New Zealand Food Safety
Haumaru Kai Aotearoa

Annual report concerning Foodborne Diseases in New Zealand 2023

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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 2023

ESR Report FW24004

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 ESR foodborne disease reports are critical, allowing NZFS to monitor trends in foodborne illness in New Zealand by describing in a 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.

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 to 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. The intention of this report is to provide data that helps our understanding of how many notified cases of a disease are associated with food. Among the reported diseases, only listeriosis is fully attributable to consumption of contaminated food.

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 molecular-based culture independent diagnostic testing (CIDT) methods. As of October 2023, community faecal specimens in all health districts are screened by CIDT for *Campylobacter spp.*, *Salmonella spp.*, *Shigella spp.*, shiga toxin-producing *E. coli* (STEC), and *Yersinia enterocolitica*. In some of the health districts all faecal specimens are also routinely screened for *Giardia spp.*, *Cryptosporidium spp.*, *Yersinia pseudotuberculosis,* and *Vibrio parahaemolyticus.*

Similarly to previous years, most of cases of foodborne disease in New Zealand are sporadic, with limited data available on where (home, premises, or event) food was prepared or consumed. There were 35 notified outbreaks of potential foodborne disease reported in EpiSurv (New Zealand's national public health surveillance database) in 2023, represented by 386 cases. The outbreaks were predominantly associated with commercial food operators: 20 outbreaks (71.4%) were associated with a common source

restaurant/cafe/bakery; 5 (14%) with food prepared at consumer's homes. Those outbreaks reported as foodborne, but for which a food source could not be identified, may be attributable to other routes of transmission, such as water or person-to-person contact.

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).

Campylobacteriosis

The reduction of human cases of foodborne campylobacteriosis by 20% from 88 to 70 per 100,000 population by the end of 2024 is 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 decreasing, albeit slowly. Importantly, the notified case rates for domestically acquired foodborne campylobacteriosis from 2020 to 2023 follow a trajectory towards the 2024 target. Progress toward this target is reported in the section entitled "Reporting against targets".

Specifically for 2023, while the total number of campylobacteriosis notifications was slightly higher than in 2022, the number of cases associated with overseas travel was twice as high resulting in a net decrease in the rate of domestically acquired foodborne campylobacteriosis from 81 cases in 2022 to 77 in 2023. This provides confidence that the 20% reduction of human cases of foodborne campylobacteriosis by the end of 2024 will be achieved.

The higher rate of campylobacteriosis in rural compared with urban areas in both 2022 and 2023 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 chicken meat, is lowered.

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. The listeriosis notification numbers and rate have been relatively stable for the past 20 years, although the number of deaths directly attributed to listeriosis, or with listeriosis as a contributing factor was the highest in 2023. NZFS continues to work with producers of ready-to-eat foods to improve *Listeria* management during food processing, as well as carrying out a targeted consumer education campaign to enable vulnerable consumers to protect themselves from listeriosis.

Vibriosis

In the previous two years there were relatively high numbers of *Vibrio parahaemolyticus* infections, which disproportionally affected Māori people, possibly due to their traditional consumption of raw seafood. In response, NZFS successfully carried out consumer education programmes and other risk-management activities to reduce the risks of *Vibrio* infection from seafood. The result in 2023 was a decrease in notified cases to the lowest levels recorded, despite an increase in the number of samples screened for *Vibrio parahaemolyticus*. This result highlights the effectiveness of regulatory activities informed by the annual foodborne illness reports.

Demographics

The many demographic groups that make up the contemporary New Zealand population are represented differently in the rates of notification for foodborne illnesses.

For campylobacteriosis and STEC infection, those identifying as of European descent have the highest notification and hospitalisation rates among demographic groups. Those

identifying as Asian and Middle Eastern are more reflected in yersiniosis notifications and hospitalisations. While those identifying as having Pacific Island ethnicity have an average rate of notification for salmonellosis, the hospitalisation rate per 100,000 people is the highest for this demographic group. This may reflect a high level of underreporting of mild cases of salmonellosis.

New Zealand Food Safety, ESR, and the National Public Health Service (Health NZ / 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.

Science for Communities
He Pūtaiao, He Tāngata

ANNUAL REPORT CONCERNING FOODBORNE DISEASE IN NEW ZEALAND 2023

Prepared for New Zealand Food Safety under
Project 406850 – Systematic reporting of epidemiology of potentially foodborne disease in New Zealand for year 2023

by

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August 2024

This report is available at www.mpi.govt.nz

Client Report FW24004

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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 2023 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 the EpiSurv database (for a description of EpiSurv, see the Methods section of this report, page 118). 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 estimates for 14 international regions [11, 12].

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

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[c]	62	77[d]	80	42
Clostridium perfringens	NE	100	100	93	98[d]	94	91
Shiga toxin-producing *Escherichia coli* (STEC) O157:H7	20	40–60[b]	60[c]	61	56[d,b]	63	40
STEC non-O157	40	40–60[b]	50[c]	60	56[d,b]	63	42
Listeria monocytogenes	88[f]	100	99	77	98[d]	99	69
Salmonella non-typhoidal	62	46–76	66[c]	63	72[d]	92	55
Shigella spp.	NE	7–36	8[c]	26	12[d]	8	NE
Staphylococcus aureus	NE	100	100	78	100	96	87
Vibrio parahaemolyticus	91	NE	74[c]	83	71[d]	NE	NE
Yersinia enterocolitica[g]	75	NE	77[c]	83	84	90	NE
Parasites							
Cryptosporidium parvum	NE	8–16	7[c]	11	10	6	12
Giardia lamblia	NE	11–14	10[c]	7	5	10	13
Viruses							
Hepatitis A virus	NE	29–42	42[c]	30	12[d]	11	11
Norovirus	33	12–26	19[c]	18	18[d]	NE	17
Sapovirus	NE	NE	13[c]	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] Estimate was derived for total STEC.

[c] 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.

[d] 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.

[f] 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.

[g] 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.

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

This report considers information for the 2023 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 it may be that additional information relevant to foodborne illness and foodborne transmission in 2023 becomes 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 disease notification, hospitalisation records, outbreak reports and 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, H, L	A04.3 Enterohaemorrhagic *Escherichia coli* infection
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), ESR laboratory data (L).

[b] International statistical classification of diseases and related health problems, 10th revision [15].

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 [13] or the EpiSurv Case Report Form (CRF) Instructions website [14].

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 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 [13]. 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.

For salmonellosis, the attribution of disease incidence to foodborne transmission is based on an expert consultation held on 5 June 2013 [2]. For campylobacteriosis, Shiga toxin-producing *Escherichia coli* (STEC) infection, and yersiniosis the attribution of disease incidence to foodborne transmission was estimated by a NZFS expert colloquium in November 2020 [2, 3]. In the current report these food attributable proportions (Table 1) have been used to estimate the number of food-associated cases of relevant diseases. The estimated proportion of travel-associated cases from reported risk factors was subtracted from the total cases before application of the food-associated proportion. A travel-associated case is a reported case who was outside New Zealand during the incubation period for the disease.

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

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

[b] International statistical classification of diseases and related health problems, 10th revision [15].

[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.

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 in affected Health Districts are screened by CIDT for *Campylobacter spp.*, *Salmonella spp.*, *Shigella spp.*, STEC, and *Yersinia enterocolitica*. In some of the affected Health Districts all faecal specimens are

also routinely screened for *Giardia* spp., *Cryptosporidium spp.*, *Yersinia pseudotuberculosis* and *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 60 in Appendix B.

For the 2023 reporting year, nationally reported notification rates are still a mixture of notifications based on CIDT and non-CIDT approaches. In June 2023, West Coast community and hospital, as well as Canterbury hospital, faecal specimen testing moved to CIDT-based methods. In October 2023 Canterbury community and South Canterbury community and hospital samples were tested using CIDT methods.

Multiple different testing related factors (e.g., change in sensitivity of methods, proportion of faecal specimens being tested) may affect the notification rates on top of any underlying changes to the incidence of diseases in New Zealand. The impact of the move to using CIDT methods on notification rates of individual diseases is disease specific and is therefore discussed in more detail in the respective sections of this report.

Initial analyses comparing notification trends for bacterial infections in areas where community laboratories changed to nucleic acid amplification-based CIDT and areas yet to change to CIDT (see Appendix B) suggest the change in methodology is having a significant impact on reporting rates for STEC infections, but not for campylobacteriosis, salmonellosis, shigellosis and yersiniosis [16]. Any observed trends in changes in STEC notification rates between 2015 and 2023 must be considered in the context of changes to testing approaches.

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 2023, the number of New Zealand residents returning from absences of less than 12 months were 88% of the numbers observed during the pre-COVID-19 years of 2018 and 2019 (Table 4). Total passenger arrivals in 2023 were 83% of the numbers observed in 2018 and 2019. The effect of reduced overseas travel on New Zealand notification rates is disease specific and is therefore discussed in the respective sections of the report.

Table 4. International travel and migration passenger arrivals in New Zealand, 2018-2023

	2018	2019	2020	2021	2022	2023
NZ resident travellers	3,020,007	3,101,427	681,893	142,879	1,327,126	2,683,654
Total passenger arrivals[a]	7,005,234	7,100,373	1,733,521	398,556	2,856,072	5,825,798

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 18 March 2024.

[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 analysis, e.g. by demographics, is based on all notified cases and not limited to those attributable to foodborne transmission.

SUMMARY OF MAIN FOODBORNE DISEASES

The incidence of the main foodborne diseases in 2023 is summarised in Table 5 below.

Table 5. Estimated proportion and incidence of the main foodborne diseases for 2023

	Total notified[a]		Estimated domestically acquired foodborne transmission[b]		
	Cases	Rate[d]	Cases	Proportion (%)[c]	Rate[d]
Campylobacteriosis	6089	116.6	4010	75	76.8
Hepatitis A	34	0.7	NE	-	-
Listeriosis	37	0.7	NE	-	-
Salmonellosis	827	15.8	325	62	6.2
STEC infection	1006	19.3	366	40[e]	7.0
Yersiniosis	1408	27.0	976	75	18.7

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

[a] The main diseases included in this table are individually specified in the New Zealand schedule of notifiable diseases [13]. 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] Estimated foodborne transmission proportions were derived from two expert consultations in 2013 and 2020, respectively [2, 3].

[d] Rate per 100,000, 2023 mid-year estimated population.

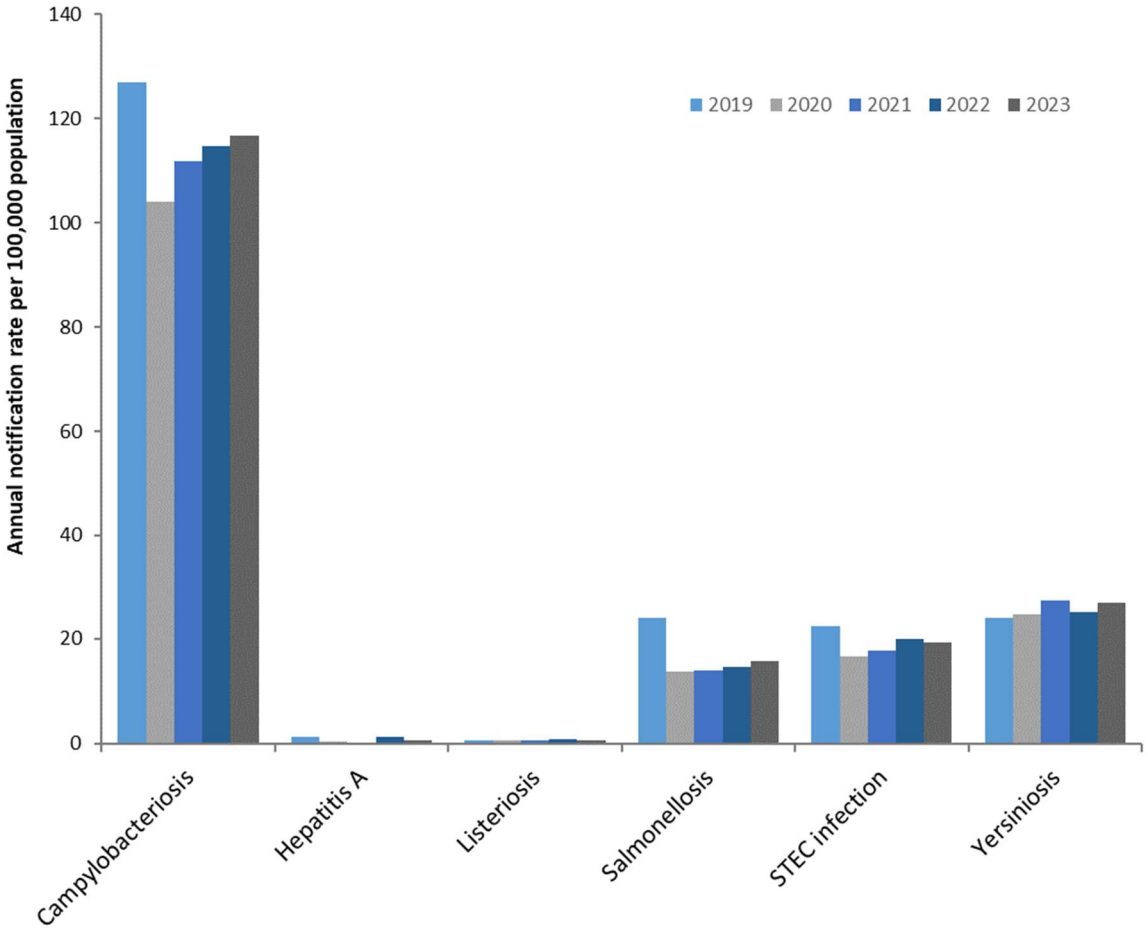
[e] The expert elicitation [3] derived separate estimates of the foodborne proportion for O157 STEC (20%) and non-O157 STEC (40%). The estimate for non-O157 STEC, the dominant set of serotypes, has been used to estimate the number of food-related cases.

In 2023, notification rates for the main foodborne diseases showed distinct disease specific temporal patterns compared to preceding years (Figure 1, Appendix Table 61). The campylobacteriosis notification rate increased from 114.9 cases per 100,000 population in 2022 to 116.6 in 2023 but remained below the 2019 rate which was pre-COVID 19. The salmonellosis notification rate also increased from 2022 to 2023 but was still lower than 2019. STEC infection notification rates decreased slightly from 2022 to 2023 (20.0 and 19.3 cases per 100,000 population, respectively). Rates of campylobacteriosis, salmonellosis and STEC infection cases listing overseas travel as a risk factor while increasing from 2022, were still lower in 2023, compared to 2019, which corresponds to the overseas travel by New Zealand residents (Table 4). Notification rates for hepatitis A decreased from 2022 to 2023 from 1.1 to 0.7 cases per 100,000 population, while yersiniosis notification rates increased from 25.3 to 27.0 per 100,000 population.

Listeriosis notification rates have been relatively stable over the last four years with between 0.6 and 0.8 listeriosis cases per 100,000 population.

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* [16].

Figure 1. Notification rates of the main foodborne diseases, 2019–2023



Reporting against targets

Performance targets for potentially foodborne diseases are reviewed by NZFS on an annual basis. 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].

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

Rationale

Campylobacteriosis is the most commonly notified potentially foodborne disease in New Zealand. A study commissioned by NZFS and conducted in 2018–2019 [17], provided updated information on 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 includes 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 ESR for the Ministry of Health [18].

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,* ESR) [18]. 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 ESR 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 [16].

The estimated incidence of domestically acquired foodborne campylobacteriosis in 2023 is given in Table 6.

Table 6. Estimated proportion and incidence of foodborne campylobacteriosis for 2023

	Cases	Proportion of total notified cases (%)	Rate (per 100,000, mid-year estimated population)
Total notified	6089	-	116.6
Total estimated as not related to overseas travel[a]	5346	87.8	102.4
Estimated domestically acquired foodborne transmission[b]	4010	65.9	76.8

[a] The number of cases listing overseas travel as a risk factor in 2023 was 315, out of 2584 completed responses (12.2%). Thus, it was estimated 87.8% of all notified campylobacteriosis infections were domestically acquired.

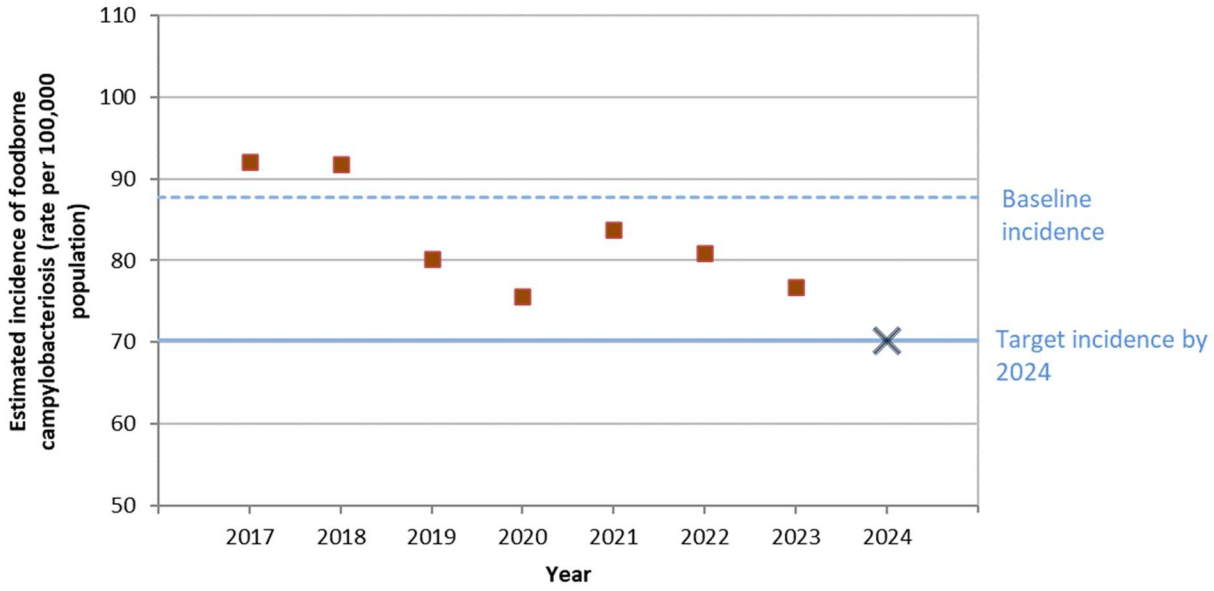
[b] From expert consultation in 2020, 75% of domestic cases are assumed to be foodborne [3].

Presentation

The trend in the estimated domestically acquired foodborne campylobacteriosis rate compared with the 2020 to 2024 performance target (blue asterisk) is shown in Figure 2. The rates observed in 2020 to 2023 are between the performance target baseline and 2024 target rates.

The total number of campylobacteriosis notifications in 2023 (6089) was higher than in 2022 (5878). However, the estimated number of overseas travel associated cases was much higher in 2023 (743) than in 2022 (347), leading to a decrease in the estimated incidence of domestically acquired foodborne campylobacteriosis from 2022 (81.0 cases per 100,000 population) to 2023 76.8 cases per 100,000 population).

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



Note:

X indicates the 2020-2024 performance target (70.2 cases per 100,000 population or less by the end of 2024).

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 ESR's Enteric Reference Laboratory, ESR's Enteric, Food and Environmental Virology/Norovirus Reference Laboratory or ESR's 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/g *Bacillus cereus* from a clinical specimen or ≥10^4/g *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 2023 by data source

During 2023, two cases of *B. cereus* intoxication were reported in EpiSurv. For one case norovirus infection was also reported.

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).

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 2023, there were three cases hospitalised (0.06 hospitalised cases per 100,000 population), all of which were reported with *B. cereus* intoxication as another relevant diagnosis. No admissions were reported with *B. cereus* intoxication as the principal diagnosis.

Outbreaks reported as caused by *Bacillus cereus*

During 2023, there was one outbreak with 12 associated cases reported in EpiSurv with *B. cereus* and *C. perfringens* confirmed as the causative agents (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, 2023

	Possible foodborne transmission with confirmed source	Total *B. cereus* outbreaks
Outbreaks	1	1
Outbreak-associated cases	12	12
Hospitalised cases	0	0

Table 8 contains details of the *B. cereus* outbreak reported in 2023 with food as the possible mode of transmission. The suspected source of the outbreak was laboratory confirmed as chicken curry from a catering service as the vehicle for the pathogen. Possible inadequate cooling of the meal at the caterer or the consumer was identified as the cause of the outbreak *C. perfringens* was also detected.

Table 8. Details of *B. cereus* outbreak reported in EpiSurv, 2023

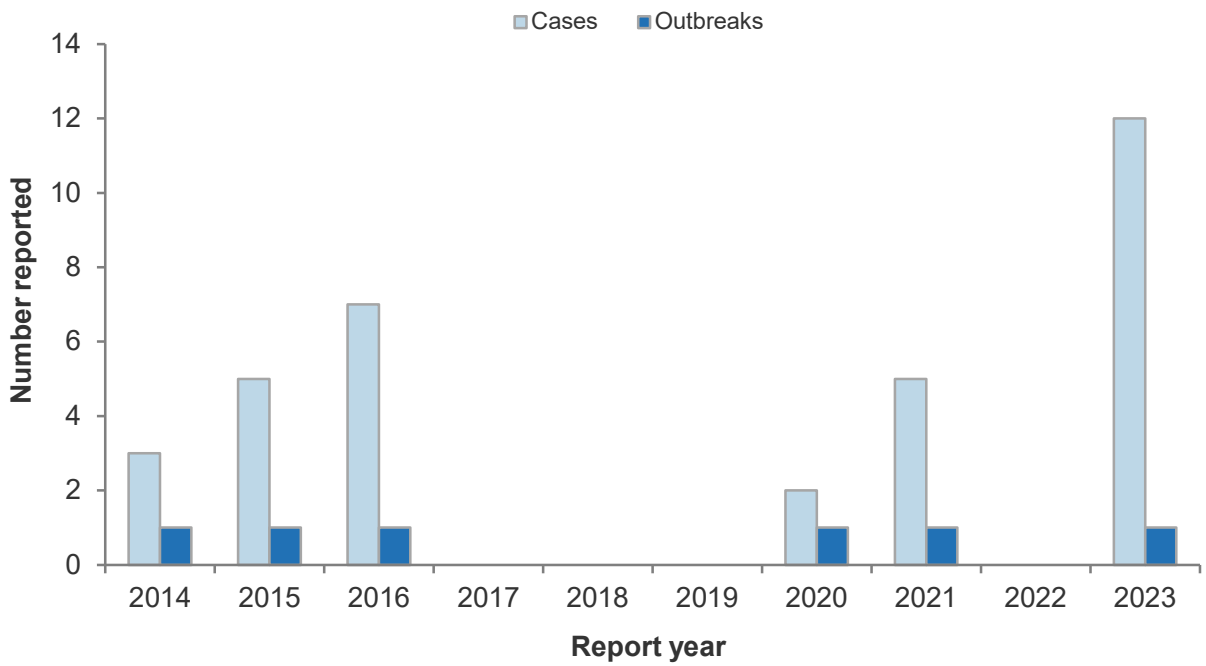
PHS	Report Month	Suspected source	Evidence	Setting	No. ill
Regional PH	October	Chicken curry	Common meal and laboratory confirmation	Home, provided by caterer	2C 10P

PHS: Public health service, PH: Public health

Number ill: C: Confirmed, P: Probable

Outbreaks of *B. cereus* intoxication are rare, with only six outbreaks reported in EpiSurv since 2014. 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, 2014–2023



Note: The figure includes data primarily from EpiSurv. The 2021 outbreak information is derived from Food Compliance Services, NZFS, records and was not recorded in EpiSurv.

Recent surveys

Nil.

Relevant New Zealand studies and publications

Journal papers

Identification and characterisation of spore-forming bacteria in bovine raw milk collected from four dairy farms in New Zealand – Gupta and Brightwell, 2023

Raw bulk-tank milk was collected from four bovine dairy farms in the Manawatu region, in December–January 2015 (summer) and July–September (winter–early spring)[1] and characterised with respect to the content, type and toxigenic potential of spore-forming bacteria [19]. *B. cereus*-like DNA sequences (99% match) were detected from one farm during the winter. However, the gene controlling production of the emetic toxin, cereulide (*ces*B) was not detected. Genes for one of the components of the haemolysin toxin was detected in the presumptive *B. cereus* isolate.

Relevant regulatory developments

No *B. cereus*-specific regulatory developments.

[1] The publication does not specify the year for winter-spring sampling and it may be either 2014 or 2015.

Campylobacteriosis

Case definition

Clinical description:	An illness of variable severity with symptoms of abdominal pain, fever and watery diarrhoea, and often bloody stools. Less frequently, *Campylobacter* can present as an invasive disease.
Laboratory test for diagnosis:	Isolation of *Campylobacter* 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 2023 are given in Table 9.

Table 9. Summary of surveillance data for campylobacteriosis, 2023

Parameter	Value in 2023	Source
Number of notified cases	6089	EpiSurv
Notification rate (per 100,000)	116.6	EpiSurv
Hospitalised cases[a]	989	NMDS
Deaths[b]	0	EpiSurv
Travel-related cases[c, d]	315	EpiSurv
Estimated domestically acquired food-related cases[e]	4010	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] Four campylobacteriosis cases were reported as having died in EpiSurv, of these, one case died of other causes and for the other three cases the cause of death was not recorded. No cases were recorded with campylobacteriosis as the primary cause of the case dying.

[c] Number of notified cases reporting overseas travel as risk factor. 2269 cases had not travelled overseas during the incubation period and for the remaining 3505 cases travel history is unknown.

[d] While New Zealand borders opened again for international travel in 2022, overseas travel in 2023 was still reduced compared to pre-COVID-19 years.

[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]. Estimate of cases acquired overseas calculated as *Total cases* X *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*.

Changes to laboratory methods

Since 2015, laboratories across New Zealand have changed the methodology for testing faecal specimens (Appendix B, page 123). In 2023, laboratories servicing community faecal specimens for Canterbury (October 2023), South Canterbury (October 2023), and West Coast (June 2023) have changed to CIDT methods. Since these changes were implemented community faecal specimens in all Health Districts are now being screened by CIDT methods for *Campylobacter* spp.

There is no evidence that campylobacteriosis notification rates have been affected by the introduction of CIDT methods by diagnostic laboratories [16].

Campylobacteriosis individual cases reported in 2023 by data source

During 2023, 6089 individual cases (116.6 cases per 100,000 population) of campylobacteriosis and no resulting deaths were reported in EpiSurv. Of the 6089 cases, the symptoms of 5910 cases (97%) were reported as fitting the clinical description for campylobacteriosis, the symptoms were unknown for 172 cases, and for seven cases the symptoms were listed as not fitting the clinical description.

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 989 hospitalised cases (18.9 hospitalised cases per 100,000 population) recorded in 2023, 803 cases were reported with campylobacteriosis as the principal diagnosis and 186 were reported with campylobacteriosis as another relevant diagnosis. Some of the 989 hospitalised cases were admitted to hospital more than once resulting in a total of 1040 hospital admissions.

