes cases where sex was not recorded.

In 2024, the highest yersiniosis notification rates and hospitalised case rates were for the <1 year age group (95.0 cases and 13.8 hospitalised cases per 100,000 population) (Table 61). The 70+ years age group had the longest hospital stays (45 cases admitted for two or more nights) (Appendix C, Table 79).

Table 61. Yersiniosis cases by age group, 2024

Age group (years)	EpiSurv notified cases		Hospitalised cases[a]	
	No.	Rate[b]	No.	Rate[b]
<1	55	95.0	8	13.8
1 to 4	131	53.7	12	4.9
5 to 9	31	9.4	2	-
10 to 14	29	8.3	1	-
15 to 19	32	9.4	5	1.5
20 to 29	127	18.5	16	2.3
30 to 39	157	19.4	20	2.5
40 to 49	147	22.1	15	2.3
50 to 59	122	18.7	19	2.9
60 to 69	136	23.3	18	3.1
70+	173	27.9	49	7.9
Total	**1140**	**21.4**	**165**	**3.1**

[a] Health New Zealand Te Whatu Ora NMDS data.
[b] Per 100,000 population in this age group (rate not calculated when fewer than five cases reported).

In 2024, the yersiniosis notification and hospitalised case rates were highest for the ethnic groups 'Asian' (31.9 cases and 4.4 hospitalised cases per 100,000 population) and MELAA (28.3 cases and 6.4 hospitalised cases per 100,000 population) (Appendix C, Table 70 and Table 71).

Geographic distribution

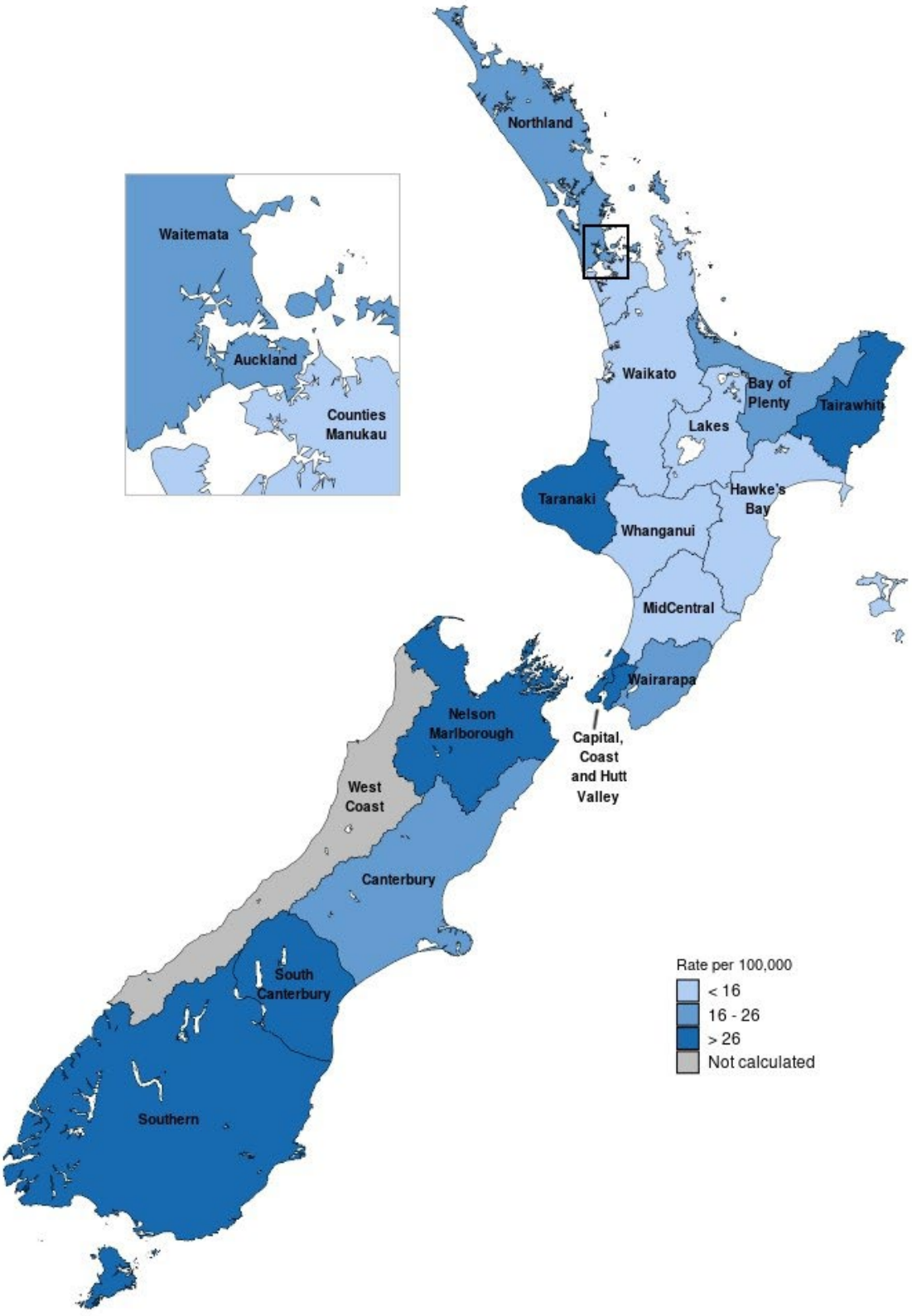
The notification rates by Health District calculated per 100,000 resident population are presented in Figure 53 (see also Appendix C, Table 83). The number of notified cases by Health District are presented in Appendix C, Table 82.

In 2024, the Health District notification rates of yersiniosis ranged from 9.3 per 100,000 population (18 cases) for MidCentral to 43.2 per 100,000 population for Tairāwhiti (23 cases). The Health Districts Tairāwhiti, Nelson Marlborough (35.8 cases per 100,000 population, 60 cases), and Capital, Coast and Hutt Valley (34.0 cases per 100,000 population, 166 cases) had the highest rates.

From 2020 to 2024, notification rates for yersiniosis have been variable across New Zealand, with the lower North Island Health Districts Capital and Coast and Hutt Valley (data from which are now combined) consistently in the highest quartile of notification rates.

Yersiniosis notification rates, stratified by 2023 Urban Rural Classification [26] of the cases' residential address and excluding cases associated with overseas travel varied across the different urban and rural areas (Appendix C, Table 84). Notification rates were highest in 'rural other' (21.7 cases per 100,000 population), 'major urban' (20.9 cases per 100,000 population) and 'medium urban' areas (20.0 per 100,000 population). The lowest notification rate was in 'rural settlement' areas (14.4 cases per 100,000 population), although these areas had the highest hospitalised case rate (5.6 hospitalised cases per 100,000 population) (Appendix C, Table 85).

Figure 53. Geographic distribution of yersiniosis notifications, 2024



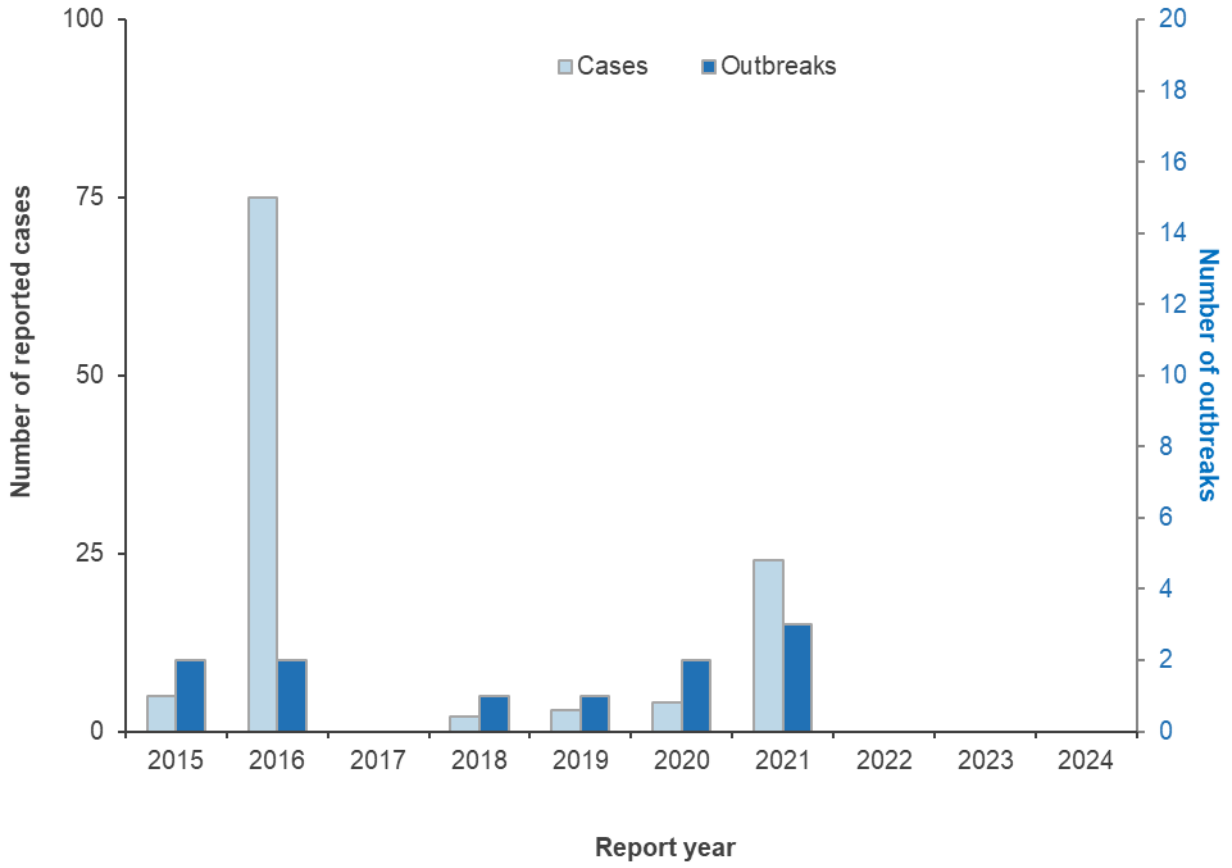
Outbreaks reported as caused by *Yersinia* spp.

In 2024, there was a single yersinosis outbreak of 18 cases notified in EpiSurv. Food was not reported as a possible mode of transmission for this outbreak that occurred in a long-term care facility. It is important to note that an outbreak may have multiple pathogens, modes of transmission, settings where exposure occurred, or settings where preparation of food was conducted.

Over the 10-year period 2015 to 2024, there were three or fewer yersiniosis outbreaks with food reported as a possible mode of transmission. The number of annual outbreak related cases ranged from two to 75 (Figure 54).

The largest outbreak in the last 10 years were an outbreak of 51 cases in 2016 with sprouts as the suspected source.

Figure 54. Yersiniosis outbreaks with food reported as a possible mode of transmission and associated cases reported by year, 2015-2024



Notes:

1. The data in this figure is based on EpiSurv records for the years up to 2021. From 2021 onwards, the graph includes foodborne outbreaks recorded in EpiSurv and any outbreaks that were referred to NZFS but were not recorded in EpiSurv as an outbreak.
2. A dual campylobacteriosis-yersiniosis 2019 outbreak of 62 cases reported in the 2023 report, has since been reclassified as not a yersiniosis outbreak and therefore the data is not included in the 2024 report figure.

Yersinia species commonly reported

In 2024, isolates from 712 out of 1140 cases (62%) of notified yersiniosis were typed by the Enteric Reference Laboratory. Table 62 shows the number of isolates typed by the Enteric Reference Laboratory at PHF Science each year, while the percentage of cases of each type is shown in Figure 55.

The table and figure need to be interpreted with some caution as:

- Not all clinical laboratories forward all *Yersinia* isolates to ERL for confirmation and typing.
- The number of isolates forwarded for confirmation and typing, as a percentage of all notifications, has decreased since the adoption of CIDT, from 92% in 2014 to 62% in 2024.
- Successful detection and identification of *Yersinia* spp. is influenced by the methods used by the laboratories. Newer nucleic acid-based methods have not been shown to be more sensitive than the historical culture-based methods. However, the use of different diagnostic CIDT panels across New Zealand (see Appendix B, page 128) results in all faecal specimens being screened for *Y. enterocolitica* but samples processed by laboratories covering more than half (55%) of the New Zealand population are no longer being screened for *Y. pseudotuberculosis*. Cases of *Y. pseudotuberculosis* in these Health Districts may be notified as acute gastroenteritis cases or not be notified. In the last 10 years, *Y. pseudotuberculosis* has been associated with less than 3% of sporadic cases of yersiniosis in each reporting year.
- Some CIDT positive samples do not provide an isolate that can be typed.

Between 2020 and 2024, each year the largest proportion of yersiniosis cases was due to *Y. enterocolitica* (Table 62 and Figure 55). The most prevalent type of *Y. enterocolitica* has been biotype 2/3, serotype O:9 in each year since 2020. This type was associated with almost 39% of the notified cases in 2024. During 2024, *Y. enterocolitica* biotype 1A accounted for 18% of yersiniosis notifications and biotype 4 accounted for 5% of yersiniosis notified cases.