It should be noted that EpiSurv and the NMDS database are separate systems and hospital admission can occur without cases being notified in EpiSurv. This means that not all cases diagnosed with campylobacteriosis in hospital are reported in EpiSurv.

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].

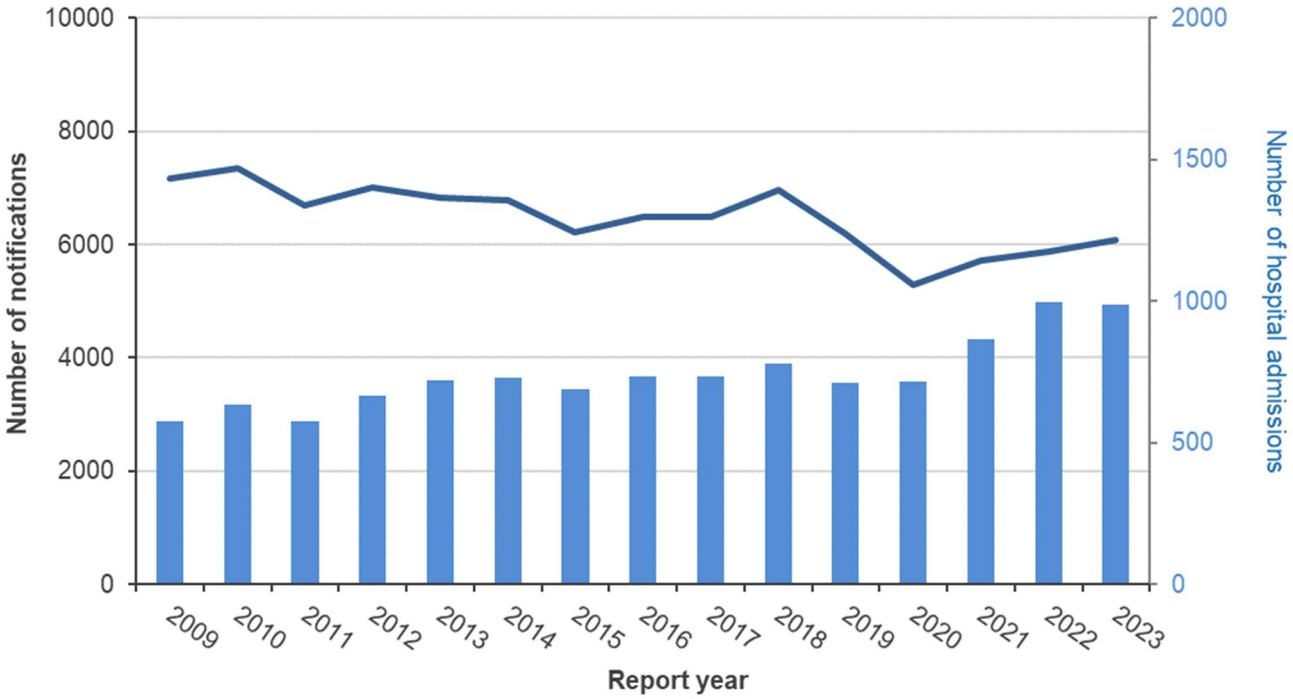
Annual data

In the past, the number of campylobacteriosis notifications reported had increased year-on-year up to the highest number recorded in 2006 (15,873 cases). Due to the measures taken by NZFS (and its predecessors) and the poultry industry, there was a significant decrease from 2006 to 2008 in the number of notified cases. Thereafter, the number and rate of notifications each year followed an overall downward trend from 2008 to 2022, with a drop in notifications in 2020 probably due to restrictions related to the COVID-19 pandemic (Figure 4 and Figure 5) [16]. The annual number of hospital admissions with campylobacteriosis as a principal or other relevant diagnosis was in the range of 574 to 780 admissions during 2009 to 2020. From 2021 there has been a higher number of hospital admissions with 1040 admissions in 2023.

The frequency of overseas travel was lower in 2020 to 2023 compared to pre-COVID-19 years (see Introduction, page 9). This is reflected in the notifications; in 2023, there were 315 campylobacteriosis notifications in EpiSurv listing overseas travel as a risk factor, compared to 394 in 2019, 66 in 2020, seven in 2021 and 128 in 2022.

The number of cases listing overseas travel as a risk factor in 2023 was 315, out of 2584 completed responses (12.2%). Thus, it was estimated 87.8% of all notified campylobacteriosis infections were domestically acquired.

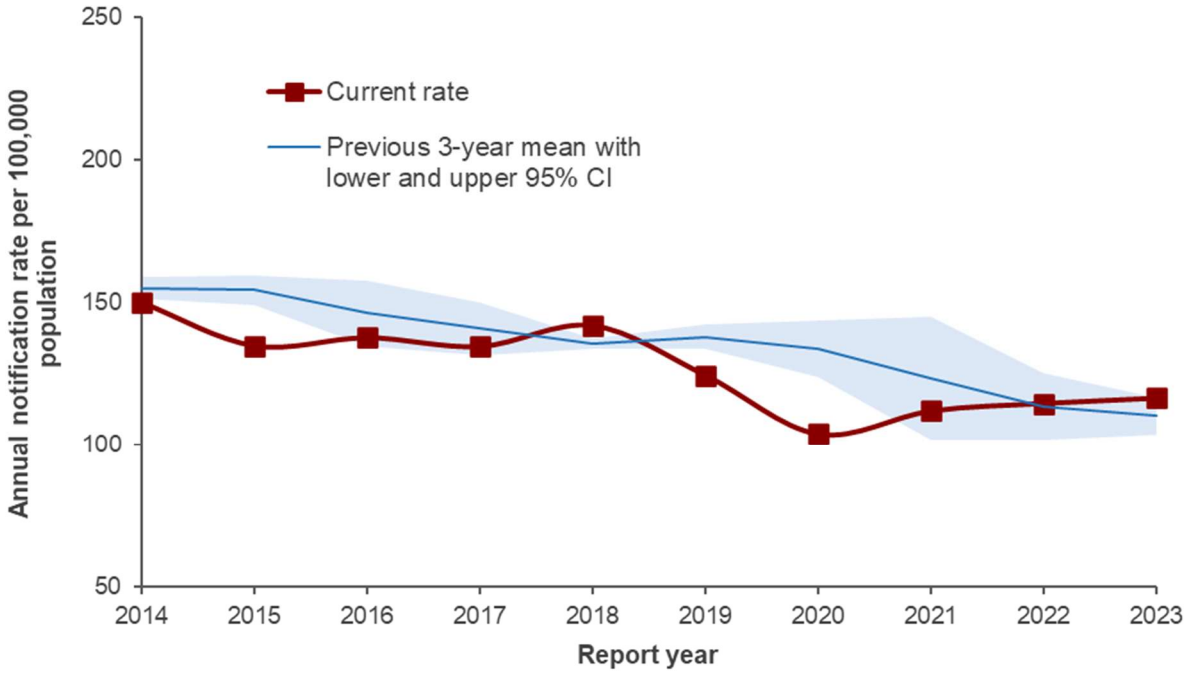
Figure 4. Campylobacteriosis EpiSurv notifications (line) and NMDS hospital admissions (bar) by year, 2009–2023



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

In 2023, the notification rate for campylobacteriosis (116.6 cases per 100,000 population) was similar (within the 95% CI) to the previous three-year mean (110.3 cases per 100,000 population). The trend for the previous three-year mean was generally downward since 2014. In 2020, the campylobacteriosis notification rate (104.0 cases per 100,000 population) was much lower compared to the previous years, probably due to the impact of COVID-19-related health measures (Figure 5).

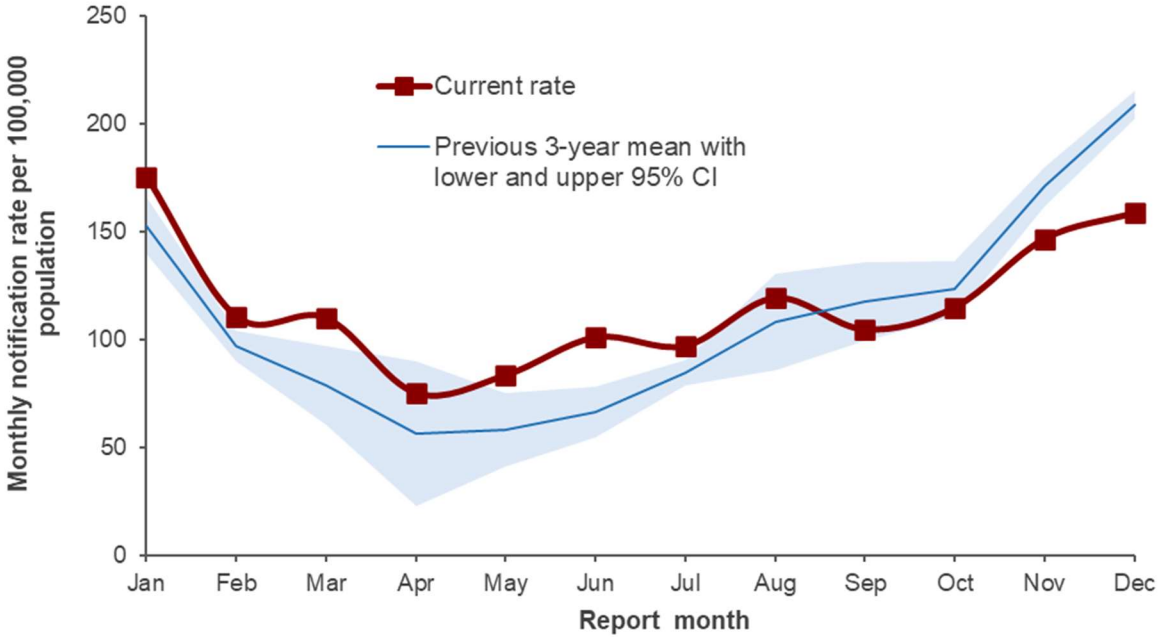
Figure 5. Campylobacteriosis notification rate by year, 2014–2023



Seasonal data

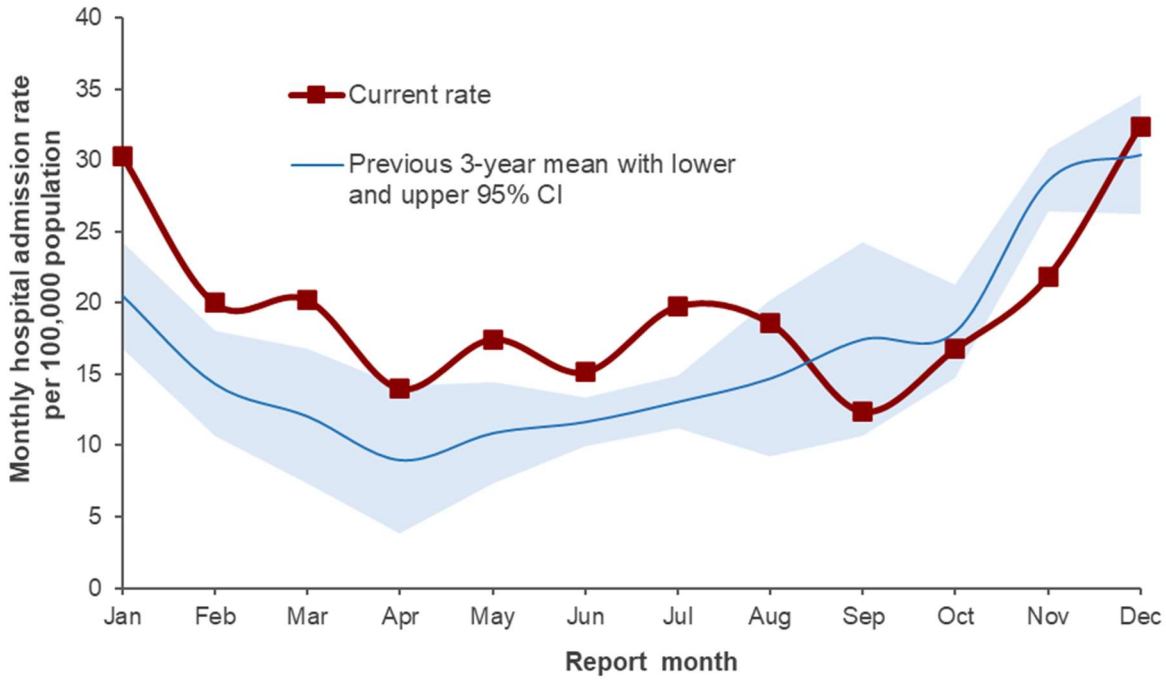
Campylobacteriosis notification rates per 100,000 population by month for 2023 are shown in Figure 6. In 2023, monthly notification rates followed a similar trend compared with previous years. The monthly number of notifications in 2023 ranged from 328 cases (April, 75.4 cases per 100,000 population) to 763 cases (January, 175.3 cases per 100,000 population).

Figure 6. Campylobacteriosis monthly notification rate (annualised), 2023



In 2023, the monthly hospital admission rates for the first seven months of the year were higher than the previous three-year mean, but similar or lower (November) rates in the remaining months (Figure 7).

Figure 7. Campylobacteriosis monthly hospital admission rate (annualised), 2023



Demographics

In 2023, the rates of notifications and hospitalised cases for campylobacteriosis were higher for males (129.7 notified cases and 20.8 hospitalised cases per 100,000 population) compared with females (103.5 notified cases and 17.1 hospitalised cases per 100,000 population) (Table 10).

Table 10. Campylobacteriosis cases by sex, 2023

Sex	EpiSurv notified cases		Hospitalised cases[a]	
	No.	Rate[b]	No.	Rate[b]
Male	3370	129.7	541	20.8
Female	2716	103.5	448	17.1
Total[c]	**6089**	**116.6**	**989**	**18.9**

[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 2023 was reported for children in the 1 to 4 years age group (206.4 cases per 100,000 population, 506 cases). The highest hospitalised case rate was for the 70 years and over age group (54.2 hospitalised cases per 100,000 population, 325 cases) (Table 11).

Table 11. Campylobacteriosis cases by age group, 2023

Age group (years)	EpiSurv notified cases		Hospitalised cases[a]	
	No.	Rate[b]	No.	Rate[b]
<1	97	169.7	15	26.2
1 to 4	506	206.4	44	17.9
5 to 9	197	60.9	14	4.3
10 to 14	187	54.5	17	5.0
15 to 19	318	97.2	50	15.3
20 to 29	847	123.9	111	16.2
30 to 39	747	96.9	102	13.2
40 to 49	585	90.8	77	12.0
50 to 59	779	119.1	100	15.3
60 to 69	822	142.8	134	23.3
70+	1003	167.2	325	54.2
Total[c]	**6089**	**116.6**	**989**	**18.9**

[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).

[c] Total includes one notification where age is unknown.

Geographic distribution

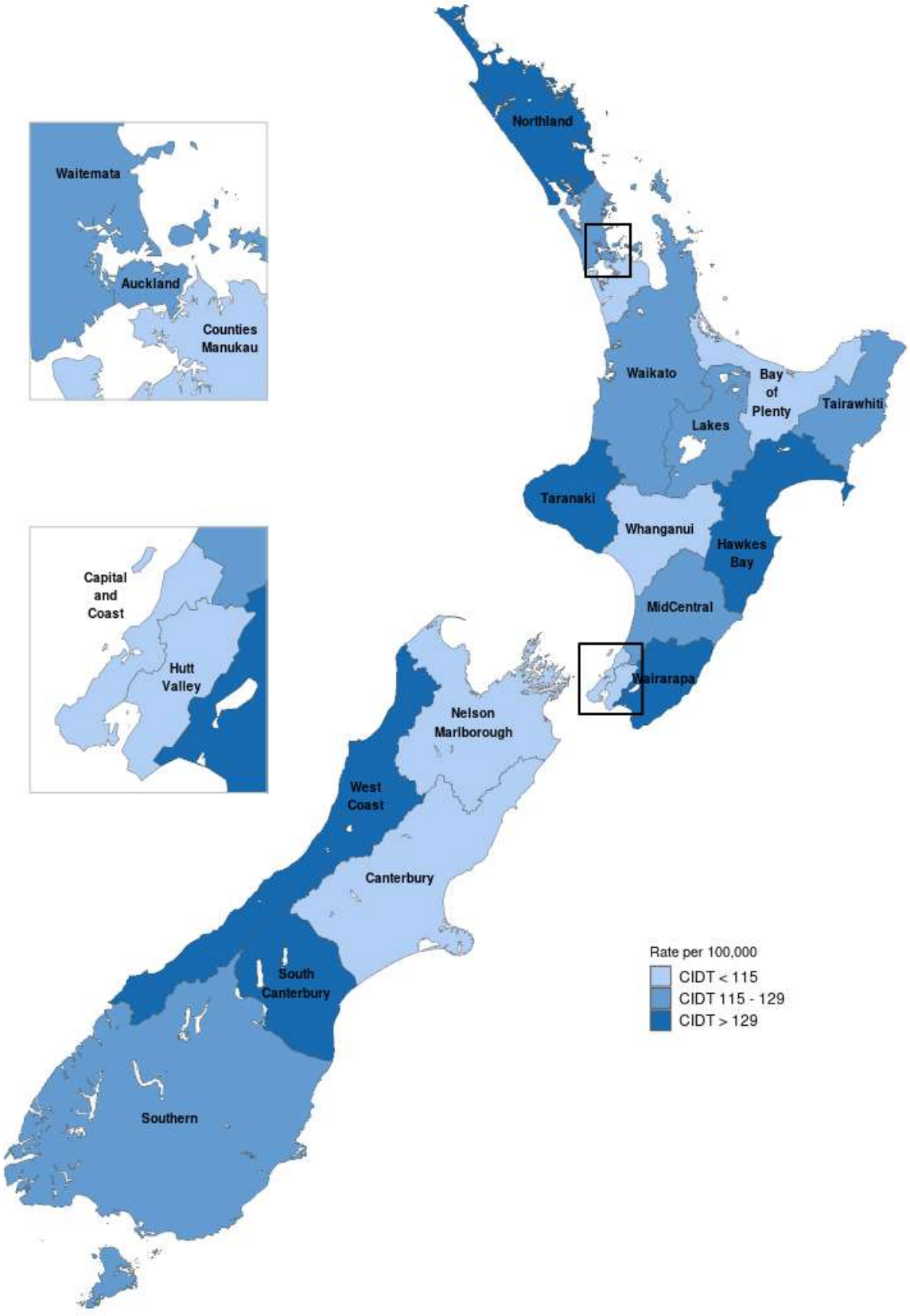
The notification rates by Health District calculated per 100,000 resident population are presented in Figure 8 (see also Table 80).

In 2023, Health District notification rates of campylobacteriosis ranged from 82.6 cases per 100,000 population (134 cases) in Hutt Valley to 193.7 cases per 100,000 population (122 cases) in South Canterbury. Taranaki Health District (180.9 cases per 100,000 population, 233 cases) had the second highest notification rate.

Historically, notification rates for campylobacteriosis have been variable across New Zealand with the Health Districts; South Canterbury, Wairarapa, and Taranaki consistently in the highest quartile of notification rates since 2017. South Canterbury Health District has had the highest rates since 2017 ranging from 193.7 cases per 100,000 population in 2023 to 246.3 cases per 100,000 population in 2018.

Campylobacteriosis notification rates, stratified by the 2023 Urban Rural Classification [20] of the cases' residential address and excluding cases associated with overseas travel, increased as the area of residence became more rural (Appendix C, Table 81). Rates of cases residing in urban areas ranged from 88.8 to 116.1 cases per 100,000 population. The highest rate was for the 'rural other' category (202.1 cases per 100,000 population).

Figure 8. Geographic distribution of campylobacteriosis notifications, 2023



Note: Canterbury and South Canterbury Health Districts changed to community laboratory testing by CIDT methods in October 2023 and the West Coast Health District in June 2023. The plotted rates in these areas will not reflect a full year of CIDT testing in 2023.

Outbreaks reported as caused by *Campylobacter* spp.

In 2023, there were a total of 15 campylobacteriosis outbreak notifications in EpiSurv, with two outbreaks (30 cases) due to infection overseas (Table 12). Five non-overseas travel related outbreaks (36%) recorded 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.

Table 12. Campylobacteriosis outbreaks reported in EpiSurv, 2023

	Possible foodborne transmission with a suspected or confirmed source	Total campylobacteriosis outbreaks
Outbreaks	5	15
Outbreak associated cases	36	124
Outbreak hospitalised cases	2	11

Table 13 contains details of the six domestic campylobacteriosis outbreaks reported in 2023 with food as a possible mode of transmission. In addition to the five outbreaks recorded in EpiSurv (Table 12), one suspected outbreak of two cases was referred to NZFS (September outbreak).

The evidence for the source being the cause of the outbreak was laboratory confirmed for one of the outbreaks. The two outbreaks associated with chicken liver pâté were referred to NZFS. While pâté could not be confirmed as a source for either outbreak, the outbreak in Auckland stopped after production of the chicken liver pâté ceased.

Laboratory evidence for the Hawke's Bay outbreak was recorded in EpiSurv, with *Campylobacter* detected in the raw milk sample. This outbreak was referred to NZFS and resulted in a consumer level recall of implicated milk batches.

Table 13. Details of campylobacteriosis outbreaks reported in EpiSurv and/or referred to NZFS with food reported as a possible mode of transmission, 2023

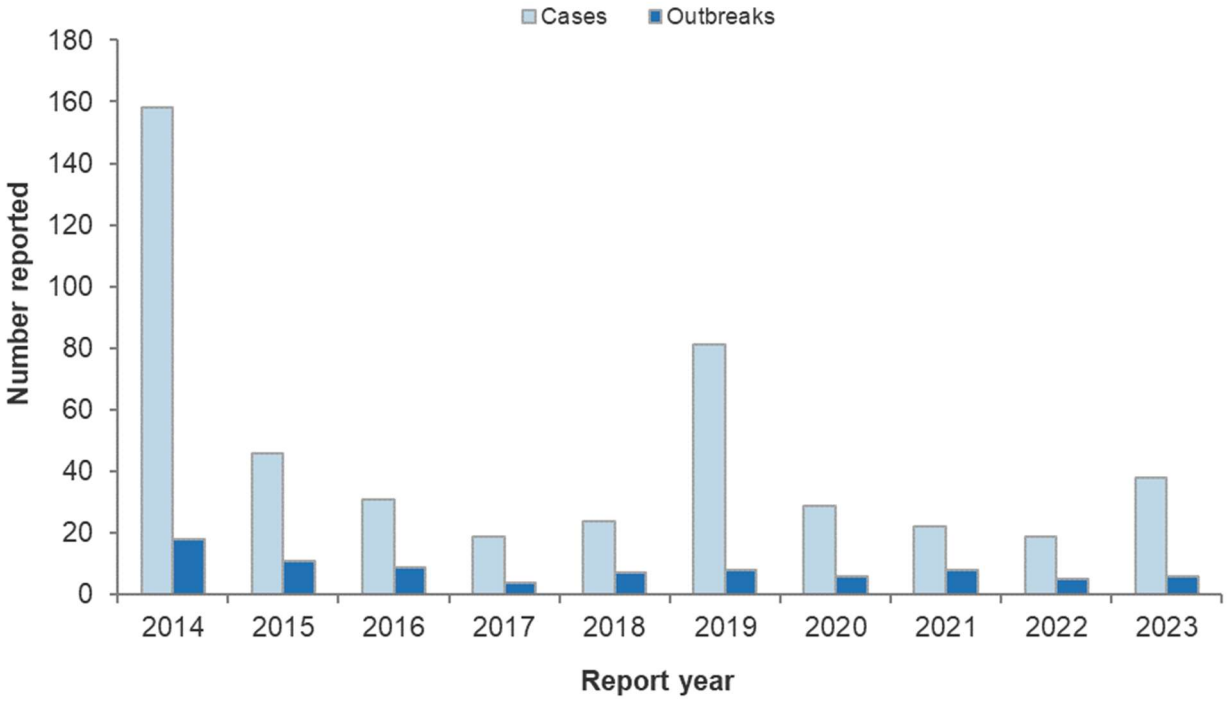
PHS	Report Month	Suspected or confirmed source	Evidence	Setting	No. ill
Northland	March	Raw milk from family farm	Common food	Home	2C
Mid Central	April	Undercooked chicken or pork at BBQ	Common meal	Home	3C 4P
Auckland Regional	June	Chicken liver pâté	Common location	Restaurant/cafe/bakery	7C 10P
Regional	September	Chicken liver parfait	Common location	Restaurant/cafe/bakery	2C
Waikato	October	Chicken liver pâté	Common event	Restaurant/cafe/bakery	2C 5P
Hawke's Bay	November	Commercial Raw milk	Common food source, laboratory evidence	Temporary or mobile service	3C

PHS: Public Health Service,

Number ill: C: confirmed, P: probable.

Between 2014 and 2023 the number of outbreaks of campylobacteriosis with food reported as a possible mode of transmission ranged from four to 18 outbreaks each year with between 19 (2017 and 2022) and 158 (2014) annual outbreak-associated cases (Figure 9). The greater number of outbreak-associated cases in 2014 was due to three outbreaks with high numbers of cases (51, 32 and 17 cases, respectively).

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), 2014–2023



Note: The figure includes data primarily from EpiSurv. From 2021, the figure includes clusters of potentially foodborne disease referred to Food Compliance Services, NZFS, that were not recorded as a potentially foodborne outbreak in EpiSurv (2021: three outbreaks, seven cases; 2022: two outbreaks, seven cases; 2023: one outbreak, two cases).

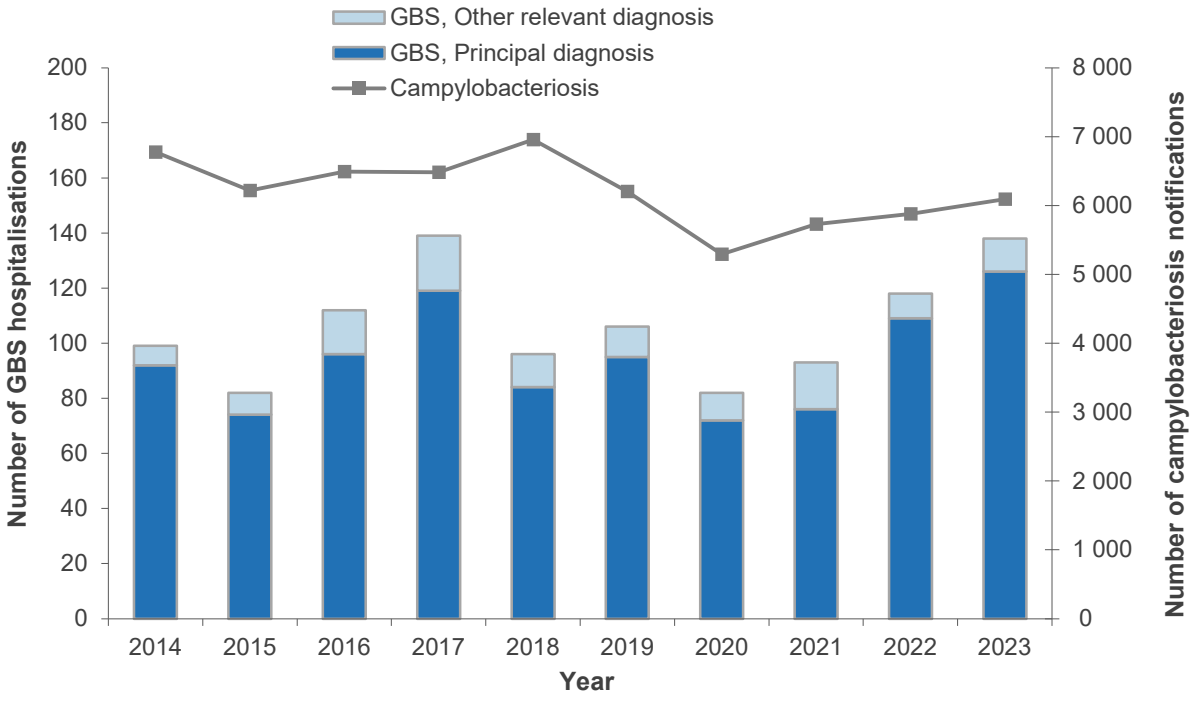
Disease sequelae - Guillain-Barré syndrome

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 a *C. jejuni* infection 1-3 weeks before onset of GBS [21].

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 2023 were considered, rather than all cases that were hospitalised in 2023. That is, if a GBS case hospitalised in 2023 had been hospitalised with GBS in a previous year, the 2023 admission was considered to be a readmission, rather than an incident case. There were 138 incident cases recorded in 2023 (2.3 hospitalised cases per 100,000 population), 126 were reported with GBS as the principal diagnosis and 12 with GBS as another relevant diagnosis.

Between 2014 and 2023, 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% [22]. 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 2014-2023 would be difficult to detect.

Figure 10. Guillain-Barré syndrome incident cases, 2014–2023



In 2023, 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 2023 (Table 10).

Table 14. Guillain-Barré syndrome incident cases by sex, 2023

Sex	Cases[a]	
	No.	Rate[b]
Male	84	3.2
Female	54	2.1
Total	**138**	**2.3**

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

[b] per 100,000 population.

In 2023, the highest rates of incident cases for GBS were in the 60 to 69 years age group, followed by the 70+ years age group (Table 15).

Table 15. Guillain-Barré syndrome incident cases by age group, 2023

Age group (years)	Cases[a]	
	No.	Rate[b]
<1	1	-
1 to 4	4	-
5 to 9	1	-
10 to 14	4	-
15 to 19	8	2.4
20 to 29	16	2.3
30 to 39	17	2.2
40 to 49	21	3.3
50 to 59	22	3.4
60 to 69	22	3.8
70+	22	3.7
Total	**138**	**2.3**

[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

Nil.

Relevant New Zealand studies and publications

Journal papers

Fecal excretion of Campylobacter jejuni by young dairy calves and the relationship with neonatal immunity and personality traits – Rapp 2023

To gain information of the carriage of *Campylobacter jejuni* by dairy cattle, 48 dairy calves were reared in indoor pens from birth to 4 weeks of life [23]. Faecal samples were collected weekly from each calf and revealed that the proportion of calves naturally contaminated with *C. jejuni* in each pen reached 70% after 3 weeks of life. High (>16 g/L) levels of IgG in the serum of neonatal calves, indicative of immunity to *C. jejuni* infection, were negatively (P = 0.04) associated with faecal detection of *C. jejuni* over the trial period. Calves that spent more time interacting with a novel object tended to be positive (P = 0.058) for *C. jejuni*.

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 2023 by data source

During 2023, 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. All three hospitalised cases (0.06 hospitalised cases per 100,000 population) recorded in 2023, were reported with ciguatera poisoning as the principal diagnosis. No admissions were reported with ciguatera poisoning as another relevant diagnosis.

It should be noted that EpiSurv and the NMDS database are separate systems and hospital admission can occur without cases being notified in EpiSurv. This means that not all cases diagnosed with ciguatera poisoning in hospital are reported in EpiSurv.

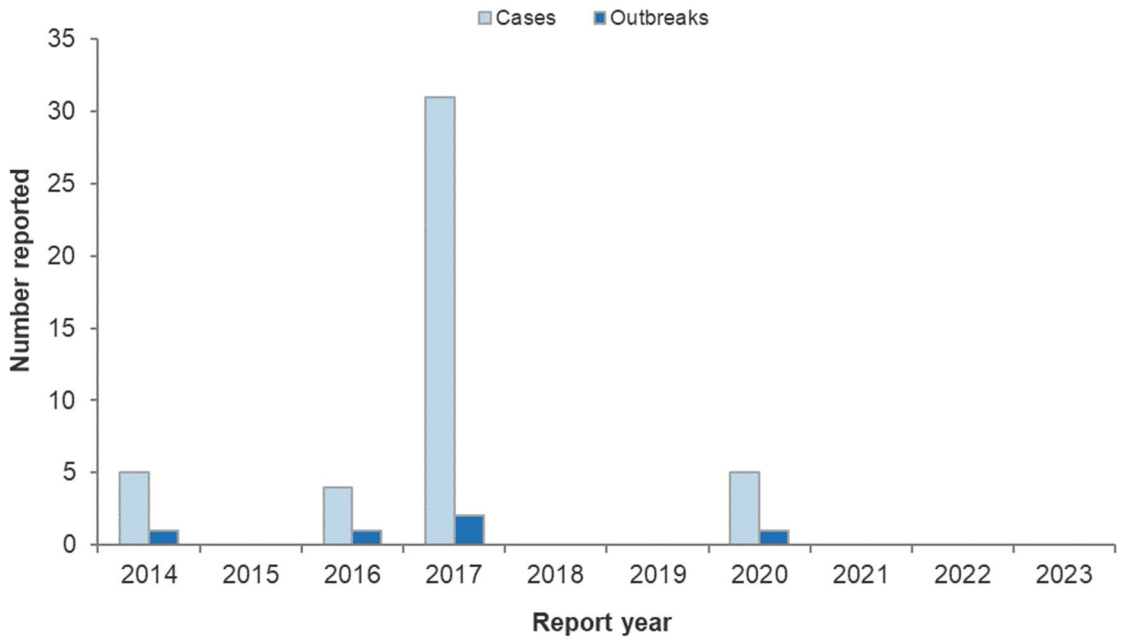
Outbreaks reported as caused by ciguatera poisoning

During 2023, 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 2014 to 2023, five outbreaks of ciguatera poisoning were reported, with no more than two outbreaks reported in a single year (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.

Figure 11. Ciguatera poisoning outbreaks reported in EpiSurv and associated cases reported by year, 2014–2023



Recent surveys

Nil.

Relevant New Zealand studies and publications

Journal papers

Sub-tropical benthic/epiphytic dinoflagellates of Aotearoa New Zealand and Rangitāhua Kermadec Islands – Rhodes 2023

Sampling and characterisation was conducted of potentially toxigenic dinoflagellates from Rangitāhua Kermadec Islands and Northland, Aotearoa New Zealand [24]. An isolate of *Gambierdiscus polynesiensis* was collected from Raoul Island, in the Kermadec group, that produced 44-methylgambierone and gambierone, and traces of ciguatoxins. No *Gambierdiscus* spp. were collected from Northland.

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/g or isolation of ≥10^5/g *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 2023 by data source

During 2023, 27 outbreak-related cases and no 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. Of the three hospitalised cases (0.06 hospitalised cases per 100,000 population) recorded in 2023, one case was reported with *C. perfringens* intoxication as the principal diagnosis and two cases with *C. perfringens* intoxication as another relevant diagnosis.

Outbreaks reported as caused by *Clostridium perfringens*

In 2023, there were three *C. perfringens* intoxication outbreaks with a total of 27 cases reported in EpiSurv, all with food as a possible mode of transmission (Table 16).

Table 16. *C. perfringens* intoxication outbreaks reported in EpiSurv, 2023

	Possible foodborne transmission with a suspected source	Possible foodborne transmission but no suspected source	Total *C. perfringens* intoxication outbreaks
Outbreaks	2	1	3
Outbreak associated cases	15	12	27
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 evidence for the source being the cause of the outbreak was inconclusive for the March and September outbreaks. The evidence linking both cases and vehicle was strong for the October outbreak with high level *C. perfringens* detected in the chicken curry. *B. cereus* was also detected. NZFS investigated all three outbreaks and found failures in food safety systems, which were subsequently resolved.

Table 17. Details of *C. perfringens* intoxication outbreaks reported in EpiSurv with food reported as a possible mode of transmission, 2023

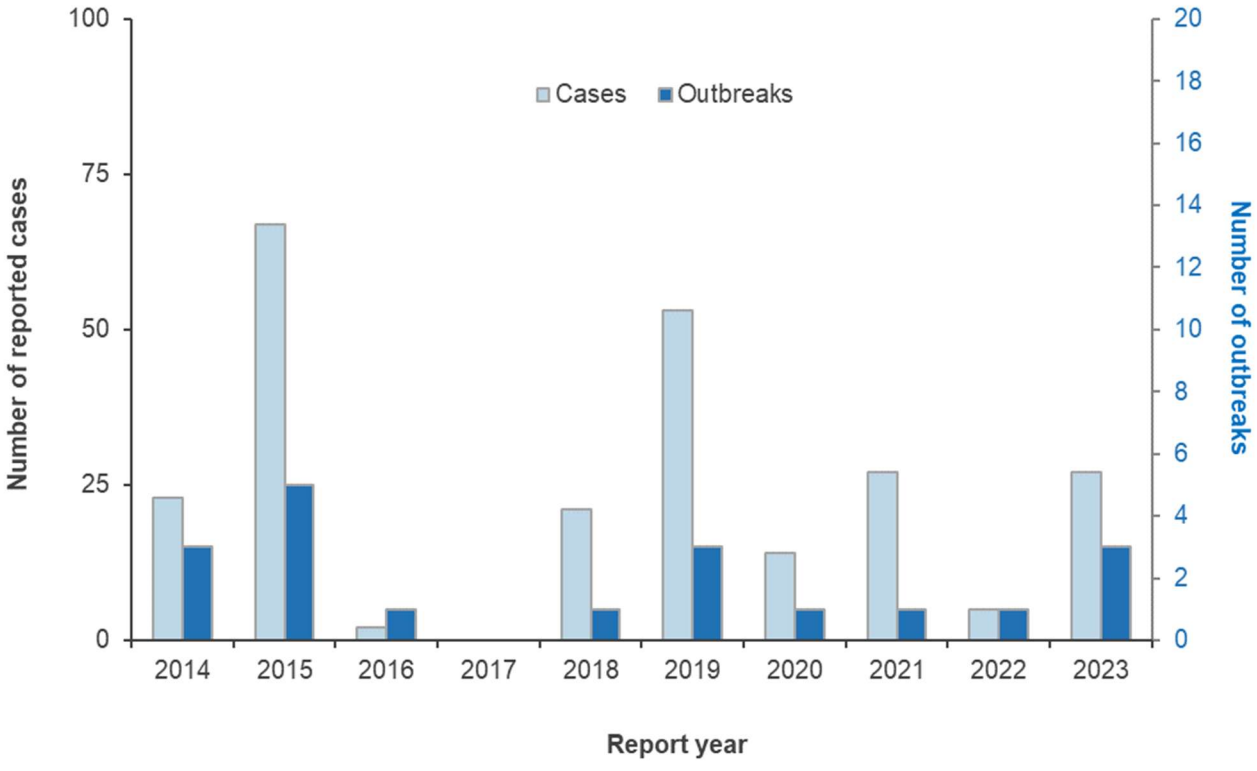
PHS	Month	Suspected source	Evidence	Setting	No. ill
Community and Public Health	March	Chicken lamb souvlaki	Common location	Food Premise	2C 1P
Regional PH	September	Unknown	Common meal	Workplace/community/ other	1C 11P
Regional PH	October	Chicken curry	Laboratory testing detected *C. perfringens.*	Meal from caterer consumed at home	2C 10P

PHS: Public Health Service, PH: Public health.

Number ill: C: confirmed, P: probable.

Over the 10-year period 2014-2023, 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 outbreak-associated cases of *C. perfringens* intoxication with possible transmission by food occurred in 2015 (67 cases).

Figure 12. *C. perfringens* intoxication outbreaks reported in EpiSurv with food reported as a possible mode of transmission and associated cases reported by year, 2014–2023



Recent surveys

Nil.

Relevant New Zealand studies and publications

Journal papers

Identification and characterisation of spore-forming bacteria in bovine raw milk collected from four dairy farms in New Zealand – Gupta 2023

Raw bulk-tank milk was collected from four bovine dairy farms in the Manawatu region, in December–January 2015 (summer) and July–September (winter–early spring) and characterised with respect to the content, type and toxigenic potential of spore-forming bacteria [19].
C. perfringens was detected by PCR in milk from two farms but only during winter. All of 27 *C. perfringens* isolates tested carried the gene for the production of the alpha toxin (*cpa*) and toxin production was verified by enzyme-linked immunosorbent assay (ELISA). Three isolates also carried the gene for the beta toxin (*cpb)* and seven carried the gene for the epsilon toxin (*etx*). While production of the epsilon toxin was confirmed by ELISA, production of the beta toxin was not.

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.
Laboratory test for diagnosis:	Detection of *Cryptosporidium parvum* 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 2023 are given in Table 18.

Table 18. Summary of surveillance data for cryptosporidiosis, 2023

Parameter	Value in 2023	Source
Number of notified cases	831	EpiSurv
Notification rate (per 100,000)	15.9	EpiSurv
Hospitalised cases[a]	67	NMDS
Deaths	0	EpiSurv
Travel-related cases[b, c]	60	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] Number of notified cases reporting overseas travel as risk factor. 461 cases had not travelled overseas during the incubation period and for the remaining 310 cases travel history is unknown.

[c] While New Zealand borders opened again for international travel in 2022, overseas travel in 2023 was still reduced compared to pre-COVID-19 years.

Changes to laboratory methods

Since 2015, laboratories across New Zealand have changed the methodology for testing faecal specimens (Appendix B, page 123). In October 2023, laboratories servicing community faecal specimens for Canterbury and South Canterbury have changed to CIDT methods, including testing for *Cryptosporidium* spp.. In 2023, community faecal specimens in all Health Districts except for Bay of Plenty, Lakes, Waikato and West Coast were screened by CIDT methods for a range of pathogens, including *Cryptosporidium* spp.. All community faecal specimens in these Health Districts are now screened for *Cryptosporidium* 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.

It is unclear at this stage how laboratory changes have affected the notification rates for cryptosporidiosis. The increased number of samples screened for *Cryptosporidium* spp. may affect the number of positive results and increase notification rates. There does not seem to be a large difference in sensitivity between EIA tests (used by most laboratories prior to enteric CIDT introduction) and nucleic acid amplification based CIDT for the detection of *Cryptosporidium* spp. [25].

Cryptosporidiosis individual cases reported in 2023 by data source

During 2023, 831 individual cases (15.9 cases per 100,000 population) of cryptosporidiosis and no resulting deaths were reported in EpiSurv. Of the 831 cases, the symptoms of 803 cases (97%) were reported as fitting the clinical description for cryptosporidiosis, the symptoms were unknown for 27 cases, and for one case the symptoms were reported as not fitting the clinical description.

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 67 hospitalised cases (1.3 hospitalised cases per 100,000 population) recorded in 2023, 56 cases were reported with cryptosporidiosis as the principal diagnosis and 11 were reported with cryptosporidiosis as another relevant diagnosis. Two of the 67 hospitalised cases were admitted to hospital twice resulting in a total of 69 hospital admissions.

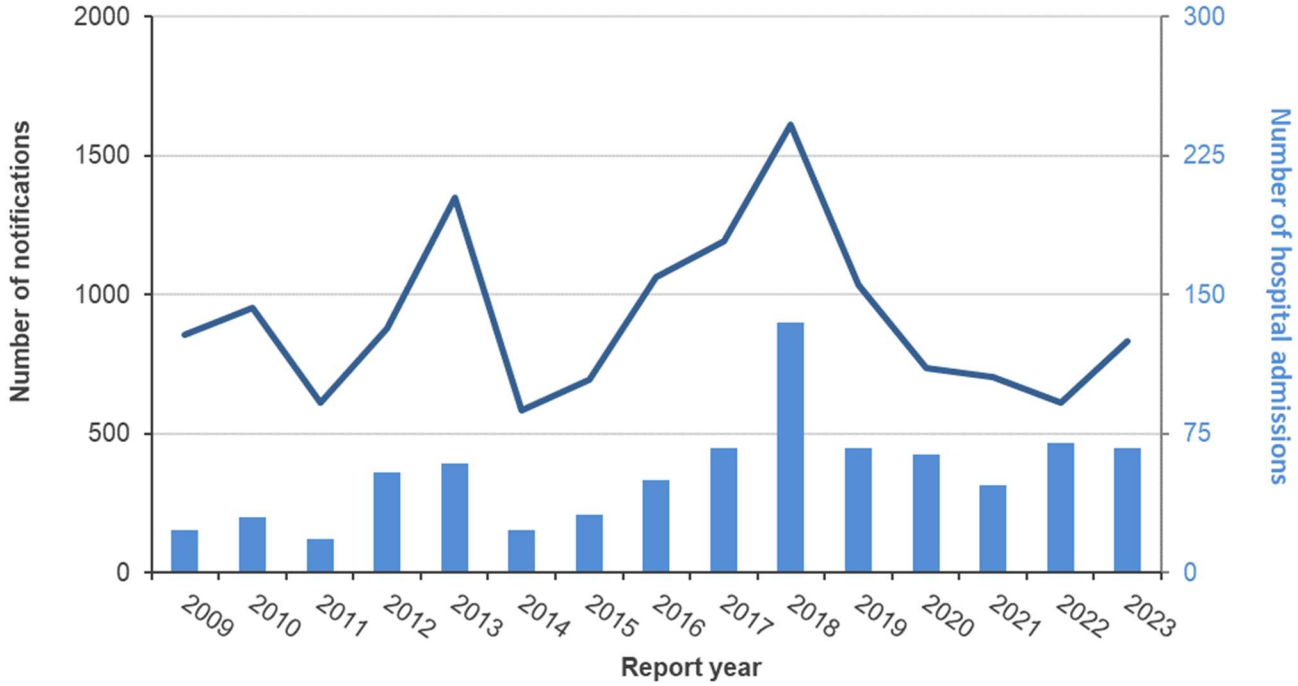
It should be noted that EpiSurv and the NMDS database are separate systems and hospital admission can occur without cases being notified in EpiSurv. This means that not all cases diagnosed with cryptosporidiosis in hospital are reported in EpiSurv.

Annual data

Over the last 15 years the number of cryptosporidiosis notifications and hospital admissions per year has been variable (Figure 13). In 2023, the number of notifications and hospital admissions were within the range seen in the previous 14 years. The number of hospital admissions with cryptosporidiosis as the principal or another relevant diagnosis varies year by year and has ranged between 18 (2011) and 135 (2018) admissions.

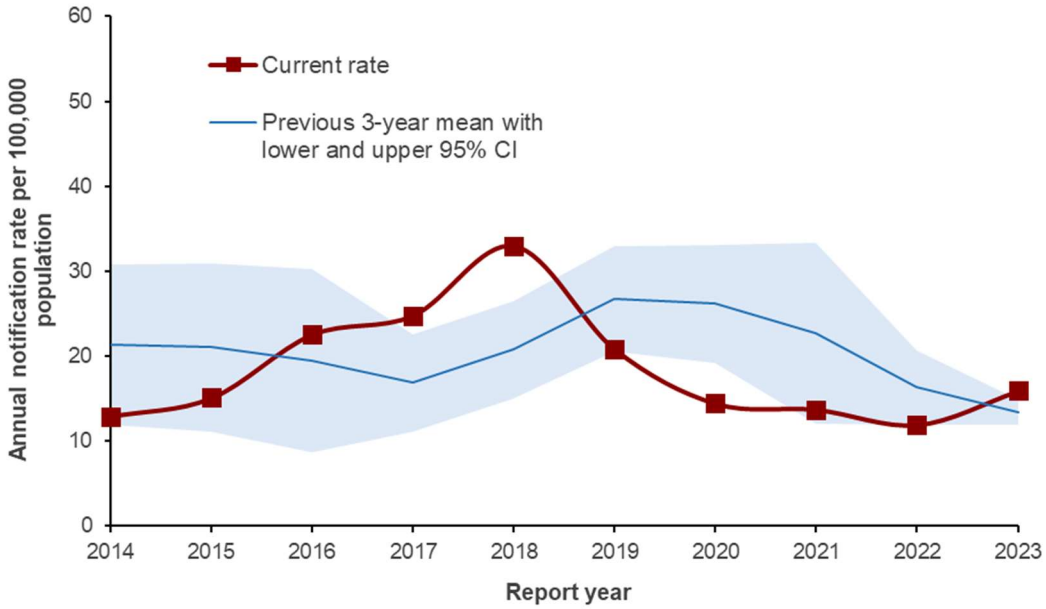
The frequency of overseas travel was lower in 2020 to 2023 compared to pre COVID-19 years (see Introduction, page 9). In 2023, there were 60 cryptosporidiosis notifications in EpiSurv listing overseas travel as a risk factor which is in line with 2019 (50 cases). Less cases listed overseas travel as a risk factor in 2020 (seven cases), 2021 (no cases) and 2022 (10 cases).

Figure 13. Cryptosporidiosis EpiSurv notifications (line) and NMDS hospital admissions (bar) by year, 2009–2023



In 2023, the notification rate for cryptosporidiosis (15.9 cases per 100,000 population) was slightly higher than the previous three-year mean (13.4 cases per 100,000 population) (Figure 14).

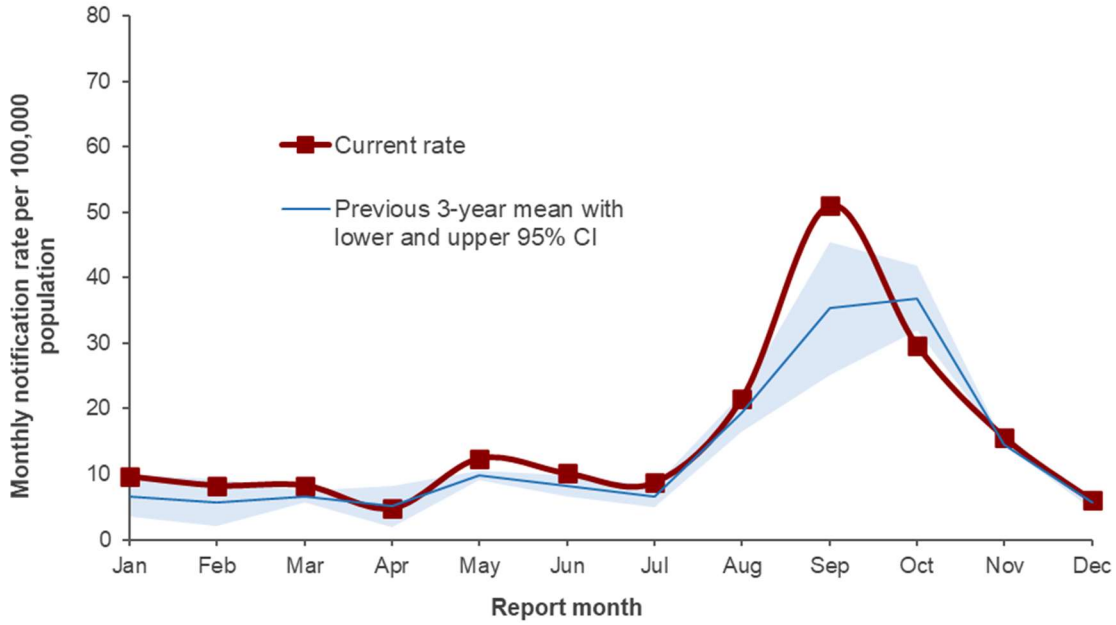
Figure 14. Cryptosporidiosis notification rate by year, 2014–2023



Seasonal data

Cryptosporidiosis notification rates per 100,000 population by month are shown in Figure 15. In 2023, monthly notification rates followed the same trend compared to previous years with a pronounced seasonal peak in spring. The monthly number of notifications in 2023 ranged from 21 notifications (April, 4.9 cases per 100,000 population) to 222 notifications (September, 51.0 cases per 100,000 population). The higher-than-normal peak in September is due to an outbreak of 101 cases in the Southern Health District.

Figure 15. Cryptosporidiosis monthly notification rate (annualised), 2023



Demographics

In 2023, the rates of notifications and hospitalised cases for cryptosporidiosis were slightly higher for females (16.6 notified cases and 1.4 hospitalised cases per 100,000 population) compared with males (15.2 notified cases and 1.1 hospitalised cases per 100,000 population) (Table 19).

Table 19. Cryptosporidiosis cases by sex, 2023

Sex	EpiSurv notified cases		Hospitalised cases[a]	
	No.	Rate[b]	No.	Rate[b]
Male	396	15.2	29	1.1
Female	435	16.6	38	1.4
Total	**831**	**15.9**	**67**	**1.3**

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

[b] Per 100,000 population.

In 2023, the highest cryptosporidiosis age-specific notification and hospitalisation rate was reported for the 1 to 4 years age group (62.0 notified cases and 6.1 hospitalised cases per 100,000 population). The lowest rates of cases were for the over 40 age groups (Table 20).

Table 20. Cryptosporidiosis cases by age group, 2023

Age group (years)	EpiSurv notified cases		Hospitalised cases[a]	
	No.	Rate[b]	No.	Rate[b]
<1	9	15.7	0	-
1 to 4	152	62.0	15	6.1
5 to 9	58	17.9	3	-
10 to 14	50	14.6	6	1.7
15 to 19	47	14.4	10	3.1
20 to 29	152	22.2	13	1.9
30 to 39	157	20.4	4	-
40 to 49	77	12.0	6	0.9
50 to 59	61	9.3	5	0.8
60 to 69	38	6.6	2	-
70+	29	4.8	3	-
Total[c]	**831**	**15.9**	**67**	**1.3**

[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).

[c] Total includes one notification where age is unknown.