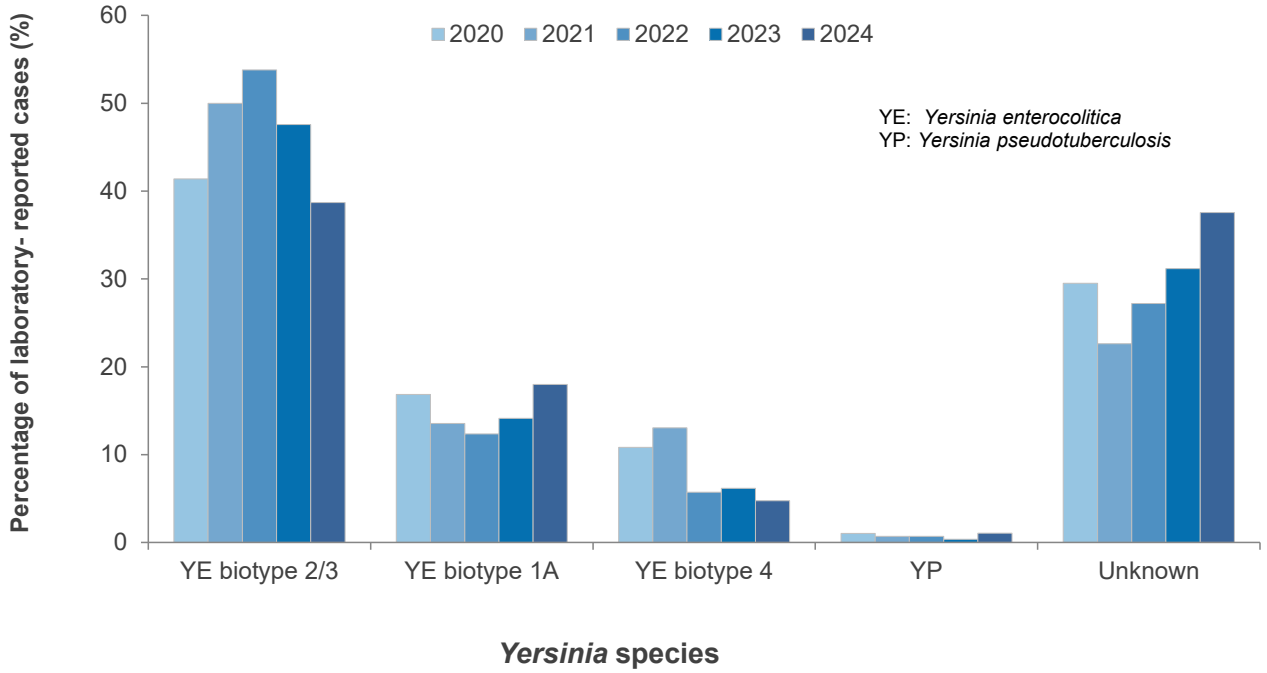
Table 62. Annual number of case notifications of different *Yersinia* spp. biotypes, serotypes and sequence types, 2020–2024

Species	2020	2021	2022	2023[a]	2024
Yersinia enterocolitica[b]	**877**	**1080**	**933**	**961**	**700**
biotype 1A	**213**	**191**	**161**	**199**	**205**
serotype O:5	38	19	19	23	5
serotype O:8	39	37	39	20	7
ST3	-	-	-	-	7
ST8	-	-	-	-	6
ST125	-	-	-	-	8
ST278	-	-	-	-	12
ST291	-	-	-	-	5
ST322	-	-	-	-	9
biotype 2/3	**523**	**705**	**695**	**670**	**441**
serotype O:5, 27 / ST14	40	27	24	20	11
serotype O:9 / ST12	483	678	670	647	429
biotype 4	**137**	**184**	**75**	**87**	**54**
serotype O:3 / ST18	137	184	75	87	54
biotype not identified	**4**	**1**	**2**	**5**	**0**
Yersinia pseudotuberculosis	**13**	**10**	**9**	**5**	**12**
ST43	-	-	-	-	9
Cases without typing information	**373**	**319**	**348**	**439**	**428**

[a] *Yersinia* isolates were identified as *Y. hibernica* for one case and *Y. frederiksenii* for another case.

[b] Prior to February 2024, *Yersinia* isolates were typed by bioserotyping. During February 2024, PHF Science implemented whole genome sequencing (WGS) of isolates. A seven gene multi locus sequence type (ST) using the McNally scheme for *Y. enterocolitica* [47] and Achtman scheme for *Y. pseudotuberculosis* [48] is now reported. Using WGS data to infer ST, it has been observed that ST12, ST14 and ST18 correlate to bioserotypes BT 2/3, O:9; BT 2/3, O:5, 27; and BT 4, O:3, respectively [49]. For these bioserotypes / sequence types, 2024 data includes isolates typed by either method. For other sequence types, the table lists those which had five or more associated cases in 2024.

Figure 55. Percentage of notified yersiniosis cases by species and biotype by year, 2020–2024



Recent surveys

Nil.

Relevant New Zealand studies and publications

Journal papers

A case-control study and molecular epidemiology of yersiniosis in Aotearoa New Zealand – Rivas et al., 2024

A risk factor questionnaire was administered to 247 notified yersiniosis cases and 258 controls from Canterbury and/or Wellington, recruited during 2021-2022 [50]. Risk of yersiniosis was significantly associated with consumption of pork (adjusted odds ratio 1.82, 95th percentile confidence interval 1.08-3.12) and cooked seafood (aOR 1.51, 95%CI 1.05-2.17). The association with pork consumption was stronger for consumption of pork mince (aOR 3.04, 95%CI 1.65-5.85). The associations were also stronger for the subset of cases with isolates typed as pathogenic *Yersinia enterocolitica* or sequence type 12. Risk factors associated with *Yersinia enterocolitica* BT 1A included the consumption of cooked seafood, sushi, tofu, and some vegetable types.

Relevant regulatory developments

No *Yersinia*-specific regulatory developments.

APPENDIX A - METHODS

This section includes descriptions of the data sources, analytical methods used and comments on the quality of data, including known limitations.

The report uses the calendar year, 1 January to 31 December 2024, for the reporting period.

Data sources

The key sources of data used in this report are detailed in the following sections. The data sources have been selected on the basis of availability of data for the specified reporting period and their accessibility within the timeframe required for the report.

Some data, such as official cause of death, are not published until several years after the end of the year in which the event occurred (although deaths may be reported as part of the case notification data recorded in EpiSurv). For this reason, these data are not available for inclusion in a report published soon after the end of the calendar year.

EpiSurv - the New Zealand notifiable disease surveillance system

Under the Health Act 1956 health professionals are required to inform their local Medical Officer of Health of any suspected or diagnosed notifiable disease. Since December 2007, laboratories have also been required to report notifiable disease cases to their local Medical Officer of Health.

Notification data are recorded using a web-based application (EpiSurv) available to staff at the 12 regional public health services (PHS) in New Zealand. The EpiSurv database is maintained and developed by the New Zealand Institute for Public Health and Forensic Science (PHF Science), formerly known as Institute of Environmental Science and Research (ESR) Ltd., which is also responsible for the collation, analysis and reporting of disease notifications on behalf of the Ministry of Health.

Data collected by PHS depends on the specific disease, but usually includes demography, outcome, basis of diagnosis, risk factors and some clinical management information. Data on risk factors reflect the frequency of exposure in the incubation period for illness and are not a measure of association with illness in comparison with the general population. For the purpose of this report, only the risk factor ‘overseas travel’ is reported.

Further information about notifiable diseases can be found in the *Notifiable Diseases in New Zealand: Annual Report* [51].

Laboratory-based surveillance

For a number of organisms (e.g., *Salmonella*, *Escherichia coli*), clinical laboratory isolates are forwarded to reference laboratories at PHF Science for confirmation and typing. The number of isolates forwarded differs by health district and organism (e.g., almost all isolates are forwarded for *Salmonella* typing but not all *Yersinia* isolates are forwarded).

Health New Zealand Te Whatu Ora

Health New Zealand Te Whatu Ora collates national data on patients admitted and discharged from publicly funded hospital events, from public and private hospitals. These data are stored as part of the National Minimum Dataset (NMDS). Cases are assigned disease codes using the tenth revision of the International Classification of Diseases (ICD-10-AM) coding system [13]. Up to 99 diagnostic, procedure, and accident codes may be assigned to each admission. The first of these is the principal diagnosis, which is the primary condition during hospitalisation. This may differ from an underlying diagnosis or initial reason for admission.

Hospital admission data are only added to the NMDS after the patient is discharged. The number of hospitalisations presented for the reported year may be under-reported due to the delay in receiving discharge summaries.

The case definitions for notifiable diseases in EpiSurv do not match the criteria used for diagnostic coding in NMDS. For this reason, the NMDS and EpiSurv hospitalisation numbers may differ. Additionally, the use of incorrect diagnostic codes can also lead to discrepancies between the two systems. EpiSurv uses the same definition for hospitalisations as the NMDS: Healthcare users who receive assessment and/or treatment for three hours or more (excluding time in a waiting room and triage), or who have had a general anaesthetic.

Hospital admission data includes repeated admissions for patients with chronic notifiable diseases or diseases which have long-term health impacts (e.g., GBS). For some diseases, the criteria for notification (clinical and laboratory or epidemiological evidence) do not match those required for diagnostic coding. For these reasons hospitalisation numbers and notifications may differ.

In this report re-admissions of cases within the calendar year were removed. The reported case numbers represent unique cases that have been hospitalised during the calendar year, not the total number of admissions due to the disease or sequelae.

Outbreak surveillance (EpiSurv, Food Compliance Services (NZFS) and PHS)

PHF Science has operated an outbreak surveillance system as an additional module in EpiSurv since mid-1997. This enables PHSs to record and report outbreaks for national reporting and analysis. It should be noted that, due to the practicalities of collecting information and laboratory resource constraints, not all cases associated with outbreaks are recorded as individual cases of notifiable disease in EpiSurv. The terms ‘setting’ and ‘suspected vehicle’ are both used in outbreak reporting to describe likely implicated sources of exposure found in epidemiological or environmental investigations.

An outbreak is classed as foodborne in this report if food was recorded as one of the likely modes of transmission applicable to the outbreak. It is important to note that a single outbreak may have multiple pathogens, modes of transmission, settings where exposure occurred, or settings where food was prepared. More information about the outbreak reporting system can be found in the *Guidelines for the Investigation and Control of Disease Outbreaks* [52]. There is considerable variability in the amount of information provided in reports from different outbreaks.

This report also provides information from Food Compliance Services, NZFS, who investigate clusters of cases of notified diseases which are potentially foodborne.

Level of evidence for outbreaks

Foodborne outbreaks have been classified as having weak or strong evidence for any given suspected vehicle. Outbreaks with strong evidence included those with a statistically significant elevated risk ratio or odds ratio (95% confidence) from an epidemiological investigation and/or laboratory evidence with the same organism and strain detected in both disease cases and vehicle (to the highest available level of identification).

Outbreaks were classified as having weak evidence when they met one or more of the following criteria:

- compelling evidence with symptoms attributable to specific organisms, e.g., scombrotoxin, ciguatoxin, etc.,
- other association but no microbial evidence for causal link, i.e., organism detected at source but not linked directly to the cases by indistinguishable DNA profiles,
- raised but not statistically significant relative risk or odds ratio,
- no evidence found but logical deduction given circumstances.

Statistics New Zealand

Population data from the Statistics New Zealand website www.stats.govt.nz were used to calculate notification and hospitalisation population rates of disease.

Statistics New Zealand also provided (i) the 2023 urban rural geographies and mapping files [26] to allow assignment of urban areas, rural settlements, other rural areas and water areas to residence of EpiSurv notified or hospitalised cases and (ii) data on arrivals into New Zealand from overseas.

University of Otago

Socioeconomic deprivation 2023 index mapping files and user manual were sourced from The University of Otago, Department of Public Health.
https://www.otago.ac.nz/wellington/research/groups/research-groups-in-the-department-of-public-health/hirp/socioeconomic-deprivation-indexes-nzdep-and-nzidep-department-of-public-health

NZFS project reports and other publications

NZFS project reports, prepared by PHF Science or other providers, and publications from the general literature were used to provide specific contextual information on the prevalence of selected pathogens in specific food types.

Relevant regulatory developments

Organism-specific regulatory developments, such as legislation (Australia New Zealand Food Standards Code, New Zealand Food Standards), notices, guidelines or other guidance documents, or instructional material produced by NZFS or Food Standards Australia New Zealand (FSANZ) were briefly summarised to provide contextual information and a single point of reference for developments in the control of pathogens in food. It should be noted that NZFS is the authority and expert in this area and the regulatory developments summarised in this report were confirmed with NZFS.

Analytical methods

Key analytical methods used include:

Dates

Notification data contained in this report are based on information recorded in EpiSurv for individual cases as at 24 February 2025. Outbreak data contained in this report are based on information recorded as an outbreak in EpiSurv as at 10 April 2025. Disease numbers are reported according to the date of notification. Hospitalisation data was extracted from the NMDS on the 9 April 2025.

Changes made to EpiSurv data by PHS staff or made to the NMDS after these dates are not reflected in this report. Consequently, future analyses of these data may produce revised results. Likewise, case notifications or rates in this report may differ slightly from previously reported figures due to data extraction dates and/or updates to the population denominator.

Case status for notifications

All notifications recorded in EpiSurv that meet the case definitions [16] are included for analysis in this report with the exception of cases classified as ‘not a case’. In some instances, the investigation of a case may not be complete, and the status may be set to ‘under investigation’. These cases are included in this report. Any changes will be reflected in future surveillance reports.

Outbreak cases can be classed as ‘laboratory confirmed’, ‘clinically confirmed’ or ‘probable’. Both ‘laboratory confirmed’ and ‘clinically confirmed’ outbreak cases are referred to as confirmed cases in the outbreak sections of the report.

Data used for calculating rates of disease

All population rates use Statistics New Zealand 2024 mid-year population estimates and are crude rates unless otherwise stated. At 30 June 2024, the New Zealand population was estimated to be 5,338,500. The population estimates for 2014 to 2023 have been revised by Statistics New Zealand, considering migration, deaths and births adjustments to 2018 Census distributions.