Geographic distribution

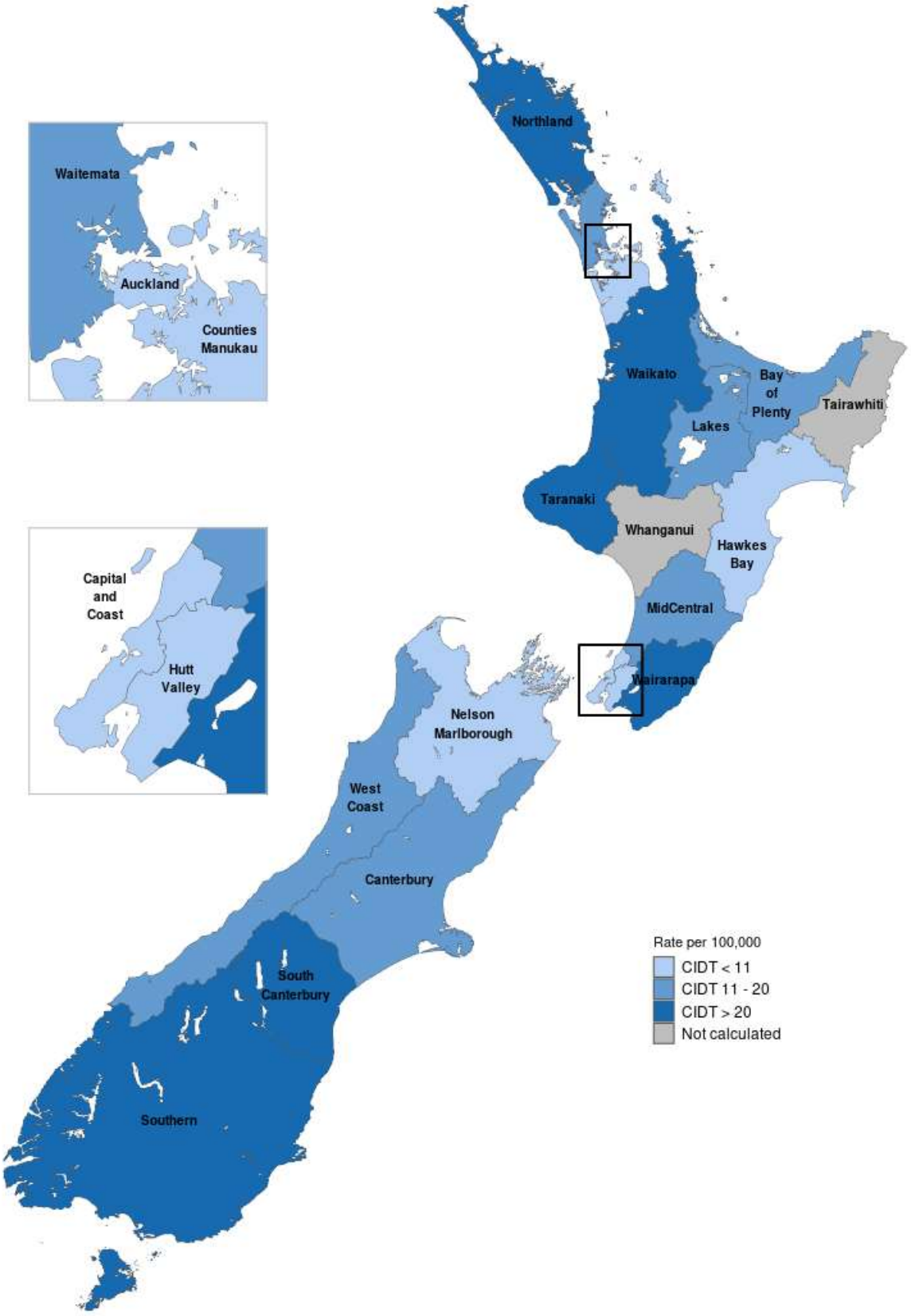
The notification rates by Health District calculated per 100,000 resident population are presented in Figure 16. The rate has not been calculated for Health Districts with fewer than five cases (grey shading): Tairāwhiti (two cases) and Whanganui (three cases).

In 2023, the Health District notification rates of cryptosporidiosis ranged from 4.9 cases per 100,000 population in Hutt Valley (eight cases) to 44.4 cases per 100,000 population (28 cases) in South Canterbury. South Canterbury, Southern (39.1 cases per 100,000 population, 141 cases), Northland (31.4 cases per 100,000 population, 64 cases) and Wairarapa (27.3 cases per 100,000 population, 14 cases) Health Districts had the highest notification rates.

Historically, notification rates for cryptosporidiosis have been variable across New Zealand with the Health Districts Waikato and Southern consistently in the highest quartile of notification rates since 2020.

Cryptosporidiosis notification rates, stratified by 2023 Urban Rural Classification [20] of the cases' residential address and excluding cases associated with overseas travel were highest in 'rural other' areas (35.8 cases per 100,000 population), and lowest in 'major urban' (8.4 cases per 100,000 population) and 'large urban' (10.3 cases per 100,000 population) areas.

Figure 16. Geographic distribution of cryptosporidiosis notifications, 2023



Note: Canterbury and South Canterbury Health Districts changed to community laboratory testing by CIDT methods in October 2023. The plotted rates in these areas will not reflect a full year of CIDT testing in 2023.

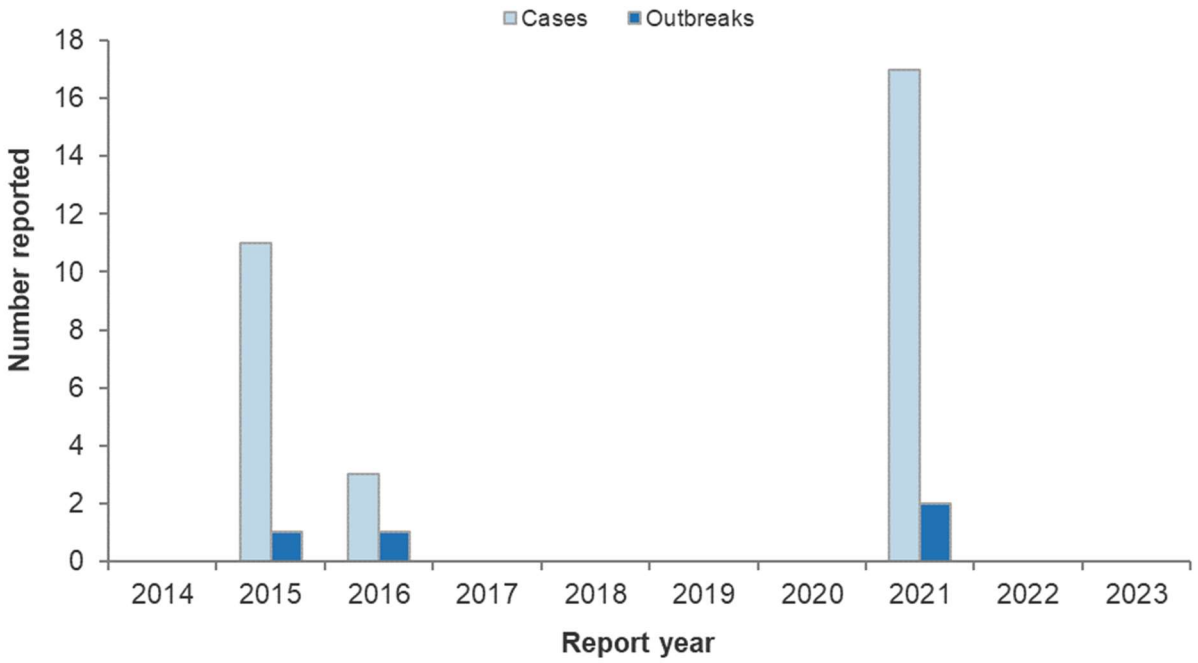
Outbreaks reported as caused by *Cryptosporidium* spp.

In 2023, there were eight cryptosporidiosis outbreaks with 163 associated cases reported in EpiSurv. Two of these outbreaks (12 cases) were associated with overseas travel. One outbreak (101 cases) reported in the Southern Health District area during August to October was still being investigated at the data extraction date for this report. The suspected but unconfirmed source of the outbreak was one of the town's drinking water supplies.

None of the domestic outbreaks reported 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 2014 and 2023 there have been a total of four outbreaks of potentially foodborne cryptosporidiosis (Figure 17), one in 2015 and 2016 and two in 20121. The annual number of cases associated with outbreaks ranged between three and 17.

Figure 17. Cryptosporidiosis outbreaks reported in EpiSurv with food reported as a possible mode of transmission and associated cases (excluding travel associated outbreaks) reported by year, 2014–2023



Recent surveys

Nil.

Relevant New Zealand studies and publications

Journal papers

A review and analysis of cryptosporidiosis outbreaks in New Zealand - Garcia-R 2023

Analysis was carried out of the details of 318 cryptosporidiosis outbreaks, involving 1634 cases, that occurred in New Zealand in the period 2010-2017 [26]. The majority of the outbreaks (260 outbreaks, 1320 cases) were considered to be due to person-to-person transmission. Only 10 outbreaks (29 cases) were considered to be due to foodborne transmission. The publication also reported on genetic analysis of samples from a sub-set of the outbreaks, including three outbreaks attributed to raw milk consumption. While *C. hominis* was reported to be the most common cause of outbreaks of cryptosporidiosis, the three outbreaks associated with raw milk were caused by *C. parvum*.

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 a specimen from the human gastrointestinal tract.
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 2023 are given in Table 21.

Table 21. Summary of surveillance data for giardiasis, 2023

Parameter	Value in 2023	Source
Number of notified cases	897	EpiSurv
Notification rate (per 100,000)	17.2	EpiSurv
Hospitalised cases[a]	43	NMDS
Deaths[b]	0	EpiSurv
Travel-related cases [c, d]	89	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] No deaths with giardiasis recorded as the primary cause of death, one giardiasis case died from other causes.

[c] Number of notified cases reporting overseas travel as risk factor. 372 cases had not travelled overseas during the incubation period and for the remaining 436 cases travel history is unknown.

[d] While New Zealand borders opened again for international travel in 2022, overseas travel in 2023 was still reduced compared to pre-COVID-19 years.

Changes to laboratory methods

Since 2015, laboratories across New Zealand have changed the methodology for testing faecal specimens (Appendix B, page 123). In October 2023, laboratories servicing community faecal specimens for Canterbury and South Canterbury have changed to CIDT methods, including testing for *Giardia* spp.. In 2023, community faecal specimens in all Health Districts except for Bay of Plenty, Lakes, Waikato and West Coast were screened by PCR methods for a range of pathogens, including *Giardia* spp.. All community faecal specimens in these Health Districts are now screened for *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.

Notification rates for giardiasis have not changed significantly since the introduction of PCR-based methods, which enabled the testing of increased numbers of samples (Figure 19). This suggests that symptoms of giardiasis were generally well recognised leading to appropriate requests for testing.

Giardiasis individual cases reported in 2023 by data source

During 2023, 897 individual cases (17.2 cases per 100,000 population) of giardiasis were reported in EpiSurv. Of the 897 cases, the symptoms of 875 cases (98%) were reported as fitting the clinical description for giardiasis, the symptoms were unknown for 21 cases, and for one case the symptoms were reported as not fitting the clinical description.

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 43 hospitalised cases (0.8 hospitalised cases per 100,000 population) recorded in 2023, 21 cases were reported with giardiasis as the principal diagnosis and 22 were reported with giardiasis as another relevant diagnosis. One hospitalised case was admitted to hospital twice resulting in a total of 44 hospital admissions.

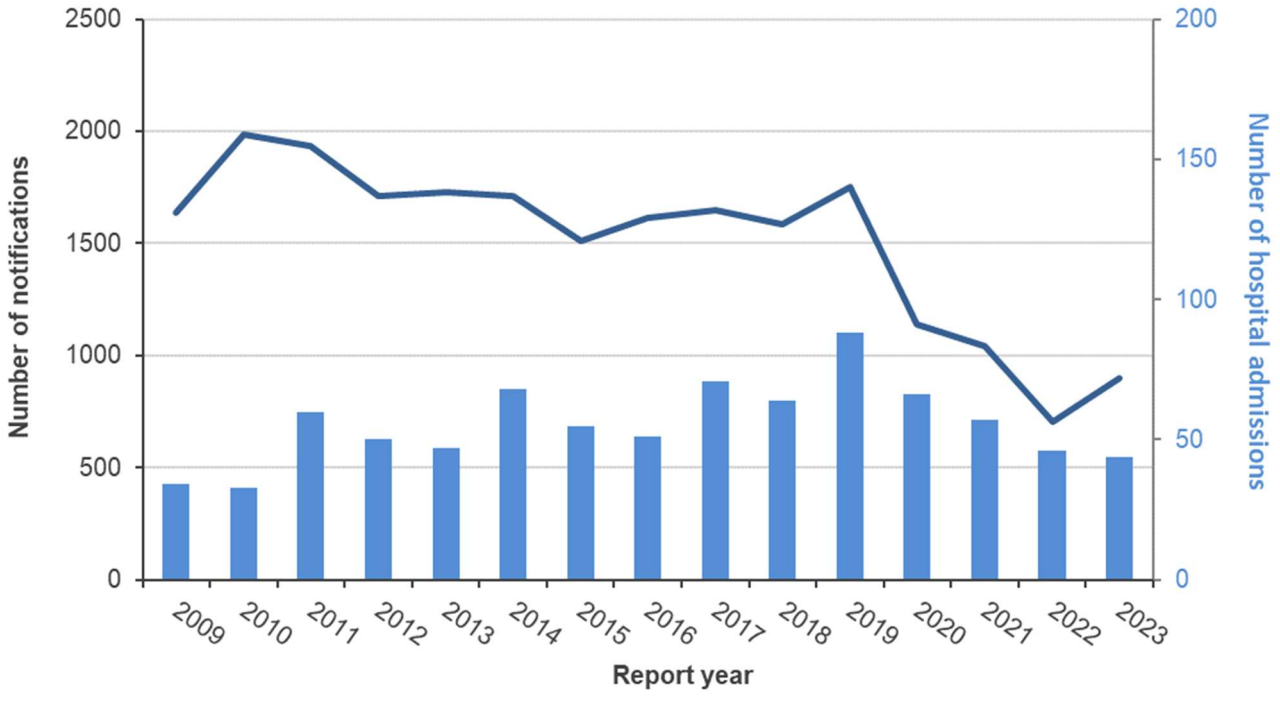
It should be noted that EpiSurv and the NMDS database are separate systems and hospital admission can occur without cases being notified in EpiSurv. This means that not all cases diagnosed with giardiasis in hospital are reported in EpiSurv.

Annual data

From 2009 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 the following years. The hospital admissions have not dropped to the same extent as the notified cases following 2019.

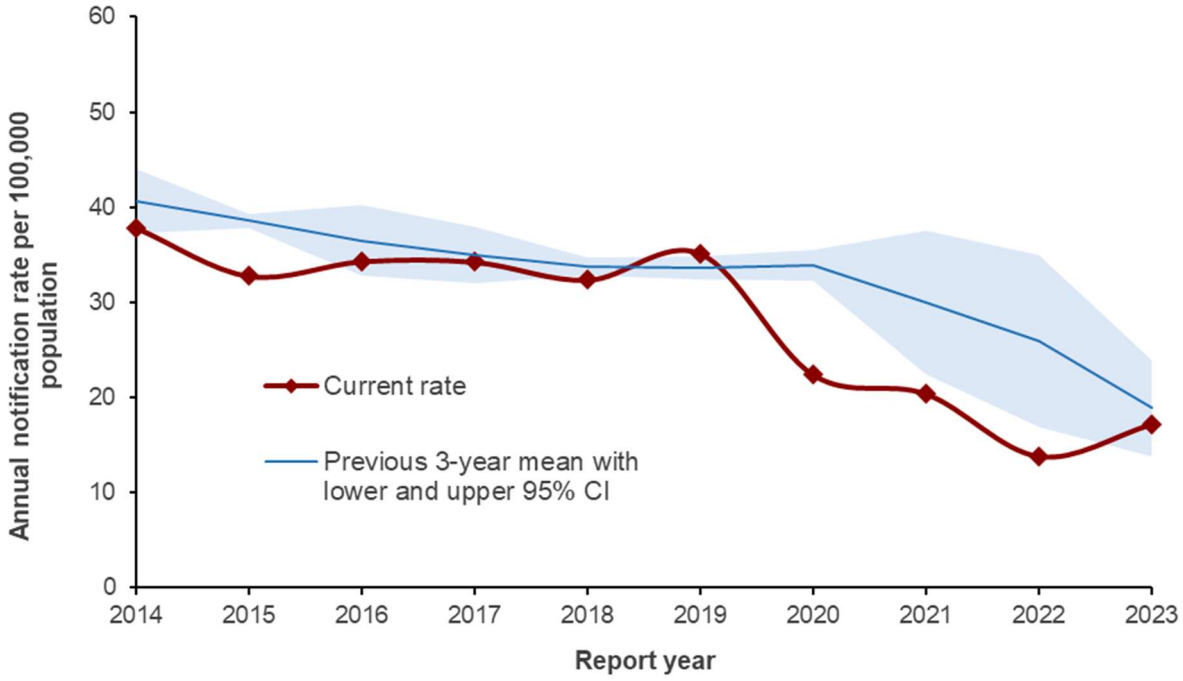
The frequency of overseas travel was lower in 2020 to 2023 compared to pre COVID-19 years (see Introduction, page 9). This is reflected in the notifications; in 2023, there were 89 giardiasis notifications in EpiSurv listing overseas travel as a risk factor, compared to 179 in 2019, 59 in 2020, six in 2021 and 35 in 2022.

Figure 18. Giardiasis EpiSurv notifications (line) and NMDS hospitalisations (bar) by year, 2009–2023



In 2023, the notification rate for giardiasis (17.2 cases per 100,000 population) was similar to the previous three-year mean (18.8 cases per 100,000 population) (Figure 19). The drop in notification rates 2020 to 2022 can be attributed to the COVID-19 pandemic [16].

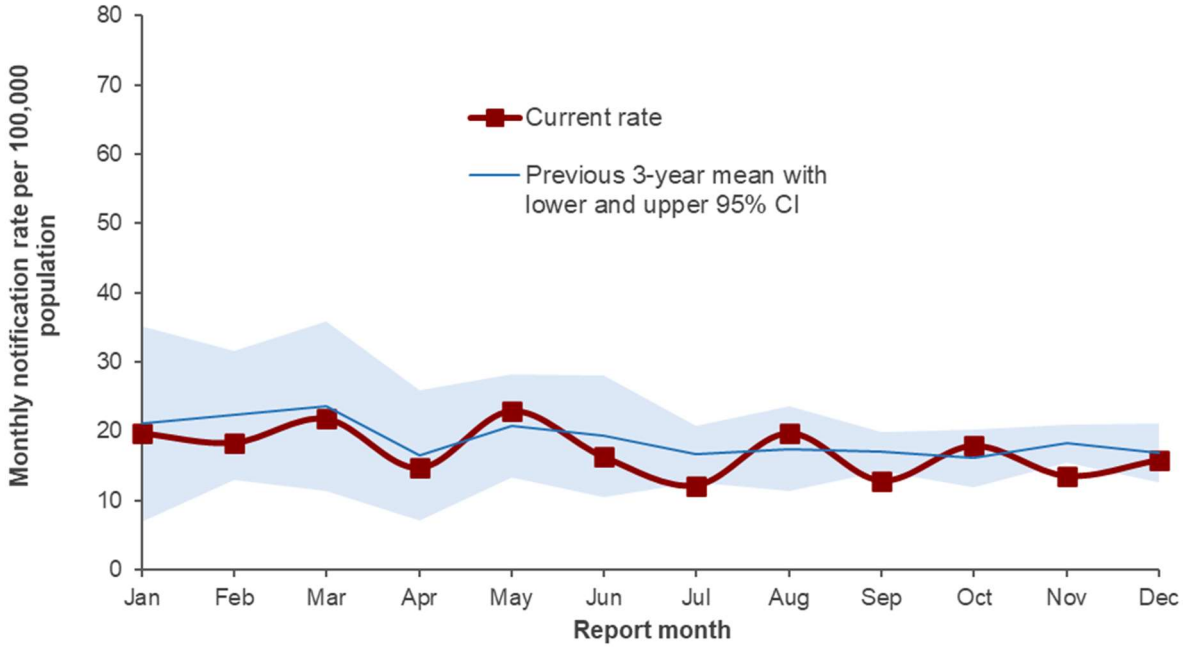
Figure 19. Giardiasis notification rate by year, 2014–2023



Seasonal data

Giardiasis notification rates per 100,000 population by month for 2023 are shown in Figure 20. There was no seasonal pattern in notification rates, similar to the three previous years. The monthly number of notifications in 2023 ranged from 53 cases (July, 12.2 cases per 100,000 population) to 100 cases (May, 23.0 cases per 100,000 population).

Figure 20. Giardiasis monthly notification rate (annualised), 2023



Demographics

In 2023, the rate of notifications for giardiasis was higher for males (18.6 cases per 100,000 population) compared with females (15.8 cases per 100,000 population). The rate of hospitalised cases was also higher for males (1.0 hospitalised cases per 100,000 population) compared to females (0.7 hospitalised cases per 100,000 population) (Table 22).

Table 22. Giardiasis cases by sex, 2023

Sex	EpiSurv notified cases		Hospitalised cases[a]	
	No.	Rate[b]	No.	Rate[b]
Male	482	18.6	25	1.0
Female	415	15.8	18	0.7
Total	**897**	**17.2**	**43**	**0.8**

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

[b] Per 100,000 population.

In 2023, the highest age-specific notification rate was for the 1 to 4 years age group (51.4 notified cases per 100,000 population) (Table 23). The highest hospitalised case rate was also reported for the 1 to 4 years age group (2.9 hospitalised cases per 100,000 population).

Table 23. Giardiasis cases by age group, 2023

Age group (years)	EpiSurv notified cases		Hospitalised cases[a]	
	No.	Rate[b]	No.	Rate[b]
<1	12	21.0	1	-
1 to 4	126	51.4	7	2.9
5 to 9	60	18.6	1	-
10 to 14	19	5.5	1	-
15 to 19	17	5.2	6	1.8
20 to 29	132	19.3	3	0.4
30 to 39	195	25.3	2	-
40 to 49	89	13.8	2	-
50 to 59	84	12.8	8	1.2
60 to 69	107	18.6	6	1.0
70+	56	9.3	6	1.0
Total	**897**	**17.2**	**43**	**0.8**

[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

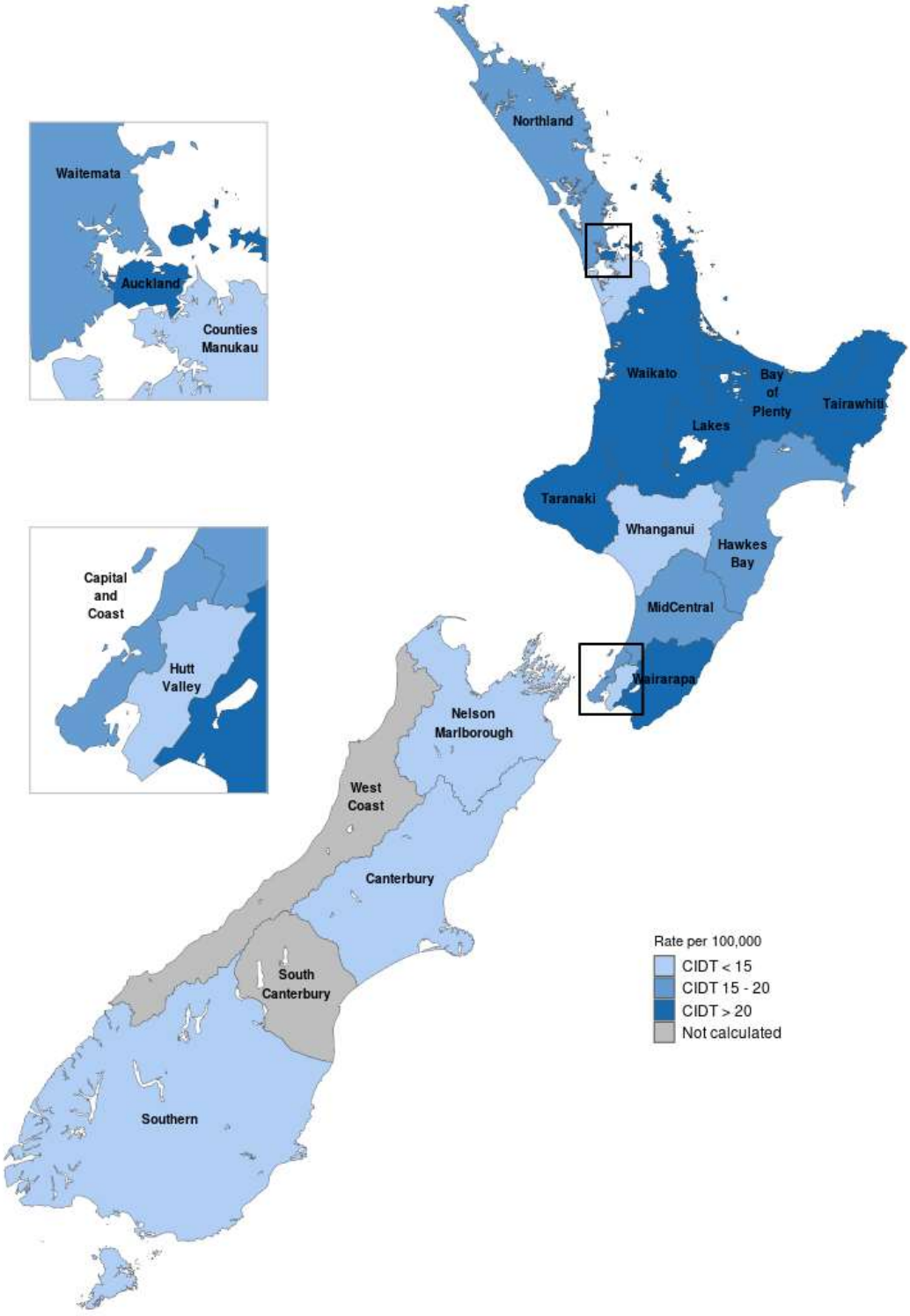
The notification rates by Health District calculated per 100,000 resident population are presented in Figure 21. The rate has not been calculated for Health Districts with fewer than five cases (grey shading): West Coast (three cases) and South Canterbury (three cases).

In 2023, the Health District notification rates for giardiasis ranged from 8.8 cases per 100,000 population (53 cases) in Canterbury to 45.6 cases per 100,000 population (24 cases) in Tairāwhiti. The Health Districts Tairāwhiti, Wairarapa (31.3 cases per 100,000 population, 16 cases) and Bay of Plenty (29.7 cases per 100,000 population, 83 cases) had the highest notification rates.

Historically, notification rates for giardiasis have been variable across New Zealand with Tairāwhiti Health District in the highest quartile consistently since 2017.

Giardiasis notification rates, stratified by 2023 Urban Rural Classification [20] of the cases' residential address and excluding cases associated with overseas travel were higher in rural areas than urban areas. Rates of cases residing in urban category areas ranged from 11.6 to 19.2 cases per 100,000 population. The highest rate was for the 'rural other' category (20.1 cases per 100,000 population).

Figure 21. Geographic distribution of giardiasis notifications, 2023



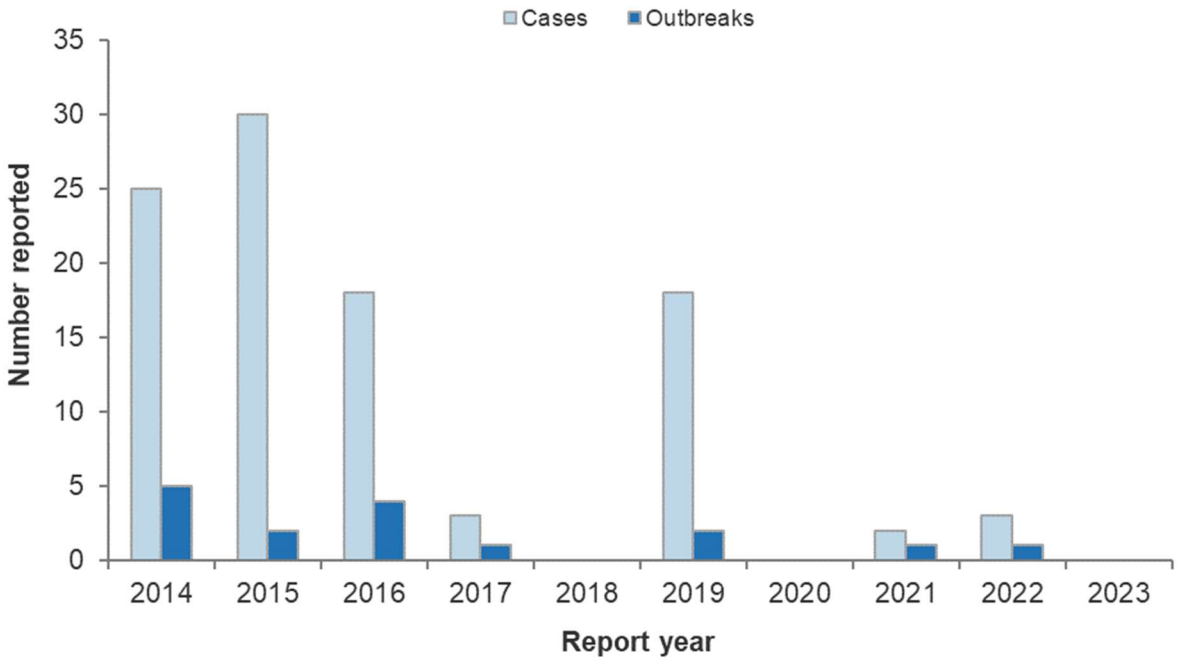
Note: Canterbury and South Canterbury Health Districts changed to community laboratory testing by CIDT methods in October 2023. The plotted rates in these areas will not reflect a full year of CIDT testing in 2023.

Outbreaks reported as caused by *Giardia spp.*

In 2023, there were 10 giardiasis outbreaks with 39 associated cases and one hospitalised case reported in EpiSurv. Two of these outbreaks (10 cases) were associated with overseas travel. None of the domestic outbreaks reported food as a possible mode of transmission.

Over the 10-year period 2014 and 2023, between zero and five giardiasis outbreaks with food reported as a possible mode of transmission were notified each year with between two 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, 2014–2023



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, elevated serum aminotransferase levels and sometimes an enlarged tender liver. 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 (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 2023 are given in Table 24.

Table 24. Summary of surveillance data for hepatitis A, 2023

Parameter	Value in 2023	Source
Number of notified cases	34	EpiSurv
Notification rate (per 100,000)	0.7	EpiSurv
Hospitalised cases[a]	32	NMDS
Deaths	0	EpiSurv
Travel-related cases[b,c]	24	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 28 cases were hospitalised with acute hepatitis A as another relevant diagnosis. Cases hospitalised may not be notified on EpiSurv.

b Number of notified cases for whom overseas travel history was reported. 10 cases had not travelled overseas during the incubation period. For all notified cases travel history was recorded.

c While New Zealand borders opened again for international travel in 2022, overseas travel in 2023 was still reduced compared to pre-COVID-19 years.

Hepatitis A individual cases reported in 2023 by data source

During 2023, 34 individual cases (0.7 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 with 71% of notified cases recorded in EpiSurv as hospitalised in 2023.

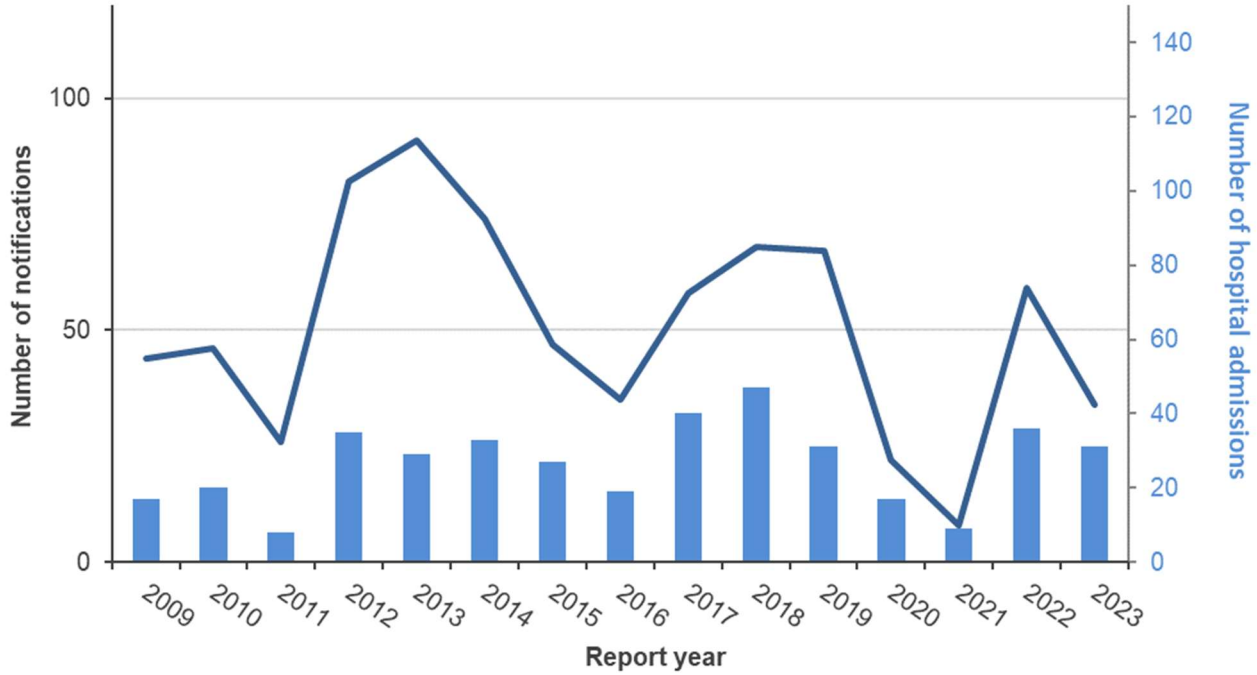
The ICD-10 code B15 was used to extract acute hepatitis A hospitalisation data from the Health New Zealand Te Whatu Ora NMDS database. There were 60 hospitalised cases (1.3 hospitalised cases per 100,000 population) recorded in the NMDS in 2023; 32 cases were reported with acute hepatitis A as the principal diagnosis and 28 cases with acute hepatitis A as another relevant diagnosis. Four of the 60 hospitalised cases were admitted to hospital more than once resulting in a total of 65 hospital admissions.

It should be noted that EpiSurv and the NMDS database are separate systems and hospital admission can occur without cases being notified in EpiSurv. Upon hospital discharge, patients are assigned disease codes using the ICD-10 coding system [15]. This may be different from the diagnoses for the patient on admission, while in hospital, or from the final diagnosis after discharge. For these reasons, hospitalisation and notification numbers may differ and not all cases recorded with hepatitis A in NMDS are reported in EpiSurv, resulting in diverging numbers between the databases.

Annual data

Between 2009 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 frequency of overseas travel was lower in 2020 to 2023 compared to pre COVID-19 years (see Introduction, page 9). This is reflected in the notifications; there were 24 hepatitis A notifications in EpiSurv listing overseas travel as a risk factor in 2023, compared to 33 in 2019, 16 in 2020 and two in 2021, and 20 in 2022.

Figure 23. Hepatitis A EpiSurv notifications (line) and NMDS hospitalisations (bar) by year, 2009–2023



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

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 2023, the rate of notifications for hepatitis A was similar for females (0.7 cases per 100,000 population) and males (0.6 cases per 100,000 population). The rate of hospitalised cases was higher for males (1.4 hospitalised cases per 100,000 population) compared to females (0.9 hospitalised cases per 100,000 population) (Table 25).

Table 25. Hepatitis A cases by sex, 2023

Sex	EpiSurv notified cases		Hospitalised cases[a]	
	No.	Rate[b]	No.	Rate[b]
Male	16	0.6	36	1.4
Female	18	0.7	24	0.9
Total	**34**	**0.7**	**60**	**1.1**

[a] Health New Zealand Te Whatu NMDS data for hospitalised cases with hepatitis A as the principal diagnosis.

[b] Per 100,000 population.

In 2023, the highest age-specific notification rate was for the 20 to 29 years age group (1.3 cases per 100,000 population) (Table 26). The highest hospitalised case rate was reported for the 70+ years age group (2.5 hospitalised cases per 100,000 population).

Table 26. Hepatitis A cases by age group, 2023

Age group (years)	EpiSurv notified cases		Hospitalised cases[a]	
	No.	Rate[b]	No.	Rate[b]
<1	0	-	0	-
1 to 4	1	-	2	-
5 to 9	4	-	2	-
10 to 14	0	-	0	-
15 to 19	4		5	1.5
20 to 29	9	1.3	7	1.0
30 to 39	7	0.9	10	1.3
40 to 49	2	-	5	0.8
50 to 59	1	-	7	1.1
60 to 69	3	-	7	1.2
70+	3	-	15	2.5
Total	**34**	**0.7**	**60**	**0.7**

[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).

Outbreaks reported as caused by hepatitis A virus

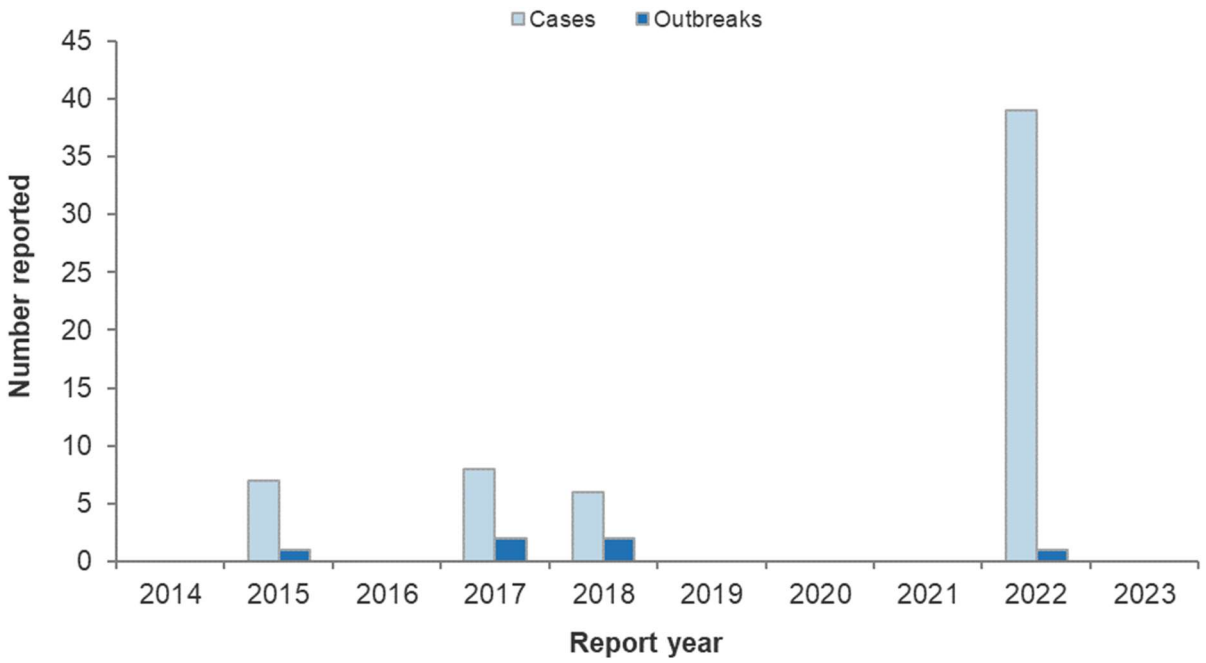
In 2023, no new hepatitis A outbreaks were reported in EpiSurv.

In 2023, a further four cases were reported for the large outbreak associated with imported frozen berries first reported in 2022. Of the 39 cases reported between June 2022 and April 2023, nine cases were likely due to secondary transmission. Hepatitis A virus of the same type as clinical isolates was detected in one opened bag of frozen berries submitted from one of the cases. NZFS

issued a public advisory message to cook imported berries before consuming and a consumer level recall of affected imported frozen berries was undertaken.

In the previous 10 years, there were seven potentially foodborne domestic outbreaks with a total of 60 associated cases (Figure 24).

Figure 24. Hepatitis A outbreaks reported in EpiSurv with food reported as a possible mode of transmission and associated cases (excluding outbreaks associated with overseas travel) reported by year, 2014–2023



Hepatitis A virus genotypes commonly reported

In 2023, faecal and/or serum/plasma specimens from 27 hepatitis A cases were submitted to ESR's Enteric, Environmental and Food Virology Laboratory for hepatitis A virus typing (Table 27). This compares to 57 hepatitis A cases in 2022 and four hepatitis A cases in 2021, respectively. The data include those cases not associated with foodborne transmission.

Table 27. Hepatitis A virus genotypes identified in case specimen by the Enteric, Environmental and Food Virology Laboratory, 2019–2023

Hepatitis A virus genotypes	2019	2020	2021	2022	2023
IA	24	10	2	35	8
IIIA	8	4	2	19	16
IB	1	2	0	2	2
Unable to genotype	1	0	0	1	0
Total	**34**	**16**	**4**	**57**	**27**

Hepatitis A virus genotypes IA, IIIA, and IB were identified in cases in 2023. While hepatitis A virus IA was the most commonly identified sub-genotype between 2019 and 2022, in 2019 and 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, particularly with III.A, was observed.

Recent surveys

Nil.

Relevant New Zealand studies and publications

Nil.

Relevant regulatory developments

No hepatitis A virus-specific regulatory developments.

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 ≥ 50mg/100g fish muscle.
Case classification:	Not applicable.

Histamine (scombroid) fish poisoning cases reported in 2023 by data source

During 2023, 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. Of the 10 hospitalised cases (0.2 hospitalised cases per 100,000 population) recorded in 2023, nine cases were reported with histamine (scombroid) fish poisoning as the principal diagnosis and one case with histamine (scombroid) fish poisoning as another relevant diagnosis.

It should be noted that EpiSurv and the NMDS database are separate systems and hospital admission can occur without cases being notified in EpiSurv. This means that not all cases diagnosed with histamine (scombroid) fish poisoning in hospital are reported in EpiSurv.

Outbreaks reported as caused by histamine (scombroid) fish poisoning

In 2023, no histamine (scombroid) fish poisoning outbreaks were reported in EpiSurv.

In addition to EpiSurv records, a single outbreak of suspected scombroid fish poisoning (two notified cases) relating to smoked fish bought from a supermarket (Table 28) was referred to NZFS. Leftover fish samples were sent to ESR for testing and histamine levels of concern were confirmed, providing strong evidence for scombroid fish poisoning. Onsite investigation occurred and control failures were resolved.

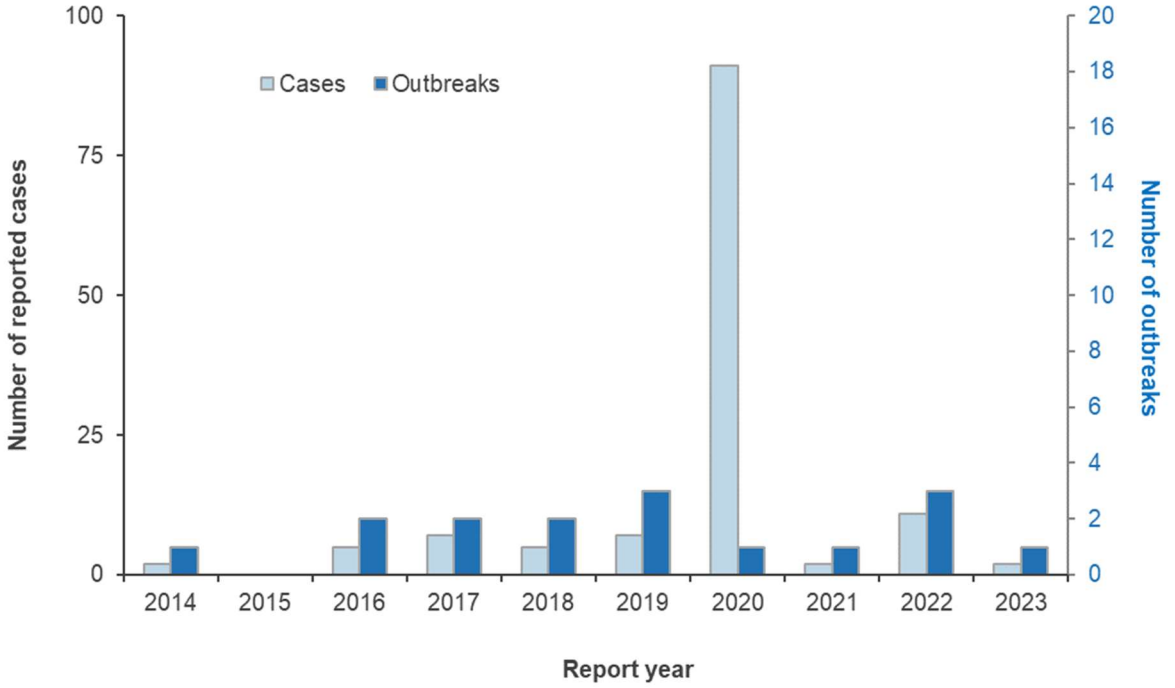
Table 28. Details of histamine (scombroid) fish poisoning outbreak referred to NZFS, 2023

PHS	Month	Suspected source	Evidence	Setting	No. ill
Auckland Regional	March	Smoked fish (kahawai)	Common food	Home	2C

PHS: Public Health Service

Over the 10-year period 2014 and 2023, 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, 2014–2023



Note: The figure includes data primarily from EpiSurv. From 2022, the figure includes clusters of potentially foodborne disease referred to Food Compliance Services, NZFS, that were not recorded as a potentially foodborne outbreak in EpiSurv (2022: two outbreaks, three and six cases; 2023: one outbreak, two cases).

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.

Summary data

Summary data for listeriosis in 2023 are given in Table 29.

Table 29. Summary of surveillance data for listeriosis, 2023

Parameter	Value in 2023	Source
Number of notified cases[a]	37	EpiSurv
Notification rate (per 100,000)	0.7	EpiSurv
Hospitalised cases[b]	40	NMDS
Deaths	7[c]	EpiSurv
Travel-related cases[d]	0	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 (34) and perinatal cases (3).

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

[c] Five non-perinatal cases and two perinatal cases died with listeriosis recorded as the primary cause of death. Four additional non-perinatal cases died but with listeriosis not recorded as the primary cause of death.

[d] Number of notified cases reporting overseas travel as risk factor. 35 cases had not travelled overseas during the incubation period and for the remaining two cases travel history is unknown. While New Zealand borders opened again for international travel in 2022, overseas travel in 2023 was still reduced compared to pre-COVID-19 years.

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

Listeriosis individual cases reported in 2023 by data source

During 2023, 37 individual cases (0.7 per 100,000 population) of listeriosis (34 non-perinatal related cases and three perinatal cases) were reported in EpiSurv with five non-perinatal resulting deaths and two perinatal deaths. An additional four non-perinatal cases in the 60+ age group died but listeriosis was not listed as the primary cause of death. Hospitalisation rates are usually very high for listeriosis with 37 notified cases recorded as hospitalised in 2023 (100%) in EpiSurv.

The ICD-10 code A32 was used to extract listeriosis hospitalisation data from the Health New Zealand Te Whatu Ora NMDS database. Of the 40 hospitalised cases (0.8 hospitalised cases per 100,000 population) recorded in 2023, 21 cases were reported with listeriosis as the principal diagnosis and 19 cases with listeriosis as another relevant diagnosis.

It should be noted that EpiSurv and the NMDS database are separate systems and hospital admission can occur without cases being notified in EpiSurv. Upon hospital discharge, patients are assigned disease codes using the ICD-10 coding system [15]. This may be different from the diagnoses for the patient on admission, while in hospital, or from the final diagnosis after discharge. For these reasons, hospitalisation and notification numbers may differ and not all cases recorded with listeriosis in NMDS are reported in EpiSurv, resulting in diverging numbers between the databases.

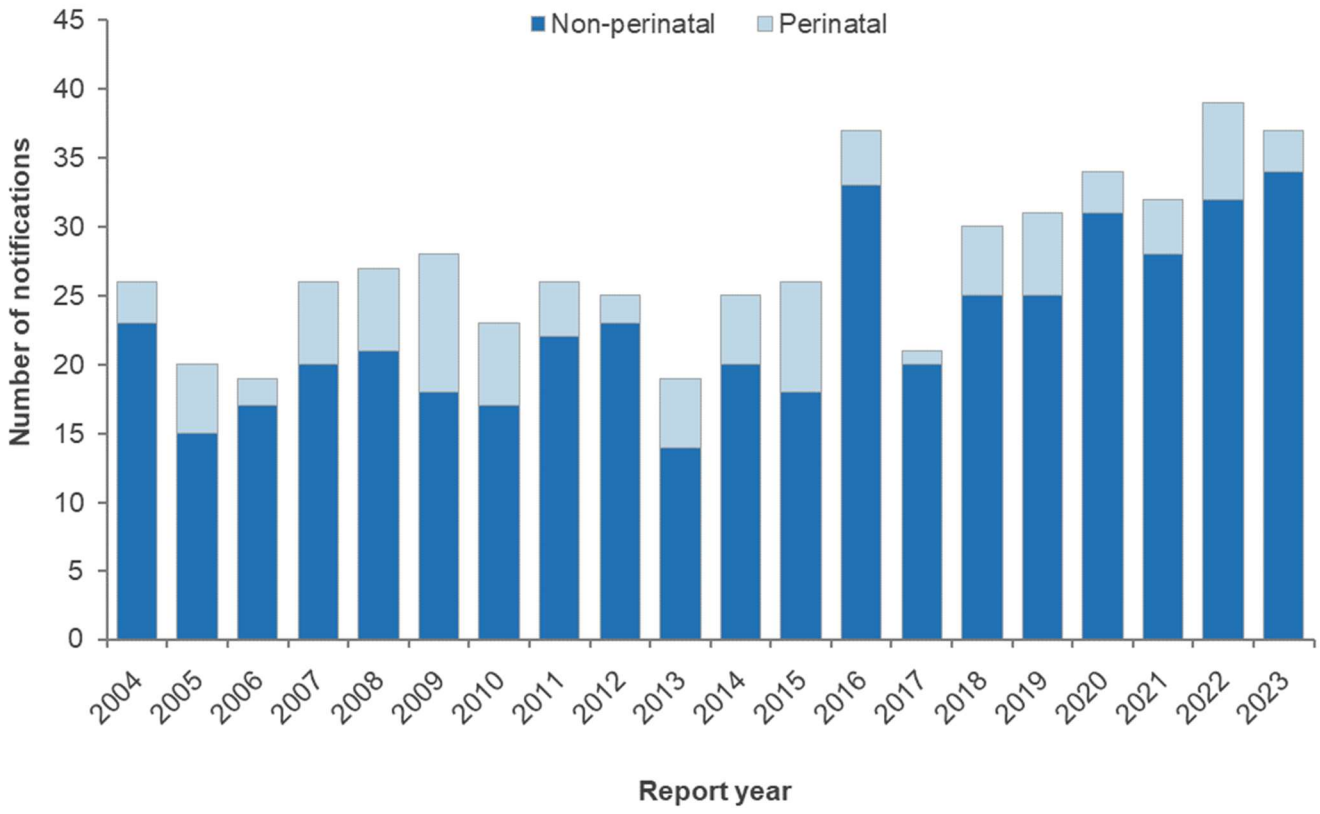
Foodborne transmission

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 2004 and 2023, 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 2023, overseas travel was not recorded as a risk factor for any of the cases.

Figure 26. Listeriosis EpiSurv non-perinatal and perinatal notifications by year, 2004–2023



Demographics

In 2023, notification and hospitalised case rates for listeriosis were higher for males (0.9 notified cases and 0.9 hospitalised cases per 100,000 population) than for females (0.5 notified cases and 0.6 hospitalised cases per 100,000 population) (Table 30). It should be noted that notification case details for perinatal cases are those for the mother, so the female cases include the three perinatal cases.

Table 30. Listeriosis cases by sex, 2023

Sex	EpiSurv notified cases		Hospitalised cases[a]	
	No.	Rate[b]	No.	Rate[b]
Male	24	0.9	23	0.9
Female	13	0.5	17	0.6
Total	**37**	**0.7**	**40**	**0.8**

[a] Health New Zealand Te Whatu Ora NMDS data. The total may include cases admitted on more than one occasion (readmissions).

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

In 2023, notification and hospitalised case rates for listeriosis were highest in the 70+ years age group (3.5 notified cases and 3.5 hospitalised cases per 100,000 population) (Table 31).

Table 31. Listeriosis cases by age group, 2023

Age group (years)	EpiSurv notified cases		Hospitalised cases[a]	
	No.[b]	Rate[c]	No.	Rate[c]
<1	0	-	0	-
1 to 4	2	-	2	-
5 to 9	0	-	0	-
10 to 14	0	-	0	-
15 to 19	0	-	1	-
20 to 29	3	-	4	-
30 to 39	1	-	3	-
40 to 49	3	-	3	-
50 to 59	2	-	1	-
60 to 69	5	0.9	5	0.9
70+	21	3.5	21	3.5
Total	**37**	**0.7**	**40**	**0.8**

[a] NMDS data for cases hospitalised with recorded diagnosis code: ICD-10 code A32.

[b] For perinatal cases the age reported is the mother's age.

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

Outbreaks reported as caused by *Listeria* spp.

In 2023, no listeriosis outbreaks were reported in EpiSurv.

Since 2006 there have been four other 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

ESR's Special Bacteriology Laboratory reported receiving 35 human isolates of *L. monocytogenes* during 2023. Table 32 shows the number of isolates and percentage of *L. monocytogenes* serotypes reported by the Special Bacteriology Laboratory at ESR between 2019 and 2023. The annual number of isolates identified to be serotype O4 or serotype O1/2 has been in the range of 15 to 24 isolates and 11 to 18 isolates, respectively, over the 5-year period. The most common sequence types since 2019 were ST1 (55 cases in total) and ST4 (17 cases in total).