Rates have not been calculated where there were fewer than five notified cases or hospitalisations in any category. Calculating rates from fewer than five cases produces unstable rates.

Geographical breakdown

As part of the New Zealand health system reform the 20 DHBs were disestablished on 30 June 2022 and their functions merged into Health New Zealand Te Whatu Ora. For 2024 this report refers to the 19 Health New Zealand Te Whatu Ora districts (Health Districts).

Urban rural classification

The urban rural classification of area of usual residence of notified EpiSurv cases was mapped via the 2025 meshblock of the residence. For hospitalised cases the mapping was via the residence 2013 Domicile code [26]. Where a meshblock/domicile code was assigned to more than one urban rural classification, the meshblock was assigned by prioritising the categories in the following order: ‘Major urban area’, ‘Large urban area’, ‘Medium urban area’, ‘Small urban area’, ‘Rural settlement’ and ‘Rural other’.

Map classification scheme

The map classification break points for the disease have been selected to divide Health District rates into three bands. The darkest colour represents the highest rates and the lightest colour the lowest rates. The grey speckled colour shows where there are insufficient data to calculate a rate (fewer than five cases).

Statistical tests

Confidence intervals have been calculated for the disease rates and displayed on the graphs. For annual and seasonal graphs, the historical mean is calculated from the previous three years’ data (2021−2023).

The confidence intervals for the percentage of cases estimated to have travelled overseas during the incubation period are calculated using a confidence interval for small finite populations based on the hypergeometric distribution.

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APPENDIX B - LABORATORIES CHANGING DETECTION METHODS FOR ENTERIC PATHOGENS

Timeline of laboratories changing to nucleic acid amplification-based detection of enteric pathogens

Since 2015, laboratories across New Zealand have changed the methodology for testing faecal specimens (see page 10). Table 63 below summarises when laboratories across New Zealand moved to nucleic acid amplification-based CIDT detection methods and which pathogens are included in the respective test panels. In 2024 there were four different commercial panels used across New Zealand.

Table 63. Dates of the change to CIDT methods for enteric pathogens by Health District (X: not changed, NS: not screened for)

Health District		*Campylobacter*	*Salmonella*	*Shigella*	STEC	*Yersinia enterocolitica*	*Yersinia pseudotuberculosis*[a]	*Giardia*[b]	*Cryptosporidium*[b]	*Vibrio parahaemolyticus*[c]
Auckland Te Toka Tumai	Hospital	Jul 2017	Jul 2017	Jul 2017	Jul 2017	Jul 2017	NS	Jul 2017	Jul 2017	Jul 2017
Auckland Te Toka Tumai	Community	Jul 2015	Jul 2015	Jul 2015	Jul 2015	Jun 2017	NS	Jul 2015	Jul 2015	Jun 2017
Bay of Plenty Hauora a Toi	Hospital	Nov 2018	Nov 2018	Nov 2018	Nov 2018	Nov 2018	NS	X	X	Nov 2018
Bay of Plenty Hauora a Toi	Community	Nov 2018	Nov 2018	Nov 2018	Nov 2018	Nov 2018	NS	X	X	Nov 2018
Canterbury Waitaha	Hospital	Jun 2023	Jun 2023	Jun 2023	Jun 2023	Jun 2023	NS	X	X	Jun 2023
Canterbury Waitaha	Community	Oct 2023	Oct 2023	Oct 2023	Oct 2023	Oct 2023	Oct 2023	Oct 2023	Oct 2023	X
Capital Coast and Hutt Valley	Hospital	Jan 2018	Jan 2018	Jan 2018	Jan 2018	Jan 2018	Jan 2018	Jan 2018	Jan 2018	X
Capital Coast and Hutt Valley	Community	Jan 2018	Jan 2018	Jan 2018	Jan 2018	Jan 2018	Jan 2018	Jan 2018	Jan 2018	X
Counties Manukau	Hospital	Nov 2015	Nov 2015	Nov 2015	Nov 2015	Nov 2015	NS	Nov 2016	Nov 2016	Dec 2017
Counties Manukau	Community	Jul 2015	Jul 2015	Jul 2015	Jul 2015	Jun 2017	NS	Jul 2015	Jul 2015	Jun 2017
Hawke's Bay Te Marau a Māui	Hospital	Oct 2022	Oct 2022	Oct 2022	Oct 2022	Oct 2022	NS	X	X	Oct 2022
Hawke's Bay Te Marau a Māui	Community	Jan 2018	Jan 2018	Jan 2018	Jan 2018	Apr 2019	Apr 2019	Dec 2014[d]	Dec 2014[d]	X
Lakes	Hospital	Nov 2018	Nov 2018	Nov 2018	Nov 2018	Nov 2018	NS	X	X	Nov 2018
Lakes	Community	Nov 2018	Nov 2018	Nov 2018	Nov 2018	Nov 2018	NS	X	X	Nov 2018
MidCentral Te Pae Hauora o Ruahine o Tararua	Hospital	May 2021	May 2021	May 2021	May 2021	May 2021	May 2021	May 2021	May 2021	X
MidCentral Te Pae Hauora o Ruahine o Tararua	Community	May 2021	May 2021	May 2021	May 2021	May 2021	May 2021	May 2021	May 2021	X

Health District		*Campylobacter*	*Salmonella*	*Shigella*	STEC	*Yersinia enterocolitica*	*Yersinia pseudotuberculosis*[a]	*Giardia*[b]	*Cryptosporidium*[b]	*Vibrio parahaemolyticus*[c]
Nelson Marlborough	Hospital	Jan 2018	Jan 2018	Jan 2018	Jan 2018	Apr 2019	Apr 2019	Dec 2014[d]	Dec 2014[d]	X
Nelson Marlborough	Community	Jan 2018	Jan 2018	Jan 2018	Jan 2018	Apr 2019	Apr 2019	Dec 2014[d]	Dec 2014[d]	X
Northland Te Tai Tokerau	Hospital	Dec 2022	Dec 2022	Dec 2022	Dec 2022	Dec 2022	NS	Dec 2022	Dec 2022	Dec 2022
Northland Te Tai Tokerau	Community	Jul 2015	Jul 2015	Jul 2015	Jul 2015	Jun 2017	NS	Jul 2015	Jul 2015	Jun 2017
South Canterbury	Hospital	Oct 2023	Oct 2023	Oct 2023	Oct 2023	Oct 2023	Oct 2023	Oct 2023	Oct 2023	X
South Canterbury	Community	Oct 2023	Oct 2023	Oct 2023	Oct 2023	Oct 2023	Oct 2023	Oct 2023	Oct 2023	X
Southern	Hospital	Jan 2017	Jan 2017	Jan 2017	Jan 2017	Apr 2019	Apr 2019	Dec 2014[d]	Dec 2014[d]	X
Southern	Community	Jan 2017	Jan 2017	Jan 2017	Jan 2017	Apr 2019	Apr 2019	Dec 2014[d]	Dec 2014[d]	X
Tairāwhiti	Hospital	May 2021	May 2021	May 2021	May 2021	May 2021	May 2021	May 2021	May 2021	X
Tairāwhiti	Community	May 2021	May 2021	May 2021	May 2021	May 2021	May 2021	May 2021	May 2021	X
Taranaki	Hospital	Feb 2020	Feb 2020	Feb 2020	Feb 2020	Feb 2020	Feb 2020	Feb 2020	Feb 2020	X
Taranaki	Community	Feb 2020	Feb 2020	Feb 2020	Feb 2020	Feb 2020	Feb 2020	Feb 2020	Feb 2020	X
Waikato	Hospital	Mar 2024	Mar 2024	Mar 2024	Mar 2024	Mar 2024	NS	X	X	Mar 2024
Waikato	Community	Nov 2018	Nov 2018	Nov 2018	Nov 2018	Nov 2018	NS	X	X	Nov 2018
Wairarapa	Hospital	Jan 2018	Jan 2018	Jan 2018	Jan 2018	Jan 2018	Jan 2018	Jan 2018	Jan 2018	X
Wairarapa	Community	Jan 2018	Jan 2018	Jan 2018	Jan 2018	Jan 2018	Jan 2018	Jan 2018	Jan 2018	X
Waitematā	Hospital	Jun 2022	Jun 2022	Jun 2022	Dec 2016	Jun 2022	NS	X	X	Jun 2022
Waitematā	Community	Jul 2015	Jul 2015	Jul 2015	Jul 2015	Jun 2017	NS	Jul 2015	Jul 2015	Jun 2017
West Coast To Tai o Poutini	Hospital	Jun 2023	Jun 2023	Jun 2023	Jun 2023	Jun 2023	NS	X	X	Jun 2023
West Coast To Tai o Poutini	Community	Jun 2023	Jun 2023	Jun 2023	Jun 2023	Jun 2023	NS	X	X	Jun 2023
Whanganui	Hospital	May 2021	May 2021	May 2021	May 2021	May 2021	May 2021	May 2021	May 2021	X
Whanganui	Community	May 2021	May 2021	May 2021	May 2021	May 2021	May 2021	May 2021	May 2021	X

Data source: New Zealand Microbiology Network CIDT testing database, personal communication, March 2025.

[a] The use of different diagnostic panels across New Zealand results in all faecal specimens being screened for *Y. enterocolitica* but samples processed by laboratories covering about half of the New Zealand population are not being screened for *Y. pseudotuberculosis*. Cases of *Y. pseudotuberculosis* in these Health Districts may be notified as acute gastroenteritis cases or not be notified. In the last 10 years, *Y. pseudotuberculosis* has been associated with less than 3% of sporadic cases of yersiniosis in each reporting year. Previous culture-based methods identified isolates as belonging to the *Yersinia* genus, followed by additional testing to identify the species.

[b] Community faecal specimens in all Health Districts except for Bay of Plenty, Lakes, Waikato and West Coast are now screened by PCR methods for *Cryptosporidium* spp. and *Giardia* spp. whereas previously only those specimens where parasite screening was requested were tested. The remainder of the Health Districts (around 17% of the New Zealand population) are still serviced by laboratories using microscopic methods or enzyme immunoassay tests (EIA) when parasite screening is specifically requested.

[c] Samples positive for the *Vibrio* species target are cultured to confirm *V. parahaemolyticus* infection. Laboratories without a CIDT *Vibrio* spp. target are testing samples with a history of shellfish consumption for *V. parahaemolyticus* via culture.

[d] Until 2018 only faecal specimens where parasite screening was requested were tested by PCR for Giardia and Cryptosporidium

Changes in culture-based testing methods

The laboratory covering faecal specimens from community-based patients for Canterbury, South Canterbury and part of the West Coast changed to nucleic acid amplification-based detection CIDT in October 2023 and used an improved culture-based testing approach for STEC infection prior to that. Since September 2018, all faecal samples submitted to that laboratory were tested for STEC with this improved, culture-based approach (plating to CHROMagar STEC, followed up with EIA *stx* testing), which identified some non-O157 serotypes but not as many as nucleic acid amplification-based CIDT.

APPENDIX C - SUMMARY TABLES

Appendix C brings together data from EpiSurv, the NMDS and international data as summary tables to facilitate comparisons between potentially foodborne diseases which have high notification rates in New Zealand (campylobacteriosis, salmonellosis, STEC infection and yersiniosis), or have been shown to have more severe outcomes when notified (hepatitis A and listeriosis). Acute gastroenteritis includes a number of diseases where food is the primary mode of transmission (*Bacillus cereus*, *Clostridium perfringens* and *Staphylococcus aureus*, ciguatera poisoning, histamine (scombroid) fish poisoning, toxic shellfish poisoning and *Vibrio parahaemolyticus* infection) and is included for comparison.

Unless specifically stated, the case numbers and rates presented in this report relate to the total number of notified cases for the disease in New Zealand and do not differentiate between mode of transmission, i.e. foodborne or person-to person. Likewise, all data analysis, e.g. by demographics, is based on all notified cases and not limited to those attributable to foodborne transmission.

National tables

Table 64. Number of cases notified in EpiSurv and rate per 100,000 population of selected notifiable diseases in New Zealand, 2023–2024

Disease	2023[a]		2024	
	Cases	Rate	Cases	Rate
Acute gastroenteritis[b]	462	8.8	441	8.3
Campylobacteriosis	6092	116.1	5801	108.7
Hepatitis A	34	0.6	68	1.3
Listeriosis	37	0.7	36	0.7
Salmonellosis	827	15.8	844	15.8
STEC infection	1005	19.2	1115	20.9
Yersiniosis	1408	26.8	1140	21.4

[a] Changes to EpiSurv records after the cut-off date for the Annual Report Concerning Foodborne Disease in New Zealand 2023 [53] and using the latest update of the population estimates mean the number of cases and rates reported in this report for the 2023 year may be different from those reported in the 2023 report.

[b] Cases with certain conditions (intoxications from the bacteria *Bacillus cereus*, *Clostridium perfringens* and *Staphylococcus aureus*, ciguatera poisoning, histamine (scombroid) fish poisoning, toxic shellfish poisoning and *Vibrio parahaemolyticus*, norovirus and sapovirus infections) are notified under the heading of acute gastroenteritis.

Not all individual cases of acute gastroenteritis are notifiable, only those when: (i) the infected person is in a high-risk category (e.g. food handler, early childhood service worker, or another person with increased risk of spreading the disease), (ii) it is an infectious gastroenteritis of public health importance such as *C. perfringens*, *V. parahaemolyticus* or (iii) there are single cases of chemical or toxic food poisoning such as botulism, histamine (scombroid) poisoning and any type of toxic shellfish poisoning [16]. Please note that other publications or reports may report botulism and toxic shellfish poisoning separately, resulting in differing case numbers for acute gastroenteritis.