Table 32. *L. monocytogenes* serotypes and sequence types of case isolates identified by the Special Bacteriology Laboratory, 2019–2023

Serotype / Sequence type (ST)	2019	2020	2021	2022	2023
Serotype O1/2	**15**	**13**	**11**	**15**	**18**
ST120	2	1	1	1	0
ST14	1	0	0	0	3
ST155	2	1	2	0	1
ST204	0	0	1	1	0
ST224	1	2	0	1	1
ST26	0	1	0	1	1
ST321	1	4	1	1	1
ST324	0	0	0	3	1
ST424	1	0	0	1	0
ST451	0	0	1	2	1
ST489	0	1	0	0	0
ST59	2	0	1	1	1
ST7	0	0	0	0	0
Other ST	3	3	2	0	8
Serotype O4	**15**	**18**	**21**	**24**	**16**
ST1	6	10	11	16	12
ST2	3	1	3	1	0
ST220	1	0	0	0	0
ST4	3	5	4	3	2
ST455	1	2	2	1	0
Other ST	1	0	1	3	2
Non-serotypable	**0**	**0**	**0**	**0**	**1**
Total	**30**	**31**	**32**	**39**	**35**

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 2023 by data source

During 2023, 49 individual cases of norovirus infection were reported in EpiSurv of which 29 were reported associated to outbreaks. A single norovirus case in the 90+ age group was recorded as dying from unknown causes in EpiSurv.

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). 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 831 hospitalised cases (15.9 hospitalised cases per 100,000 population) recorded in 2023, 410 cases were reported with norovirus infection as the principal diagnosis and 421 were reported with norovirus infection as another relevant diagnosis. Of the 831 hospitalised cases, 92 were in the 1 to 4 years age group and 353 were in the 70+ years age group.

It should be noted that EpiSurv and the NMDS database are separate systems and hospital admission can occur without cases being notified in EpiSurv. This means that not all cases diagnosed with norovirus infection in hospital are reported in EpiSurv.

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 2023, there were six notified outbreaks of norovirus infection recorded in EpiSurv which reported food or a food handler as one of the possible modes of transmission (Table 33). There were no 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 33. Norovirus infection outbreaks reported in EpiSurv, 2023

	Possible foodborne transmission with a suspected or confirmed source	Possible foodborne transmission but no suspected source	Total norovirus infection outbreaks
Outbreaks	3	3	245
Outbreak associated cases	67	70	6341
Outbreak hospitalised cases	0	0	89

Table 34 contains details of the six norovirus infection outbreaks with food reported as a possible mode of transmission in 2023. The evidence for foodborne transmission was weak for all six outbreaks. The March and June outbreaks were referred to NZFS and it was determined that unwell food handlers were likely to be the source of the illness.

The April outbreak was related to a family event. Eighty-five people completed a risk factor questionnaire which established an elevated risk of illness from consuming homemade crayfish sandwiches.

Table 34. Details of norovirus infection outbreaks in EpiSurv with food or food handling reported as a possible mode of transmission, 2023

PHS	Month	Suspected source	Evidence	Setting	No. Ill	Norovirus genotype
Auckland	March	Food handler	Common event	Restaurant/café/ bakery	2C 12P	GII.3 [P12]
Regional	April	Crayfish sandwiches	Common meal	Home	4C 52P	GII.3 [P12]
Auckland	June	Food handler	Common location	Restaurant/café/ bakery	2C 31P	GI.6 [P11]
Northland	August	Unknown	Common location	Workplace cafe	4C 19P	GII.7 [P7]
Hawke's Bay	September	Ham and egg sandwiches / food handler	Common meal	Restaurant/café/ bakery	7C	GII.4 Sydney[P16] & GII.7 [P7]
C and PH	October	Beef rissoles, potatoes, vegetables	Common meal	Home	4C	GII.7 [P7]

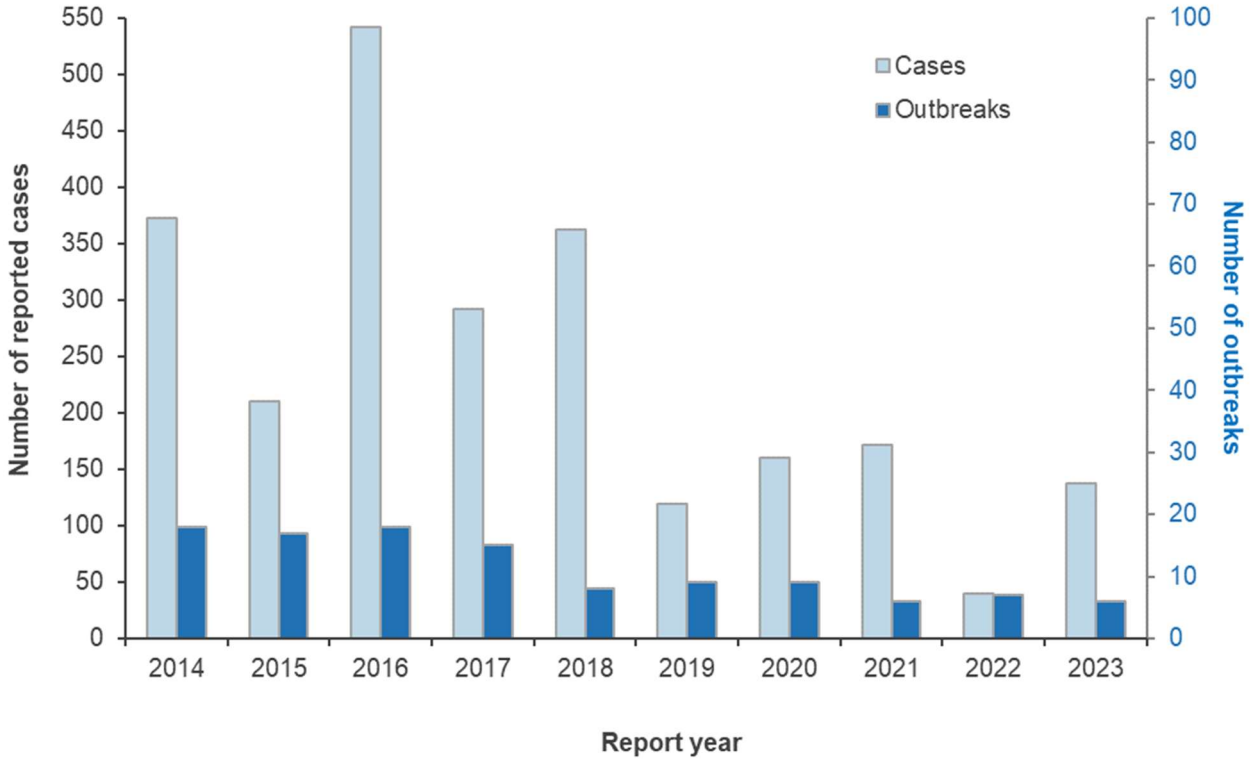
PHS: Public health service, Auckland: Auckland Regional Public Health Service, C and PH: Community and Public Health.

Number ill: C: confirmed, P: probable.

During investigation of suspected foodborne illness outbreaks by ESR's Public Health Laboratory and the Enteric, Food and Environmental Virology/Norovirus Reference Laboratory (NRL), faecal specimens relating to six outbreaks (Table 34) were received for norovirus testing. Norovirus was detected in faecal samples from those outbreaks. The outbreaks were associated with GII.4 Sydney[P16] (x1), GI.6[P11] (x1), GII.3[P12] (x2), GII.7[P7] (x3), with the September outbreak associated with two GII genotypes.

Over the 10-year period 2014 to 2023, 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 (2014 and 2016) (Figure 27). The total number of cases associated with these outbreaks each year ranged from 40 (2022) to 542 cases (2016).

Figure 27. Norovirus infection outbreaks with food reported as a possible mode of transmission and associated cases reported by year, 2014–2023



Note: The figure includes data primarily from EpiSurv. The figure includes clusters of potentially foodborne disease recorded by Food Compliance Services, NZFS, that were not recorded as an outbreak in EpiSurv (2022: two outbreaks, 17 cases).

Norovirus types commonly reported

Norovirus genotyping data from the NRL are shown in Table 35. 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 ESR for genotyping and not all gastroenteritis outbreaks caused by norovirus are reported as norovirus outbreaks in EpiSurv.

In 2023, 185 norovirus outbreaks were ESR laboratory-confirmed. Norovirus genogroup II (GII) was identified in 135/185 (73.0%) outbreaks. In the previous four years (2019-2022), GII was also the predominant norovirus genogroup being identified in between 77.3% (2021) and 91.3% (2022) of outbreaks.

The norovirus genotype was determined for 181/185 (97.8%) of ESR laboratory-confirmed norovirus outbreaks. GII.4 Sydney[P16] was the most common (82/185, 44.3% of outbreaks) genotype identified.

Table 35. Norovirus genotypes identified in outbreak-related cases by the Norovirus Reference Laboratory, 2019–2023

Norovirus genotypes	2019	2020	2021	2022	2023
Genogroup I	**32**	**33**	**22**	**10**	**49**
GI untyped	1	2	2	-	1
GI.1[P1]	-	-	-	-	1
GI.2[P2]	1	-	-	5	3
GI.3[P3]	9	5	-	-	8
GI.3[P13]	4	8	14	2	-
GI.4[P4]	5	-	-	1	1
GI.5[P4]	5	14	1	-	-
GI.5[P5]	1	-	-	2	25
GI.5[P12]	-	1	-	-	-
GI.6[P6]	4	-	-	-	
GI.6[P11]	1	3	5	-	8
GI.7[P7]	-	-	-	-	2
GI.8[P8]	-	-	-	-	-
GI.9[P9]	1	-	-	-	
Genogroup II	**147**	**125**	**75**	**126**	**135**
GII.2[P16]	17	93	35	5	4
GII.3[P12]	20	5	-	11	13
GII.4 Sydney[P16][a]	49	6	-	18	82
GII.4 Sydney[P31][a]	21	-	34	28	5
GII.4 Sydney[P4 New Orleans][a]	13	1	-	-	-
GII.6[P7]	13	3	2	54	1
GII.7[P7]	1	2	-	1	15
GII.8[P8]	-	1	-	-	2
GII.9[P7]	2	-	-	-	-
GII.10[P16]	3	-	-	-	-
GII.14[P7]	2	1	-	-	-
GII.17[P17]	1	6	2	2	8
Other[b]	5	7	2	7	5
Mixed GI and GII	**3**	**2**	-	**1**	**1**
Genogroup GIX[c]	-	**1**	-	**1**	-
Total outbreaks[d]	**182**	**161**	**97**	**138**	**185**

[a] GII.4 variants.

[b] 'Other' includes GII untyped, Mixed GII types, GII.3[P16], GII.3[P21], 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 ESR 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

Nil.

Relevant regulatory developments

No norovirus-specific regulatory developments.

Salmonellosis

Case definition

Clinical description:	Salmonellosis presents as gastroenteritis, with abdominal pains, diarrhoea (occasionally bloody), fever, nausea and vomiting. Asymptomatic infections may occur.
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	A clinically compatible illness that is laboratory confirmed.

Summary data

Summary data for salmonellosis in 2023 are given in Table 36. 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 36. Summary of surveillance data for salmonellosis, 2023

Parameter	Value in 2023	Source
Number of notified cases	827	EpiSurv
Notification rate (per 100,000)	15.8	EpiSurv
Hospitalised cases[a]	218	NMDS
Deaths[b]	0	EpiSurv
Travel-related cases[c, d]	256	EpiSurv
Estimated domestically acquired food-related cases[e]	325	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] One salmonellosis case was reported as having died in EpiSurv from a cause other than salmonellosis.

[c] Number of notified cases reporting overseas travel as risk factor. 445 cases had not travelled overseas during the incubation period and for the remaining 126 cases travel history is unknown.

[d] While New Zealand borders opened again for international travel in 2022, overseas travel in 2023 was still reduced compared to pre-COVID-19 years.

[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]. Estimate of cases acquired overseas calculated as Total cases X 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*.

Changes to laboratory methods

Since 2015, laboratories across New Zealand have changed the methodology for testing faecal specimens (Appendix B, page 123). In 2023, laboratories servicing community faecal specimens for Canterbury (October 2023), South Canterbury (October 2023), and West Coast (June 2023) have changed to CIDT methods. Since these changes were implemented community faecal specimens in all Health Districts were screened by CDIT for a range of pathogens, including *Salmonella* spp.

Following the introduction of CIDT methods there was no sustained increase in notification rates for salmonellosis [27].

Salmonellosis individual cases reported in 2023 by data source

During 2023, 827 individual cases (15.8 per 100,000 population) of salmonellosis were reported in EpiSurv. Of the 827 cases, the symptoms of 812 cases (98%) were reported as fitting the clinical description for salmonellosis, the symptoms were unknown for 12 cases, and for three cases the symptoms were reported as not fitting the clinical description. One salmonellosis case was recorded in EpiSurv as having died from a cause other than salmonellosis.

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 218 hospitalised cases (4.2 hospitalised cases per 100,000 population) recorded in 2023, 161 cases were reported with salmonellosis as the principal diagnosis and 57 were reported with salmonellosis as another relevant diagnosis. Eighteen of the 218 hospitalised cases were admitted to hospital more than once resulting in a total of 238 hospital admissions.

It should be noted that EpiSurv and NMDS database are separate systems and hospital admission can occur without cases being notified in EpiSurv. This means that not all cases diagnosed with salmonellosis in hospital are reported in EpiSurv.

Foodborne transmission

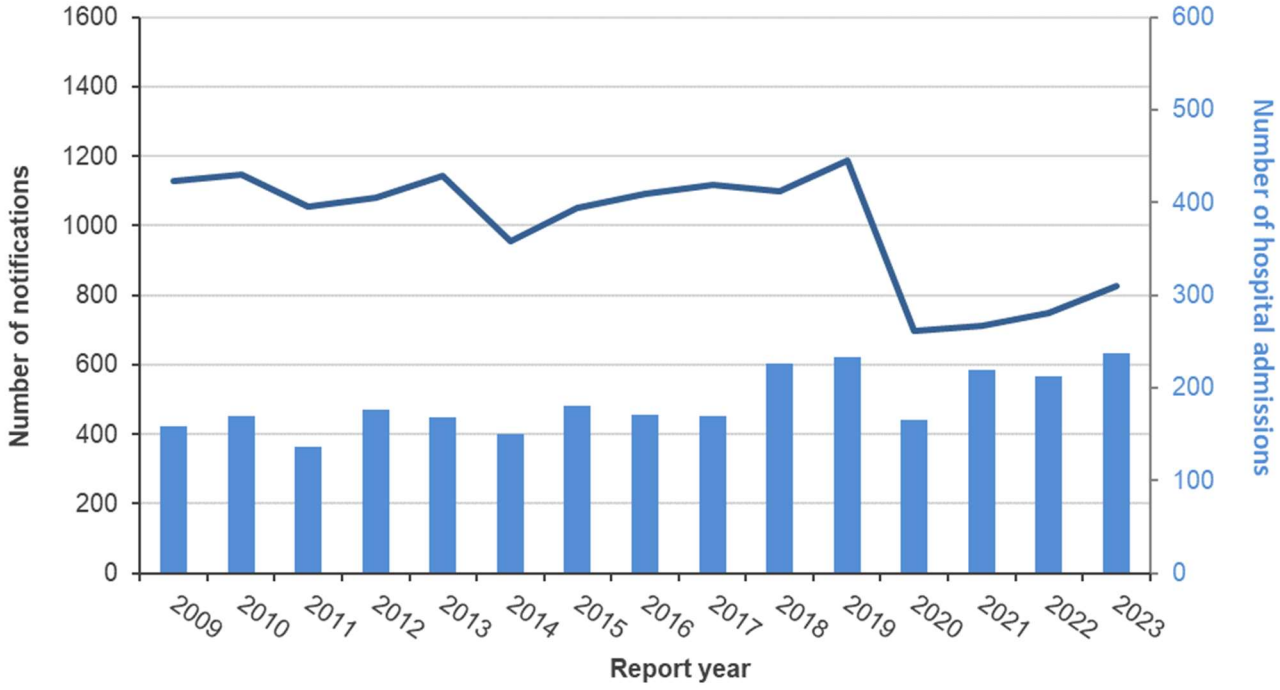
It has been estimated by expert consultation that 62.1% (95th percentile credible interval: 35.2% to 86.4%) of salmonellosis incidence is due to foodborne transmission. It was further estimated that approximately 19% of foodborne salmonellosis was due to transmission via poultry [2].

Annual data

Between 2009 and 2019 the number of salmonellosis notifications per year ranged between 955 (2014) and 1190 (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 [16] and the reduction in overseas travel (see Introduction, page 9). In 2023, there were 256 salmonellosis notifications in EpiSurv listing overseas travel as a risk factor, compared to 351 in the pre-COVID-19 year 2019, 49 in 2020, none in 2021 and 123 in 2022.

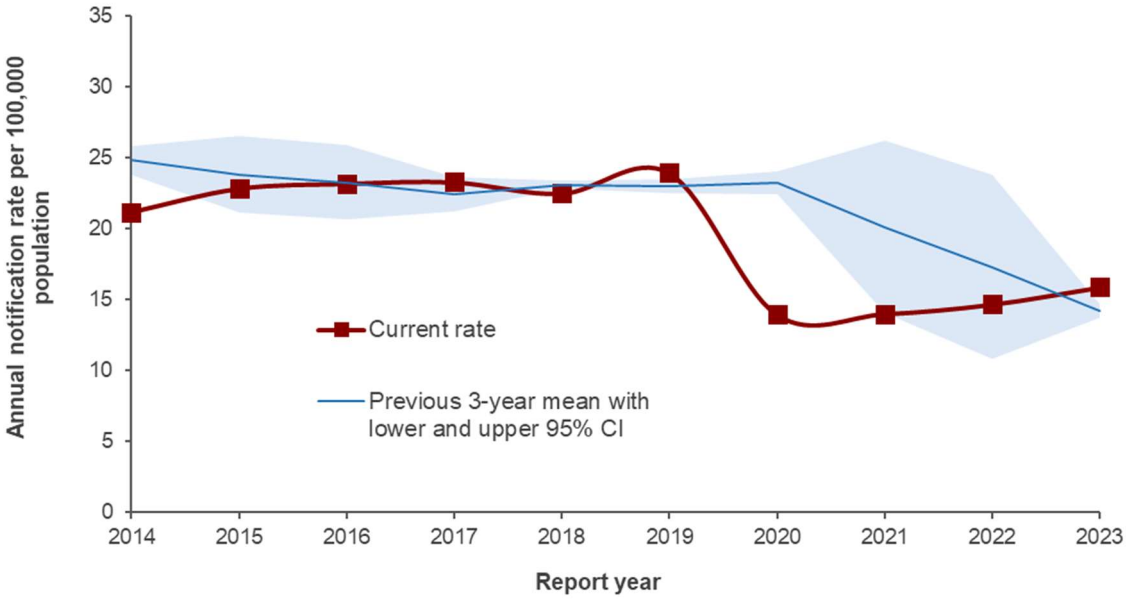
The number of hospital admissions with salmonellosis as a principal or other relevant diagnosis varied slightly year by year but did not show the same pronounced reduction in the years 2020 to 2023 as the number of annual notifications.

Figure 28. Salmonellosis EpiSurv notifications (line) and NMDS hospitalisations (bar) by year, 2009–2023



The notification rate in 2023 (15.8 cases per 100,000 population) was slightly higher than the previous three-year mean (14.2 cases per 100,000 population) (Figure 29).

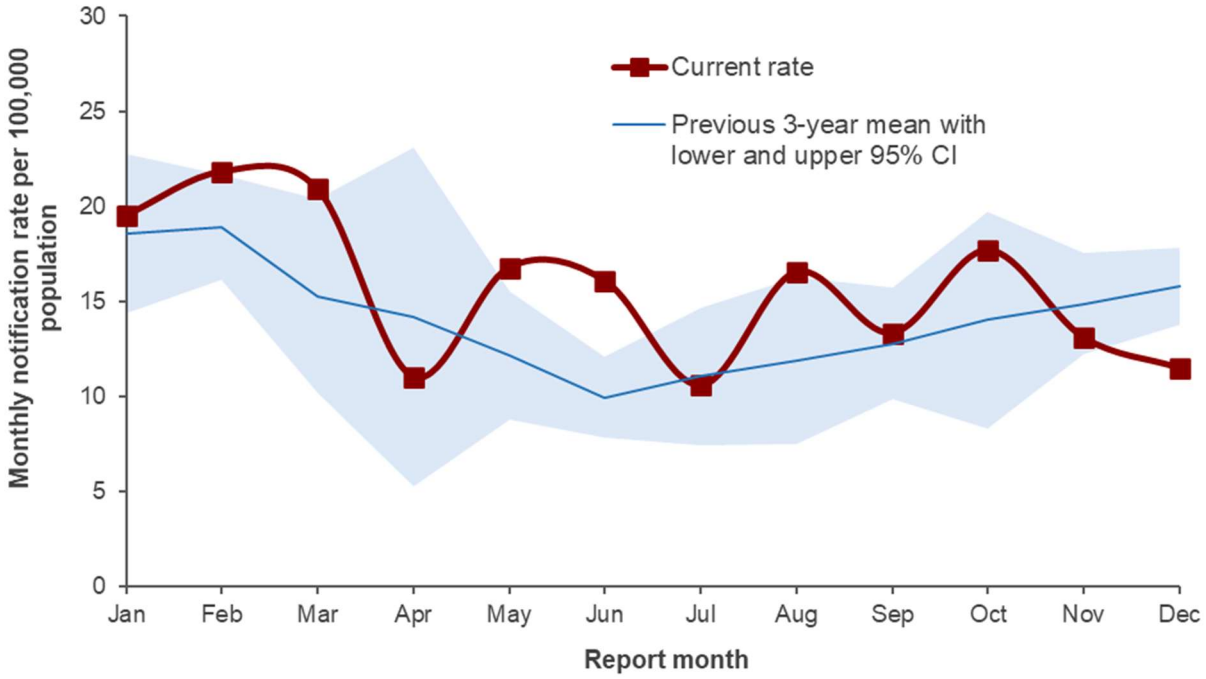
Figure 29. Salmonellosis notification rate by year, 2014–2023



Seasonal data

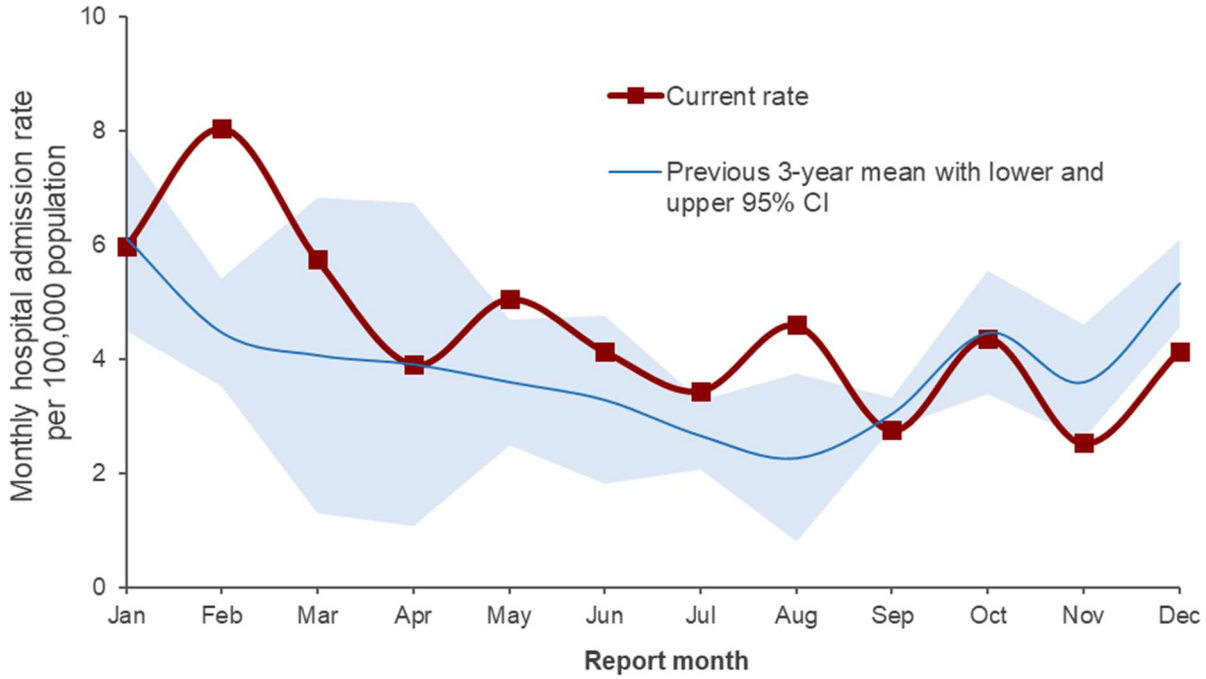
Salmonellosis case notification rates per 100,000 population by month for 2023 are shown in Figure 30. The monthly number of notifications in 2023 ranged from 46 cases (July, 10.6 cases per 100,000 population) to 95 cases (February, 21.8 cases per 100,000 population).

Figure 30. Salmonellosis monthly notification rate (annualised), 2023



In 2023, monthly hospital admission rates varied over the year (Figure 31) and followed a similar seasonal pattern to the previous three years, with slightly higher rates in February.

Figure 31. Salmonellosis monthly hospital admission rate (annualised), 2023



Demographics

In 2023, the notification rate for males was slightly higher (16.3 cases per 100,000 population, 424 cases) than for females (15.3 cases per 100,000 population, 401 cases). The rate of hospitalised cases was higher for females (4.4 hospitalised cases per 100,000 population, 116 hospitalised cases) compared to males (3.9 hospitalised cases per 100,000 population, 102 hospitalised cases) (Table 37).

Table 37. Salmonellosis cases by sex, 2023

Sex	EpiSurv notified cases		Hospitalised cases[a]	
	No.	Rate[b]	No.	Rate[b]
Male	424	16.3	102	3.9
Female	401	15.3	116	4.4
Total[c]	**827**	**15.8**	**218**	**4.2**

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

[b] Per 100,000 population.

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

In 2023, notification and hospital admission rates of salmonellosis were highest for children in the <1 years age group (73.5 cases and 19.2 hospitalised cases per 100,000 population) (Table 38).

Table 38. Salmonellosis cases by age group, 2023

Age group (years)	EpiSurv notified cases		Hospitalised cases[a]	
	No.	Rate[b]	No.	Rate[b]
< 1	42	73.5	11	19.2
1 to 4	114	46.5	20	8.2
5 to 9	48	14.8	7	2.2
10 to 14	28	8.2	4	-
15 to 19	38	11.6	6	1.8
20 to 29	74	10.8	20	2.9
30 to 39	88	11.4	23	3
40 to 49	78	12.1	18	2.8
50 to 59	105	16.1	25	3.8
60 to 69	107	18.6	38	6.6
70+	104	17.3	46	7.7
Total[c]	**827**	**15.8**	**218**	**4.2**

[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).

[c] Total includes one EpiSurv notification where age is unknown.