Table 65. Rate per 100,000 population of selected notifiable diseases in New Zealand and other selected countries

Disease	Country/Region (year data relate to)						
	New Zealand (2024)	Australia[a] (2024)	USA[b,c] (2023)	Canada[d] (2022)	UK[e] (2024)	EU Total[f,g] (2023)	Other high
Campylobacteriosis	108.7	145	23.4	18.7	121.9	45.7	129.4 (Luxembourg)[f] 125.2 (Czechia)[f]
Hepatitis A	1.3	0.90	0.68[c]	0.63	NR	1.0[g]	5.5 (Hungary)[g] 5.3 (Croatia)[g]
Listeriosis	0.7	0.23	0.3	0.50	0.29	0.66	1.7 (Finland)[f] 1.2 (Sweden)[f]
Salmonellosis	15.8	46	16.6	11.6	18.0	18.0	73.7 (Slovakia)[f] 69.1 (Czechia)[f]
STEC infection	20.9	4	6.6	2.7	3.5	3.1	24.1 (Denmark)[f] 20.2 (Liechtenstein)[f]
Yersiniosis	21.4	NN	2.8	NN	NN	2.4	20.2 (Denmark)[f] 5.7 (Czechia)[f]

NN: Not notifiable, NR: not reported

[a] The Australian National Notifiable Diseases Surveillance System (NNDSS, https://nindss.health.gov.au/pbi-dashboard/).

[b] FoodNet – Foodborne Diseases Active Surveillance Network http://www.cdc.gov/foodnet/.

[c] U.S. Centers for Disease Control and Prevention. Summary of notifiable disease https:// https://wonder.cdc.gov/nndss-annual-summary.html (CDC data presented here relate to the 2022 year).

[d] Canadian Notifiable Disease Surveillance System (CNDSS) https://diseases.canada.ca/notifiable/.

[e] Following the UK exit from the European Union, notifiable disease rates for the UK are not included in the EU report for 2023. Disease rates for some potentially foodborne diseases are reported individually by the UK Health Security Agency https://www.gov.uk/health-and-social-care/health-protection-infectious-diseases#research_and_statistics. STEC rate is for 2023. While hepatitis A case numbers are reported on a quarterly basis, no annual rates are reported.

[f] European Food Safety Authority and European Centre for Disease Prevention and Control (ECDC). The European Union One Health 2023 Zoonoses Report https://www.efsa.europa.eu/en/efsajournal/pub/9106.

[g] European Centre for Disease Prevention and Control (ECDC). Annual epidemiological report on communicable diseases in Europe https://www.ecdc.europa.eu/en/publications-data/monitoring/all-annual-epidemiological-reports. ECDC data presented here relate to the 2022 year for hepatitis A, except for the rate for the UK, which is from the 2019 report.

Table 66. Number of cases of selected notifiable diseases recorded in EpiSurv by year, 1995–2024

Disease	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009
Acute gastroenteritis[a]	-	555	316	493	608	730	942	1088	1030	1362	559	926	617	676	713
Campylobacteriosis	7442	7635	8924	11,572	8161	8418	10,146	12,493	14,788	12,215	13,836	15,873	12,778	6692	7177
Hepatitis A	338	311	347	144	119	107	61	106	70	49	51	123	42	89	44
Listeriosis	13	10	35	17	19	22	18	19	24	26	20	19	26	27	28
Salmonellosis	1334	1141	1177	2069	2077	1795	2417	1880	1401	1081	1382	1335	1275	1337	1128
STEC infection[b]	6	7	13	48	64	67	76	73	104	89	92	87	100	122	143
Yersiniosis[b]	-	330	488	546	503	396	429	472	436	407	383	453	502	508	430

Disease	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024
Acute gastroenteritis	502	570	765	558	775	506	513	324	231	486	357	244	331	462	441
Campylobacteriosis	7346	6686	7016	6837	6782	6218	7457	6482	6957	6203	5292	5729	5878	6092	5801
Hepatitis A	46	26	82	91	74	47	35	58	68	67	21	8	58	34	68
Listeriosis	23	26	25	19	25	26	36	21	30	31	35	32	39	37	36
Salmonellosis	1146	1055	1081	1143	955	1051	1091	1127	1100	1190	709	714	749	827	844
STEC infection	138	153	147	205	187	330	417	547	925	1103	845	912	1022	1005	1115
Yersiniosis	406	513	514	483	680	634	858	917	1201	1185	1260	1410	1294	1408	1140

[a] Cases with certain conditions (intoxications from the bacteria *Bacillus cereus*, *Clostridium perfringens* and *Staphylococcus aureus*, ciguatera poisoning, histamine (scombroid) fish poisoning, toxic shellfish poisoning and *Vibrio parahaemolyticus,* norovirus and sapovirus infections) are notified under the heading of acute gastroenteritis.

Not all individual cases of acute gastroenteritis are notifiable, only those when: (i) the infected person is in a high-risk category (e.g. food handler, early childhood service worker, or another person with increased risk of spreading the disease), (ii) it is an infectious gastroenteritis of public health importance such as *C. perfringens* and *V. parahaemolyticus* or (iii) there are single cases of chemical or toxic food poisoning such as botulism, histamine (scombroid) poisoning and any type of toxic shellfish poisoning [16]. Please note that other publications or reports may report botulism and toxic shellfish poisoning separately, resulting in differing case numbers for acute gastroenteritis. Please note that other publications or reports may report botulism and toxic shellfish poisoning separately, resulting in differing case numbers for acute gastroenteritis.

[b] STEC infection and yersiniosis were added to the Health Act 1956 notification schedule in June 1996, cell marked "-" where data are unavailable.

Table 67. Deaths due to selected notifiable diseases recorded in EpiSurv[a], 2005–2024

Disease	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024
Acute gastroenteritis[b]	0	0	0	0	0	0	0	0	0	2	0	1	0	0	0	0	0	0	0	0
Campylobacteriosis	1	1	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	1[c]
Listeriosis - non perinatal	1	0	2	3	2	3	1	4	2	3	1	0	0	2	0	1	3	4	5	0[d]
Listeriosis - perinatal	4	1	2	2	2	4	0	2	3	2	3	2	0	0	4	1	1	2	2	1
Salmonellosis	1	1	1	1	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0[e]
STEC infection	0	0	0	0	1	0	0	0	0	1	0	0	0	2	1	0	0	1	0	0[f]
Yersiniosis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0[g]

[a] The numbers in this table are those recorded in EpiSurv where the notifiable disease was recorded as the primary cause of death. Deaths recorded in EpiSurv with the cause unknown or not from the disease, are not included in the table.

[b] Cases with certain conditions (intoxications from the bacteria *Bacillus cereus, Clostridium perfringens* and *Staphylococcus aureus*, ciguatera poisoning, histamine (scombroid) fish poisoning, toxic shellfish poisoning and *Vibrio parahaemolyticus*, norovirus and sapovirus infections) are notified under the heading of acute gastroenteritis.

Not all individual cases of acute gastroenteritis are notifiable, only those when: (i) the infected person is in a high-risk category (e.g. food handler, early childhood service worker, or another person with increased risk of spreading the disease), (ii) it is an infectious gastroenteritis of public health importance such as *C. perfringens, V. parahaemolyticus* or (iii) there are single cases of chemical or toxic food poisoning such as botulism, histamine (scombroid) poisoning and any type of toxic shellfish poisoning [16]. Please note that other publications or reports may report botulism and toxic shellfish poisoning separately, resulting in differing case numbers for acute gastroenteritis.

[c] In 2024, there were seven deaths of campylobacteriosis cases recorded in EpiSurv; one case died from campylobacteriosis. Three cases died from a cause other than campylobacteriosis and the cause of death was not recorded for the other three cases.

[d] In 2024, there were four deaths of listeriosis (non-perinatal) cases (60+ age group) recorded in EpiSurv. One case died from a cause other than listeriosis. The cause of death was not recorded for the three other listeriosis cases who died.

[e] In 2024, there were three deaths of salmonellosis cases recorded in EpiSurv. Two cases died from a cause other than salmonellosis and the cause of death was not recorded for the other case.

[f] In 2024, there were six deaths of STEC infection cases recorded in EpiSurv. All six cases died from a cause other than STEC infection.

[g] In 2024, there were five deaths of yersiniosis cases was recorded in EpiSurv, but none were recorded as due to yersiniosis. Three cases died from a cause other than yersinosis and the cause of death was not recorded for the other two cases.

Table 68. Hospitalised cases of selected notifiable diseases, 2023–2024

Disease	Source[a]	ICD-10 Codes	2023[b]			2024		
			Principal diagnosis	Other relevant diagnosis	Total	Principal diagnosis	Other relevant diagnosis	Total
Campylobacteriosis	NMDS	A04.5	803	185	**988**	874	164	**1038**
Hepatitis A	NMDS	B15	32	27	**59**	51	31	**82**
Listeriosis[c]	NMDS	A32	21	19	**40**	16	17	**33**
	EpiSurv	NA	NA	NA	**37**	NA	NA	**36**
Salmonellosis[d]	NMDS	A02.0	162	56	**218**	172	41	**213**
STEC infection[e]	NMDS	A04.3	23	19	**42**	37	31	**68**
	EpiSurv	NA	NA	NA	**235**	NA	NA	**291**
Yersiniosis	NMDS	A04.6	115	90	**205**	84	81	**165**

[a] NMDS data records hospital events when patients were treated in an emergency department, observation unit, acute assessment unit, short stay unit and/or admitted to a ward for three hours or more. This time includes observation and treatment but excludes time in the waiting room or triage. This table gives the number of cases who were hospitalised at least once with the associated ICD-10 code during the reporting year. Cases hospitalised more than once during the year are only included once. Patients with at least one hospital stay with the code as the principal diagnosis are captured in the 'Principal diagnosis' column.

[b] Changes to NMDS records after the extraction date for the Annual Report Concerning Foodborne Disease in New Zealand 2023 [53] mean the number of cases for the 2023 year may be different from those reported in the 2023 report.

[c] For previous reports for reporting years 2023 and prior, the A32 code for listeriosis was used to identify hospital admissions data for listeriosis cases. In the past this code consistently reported more cases hospitalised compared with EpiSurv. For reporting year 2024, less cases were recorded as hospitalised in NMDS while all notified cases were recorded as hospitalised in EpiSurv.

[d] *Salmonella* enterocolitis.

[e] For previous reports for reporting years 2022 and before, the A04.3 code for Enterohaemorrhagic *Escherichia coli* infection was used to identify hospital admissions data for STEC infection cases. A new 2024 study [15] has shown that ICD-10 code A04.3 alone does not capture all the cases hospitalised due to STEC infection. In 2024, 291 cases were listed as hospitalised in EpiSurv, compared with 68 cases identified using the A04.3 code.

NA: Not applicable.

Table 69. Hospitalisation and duration in hospital or intensive care unit (ICU) for cases of selected notifiable diseases, reported in NMDS, 2024

Disease	ICD 10 Codes	NMDS[a] Hospitalised cases	Total nights in hospital[b]			Admission to ICU[c]	
			0 to 1	2 to 6	7+	Cases (% of hospitalised)[b]	Total hours in ICU[c] Median [Range] or values
Campylobacteriosis	A04.5	1038	397	544	97	22 (2.1%)	67 [8 to 266]
Hepatitis A	B15	82	40	33	9	0 (0.0%)	NA
Listeriosis	A32	33 (36)[d]	0	12	21	4 (12.1%)	76 [51 to 681]
Salmonellosis[e]	A02.0	213	73	113	27	4 (1.9%)	54 [37 to 168]
STEC infection	A04.3	68 (291)[f]	14	31	23	9 (13.2%)	112 [3 to 150]
Yersiniosis	A04.6	165	37	78	50	8 (4.9%)	91 [25 to 221]

[a] NMDS data records hospital events when individuals were treated in an emergency department, observation unit, acute assessment unit, short stay unit and/or admitted to a ward for three hours or more. This time includes observation and treatment but excludes time in the waiting room or triage. This table includes counts of individuals who were diagnosed with the disease as the principal or other relevant diagnosis.

[b] Total nights in hospital equates to the total number of midnights spent in hospital by an individual during one or more admissions, with the first admission in 2024.

[c] ICU data relates to admissions to an intensive care unit. It does not include time in a high dependency or neonatal intensive care unit. The hours are the total duration in ICU, which may include more than one period in the ICU. Incomplete hours are rounded up to the next hour. Median and range are given if three cases or more were admitted. For less than three cases the number of hours for the individual cases are listed.

[d] 33 is the number of cases admitted to hospital, with an associated ICD-10 diagnosis code of A32 (listeriosis). For previous reports for reporting years 2023 and prior, the A32 code for listeriosis was used to identify hospital admissions data for listeriosis cases. In the past this code consistently reported more cases hospitalised compared with EpiSurv. For reporting year 2024, less cases were recorded as hospitalised in NMDS while all notified cases were recorded as hospitalised in EpiSurv.

[e] *Salmonella* enterocolitis.

[f] 68 is the number of cases admitted to hospital, with an associated ICD-10 diagnosis code of A04.3 (enterohaemorrhagic *Escherichia coli* infection). A 2024 study [15] has shown that ICD-10 code A04.3 alone does not capture all the cases hospitalised due to STEC infection. 291 is the number of cases recorded as hospitalised in EpiSurv. Note the severity information (nights in hospital and admission to ICU) is for hospitalised cases associated with code A04.3.

Ethnicity tables

Table 70. Number of cases notified in EpiSurv and rate per 100,000 population of selected notifiable diseases by ethnic group[a], 2024

Disease	Notified Cases						Rate per 100,000 population					
	Māori	Pacific peoples	Asian	MELAA[b]	European or Other	Total[c]	Māori	Pacific peoples	Asian	MELAA[b]	European or Other	Total[c]
Acute gastroenteritis[d]	60	19	55	6	294	441	6.7	5.3	6.8	7.7	9.2	8.3
Campylobacteriosis	594	186	585	84	4092	5801	66.8	51.7	72.1	108.1	127.9	108.7
Hepatitis A	13	3	36	6	9	68	1.5	-	4.4	7.7	0.3	1.3
Listeriosis	9	4	6	0	17	36	1.0	-	0.7	-	0.5	0.7
Salmonellosis	129	64	110	10	525	844	14.5	17.8	13.6	12.9	16.4	15.8
STEC infection	144	27	66	19	849	1115	16.2	7.5	8.1	24.4	26.5	20.9
Yersiniosis	124	37	259	22	694	1140	13.9	10.3	31.9	28.3	21.7	21.4

Note: Where fewer than five cases have been notified, a rate has not been calculated (-).

[a] In the data analyses ethnicity is prioritised in the following order: Māori, Pacific peoples, Asian, MELAA, European or Other Ethnicity (including New Zealander).

[b] MELAA: Middle Eastern, Latin American and African.

[c] Total includes cases where ethnicity was unknown.

[d] Cases with certain conditions (intoxications from the bacteria *Bacillus cereus*, *Clostridium perfringens* and *Staphylococcus aureus*, ciguatera poisoning, histamine (scombroid) fish poisoning, toxic shellfish poisoning and *Vibrio parahaemolyticus,* norovirus and sapovirus infections) are notified under the heading of acute gastroenteritis.

Not all individual cases of acute gastroenteritis are notifiable, only those when: (i) the infected person is in a high-risk category (e.g. food handler, early childhood service worker, or another person with increased risk of spreading the disease), (ii) it is an infectious gastroenteritis of public health importance such as *C. perfringens, V. parahaemolyticus* or (iii) there are single cases of chemical or toxic food poisoning such as botulism, histamine (scombroid) poisoning and any type of toxic shellfish poisoning [16]. Please note that other publications or reports may report botulism and toxic shellfish poisoning separately, resulting in differing case numbers for acute gastroenteritis.

Table 71. Hospitalised cases[a] and rate per 100,000 population of selected notifiable diseases by ethnic group[b], 2024

Disease	Source	Hospitalised cases[a]						Rate per 100,000 population					
		Māori	Pacific peoples	Asian	MELAA[c]	European or Other	Total[d]	Māori	Pacific peoples	Asian	MELAA[c]	European or Other	Total[d]
Campylobacteriosis	NMDS	129	65	95	18	727	1038	14.5	18.1	11.7	23.2	22.7	19.4
Hepatitis A	NMDS	10	8	33	8	23	82	1.1	2.2	4.1	10.3	0.7	1.5
Listeriosis	EpiSurv[e]	9	4	6	0	17	36	1.0	-	0.7	-	0.5	0.7
Salmonellosis	NMDS	37	34	33	3	106	213	4.2	9.4	4.1	-	3.3	4.0
STEC infection	EpiSurv[f]	46	13	18	4	208	291	5.2	3.6	2.2	-	6.5	5.5
Yersiniosis	NMDS	22	12	36	5	89	165	2.5	3.3	4.4	6.4	2.8	3.1

[a] NMDS data records hospital events when individuals were treated in an emergency department, observation unit, acute assessment unit, short stay unit and/or admitted to a ward for three hours or more. This time includes observation and treatment but excludes time in the waiting room or triage. This table includes counts of individuals who were diagnosed with the disease as the principal or other relevant diagnosis. Where fewer than five cases have been notified, a rate has not been calculated '-'.

[b] In the data analyses ethnicity is prioritised in the following order: Māori, Pacific Peoples, Asian, MELAA, European or Other Ethnicity (including New Zealander).

[c] MELAA: Middle Eastern, Latin American and African.

[d] Total includes cases where ethnicity was unknown.

[e] For previous reports for reporting years 2023 and prior, the A32 code for listeriosis was used to identify hospital admissions data for listeriosis cases. In the past this code consistently reported more cases hospitalised compared with EpiSurv. For reporting year 2024, less cases were recorded as hospitalised in NMDS while all notified cases were recorded as hospitalised in EpiSurv.

[f] A 2024 study [15] has shown the ICD-10 code used in previous years reports, A04.3 (Enterohaemorrhagic *Escherichia coli* infection), does not capture all the cases hospitalised due to STEC infection. This table gives the number of STEC infection cases listed as hospitalised in EpiSurv by ethnic group, rather than reporting the NMDS data.

Table 72. NMDS[a] length of hospital stay of cases of selected notifiable diseases by ethnic group[b], 2024

Disease	ICD 10 Codes	Cases staying in hospital[c]														
		Māori			Pacific peoples			Asian			MELAA[d]			European or Other		
		0 to 1 nights	2 to 6 nights	7+ nights	0 to 1 nights	2 to 6 nights	7+ nights	0 to 1 nights	2 to 6 nights	7+ nights	0 to 1 nights	2 to 6 nights	7+ nights	0 to 1 nights	2 to 6 nights	7+ nights
Campylobacteriosis	A04.5	48	72	9	23	36	6	45	45	5	8	9	1	273	378	76
Hepatitis A	B15	5	3	2	1	6	1	16	14	3	6	2	0	12	8	3
Listeriosis	A32	0	1	6	0	1	1	0	2	2	0	0	0	0	8	12
Salmonellosis[e]	A02.0	12	21	4	4	25	5	17	12	4	2	0	1	38	55	13
STEC infection[f]	A04.3	4	7	4	1	0	2	0	2	1	0	0	0	8	22	16
Yersiniosis	A04.6	8	9	5	3	8	1	11	22	3	1	3	1	14	36	39

[a] NMDS data records hospital events when individuals were treated in an emergency department, observation unit, acute assessment unit, short stay unit and/or admitted to a ward for three hours or more. This time includes observation and treatment but excludes time in the waiting room or triage. This table includes counts of individuals who were diagnosed with the disease as the principal or other relevant diagnosis.

[b] In the data analyses ethnicity is prioritised in the following order: Māori, Pacific Peoples, Asian, MELAA, European or Other Ethnicity (including New Zealander).

[c] Nights admitted equates to the total number of midnights spent in hospital by an individual during one or more admissions in 2023.

[d] MELAA: Middle Eastern, Latin American and African.

[e] *Salmonella* enterocolitis.

[f] Enterohaemorrhagic *Escherichia coli* infection. (ICD-10 code A04.3). A 2024 study [15] has shown that ICD-10 code A04.3 alone does not capture all the cases hospitalised due to STEC infection. The data in the table reflects the case severity for those STEC infection cases who were coded to diagnosis code A04.3.

Table 73. NMDS ICU admissions and duration of stay of selected notifiable diseases by ethnic group[a], 2024

Disease	Cases admitted to ICU[b] during hospitalisation						Hours admitted to ICU[b] Median [Range] or values if 1 or 2 admissions				
	Māori	Pacific peoples	Asian	MELAA[c]	European or Other	Total	Māori	Pacific peoples	Asian	MELAA[c]	European or Other
Campylobacteriosis	2	3	2	0	15	**22**	28 and 266	135 [55 to 146]	25 and 230	NA	63 [8 to 84]
Hepatitis A	0	0	0	0	0	**0**	NA	NA	NA	NA	NA
Listeriosis	1	1	0	0	2	**4**	NA	681	NA	NA	51 and 86
Salmonellosis[d]	1	0	1	0	2	**4**	46	NA	168	NA	37 and 62
STEC infection[e]	2	0	0	0	7	**9**	112 and 143	NA	NA	NA	41 [3 to 150]
Yersiniosis	1	1	0	0	6	**8**	65	25	NA	NA	129 [29 to 221]

[a] In the data analyses ethnicity is prioritised in the following order: Māori, Pacific Peoples, Asian, MELAA, European or Other Ethnicity (including New Zealander).

[b] ICU data relates to admissions to an intensive care unit. It does not include time in a high dependency or neonatal intensive care unit. The hours are the total duration in ICU, which may include more than one period in the ICU. Incomplete hours are rounded up to the next hour. Median and range are given if three cases or more were admitted. For less than three cases the number of hours for the individual cases are listed. '-' no data as no ICU admissions were recorded

[c] MELAA: Middle Eastern, Latin American and African.

[d] *Salmonella* enterocolitis.

[e] Enterohaemorrhagic *Escherichia coli* infection (ICD-10 code A04.3). A 2024 study [15] has shown that ICD-10 code A04.3 alone does not capture all the cases hospitalised due to STEC infection. The data in the table reflects the case severity for those STEC infection cases who were coded to diagnosis code A04.3.

Sex tables

Table 74. Number of EpiSurv cases and rate per 100,000 population of selected notifiable diseases by sex, 2024

Disease	Sex					
	Male		Female		Total[a]	
	Cases	Rate	Cases	Rate	Cases	Rate
Acute gastroenteritis[b]	197	7.4	243	9.1	441	8.3
Campylobacteriosis	3210	120.8	2589	96.5	5801	108.7
Hepatitis A	34	1.3	34	1.3	68	1.3
Listeriosis[c]	13	0.5	23	0.9	36	0.7
Salmonellosis	418	15.7	425	15.8	844	15.8
STEC infection	529	19.9	585	21.8	1115	20.9
Yersiniosis	527	19.8	611	22.8	1140	21.4

[a] Total includes EpiSurv notifications where sex is unknown.

[b] Cases with certain conditions (intoxications from the bacteria *Bacillus cereus, Clostridium perfringens* and *Staphylococcus aureus*, ciguatera poisoning, histamine (scombroid) fish poisoning, toxic shellfish poisoning and *Vibrio parahaemolyticus*, norovirus and sapovirus infections) are notified under the heading of acute gastroenteritis.

Not all individual cases of acute gastroenteritis are notifiable, only those when: (i) the infected person is in a high-risk category (e.g. food handler, early childhood service worker, or another person with increased risk of spreading the disease), (ii) it is an infectious gastroenteritis of public health importance such as *C. perfringens* and *V. parahaemolyticus* or (iii) there are single cases of chemical or toxic food poisoning such as botulism, histamine (scombroid) poisoning and any type of toxic shellfish poisoning [16]. Please note that other publications or reports may report botulism and toxic shellfish poisoning separately, resulting in differing case numbers for acute gastroenteritis. Please note that other publications or reports may report botulism and toxic shellfish poisoning separately, resulting in differing case numbers for acute gastroenteritis.

[c] Case details for the five perinatal cases are those for the mother.

Table 75. NMDS hospital data[a] of selected notifiable diseases by sex, 2024

Disease	Sex							
	Male				Female			
	Cases admitted to hospital	Nights in hospital[b] { 0-1, 2-6, 7+ }	Cases admitted to ICU[c]	ICU hours[c] Median [Range] or values	Cases admitted to hospital	Nights in hospital[b] { 0-1, 2-6, 7+ }	Cases admitted to ICU[c]	ICU hours[c] Median [Range] or values
Campylobacteriosis	569	{227, 292, 50}	15	60 [8 to 230]	469	{170, 252,47}	7	72 [25 to 266]
Hepatitis A	43	{20, 18, 5}	0	NA	39	{20, 15, 4}	0	NA
Listeriosis[d]	9 (13)	{0 ,3 ,6}	1	51	24 (23)	{0, 9, 15}	3	86 [64 to 681]
Salmonellosis[e]	106	{34, 59, 13)	3	62 [37 to 168]	107	{39, 54, 14}	1	46
STEC infection[f]	33 (141)[f]	{7, 16, 10}	3	112 [3 to 122]	35 (150)	{7, 15, 13}	6	86 [11 to 150]
Yersiniosis	66	{14, 32, 20}	3	29 [25 to 65]	99	{23, 46, 30}	5	141 [47 to 221]

[a] NMDS data records hospital events when individuals were treated in an emergency department, observation unit, acute assessment unit, short stay unit and/or admitted to a ward for three hours or more. This time includes observation and treatment but excludes time in the waiting room or triage. This table includes counts of individual cases who were diagnosed with the disease as the principal or other relevant diagnosis.

[b] Nights admitted equates to the total number of midnights spent in hospital by an individual during one or more admissions.

[c] ICU data relates to admissions to an intensive care unit. It does not include time in a high dependency or neonatal intensive care unit. The hours are the total duration in ICU during the hospital admission event, which may include more than one period in the ICU. Incomplete hours are rounded up to the next hour. '-' no data as no ICU admissions were recorded.

[d] Case details for the five perinatal cases are those for the mother. X (Y): X is the number of cases admitted to hospital, with an associated ICD-10 diagnosis code of A32 (listeriosis) for males or females. All the severity information is for cases hospitalised associated with code A32. Y is the number of cases recorded as hospitalised in EpiSurv for males or females.

[e] *Salmonella* enterocolitis.

[f] X (Y): X is the number of cases admitted to hospital, with an associated ICD-10 diagnosis code of A04.3 (Enterohaemorrhagic *Escherichia coli* infection) for males or females. All the severity information is for cases hospitalised associated with code A04.3. A 2024 study [15] has shown that ICD-10 code A04.3 alone does not capture all the cases hospitalised due to STEC infection. Y is the number of cases recorded as hospitalised in EpiSurv for male or females.