Geographic distribution

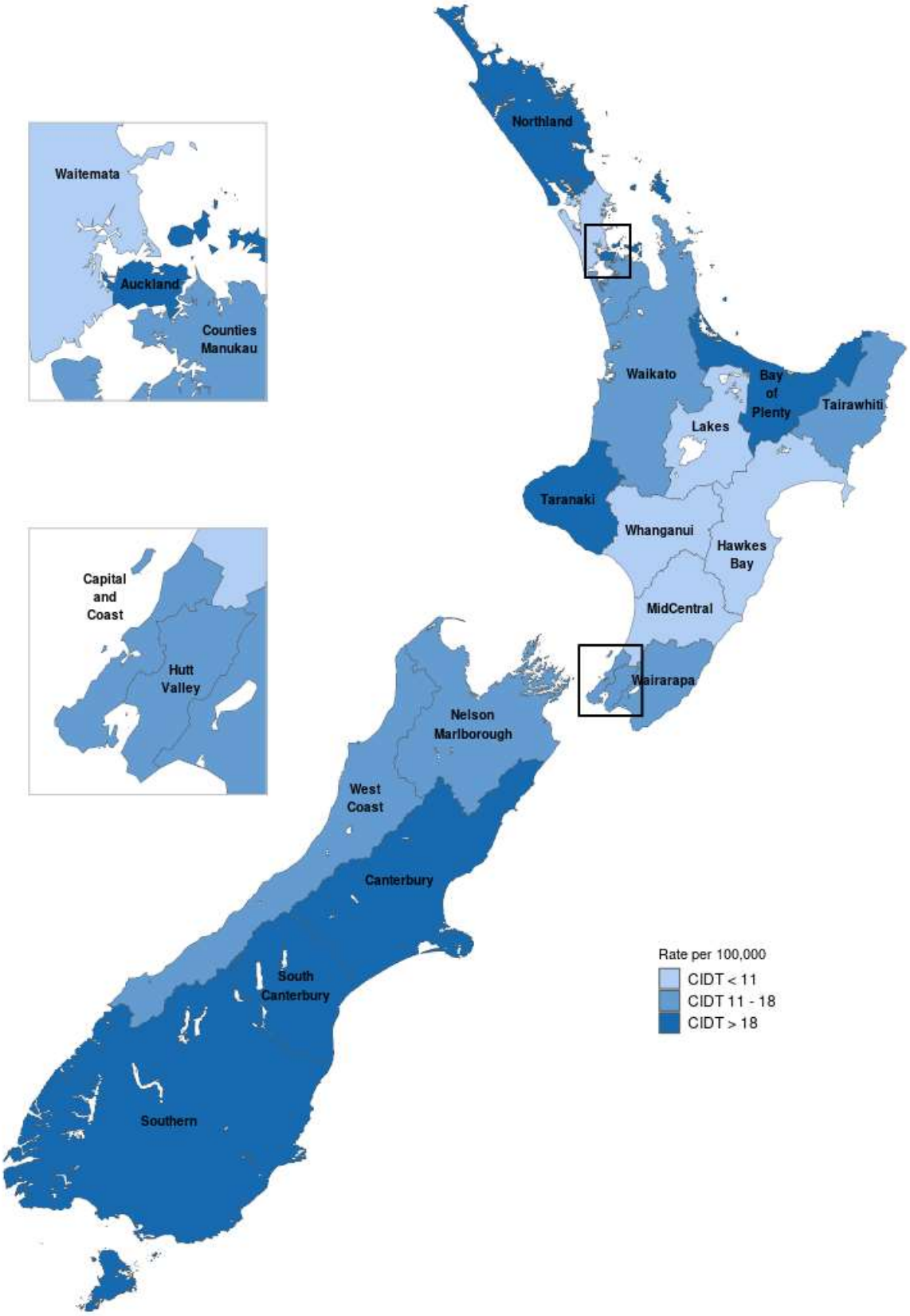
The notification rates by Health District calculated per 100,000 resident population are presented in Figure 32 (see also Table 80).

In 2023, the Health District notification rates of salmonellosis ranged from 9.2 per 100,000 population in Lakes (11 cases) to 38.1 cases per 100,000 population (24 cases) in South Canterbury. The Health Districts South Canterbury, Taranaki (29 cases), Canterbury (135 cases), Bay of Plenty (61 cases) and Southern (78 cases) had the next highest notification rates (21.6 to 22.5 cases per 100,000 population).

Historically, notification rates for salmonellosis have been highest in the lower half of the South Island. South Canterbury and Southern Health Districts have had rates in the highest quartile of notification rates since 2019. West Coast Health District has been in the highest quartile of notification rates from 2018 to 2021.

Salmonellosis notification rates, stratified by 2023 Urban Rural Classification [20] of the cases' residential address and excluding cases associated with overseas travel, were lower for urban area categories compared to rural categories (Appendix C Table 81). Rates for urban categories ranged from 8.7 to 11.8 per 100,000 population, while rates for rural categories were 14.0 cases per 100,000 population for 'rural settlement' areas and 19.8 cases per 100,000 population for 'rural other' areas.

Figure 32. Geographic distribution of salmonellosis notifications, 2023



Note: Canterbury and South Canterbury Health Districts changed to community laboratory testing by CIDT methods in October 2023 and the West Coast Health District in June 2023. The plotted rates in these areas will not reflect a full year of CIDT testing in 2023.

Outbreaks reported as caused by *Salmonella*

In 2023, there were four salmonellosis outbreaks notified in EpiSurv (29 cases and one hospitalisation), none of which were reported as potentially foodborne. While not being reported as potentially foodborne in EpiSurv, two outbreaks listed foodborne risk factors: One outbreak affecting two children from the same household listed handling raw meat and chicken during meal preparation as a risk factor, no other risk factors identified. A second outbreak of 15 cases was associated with a common community event that included a shared “bring a plate” meal. The community outbreak was listed as possibly due to person-to-person transmission in the outbreak report.

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 addition to EpiSurv records, one further salmonellosis outbreak due to a suspected food was referred to NZFS. This outbreak of two cases was suspected to be related to a milkshake or home cooked pork, but the source could not be confirmed.

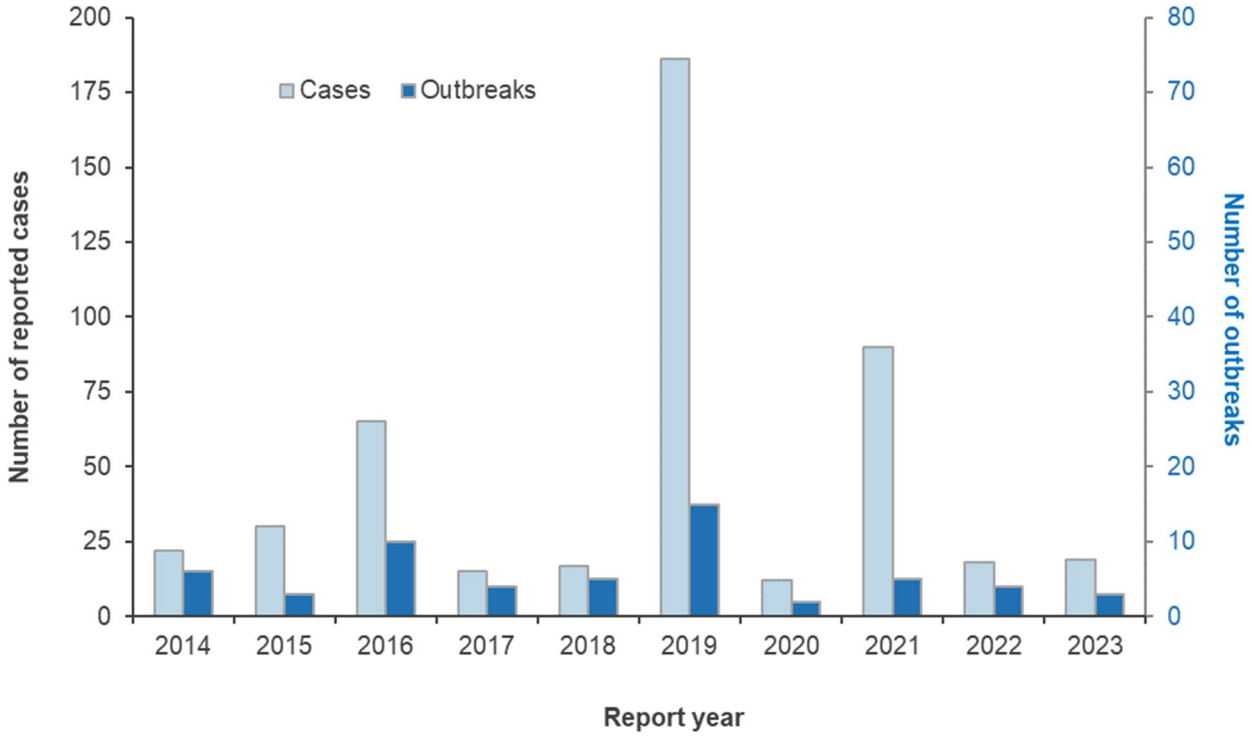
Table 39. Details of the suspected salmonellosis outbreaks with food reported as a possible mode of transmission, 2023

PHS	Month	Suspected source	Evidence	Setting	No. ill
PH South	March	Undercooked pork at home/ purchased milk shake	Common food	Home and takeaway	1C 1P

PHS: Public Health Service

Over the 10-year period 2014 to 2023, 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 5 (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, 2014–2023



Note: The figure includes data primarily from EpiSurv. The figure includes clusters of potentially foodborne disease referred to Food Compliance Services, NZFS, that were not recorded with food as a possible mode of transmission in EpiSurv (2022: two outbreaks, five cases, 2023: one outbreak, two cases).

Salmonella types commonly reported

Human isolates

In 2023, isolates from 827 notified cases with non-typhoidal *Salmonella* infections were typed by the ESR Enteric Reference Laboratory (Table 40). *S.* Typhimurium (237 cases) and *S.* Enteritidis (92 cases) were the most common serotypes identified. Other serotypes commonly reported were *S.* Stanley (27 cases), *S.* Saintpaul (26 cases), S. Weltevreden (25 cases), S. Bovismorbificans (24 cases) and *S.* Brandenburg (24 cases).

Table 40. Annual number of case notifications with different *Salmonella* serotypes identified by the Enteric Reference Laboratory, 2019–2023

Serotype[a]	2019	2020	2021	2022	2023	Count of cases with overseas travel history (%), 2023[b]	Count of cases with unknown travel history (%), 2023[c]
S. Typhimurium[d]	438	329	310	348	237	28 (12)	45 (19)
S. Enteritidis[d]	154	70	131	73	92	41 (45)	9 (10)
S. Agona	13	4	4	9	18	13 (72)	0
S. Bareilly	5	1	1	5	6	3 (50)	0
S. Bovismorbificans	47	60	50	43	24	1 (4)	3 (13)
S. Brandenburg	37	36	39	20	24	0	7 (29)
S. Chester	1	1	2	2	15	10 (67)	0
S. Give	1	5	2	9	2	0	1 (50)
S. Hvittingfoss	5	1	6	3	5	3 (60)	0
S. Infantis	27	7	9	5	8	2 (25)	0
S. Javiana	5	2	1	8	9	6 (67)	1 (11)
Monophasic *S.* Paratyphi B var. Java	0	1	0	2	8	3 (38)	3 (38)
Monophasic *S.* Typhimurium[d]	0	1	2	1	15	9 (60)	1 (7)
S. Mississippi	15	17	7	14	19	3 (16)	3 (16)
S. Newport	10	3	1	2	14	8 (57)	1 (7)
S. Paratyphi B var. Java	26	8	3	3	20	15 (75)	4 (20)
S. Pensacola	6	1	8	6	5	0	0
S. Sandiego	2	0	0	5	3	4 (15)	4 (15)
S. Saintpaul	22	26	29	21	26	3 (100)	0
S. Stanley	41	11	9	18	27	23 (85)	1 (4)
S. Thompson	11	11	10	11	12	0	3 (25)
S. Virchow	7	3	0	9	5	4 (80)	0
S. Weltevreden	19	11	3	6	25	13 (52)	2 (8)
Other[e]	187	37	33	55	88	34 (39)	5 (6)
Unknown[f]	111	63	54	72	121	30 (25)	31 (26)
Total Cases	**1188**	**709**	**714**	**750**	**827[g]**		

[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 2023 or had more than 10 annual cases in the previous three years.

[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 [28], 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] From 1st November 2019, all phage typing of *Salmonella* isolates ceased. From this time, serotypes that were historically phage typed (Typhimurium and Enteritidis) have all been typed using whole genome sequencing. *Salmonella* Subsp. (I) ser. 4,5,12 : i : - is being reported as monophasic *Salmonella* Typhimurium.

[e] Serotypes were able to be determined, but there were three or fewer associated notified cases in 2023.

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

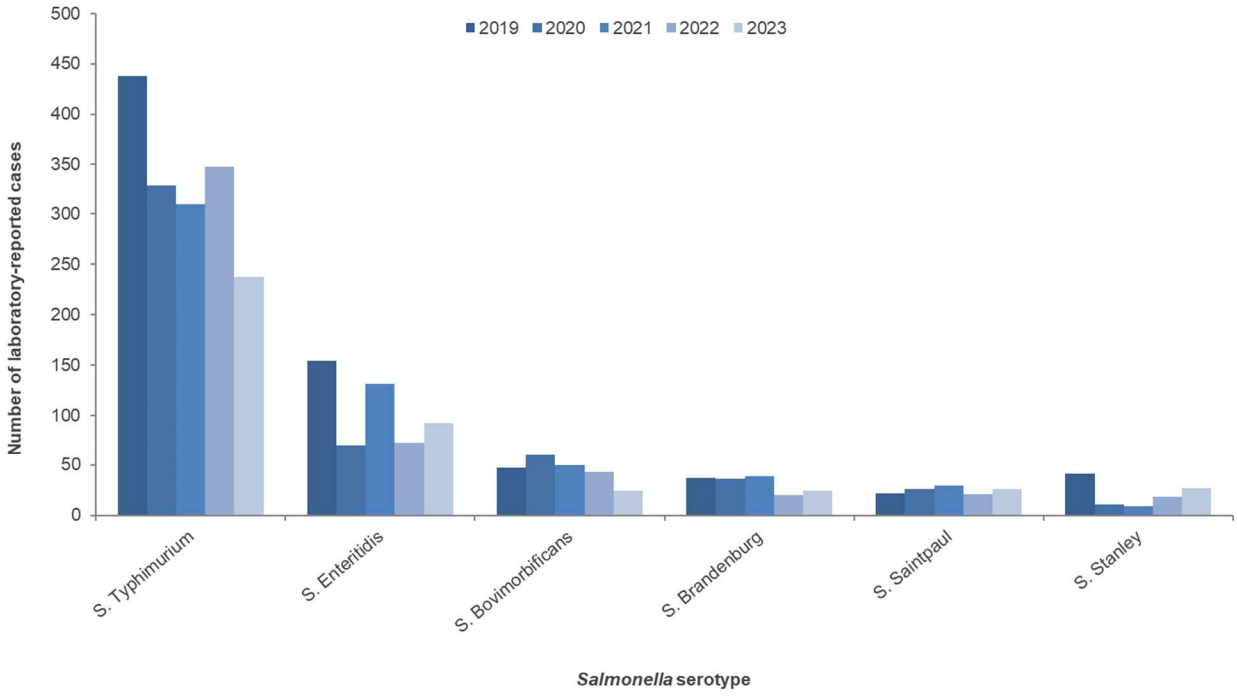
[g] One case in 2023 had a mixed infection, i.e., an individual case was represented by two *Salmonella* serotypes.

EpiSurv records for 2023 indicate that 31% of cases infected with *S*. Typhimurium were recorded as hospitalised. About 50% of cases infected with *S*. Anatum, *S.* Give and *S.* Infantis were hospitalised with hospitalisation status reported for most (83-100%) of these cases. In contrast, hospitalised case rates for cases infected with *S*. Enteritidis or *S*. Saintpaul were lower (24% and 12%, with hospitalisation status reported for 96% and 100% of these cases, respectively).

Figure 34 shows the annual trend for selected *Salmonella* serotypes from 2019 to 2023. For the types shown, there is within-type variation year to year. *S*. Typhimurium was the most prevalent serotype isolated from notified cases. The high number of cases of *S*. Typhimurium in 2019 compared to 2020 to 2023, is due to a large number of outbreak cases reported in 2019.

There was a drop in *S*. Enteritidis cases from 2019 to 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 to 2020. Of the 92 *S*. Enteritidis cases in 2023, 45% had recorded overseas travel.

Figure 34. Number of laboratory-reported case related isolates for selected *Salmonella* serotypes by year, 2019–2023



Non-human isolates

A total of 626 non-human *Salmonella* isolates were serotyped by the Enteric Reference Laboratory during 2023. *S.* Typhimurium (190 isolates) was the most common serotype in non-human samples in 2023. The next most common serotypes were *S*. Bovismorbificans (114 isolates), Hindmarsh (62 isolates) and *S*. Give (57 isolates) (Table 41). 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 41. *Salmonella* serotypes from non-human sources recorded by the Enteric Reference Laboratory, 2019–2023

Serotype	2019	2020	2021	2022	2023	Major sources, 2022
S. Typhimurium	**320**	**336**	**330**	**248**	**190**	Bovine (116), feline (17), canine (13), equine (11), ovine (7), poultry environmental (7), avian (5), and poultry miscellaneous[c] (4)
S. Enteritidis	**8**	**5**	**188[a]**	**101[a,b]**	**29**	Poultry miscellaneous (11), poultry environmental[c] (5), and bovine (4)
Other serotypes	**598**	**492**	**497**	**436**	**407**	-
S. Agona	9	9	7	30	14	Meat/bone meal (4)
S. Bovismorbificans	309	247	127	100	114	Bovine (93), poultry environmental (9)
S. Brandenburg	133	91	89	23	39	Bovine (22), ovine (7), canine (5), food[d] (5)
S. Emek	7	4	12	9	16	Bovine (12)
S. Give	12	78	88	102	57	Bovine (29), food[d] (9), poultry miscellaneous[b] (5), meat/bone meal (4), feed (4)
S. Hindmarsh	28	8	23	17	62	Ovine (56), bovine (4)
S. Infantis	3	3	17	14	7	Poultry miscellaneous[b] (2), poultry feed (2)
S. Livingstone	0	0	1	24	17	Canine (16)
S. Mbandaka	16	7	39	19	9	Feed (3), bovine (2)
S. Montevideo	0	1	0	1	8	Food[d] (6)
S. Saintpaul	14	8	9	15	15	Avian (5) and canine (5)
S. Senftenberg	8	2	7	19	5	Poultry miscellaneous[c] (3)
S. Thompson	6	1	46	4	8	Canine (7)
Other or unknown serotypes	53	33	32	59	36	-
Total	**926**	**833**	**1015**	**785**	**626**	-

[a] 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.

[b] 74 of the 101 S. Enteritidis isolates were typed by a different laboratory.

[c] Including product.

[d] Includes animal carcasses from meat works.

Recent surveys

Nil.

Relevant New Zealand studies and publications

Nil.

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 bivalve molluscan shellfish is the only food 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 2023 by data source

During 2023, four individual cases of sapovirus infection were reported in EpiSurv. None of these four cases were listed 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).

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 can't be reported.

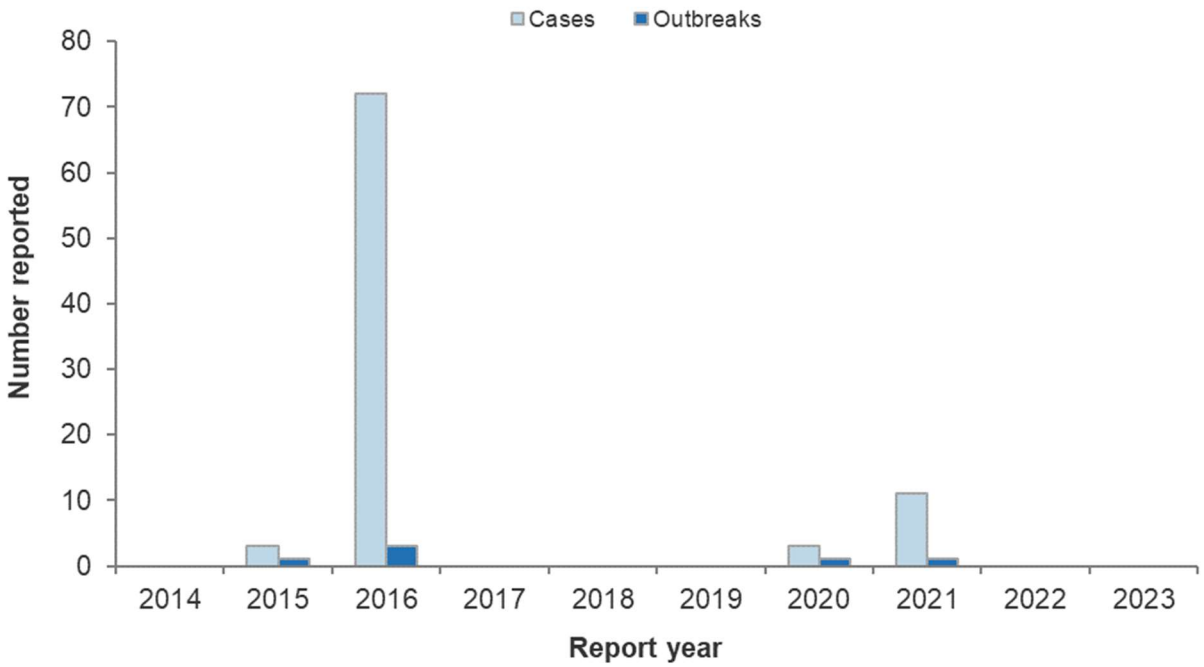
Outbreaks reported as caused by sapovirus

In 2023, there were 13 sapovirus infection outbreaks with 218 associated cases and one hospitalised case 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 person-to-person transmission or indirect contact via eating leafy greens or fruit salad at the hotel.

Figure 35. Sapovirus infection outbreaks reported in EpiSurv with food reported as a possible mode of transmission and associated cases reported by year, 2014–2023



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 and a high secondary attack rate among contacts.
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 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 shigellosis in 2023 are given in Table 42.

Table 42. Summary of surveillance data for shigellosis, 2023

Parameter	Value in 2023	Source
Number of notified cases	122	EpiSurv
Notification rate (per 100,000)	2.3	EpiSurv
Hospitalised cases[a]	77	NMDS
Deaths	0	EpiSurv
Travel-related cases [b, c]	70	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] Number of notified cases reporting overseas travel as risk factor. 48 cases had not travelled overseas during the incubation period and for the remaining four cases travel history is unknown.

[c] While New Zealand borders opened again for international travel in 2022, overseas travel in 2023 was still reduced compared to pre-COVID-19 years.

Changes to laboratory methods

Since 2015, laboratories across New Zealand have changed the methodology for testing faecal specimens (Appendix B, page 123). In 2023, laboratories servicing community faecal specimens for Canterbury (October 2023), South Canterbury (October 2023), and West Coast (June 2023) have changed to CIDT methods. Since these changes were implemented community faecal specimens in all Health Districts were screened by CIDT for a range of pathogens, including *Shigella* spp. Following the introduction of CIDT methods there was no sustained increase in notification rates for shigellosis [16].

Shigellosis individual cases reported in 2023 by data source

In 2023, 122 individual cases (2.3 per 100,000 population) of shigellosis and no resulting deaths were reported in EpiSurv. Of the 122 cases, the symptoms of 119 cases (98%) were reported as fitting the clinical description for shigellosis while for the three remaining cases the symptoms were reported as not fitting the clinical description.

The ICD-10 code A03 was used to extract shigellosis hospitalisation data from the Health New Zealand Te Whatu Ora NMDS database. Of the 77 hospitalised cases (1.5 hospitalised cases per 100,000 population) recorded in 2023, 41 were reported with shigellosis as the principal diagnosis and 36 with shigellosis as another relevant diagnosis. Five of the 77 hospitalised cases were admitted to hospital twice resulting in a total of 82 hospital admissions.

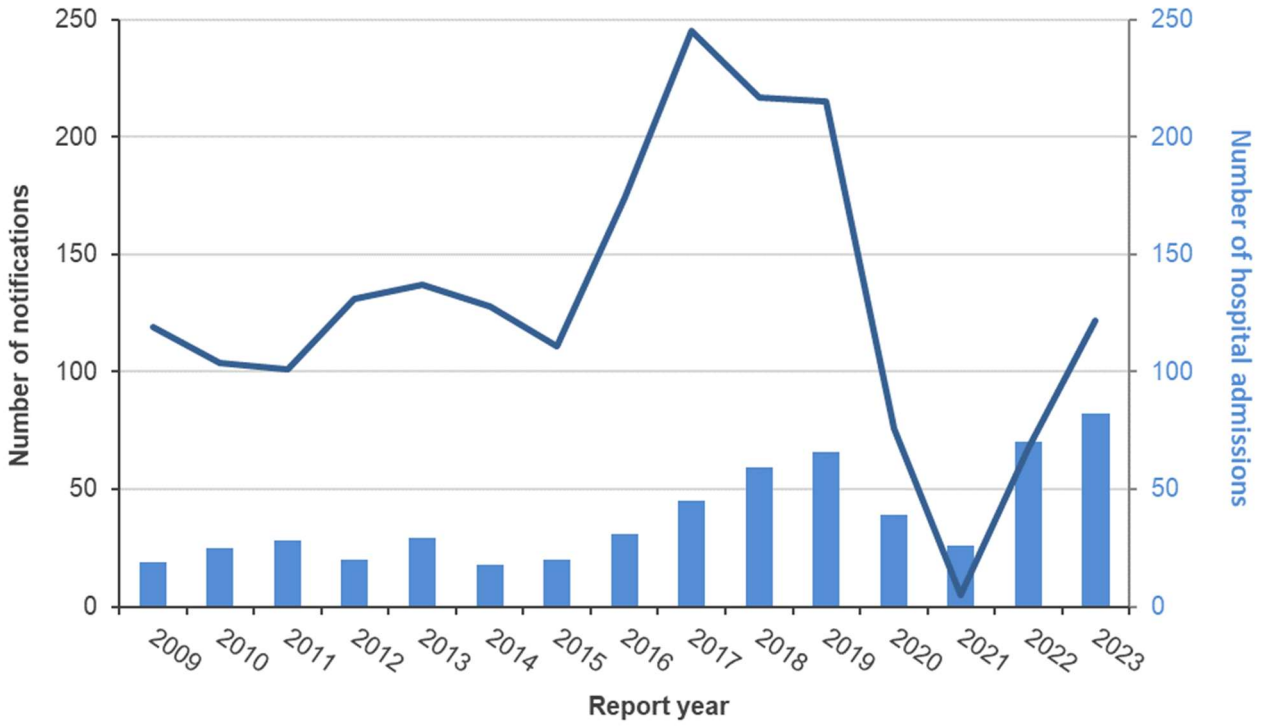
It should be noted that EpiSurv and the NMDS database are separate systems and hospital admission can occur without cases being notified in EpiSurv.