Table 76. Number of EpiSurv cases of selected notifiable diseases by age group, 2024

Disease	Age Group											
	<1	1 to 4	5 to 9	10 to 14	15 to 19	20 to 29	30 to 39	40 to 49	50 to 59	60 to 69	70+	Total[a]
Acute gastroenteritis[b]	7	29	16	9	20	61	66	58	67	48	52	**441**
Campylobacteriosis	102	474	205	186	295	738	633	594	724	828	1022	**5801**
Hepatitis A	0	6	8	6	5	17	11	8	1	3	3	**68**
Listeriosis[c]	0	1	0	1	1	3	2	0	5	5	18	**36**
Salmonellosis	46	82	42	28	25	95	95	103	124	114	90	**844**
STEC infection	40	163	51	38	47	100	82	84	120	145	245	**1115**
Yersiniosis	55	131	31	29	32	127	157	147	122	136	173	**1140**

[a] Total includes cases where age was unknown.

[b] Cases with certain conditions (intoxications from the bacteria *Bacillus cereus*, *Clostridium perfringens* and *Staphylococcus aureus*, ciguatera poisoning, histamine (scombroid) fish poisoning, toxic shellfish poisoning and *Vibrio parahaemolyticus,* norovirus and sapovirus infections) are notified under the heading of acute gastroenteritis.

Not all individual cases of acute gastroenteritis are notifiable, only those when: (i) the infected person is in a high-risk category (e.g. food handler, early childhood service worker, or another person with increased risk of spreading the disease), (ii) it is an infectious gastroenteritis of public health importance such as *C. perfringens* and *V. parahaemolyticus* or (iii) there are single cases of chemical or toxic food poisoning such as botulism, histamine (scombroid) poisoning and any type of toxic shellfish poisoning [16]. Please note that other publications or reports may report botulism and toxic shellfish poisoning separately, resulting in differing case numbers for acute gastroenteritis. Please note that other publications or reports may report botulism and toxic shellfish poisoning separately, resulting in differing case numbers for acute gastroenteritis.

[c] Case details for the five perinatal cases are those for the mother (one in the 15 to 19 age group, two in the 20 to 29 age group, and two in the 30 to 39 age group).

Table 77. Rate per 100,000 population of selected notifiable diseases by age group, 2024

Disease	Age Group											
	<1	1 to 4	5 to 9	10 to 14	15 to 19	20 to 29	30 to 39	40 to 49	50 to 59	60 to 69	70+	Total[a]
Acute gastroenteritis[b]	12.1	11.9	4.9	2.6	5.9	8.9	8.2	8.7	10.3	8.2	8.4	**8.3**
Campylobacteriosis	176.3	194.3	62.4	53.3	86.5	107.5	78.3	89.2	111.0	141.6	164.9	**108.7**
Hepatitis A	-	2.5	2.4	1.7	1.5	2.5	1.4	1.2	-	-	-	**1.3**
Listeriosis[c]	-	-	-	-	-	-	-	-	0.8	0.9	2.9	**0.7**
Salmonellosis	79.5	33.6	12.8	8.0	7.3	13.8	11.7	15.5	19.0	19.5	14.5	**15.8**
STEC infection	69.1	66.8	15.5	10.9	13.8	14.6	10.1	12.6	18.4	24.8	39.5	**20.9**
Yersiniosis	95.0	53.7	9.4	8.3	9.4	18.5	19.4	22.1	18.7	23.3	27.9	**21.4**

[a] Total includes cases where age was unknown.

[b] Cases with certain conditions (intoxications from the bacteria *Bacillus cereus*, *Clostridium perfringens* and *Staphylococcus aureus*, ciguatera poisoning, histamine (scombroid) fish poisoning, toxic shellfish poisoning and *Vibrio parahaemolyticus,* norovirus and sapovirus infections) are notified under the heading of acute gastroenteritis.

Not all individual cases of acute gastroenteritis are notifiable, only those when: (i) the infected person is in a high-risk category (e.g. food handler, early childhood service worker, or another person with increased risk of spreading the disease), (ii) it is an infectious gastroenteritis of public health importance such as *C. perfringens* and *V. parahaemolyticus* or (iii) there are single cases of chemical or toxic food poisoning such as botulism, histamine (scombroid) poisoning and any type of toxic shellfish poisoning [16]. Please note that other publications or reports may report botulism and toxic shellfish poisoning separately, resulting in differing case numbers for acute gastroenteritis. Please note that other publications or reports may report botulism and toxic shellfish poisoning separately, resulting in differing case numbers for acute gastroenteritis.

[c] Case details for the five perinatal cases are those for the mother, not identified in rates as less than 5 cases in the mothers age group.

Fewer than five cases in a cell or less than a national total of 100 cases for the year, '-' indicates rates were not calculated as there were less than 5 cases.

First band (lower than 25th percentile)

Second (middle) band

Third band (above 75th percentile)

Table 78. Hospitalised cases[a] of selected notifiable diseases by age group, 2024

Disease	Source[a]	Age Group (years)											
		<1	1 to 4	5 to 9	10 to 14	15 to 19	20 to 29	30 to 39	40 to 49	50 to 59	60 to 69	70+	Total
Campylobacteriosis	NMDS	21	50	22	20	43	115	93	88	119	139	328	**1038**
Hepatitis A	NMDS	0	2	6	5	5	14	17	9	5	6	13	**82**
Listeriosis[b]	EpiSurv	0	1	0	1	1	3	2	0	5	5	18	**36**
Salmonellosis	NMDS	9	21	13	5	3	22	19	25	32	28	36	**213**
STEC infection	EpiSurv	10	47	19	7	6	24	16	12	32	35	83	**291**
Yersiniosis	NMDS	8	12	2	1	5	16	20	15	19	18	49	**165**

[a] NMDS data records hospital events when individuals were treated in an emergency department, observation unit, acute assessment unit, short stay unit and/or admitted to a ward for three hours or more. This time includes observation and treatment but excludes time in the waiting room or triage. This table includes counts of individuals who were diagnosed with the disease as the principal or other relevant diagnosis.

A 2024 study [15] has shown the ICD-10 code used in previous years reports, A04.3 (Enterohaemorrhagic *Escherichia coli* infection), does not capture all the cases hospitalised due to STEC infection. This table gives the number of STEC infection cases listed as hospitalised in EpiSurv for age group, rather than reporting the NMDS data.

[b] Case details for the five perinatal cases are those for the mother (one in 15 to 19 age group. two in the 20 to 29 age group, and two in the 30 to 39 age group).

Table 79. NMDS hospitalised cases[a] of selected notifiable diseases by nights admitted and age group, 2024

Nights Admitted	Disease	Age Group (years)											
		<1	1 to 4	5 to 9	10 to 14	15 to 19	20 to 29	30 to 39	40 to 49	50 to 59	60 to 69	70+	Total
0 to 1	Campylobacteriosis	12	26	11	15	24	67	53	39	48	45	57	**397**
	Hepatitis A	0	1	3	2	3	10	8	4	2	1	6	**40**
	Listeriosis	0	0	0	0	0	0	0	0	0	0	0	**0**
	Salmonellosis	5	11	4	3	3	14	6	9	8	4	6	**73**
	STEC infection	1	2	1	0	1	3	1	2	0	2	1	**14**
	Yersiniosis	3	5	1	0	0	5	8	5	2	4	4	**37**
2 to 6	Campylobacteriosis	9	21	9	5	18	46	39	45	62	79	211	**544**
	Hepatitis A	0	1	3	3	2	4	8	5	2	2	3	**33**
	Listeriosis[b]	0	0	0	0	0	4	3	0	1	0	4	**12**
	Salmonellosis	3	9	9	2	0	6	12	12	21	17	22	**113**
	STEC infection	1	3	1	3	1	0	1	3	3	5	10	**31**
	Yersiniosis	4	7	1	1	5	10	9	6	12	3	20	**78**
7+	Campylobacteriosis	0	3	2	0	1	2	1	4	9	15	60	**97**
	Hepatitis A	0	0	0	0	0	0	1	0	1	3	4	**9**
	Listeriosis[b]	0	0	0	0	1	0	1	0	1	5	13	**21**
	Salmonellosis	1	1	0	0	0	2	1	4	3	7	8	**27**
	STEC infection	1	5	1	2	0	0	0	0	1	4	9	**23**
	Yersiniosis	1	0	0	0	0	1	3	4	5	11	25	**50**

[a] NMDS data records hospital events when individuals were treated in an emergency department, observation unit, acute assessment unit, short stay unit and/or admitted to a ward for three hours or more. This time includes observation and treatment but excludes time in the waiting room or triage. This table includes counts of individuals who were diagnosed with the disease as the principal or other relevant diagnosis Nights admitted equates to the total number of midnights spent in hospital by an individual during one or more admissions.

[b] Case details for the five perinatal cases are those for the mother (one in the 15 to 19 age group, two in the 20 to 29 age group, and two in the 30 to 39 age group).

Table 80. NMDS hospitalised cases[a] admitted to an intensive care unit (ICU)[b] of selected notifiable disease by age group, 2024

Disease	Age Group (years)											
	<1	1 to 4	5 to 9	10 to 14	15 to 19	20 to 29	30 to 39	40 to 49	50 to 59	60 to 69	70+	Total
Campylobacteriosis	0	1	0	0	0	1	0	0	3	4	13	**22**
Hepatitis A	0	0	0	0	0	0	0	0	0	0	0	**0**
Listeriosis	0	0	0	0	0	0	0	0	0	3	1	**4**
Salmonellosis	0	0	0	0	0	1	1	0	0	1	1	**4**
STEC infection	1	1	0	2	0	0	0	0	0	3	2	**9**
Yersiniosis	0	0	0	0	0	0	1	0	3	3	1	**8**

[a] NMDS data records hospital events when individuals were treated in an emergency department, observation unit, acute assessment unit, short stay unit and/or admitted to a ward for three hours or more. This time includes observation and treatment but excludes time in the waiting room or triage. This table includes counts of individuals who were diagnosed with the disease as the principal or other relevant diagnosis.

[b] ICU data relates to admissions to an intensive care unit. It does not include time in a high dependency or neonatal intensive care unit.

Table 81. NMDS ICU[a] duration (hours, median [range] or values)[b] of selected notifiable diseases by age group, 2024

Disease	Age group (years)										
	<1	1 to 4	5 to 9	10 to 14	15 to 19	20 to 29	30 to 39	40 to 49	50 to 59	60 to 69	70+
Campylobacteriosis	NA	28	NA	NA	NA	70	NA	NA	48 [25 to 83]	51 [13 to 266]	73 [8 to 230]
Hepatitis A	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Listeriosis	NA	NA	NA	NA	NA	NA	NA	NA	NA	64 [51 to 681]	86
Salmonellosis	NA	NA	NA	NA	NA	168	46	NA	NA	62	37
STEC infection	122	131	NA	11, 41	NA	NA	NA	NA	NA	143 [18 to 150]	3, 112
Yersiniosis	NA	NA	NA	NA	NA	NA	25	NA	65 [29 to 221]	118 [47 to 182]	141

[a] NMDS data records hospital events when individuals were treated in an emergency department, observation unit, acute assessment unit, short stay unit and/or admitted to a ward for three hours or more. This time includes observation and treatment but excludes time in the waiting room or triage. This table includes counts of individuals who were diagnosed with the disease as the principal or other relevant diagnosis.

ICU data relates to admissions to an intensive care unit. It does not include time in a high dependency or neonatal intensive care unit. The hours are the total duration in ICU during the hospital admission event, which may include more than one period in the ICU. Incomplete hours are rounded up to the next hour. '-' no data as no ICU admissions were recorded.

[b] Median and range are given if three cases or more were admitted. For less than three cases the number of hours for the individual cases are listed.

Table 82. Number of EpiSurv cases of selected notifiable diseases by Health District, 2024

Disease	Northern Region				Te Manawa Taki Region					Central Region					Te Waipounamu Region					Total
	Northland	Waitematā	Auckland	Counties Manukau	Waikato	Lakes	Bay of Plenty	Tairāwhiti	Taranaki	Hawke's Bay	Whanganui	MidCentral	Capital, Coast and Hutt Valley	Wairarapa	Nelson Marlborough	West Coast	Canterbury	South Canterbury	Southern	
Acute gastroenteritis[a]	28	9	15	6	104	27	57	0	1	4	6	0	43	1	6	9	94	2	29	**441**
Campylobacteriosis	270	713	523	552	592	126	285	61	228	192	65	200	424	72	177	47	649	117	508	**5801**
Hepatitis A	2	4	6	10	9	0	7	0	0	4	0	3	7	0	1	0	13	0	2	**68**
Listeriosis	1	7	6	5	1	1	4	0	1	0	0	1	0	0	0	0	5	1	3	**36**
Salmonellosis	37	97	93	74	71	15	40	2	23	36	10	18	84	6	19	4	120	18	77	**844**
STEC infection	75	64	36	62	112	22	56	9	56	53	16	31	90	23	38	7	159	49	157	**1115**
Yersiniosis	40	114	112	94	66	17	72	23	42	20	7	18	166	13	60	4	133	19	120	**1140**

[a] Cases with certain conditions (intoxications from the bacteria *Bacillus cereus*, *Clostridium perfringens* and *Staphylococcus aureus*, ciguatera poisoning, histamine (scombroid) fish poisoning, toxic shellfish poisoning and *Vibrio parahaemolyticus,* norovirus and sapovirus infections) are notified under the heading of acute gastroenteritis.

Not all individual cases of acute gastroenteritis are notifiable, only those when: (i) the infected person is in a high-risk category (e.g. food handler, early childhood service worker, or another person with increased risk of spreading the disease), (ii) it is an infectious gastroenteritis of public health importance such as *C. perfringens* and *V. parahaemolyticus* or (iii) there are single cases of chemical or toxic food poisoning such as botulism, histamine (scombroid) poisoning and any type of toxic shellfish poisoning [16]. Please note that other publications or reports may report botulism and toxic shellfish poisoning separately, resulting in differing case numbers for acute gastroenteritis. Please note that other publications or reports may report botulism and toxic shellfish poisoning separately, resulting in differing case numbers for acute gastroenteritis.

Table 83. Rate per 100,000 population of selected notifiable diseases by Health District, 2024

Disease	Northern Region				Te Manawa Taki Region					Central Region					Te Waipounamu Region					Total
	Northland	Waitematā	Auckland	Counties Manukau	Waikato	Lakes	Bay of Plenty	Tairāwhiti	Taranaki	Hawke's Bay	Whanganui	MidCentral	Capital, Coast and Hutt Valley	Wairarapa	Nelson Marlborough	West Coast	Canterbury	South Canterbury	Southern	
Acute gastroenteritis[a]	13.7	1.3	2.9	0.9	22.1	22.4	20.3	-	-	-	8.5	-	8.8	-	3.6	25.9	15.0	-	7.9	8.3
Campylobacteriosis	131.8	105.6	102.3	86.4	125.6	104.7	101.3	114.4	174.0	103.6	92.5	102.8	86.8	138.5	105.6	135.1	103.3	180.6	139.0	108.7
Hepatitis A	-	-	1.2	1.6	1.9	-	2.5	-	-	-	-	-	1.4	-	-	-	2.1	-	-	1.3
Listeriosis	-	1.0	1.2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0.7
Salmonellosis	18.1	14.4	18.2	11.6	15.1	12.5	14.2	-	17.6	19.4	14.2	9.3	17.2	11.5	11.3	-	19.1	27.8	21.1	15.8
STEC infection	36.6	9.5	7.0	9.7	23.8	18.3	19.9	16.9	42.7	28.6	22.8	15.9	18.4	44.2	22.7	20.1	25.3	75.6	43.0	20.9
Yersiniosis	19.5	16.9	21.9	14.7	14.0	14.1	25.6	43.2	32.1	10.8	10.0	9.3	34.0	25.0	35.8	-	21.2	29.3	32.8	21.4

[a] Cases with certain conditions (intoxications from the bacteria *Bacillus cereus*, *Clostridium perfringens* and *Staphylococcus aureus*, ciguatera poisoning, histamine (scombroid) fish poisoning, toxic shellfish poisoning and *Vibrio parahaemolyticus,* norovirus and sapovirus infections) are notified under the heading of acute gastroenteritis.

Not all individual cases of acute gastroenteritis are notifiable, only those when: (i) the infected person is in a high-risk category (e.g. food handler, early childhood service worker, or another person with increased risk of spreading the disease), (ii) it is an infectious gastroenteritis of public health importance such as *C. perfringens* and *V. parahaemolyticus* or (iii) there are single cases of chemical or toxic food poisoning such as botulism, histamine (scombroid) poisoning and any type of toxic shellfish poisoning [16]. Please note that other publications or reports may report botulism and toxic shellfish poisoning separately, resulting in differing case numbers for acute gastroenteritis. Please note that other publications or reports may report botulism and toxic shellfish poisoning separately, resulting in differing case numbers for acute gastroenteritis.

Fewer than five cases in a cell or less than a national total of 100 cases for the year, '-' indicates rates were not calculated as there were less than 5 cases.

First band (lower than 25th percentile)

Second (middle) band

Third band (above 75th percentile)

Table 84. Number of EpiSurv cases and rate per 100,000 population of selected notifiable diseases by urban rural residence group[a] (excluding notifications with overseas travel as a risk factor), 2024

Disease	Cases								Rate per 100,000 population[b]						
	Major urban area	Large urban area	Medium urban area	Small urban area	Rural settlement	Rural other	Overseas Tourist/ Unknown address[a]	Total[c]	Major urban area	Large urban area	Medium urban area	Small urban area	Rural settlement	Rural other	Total[c]
Acute gastroenteritis[d]	129	35	23	30	9	41	25	**292**	4.7	4.8	4.8	5.4	5.6	6.1	**5.5**
Campylobacteriosis	2193	635	414	620	170	1302	161	**5495**	80.5	86.3	86.2	110.6	106.4	192.3	**102.9**
Hepatitis A	12	2	3	6	0	3	1	**27**	0.4	-	-	1.1	-	-	**0.5**
Listeriosis	15	3	3	3	2	4	1	**31**	0.6	-	-	-	-	-	**0.6**
Salmonellosis	221	52	53	49	19	105	17	**516**	8.1	7.1	11	8.7	11.9	15.5	**9.7**
STEC infection	267	117	104	139	31	332	39	**1029**	9.8	15.9	21.7	24.8	19.4	49	**19.3**
Yersiniosis	569	139	96	105	23	147	23	**1102**	20.9	18.9	20	18.7	14.4	21.7	**20.6**

[a] Cases usual residential address mapped to 2025 mesh blocks, for addresses classified as “exact” to “street” level of accuracy. Addresses accurate to the territorial authority or PH office accuracy are classed as “Unknown address”. 2023 Urban Rural Classification is classified by 2025 mesh block.

[b] Where fewer than five cases have been notified, a rate has not been calculated, indicated by ‘-‘.

[c] Total cases notified in EpiSurv which did not record the person being overseas during the incubation period for the disease, i.e. all notifications with overseas travel recorded as a risk factor have been excluded.

[d] Cases with certain conditions (intoxications from the bacteria *Bacillus cereus*, *Clostridium perfringens* and *Staphylococcus aureus*, ciguatera poisoning, histamine (scombroid) fish poisoning, toxic shellfish poisoning and *Vibrio parahaemolyticus*, norovirus and sapovirus infections) are notified under the heading of acute gastroenteritis.

Not all individual cases of acute gastroenteritis are notifiable, only those when: (i) the infected person is in a high-risk category (e.g. food handler, early childhood service worker, or another person with increased risk of spreading the disease), (ii) it is an infectious gastroenteritis of public health importance such as *C. perfringens* and *V. parahaemolyticus* or (iii) there are single cases of chemical or toxic food poisoning such as botulism, histamine (scombroid) poisoning and any type of toxic shellfish poisoning[16]. Please note that other publications or reports may report botulism and toxic shellfish poisoning separately, resulting in differing case numbers for acute gastroenteritis.

Table 85. Hospitalised cases[a] and rate per 100,000 population of selected notifiable diseases by urban rural residence group[b], 2024

Disease	Source[a]	Hospitalised cases							Hospitalised cases per 100,000 population[c]						
		Major urban area	Large urban area	Medium urban area	Small urban area	Rural settlement	Rural other	Overseas Tourist / unknown address	Major urban area	Large urban area	Medium urban area	Small urban area	Rural settlement	Rural other	Total
Campylobacteriosis	NMDS	473	153	90	185	77	49	11	17.4	20.8	18.7	33.0	48.2	7.2	**19.4**
Hepatitis A	NMDS	52	11	7	6	5	1	0	1.9	1.5	1.5	1.1	3.1	-	**1.5**
Listeriosis	EpiSurv	16	3	3	4	2	6	2	0.6	-	-	-	-	0.9	**0.7**
Salmonellosis	NMDS	111	20	30	24	14	12	2	4.1	2.7	6.2	4.3	8.8	1.8	**4.0**
STEC infection	EpiSurv	80	31	25	43	10	83	19	2.9	2.9	5.2	7.7	6.3	12.3	**5.5**
Yersiniosis	NMDS	103	19	14	13	9	6	1	3.8	2.6	2.9	2.3	5.6	0.9	**3.1**

[a] NMDS data records hospital events when individuals were treated in an emergency department, observation unit, acute assessment unit, short stay unit and/or admitted to a ward for three hours or more. This time includes observation and treatment but excludes time in the waiting room or triage. This table includes counts of individuals in the NMDS who were diagnosed with the disease as the principal or other relevant diagnosis.

A 2024 study [15] has shown the ICD-10 code used in previous years reports, A04.3 (Enterohaemorrhagic *Escherichia coli* infection), does not capture all the cases hospitalised due to STEC infection. This table gives the number of STEC infection cases listed as hospitalised in EpiSurv for urban rural residence group, rather than reporting the NMDS data.

[b] Mapping to 2023 Urban Rural Classification is via Domicile 2013 areas. Some of the areas are assigned to more than one urban rural classification. In the data analyses urban rural classification is prioritised in the following order; major urban area, large urban area, medium urban area, small urban area, rural settlement and rural other.

[c] Where fewer than five cases have been notified, a rate has not been calculated, indicated by '-'.

Table 86. Number of EpiSurv cases of selected notifiable diseases by the 2023 Deprivation Index of area of residence[a] (excluding notifications with overseas travel as a risk factor), 2024

Disease	2023 Deprivation Index of area of residence of case[a] (1 represents areas with least deprived scores and 10 areas with most deprived scores)						
	Unknown	1 & 2	3 & 4	5 & 6	7 & 8	9 & 10	Total[b]
Acute gastroenteritis[c]	27	63	47	48	60	47	**292**
Campylobacteriosis	181	1151	1091	1161	1088	823	**5495**
Hepatitis A	1	7	1	4	3	11	**27**
Listeriosis	1	3	6	5	6	10	**31**
Salmonellosis	18	112	90	104	95	97	**516**
STEC infection	42	186	195	237	205	164	**1029**
Yersiniosis	28	244	223	249	186	172	**1102**

[a] The Deprivation Index scale divides New Zealand into tenths of a distribution generated from first principle component analysis of census variables including; access to internet in the home, income levels, employment status, qualification status, home ownership, living space and conditions [54].

[b] Total cases notified in EpiSurv which did not record the person being overseas during the incubation period for the disease, i.e. all notifications with overseas travel recorded as a risk factor have been excluded.

[c] Cases with certain conditions (intoxications from the bacteria *Bacillus cereus*, *Clostridium perfringens* and *Staphylococcus aureus*, ciguatera poisoning, histamine (scombroid) fish poisoning, toxic shellfish poisoning and *Vibrio parahaemolyticus,* norovirus and sapovirus infections) are notified under the heading of acute gastroenteritis.

Not all individual cases of acute gastroenteritis are notifiable, only those when: (i) the infected person is in a high-risk category (e.g. food handler, early childhood service worker, or another person with increased risk of spreading the disease), (ii) it is an infectious gastroenteritis of public health importance such as *C. perfringens* and *V. parahaemolyticus* or (iii) there are single cases of chemical or toxic food poisoning such as botulism, histamine (scombroid) poisoning and any type of toxic shellfish poisoning [16]. Please note that other publications or reports may report botulism and toxic shellfish poisoning separately, resulting in differing case numbers for acute gastroenteritis.

Table 87. Percentage of total EpiSurv cases of selected notifiable diseases by 2023 Deprivation Index of area of residence[a] (excluding notifications with overseas travel as a risk factor), 2024

Disease	2023 Deprivation Index of area of residence of case[a] (1 represents areas with least deprived scores and 10 areas with most deprived scores)					
	Unknown	1 & 2	3 & 4	5 & 6	7 & 8	9 & 10
Acute gastroenteritis[b]	9.2	21.6	16.1	16.4	20.5	16.1
Campylobacteriosis	3.3	20.9	19.9	21.1	19.8	15.0
Salmonellosis	3.5	21.7	17.4	20.2	18.4	18.8
STEC infection	4.1	18.1	19.0	23.0	19.9	15.9
Yersiniosis	2.5	22.1	20.2	22.6	16.9	15.6

Hepatitis A and listeriosis cases are not included in the table due to the low number of cases associated with each index level.

Total cases notified in EpiSurv which did not record the person being overseas during the incubation period for the disease, i.e. all notifications with overseas travel recorded as a risk factor have been excluded.

While the Deprivation Index is based on area units instead of population size, at a national level there should be approximately equal proportions of the New Zealand population in each of the 10 index levels. If there were no unassigned cases and there was no relationship between Deprivation Index of area of residence and likelihood of becoming a notified case, a case would be equally likely to reside in an area assigned to each of the 10 levels. In this scenario, each of the cells (excluding the 'Unknown' column) in the above table would have an expected value of 20%.

[a] The Deprivation Index scale divides New Zealand into tenths of a distribution generated from first principle component analysis of census variables including; access to internet in the home, income levels, employment status, qualification status, home ownership, living space and conditions [54].

[b] Cases with certain conditions (intoxications from the bacteria *Bacillus cereus*, *Clostridium perfringens* and *Staphylococcus aureus*, ciguatera poisoning, histamine (scombroid) fish poisoning, toxic shellfish poisoning and *Vibrio parahaemolyticus,* norovirus and sapovirus infections) are notified under the heading of acute gastroenteritis.

Not all individual cases of acute gastroenteritis are notifiable, only those when: (i) the infected person is in a high-risk category (e.g. food handler, early childhood service worker, or another person with increased risk of spreading the disease), (ii) it is an infectious gastroenteritis of public health importance such as *C. perfringens* and *V. parahaemolyticus* or (iii) there are single cases of chemical or toxic food poisoning such as botulism, histamine (scombroid) poisoning and any type of toxic shellfish poisoning [16]. Please note that other publications or reports may report botulism and toxic shellfish poisoning separately, resulting in differing case numbers for acute gastroenteritis.

Table 88. Hospitalised cases[a] of selected notifiable diseases by the 2023 Deprivation Index of area of residence[b], 2024

Disease	Source[a]	2023 Deprivation Index of area of residence of case[b] (1 represents areas with least deprived scores and 10 areas with most deprived scores)						
		Unknown	1 & 2	3 & 4	5 & 6	7 & 8	9 & 10	Total
Campylobacteriosis	NMDS	13	187	212	219	213	194	**1038**
Hepatitis A	NMDS	0	9	9	22	13	29	**82**
Listeriosis	EpiSurv	2	4	6	6	7	11	**36**
Salmonellosis	NMDS	3	48	41	35	39	47	**213**
STEC infection	EpiSurv	20	53	54	56	62	46	**291**
Yersiniosis	NMDS	2	24	36	33	35	35	**165**

[a] NMDS data records hospital events when individuals were treated in an emergency department, observation unit, acute assessment unit, short stay unit and/or admitted to a ward for three hours or more. This time includes observation and treatment but excludes time in the waiting room or triage. This table includes counts of individuals in the NMDS who were diagnosed with the disease as the principal or other relevant diagnosis.

A 2024 study [15] has shown the ICD-10 code used in previous years' reports, A04.3 (Enterohaemorrhagic *Escherichia coli* infection), does not capture all the cases hospitalised due to STEC infection. Table 88 gives the number of STEC infection cases listed as hospitalised in EpiSurv for Deprivation Index of area of residence group, rather than reporting the NMDS data.

[b] The Deprivation Index scale divides New Zealand into tenths of a distribution generated from first principle component analysis of census variables including; access to internet in the home, income levels, employment status, qualification status, home ownership, living space and conditions [54].

Table 89. Percentage of hospitalised cases of selected notifiable diseases by the 2023 Deprivation Index of area of residence, 2024

Disease	2023 Deprivation Index of area of residence of case [a] (1 represents areas with least deprived scores and 10 areas with most deprived scores)					
	Unknown	1 & 2	3 & 4	5 & 6	7 & 8	9 & 10
Campylobacteriosis	1.3	18.0	20.4	21.1	20.5	18.7
Salmonellosis	1.4	22.5	19.2	16.4	18.3	22.1
STEC infection[b]	0.7	18.2	18.6	19.2	21.3	15.8
Yersiniosis	1.2	14.5	21.8	20.0	21.2	21.2

Hepatitis A and listeriosis cases are not included in the table due to the low number of cases associated with each index level.

While the Deprivation Index is based on area units instead of population size, at a national level there should be approximately equal proportions of the New Zealand population in each of the 10 index levels. If there were no unassigned cases and there was no relationship between Deprivation Index of area of residence and likelihood of becoming a notified case, a case would be equally likely to reside in an area assigned to each of the 10 levels. In this scenario, each of the cells (excluding the 'Unknown' column) in the above table would have an expected value of 20%.

[a] The Deprivation Index scale divides New Zealand into tenths of a distribution generated from first principle component analysis of census variables including; access to internet in the home, income levels, employment status, qualification status, home ownership, living space and conditions [54].

[b] A 2024 study [15] has shown the ICD-10 code used in previous years reports, A04.3 (Enterohaemorrhagic *Escherichia coli* infection), does not capture all the cases hospitalised due to STEC infection. This table gives the number of STEC infection cases listed as hospitalised in EpiSurv, rather than reporting the NMDS data.

Table 90. Potential foodborne outbreaks with a common source and associated cases by pathogen/condition as reported in EpiSurv, 2024

Pathogen/Condition	Outbreaks (n = 39)		Cases (n = 920)	
	No.	%[a]	No.	%[b]
Norovirus infection	10	25.6	563	61.2
Campylobacteriosis	4	10.3	25	2.7
Clostridium perfringens intoxication	3	7.7	180	19.6
Histamine (scombroid) fish poisoning	3	7.7	10	1.1
Salmonellosis	2	5.1	36	3.9
ETEC infection	2	5.1	26	2.8
STEC infection	1	2.6	5	0.5
Bacillus cereus	1	2.6	2	0.2
Pathogen not identified [c]	13	33.3	73	7.9

An outbreak is classed as foodborne in this report if food was recorded as one of the likely modes of transmission. It is important to note that a single outbreak may have multiple pathogens, modes of transmission, settings where exposure occurred, or settings where preparation of food was conducted.

[a] Percentage of outbreaks for each pathogen/condition, calculated using the total number of foodborne outbreaks (39).

[b] Percentage of cases for each pathogen/condition, calculated using the total number of associated cases (920).

[c] All enteric outbreaks with no pathogen identified in 2024 were recorded as gastroenteritis.

Table 91. Potential foodborne outbreaks with a common source and associated cases by exposure setting as reported in EpiSurv, 2024

Exposure setting	Outbreaks (n = 39)		Cases (n = 920)	
	No.	%[a]	No.	%[b]
Commercial food operators	**25**	**64.1**	**169**	**18.4**
Restaurant/cafe/bakery	21	53.8	145	15.8
Caterers	2	5.1	17	1.8
Supermarket	2	5.1	7	0.8
Institutions	**8**	**20.5**	**685**	**74.5**
School	2	5.1	357	38.8
Hostel/boarding house	1	2.6	171	18.6
Workplace	2	5.1	77	8.4
Marae	1	2.6	59	6.4
Prison	1	2.6	17	1.8
Long term care facility	1	2.6	4	0.4
Other	**6**	**15.4**	**66**	**7.2**
Community event	2	5.1	24	2.6
Camp/home	1	2.6	21	2.3
Farm	1	2.6	12	1.3
Home	2	5.1	9	1.0

An outbreak has been classed as foodborne in this report if food was recorded as one of the likely modes of transmission and is not associated with overseas travel. It is important to note that a single outbreak may have multiple pathogens, modes of transmission, settings where exposure occurred, or settings where preparation of food was conducted.

[a] Percentage of outbreaks for each exposure setting, calculated using the total number of foodborne outbreaks (39).

[b] Percentage of cases for each exposure setting, calculated using the total number of associated cases (920).

Table 92. Potential foodborne outbreaks with a common source and associated cases by preparation setting as reported in EpiSurv, 2024

Preparation setting	Outbreaks (n = 39)		Cases (n = 920)	
	No.	%[a]	No.	%[b]
Commercial food operators	**28**	**71.8**	**596**	**64.8**
Restaurant/cafe/bakery	21	53.8	145	15.8
Caterers	5	12.8	444	48.3
Food processor	1	2.6	5	0.5
Supermarket	1	2.6	2	0.2
Institutions	**5**	**12.8**	**258**	**28.0**
Hostel/boarding house	1	2.6	171	18.6
Marae	1	2.6	59	6.4
Prison	1	2.6	17	1.8
Workplace	1	2.6	7	0.8
Long term care facility	1	2.6	4	0.4
Other	**6**	**15.4**	**66**	**7.2**
Camp/home	1	2.6	21	2.3
Home	3	7.7	18	2.0
Community event	1	2.6	15	1.6
Farm	1	2.6	12	1.3

Note: Percentages may not add up to 100% due to rounding.

An outbreak has been classed as foodborne in this report if food was recorded as one of the likely modes of transmission. It is important to note that a single outbreak may have multiple pathogens, modes of transmission, settings where exposure occurred, or settings where preparation of food was conducted.

[a] Percentage of outbreaks for each preparation setting, calculated using the total number of foodborne outbreaks (39).

[b] Percentage of cases for each preparation setting, calculated using the total number of associated cases (920).

Table 93. All non-O157 STEC serotypes identified from human isolates by the Enteric Reference Laboratory, 2020–2024

Note: This table gives the frequency of types from all human isolates typed by the Enteric Reference Laboratory (PHF Science) in a calendar year. These frequencies may be different to the frequency of types only associated with notified cases (Table 54), which are reported in the calendar year of their report date. This table also includes data relating to human isolates where the person's symptoms did not meet the case definition and the person would not become a notified case.

Serotype	2020	2021	2022	2023	2024
O1:H7	0	2	0	0	1
O2:H6	1	0	3	1	1
O2:H29	0	1	0	0	1
O3:H12	0	0	1	0	0
O5:H19	3	1	2	4	4
O5:HNT	13	12	9	6	4
O6:H10	1	0	0	1	0
O7:H14	0	1	1	3	0
O8:H4	0	0	0	0	1
O8:H8	0	0	1	4	0
O8:H9	1	1	1	1	1
O8:H16	2	1	3	1	4
O8/O30:H25	0	3	2	0	2
O8:H19	0	0	0	1	0
O8:H21	0	0	0	1	0
O9:H30	0	1	1	0	2
O11:H25	1	0	0	0	0
O15:H2	3	2	1	0	2
O15:H4	0	0	2	0	0
O15:H16	0	0	0	1	0
O15:H18	0	0	0	1	0
O15:H27	1	0	2	0	0
O16:H5	0	0	0	0	1
O17:H18	1	1	1	0	0
O17/O106:H45	1	0	0	0	0
O18:H5	0	1	0	0	0
O18:H7	0	1	0	0	0
O21:H2	0	1	0	0	0
O21:H21	0	0	1	0	1
O22:H16	0	1	0	0	0
O26:H11	121	131	109	120	140
O38:H26	33	27	38	35	33
O42/O28ac:H20	0	0	0	1	0
O43:H2	0	1	1	0	0
O45:H2	1	0	0	0	0
O45:H19	0	1	0	0	0
O51:H24	2	0	0	0	0
O53:H45	1	0	0	0	0
O54:H4	0	0	0	1	0
O54:H45	0	0	0	1	0
O55:H12	2	4	3	2	2
O64:H20	5	5	5	8	5
O65:H2	0	0	0	1	0
O66:H25	0	1	1	1	1
O74:H20	1	0	0	0	0
O75:H5	1	0	0	0	0
O75:H7	2	0	0	0	1
O75:H8	0	3	1	3	1
O76:H19	0	2	0	0	3
O78:H4	1	1	0	0	0
O80:H2	0	0	1	0	0
O81:H21	0	0	0	0	1
O83:H27	1	0	0	0	0
O84:H2	10	10	10	13	11
O85:H49	1	1	3	1	0
O87:H16	0	1	1	2	1
O88:H8	7	11	8	10	4
O91:H7	0	0	0	0	1
O91:H14	12	28	19	30	49
O91:H21	1	0	2	2	2
O91:HNT	0	0	1	0	0
O93:H28	0	1	1	0	3

Serotype	2020	2021	2022	2023	2024
O93:H46	1	0	0	0	0
O98:H21	0	0	0	1	0
O100:H20	0	0	1	0	1
O103:H2	0	20	11	15	22
O103:H8	0	0	1	1	0
O103:H25	1	5	10	3	8
O104:H7	1	5	2	7	1
O107/O117:H7	0	1	0	0	0
O108:H21	0	0	1	0	0
O108:H25	0	0	0	2	0
O100/O154:H25	0	0	3	1	1
O111:H2	1	0	1	1	0
O111:H8	0	0	2	5	2
O111:H11	0	0	0	1	0
O112:H2	0	0	0	1	0
O112:H9	5	7	7	8	6
O112:H19	0	0	1	1	0
O113:H4	1	0	0	0	0
O113:H21	1	0	4	4	3
O117:H4	1	1	0	1	0
O117:H7	4	1	0	10	13
O117:H21	0	0	1	0	1
O120:H56	0	0	0	1	0
O121:H19	0	1	0	0	0
O123:H2	1	1	2	2	1
O123:H10	11	4	9	16	14
O123:H11	0	0	1	0	0
O124,O8:H19	0	1	0	0	0
O127:H40	0	0	0	1	0
O128:H2	79	82	82	91	85
O128:H15	0	0	0	0	1
O129:H4	0	0	0	0	1
O129:H21	0	1	0	1	0
O130:H11	11	8	6	6	4
O134:H31	0	0	0	1	0
O136:H20	1	0	0	1	0
O145:H2	0	3	1	0	1

Serotype	2020	2021	2022	2023	2024
O145:HNT	0	1	3	1	1
O146:H8	0	0	0	0	1
O146:H21	28	27	44	27	35
O146:H28	4	3	2	9	5
O150:H8	0	0	1	0	0
O151/O118:H2	0	0	0	1	0
O152:H7	0	0	1	0	0
O153:H2	8	8	6	10	6
O153:H7	1	0	0	0	0
O153:H21	1	1	0	0	0
O153:H25	0	0	0	1	0
O153/O178:H7	0	1	2	1	3
O153/O178:H23	1	0	0	0	0
O156:H25	0	1	0	1	1
O159:H4	0	2	0	1	0
O162/O101:H33	0	0	0	1	0
O163:H19	1	11	2	3	2
O165:H7	2	2	0	0	0
O165:H25	1	2	3	1	3
O166:H15	0	0	1	0	1
O171:H2	1	0	0	0	2
O174:H2	0	0	0	0	1
O174:H8	10	14	16	9	13
O174:H21	7	1	3	2	2
O176:H4	16	14	24	19	16
O177:H2	1	0	0	0	0
O177:H25	3	4	4	4	6
O179:H8	0	2	0	0	0
O182:H25	7	5	5	5	4
O183:H18	1	1	6	5	4
O185:H7	0	0	0	0	1
O187:H52	0	2	0	1	1
ONT:H7	0	0	0	0	1
ONT:H8	0	0	0	0	1
ONT:H19	0	0	0	1	0
ONT:H20	0	0	0	1	0
ONT:H25	1	0	0	0	0

Serotype	2020	2021	2022	2023	2024
ONT:H45	0	1	0	0	0
ONT:H49	0	1	1	1	1
Onovel1:H16	1	0	0	0	0
Onovel1:H27	0	0	0	1	0
Onovel2:H49	0	1	2	0	0
Onovel5:H21	1	1	0	0	0
Onovel8:H21	0	0	0	1	0
Onovel12:H32	0	0	0	0	2
Onovel14,O9:H7	0	0	0	0	1
Onovel14:H18	0	0	0	0	1
Onovel21:H14	0	4	4	3	4
Onovel27:H16	1	0	0	0	0
Onovel32:H10	0	0	0	1	0

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