Annual data

Between 2009 and 2015 the number of shigellosis notifications was in the range of 101 to 135 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 2021 (Figure 36 and Figure 37). The frequency of overseas travel was lower in 2020 to 2023 compared to pre COVID-19 years (see Introduction, page 9). In 2023 there were 122 shigella notifications in EpiSurv, of these 70 listed overseas travel as a risk factor, compared to 82 in the pre-COVID-19 year 2019, 26 in 2020, none in 2021 and 43 in 2022.

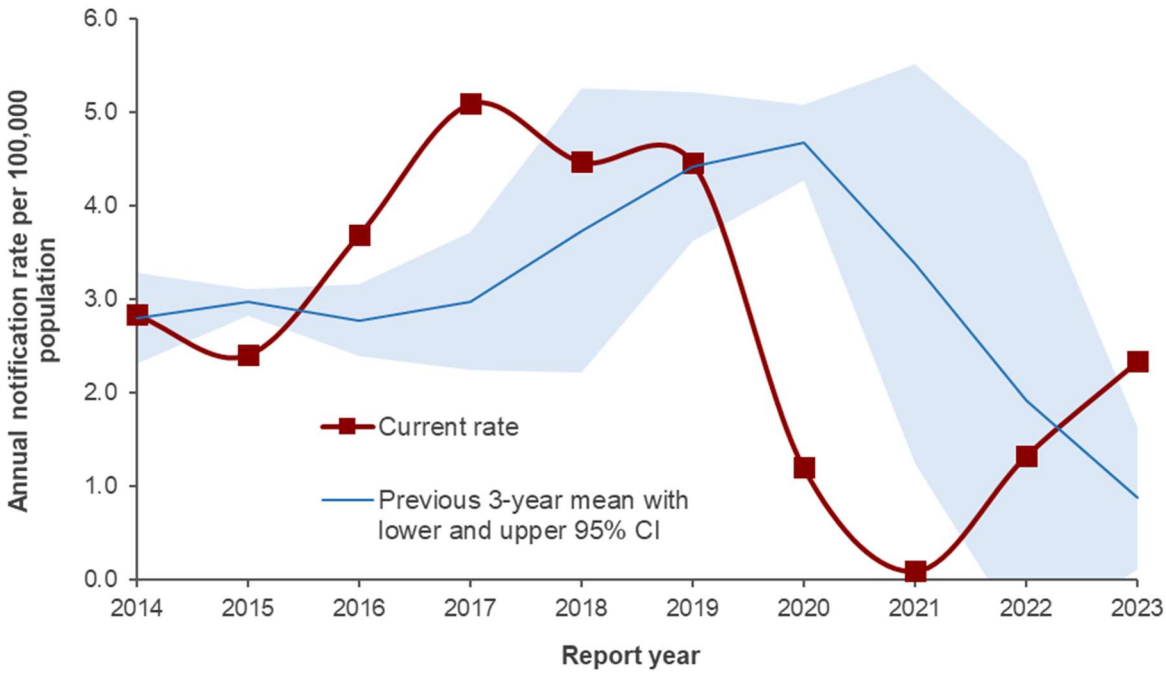
The number of hospital admissions with shigellosis as a principal or other relevant diagnosis varied year by year, following a similar pattern to the number of annual notifications. The number of hospital admissions in 2023 was higher than observed in previous years.

Figure 36. Shigellosis EpiSurv notifications (line) and NMDS hospital admissions (bar) by year, 2009–2023



The notification rate in 2023 (2.3 cases per 100,000 population) was higher than the previous three-year mean (0.9 cases per 100,000 population) (Figure 37). The drop in notification rates since 2019 can be attributed to the COVID-19 pandemic and major travel restrictions in 2020 and 2021. Increasing rates in 2022 are due to re-opening of borders and increasing travel.

Figure 37. Shigellosis notification rate by year, 2014–2023



Demographics

In 2023, notification rates were higher for males than females (2.9 compared to 1.8 cases per 100,0000 population). Hospitalised case rates were the same for males and females (1.5 hospitalised cases per 100,000 population) (Table 43).

Table 43. Shigellosis cases by sex, 2023

Sex	EpiSurv notified cases		Hospitalised cases[a]	
	No.	Rate[b]	No.	Rate[b]
Male	75	2.9	38	1.5
Female	47	1.8	39	1.5
Total	**122**	**2.3**	**77**	**1.5**

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

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

In 2023, shigellosis notification rates were highest for the 1 to 4 years age group (4.1 cases per 100,000 population) and 30 to 39 age group (3.9 cases per 100,000) (Table 44). Hospitalised case rates were also highest for the 1 to 4 years age group (4.1 hospitalised cases per 100,000 population).

Table 44. Shigellosis cases by age group, 2023

Age group (years)	EpiSurv notified cases		Hospitalised cases[a]	
	No.	Rate[b]	No.	Rate[b]
<1	1	-	1	-
1 to 4	10	4.1	10	4.1
5 to 9	6	1.9	3	-
10 to 14	4	-	3	-
15 to 19	4	-	2	-
20 to 29	19	2.8	8	1.2
30 to 39	30	3.9	8	1.0
40 to 49	13	2.0	7	1.1
50 to 59	12	1.8	9	1.4
60 to 69	16	2.8	12	2.1
70+	7	1.2	14	2.3
Total	**122**	**2.3**	**77**	**1.5**

[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 2023, there were two shigellosis outbreaks reported in EpiSurv, both of which had strong evidence of being associated with overseas travel. One outbreak of two notified cases was part of an international outbreak associated with a flight from the United Arab Emirates. Food on the aeroplane was the suspected source of the illness. The other outbreak was a family group of six cases who were overseas during the incubation period and at the time of symptom onset.

In addition to the outbreaks recorded in EpiSurv one shigellosis outbreak of three cases was referred to NZFS. This outbreak was associated with imported raw kina (Table 45). *Shigella* spp. were not detected in kina samples tested at ESR.

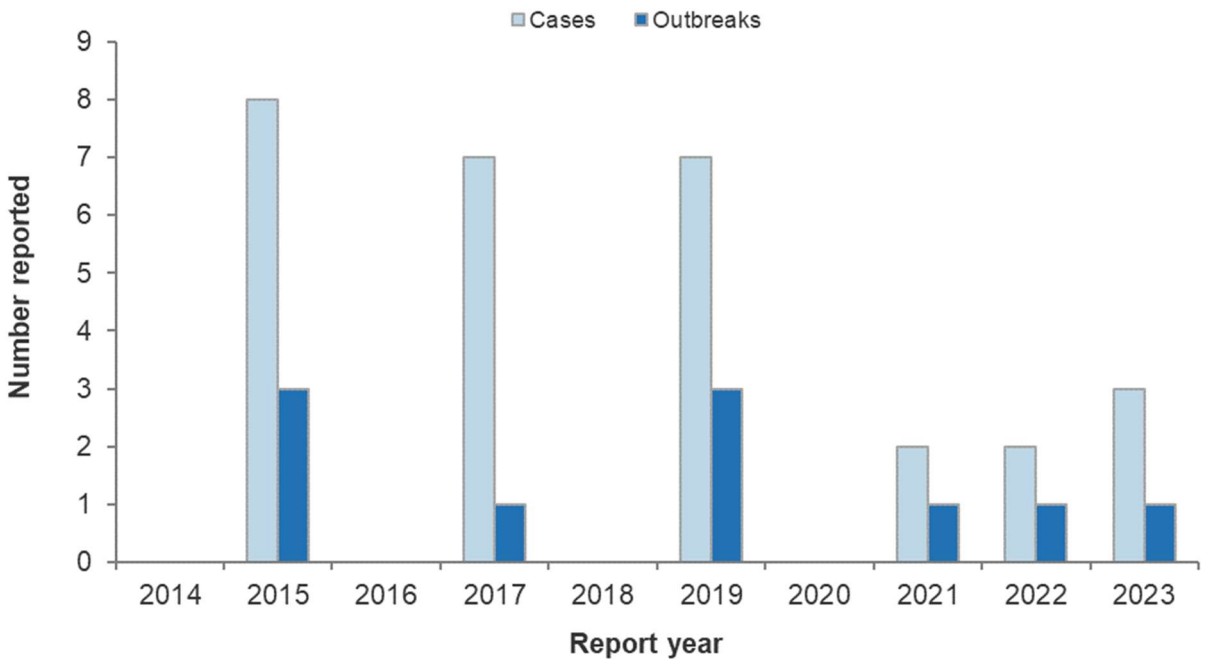
Table 45. Details of shigellosis outbreak referred to NZFS with food reported as a possible mode of transmission, 2023.

PHS	Month	Suspected source	Evidence	Setting	No. ill
Auckland Regional	July/ August	Imported frozen raw kina	Common food	Home	3C

PHS: Public Health Service

Over the 10-year period 2014–2023, the annual number of shigellosis outbreaks with food reported as a possible mode of transmission has ranged between one and three outbreaks each year in six years outbreaks were reported. Outbreaks ranged in size from two to eight associated 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), 2014–2023



Note: The figure includes data primarily from EpiSurv and includes a cluster of potentially foodborne disease referred to Food Compliance Services, NZFS, that was not recorded as a potentially foodborne outbreak in EpiSurv (2023: one outbreak of three cases).

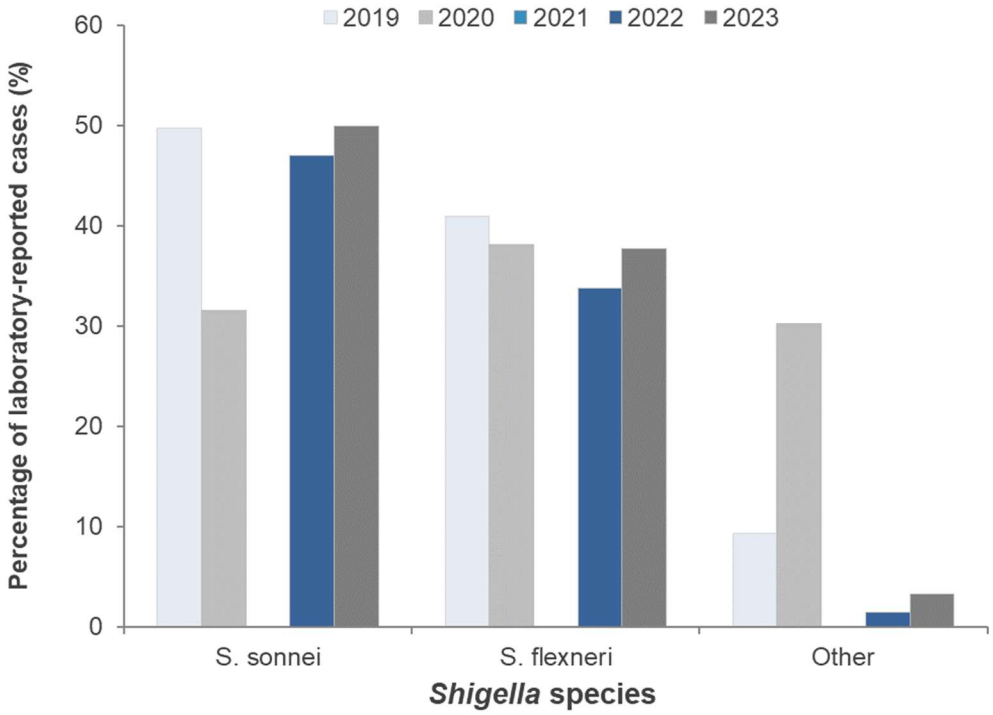
Shigella species commonly reported

In 2023, isolates from 112 out of the 122 notified cases infected with *Shigella* spp. (92%) were typed by the Enteric Reference Laboratory at ESR. *S. sonnei* was isolated most frequently (61 cases) followed by *S. flexneri* (46 cases), which is similar in relative proportions to 2022 and the pre-COVID year 2019 (Table 46, Figure 39).

Table 46. *Shigella* species and subtypes for notified cases of shigellosis, identified by the Enteric Reference Laboratory, 2019–2023

Species	2019	2020	2021	2022	2023
S. sonnei	**107**	**23**	**0**	**32**	**61**
biotype a	35	6	0	17	8
biotype f	1	1	0	2	2
biotype g	71	15	0	13	30
Unknown	0	1	0	0	21
S. flexneri	**88**	**28**	**3**	**24**	**46**
1b	13	2	0	2	3
1c	8	1	1	3	2
2a	20	11	0	5	16
2b	6	4	0	1	5
3a	5	1	0	2	4
3b	5	2	0	1	1
4av	2	0	0	3	1
6 biotype Boyd 88	13	0	0	4	1
Unknown	23	10	1	7	13
Other	**8**	**2**	**1**	**1**	**4**
S. boydii	2	2	1	0	4
S. dysenteriae	3	0	0	1	0
Shigella species not identified	3	1	0	0	1
Total	**203**	**55**	**4**	**57**	**112**

Figure 39. Percentage of notified shigellosis cases by species by year, 2019-2023



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 vomiting or diarrhoea.
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 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 2023 by data source

In 2023, 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).

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. There were two hospitalised cases (0.04 hospitalised cases per 100,000 population) recorded in 2023 with *S. aureus* intoxication as the principal diagnosis and no admissions were reported with *S. aureus* intoxication as another relevant diagnosis.

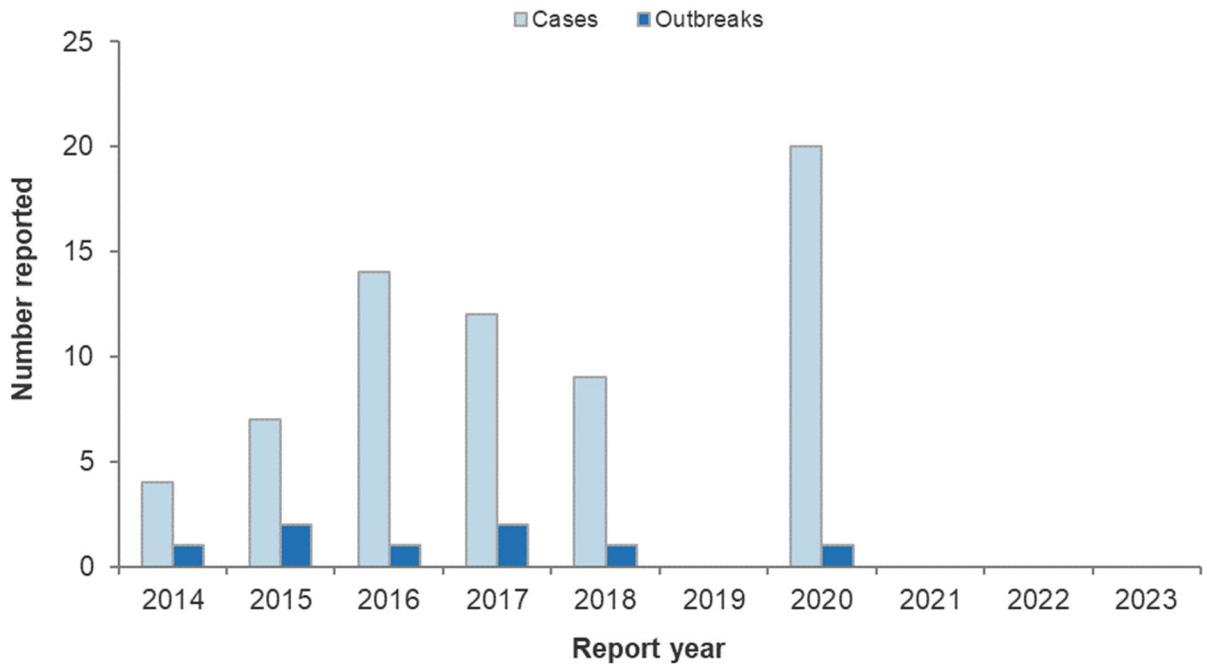
It should be noted that EpiSurv and the NMDS database are separate systems and hospital admission can occur without cases being notified in EpiSurv. This means that not all cases diagnosed with staphylococcal intoxication in hospital are reported in EpiSurv.

Outbreaks reported as caused by *Staphylococcus aureus*

During 2023, no outbreaks of *S. aureus* intoxication were reported in EpiSurv. 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 2014 to 2023, the annual number of *S. aureus* intoxication outbreaks with food reported as a possible mode of transmission ranged from zero to two, with between four and 20 associated cases in years when outbreaks were reported (Figure 40).

Figure 40. *S. aureus* intoxication outbreaks reported in EpiSurv with food reported as a possible mode of transmission and associated cases reported by year, 2014–2023



Recent surveys

Nil.

Relevant New Zealand studies and publications

Journal papers

Bovine-mastitis-causing *S. aureus* isolates (*n* = 188), obtained over a 17-year period from more than 65 dairy farms across New Zealand, were analysed by whole-genome sequencing [29]. The analysis revealed a dominant sequence type over the entire period of study, clonal complex 1, sequence type 1 (CC1/ST1), which accounted for ~75% of the isolates. CC1/ST1 was also the commonest lineage infecting humans in New Zealand in the same period. However, most bovine CC1/ST1 analysed in this study carried genes coding for the bovine-adaptive bicomponent leucocidin lukF and lukM and lacked the corresponding human-adaptive *lukF-PV* and *lukS-PV* genes. This suggests that these isolates are well adapted to the bovine environment but less likely to cause disease in humans.

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 (verotoxin)-producing *Escherichia coli* OR detection of the genes 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. Any positive toxin test should be reported as a confirmed case of STEC.
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 2023 are given in Table 47.

Table 47. Summary of surveillance data for STEC infection, 2023

Parameter	Value in 2023	Source
Number of notified cases	1006	EpiSurv
Notification rate (per 100,000)	19.3	EpiSurv
Hospitalised cases[a]	235	EpiSurv
Deaths[b]	0	EpiSurv
Travel-related cases[c]	72	EpiSurv
Estimated domestically acquired food-related cases [c,d]	366	Expert consultation and EpiSurv

[a] Cases recorded as admitted to hospital in EpiSurv. In previous reporting years, 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 [30] has shown that ICD-10 code A04.3 alone does not capture all the cases hospitalised due to STEC infection.

[b] Two STEC infection cases were reported as having died in EpiSurv, of these, one case died of other causes and for one case the cause of death was not recorded. No cases were recorded with STEC infection as the primary cause of the case dying.

[c] Number of notified cases reporting overseas travel as risk factor. 719 cases had not travelled overseas during the incubation period and for the remaining 215 cases travel history is unknown. While New Zealand borders opened again for international travel in 2022, overseas travel in 2023 was still reduced compared to pre-COVID-19 years.

[d] 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 consultation [3]. Estimate of cases acquired overseas calculated as *Total cases* X *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*.

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.

Changes to laboratory methods

Since 2015, laboratories across New Zealand have gradually changed the methodology for testing faecal specimens (Appendix B, page 123). As of October 2023, community faecal specimens in all Health Districts are screened by CIDT for a range of pathogens, including STEC.

In 2023, laboratories servicing community faecal specimens for Canterbury (October 2023), South Canterbury (October 2023), and West Coast (June 2023) have changed to CIDT methods. In these health districts since September 2018, all faecal samples submitted to the community laboratory were tested for STEC with a 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.

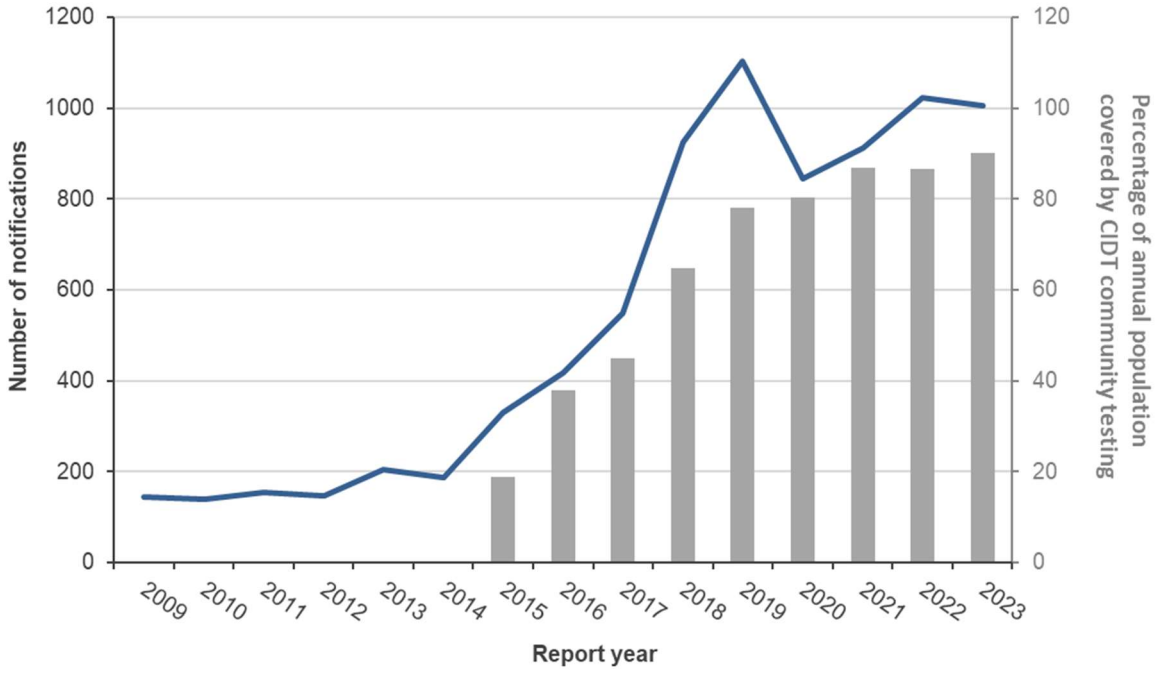
Prior to the changes in methodology, only specimens from patients meeting certain epidemiological or clinical criteria (e.g., aged less than 5 years, presence of haemolytic uraemic syndrome (HUS), or bloody diarrhoea) were tested for STEC infection, particularly O157. With CIDT testing, all faecal samples are screened for all STEC serotypes, approximately doubling the number of samples tested (Michael Addidle, ESR, 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. Identified non-O157 cases are now four-fold higher than O157 cases. Where STEC is detected by

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

screening CIDT, cultures are referred to the Enteric Reference Laboratory at ESR to attempt to isolate STEC for serotyping. In 2023, isolates were recovered for 60% of notified cases.

Between 2015 and 2019, the annual increases in STEC infection notifications correspond to the increase in the population being tested by community laboratory CIDT (Appendix B page 125) (Figure 41). The increased sensitivity of CIDT to detect non-O157 STEC serotypes (Table 51) and the increased number of samples routinely tested for STEC appears to have caused the majority of the increase in STEC notifications [31]. Areas and time periods that have not used CIDT or increased screening for STEC, show no increase in notification rates for STEC [16].

Figure 41. STEC infection EpiSurv notifications (line) and proportion of the NZ population covered by community CIDT (bar) by year, 2009–2023



STEC individual cases reported in 2023 by data source

During 2023, 1006 individual cases (19.3 cases per 100,000 population) of STEC were reported in EpiSurv. Of the 1006 cases, the symptoms of 997 cases (99%) were reported as fitting the clinical description for STEC infection while for the remaining nine cases the symptoms were unknown. Two cases were reported in EpiSurv as having died, one from a cause other than STEC infection and one in the over 70 age group from an unknown cause.

In previous report years, hospital data was presented based on ICD-10 code A04.3 (enterohaemorrhagic *E. coli* (EHEC) infection) diagnoses in the hospitalisation data from the Health New Zealand Te Whatu Ora NMDS database. EHEC and STEC are synonymous [32], 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 [30]. For this reason, 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 936 cases (93%). Of these 936 cases, 235 were reported as being hospitalised (4.6 hospitalised cases per 100,000 population).

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].

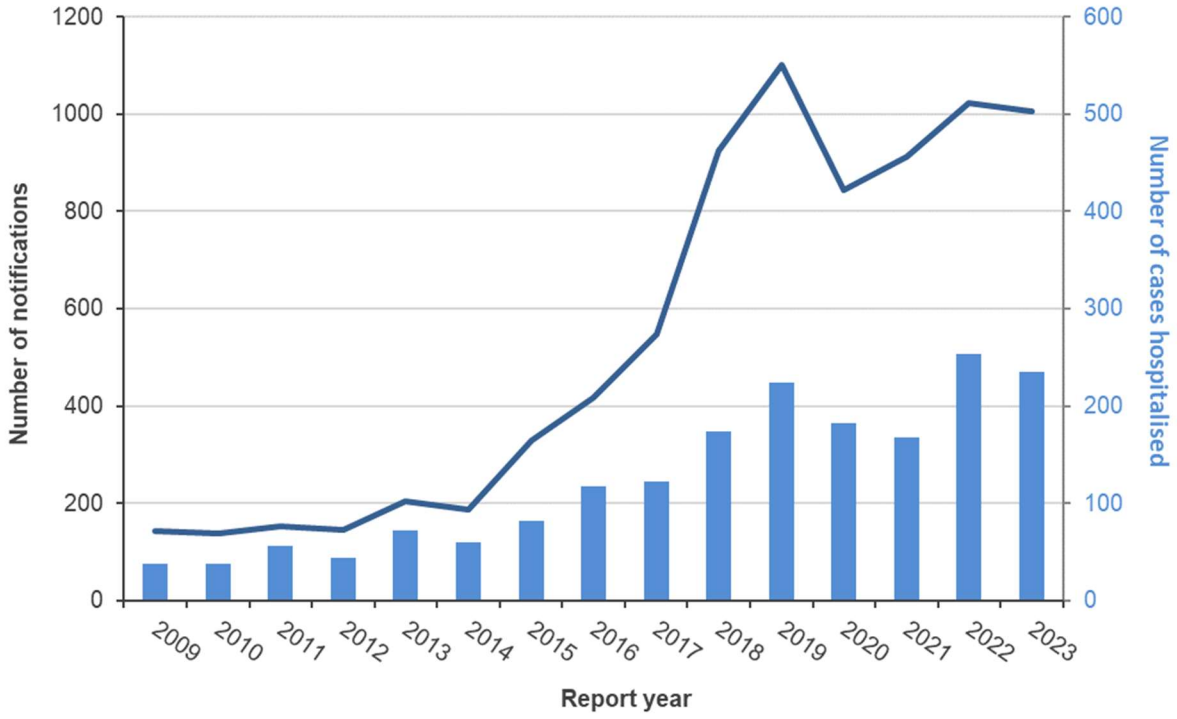
Annual data

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 community laboratory CIDT (Figure 41). A small drop in case numbers in 2020 and 2021 was followed by higher case numbers in 2022 and 2023 (Figure 42). The decrease in 2020 and 2021 compared to 2019 data is related to the reduction in reported cases during months with COVID-19 Alert Level restrictions [16].

The last six years (2018-2023) have seen hospitalised cases recorded in EpiSurv being consistently higher than prior to 2018. Of the hospitalisations recorded in EpiSurv in 2023, 22% were identified with the O157:H7 serotype, 14% with the O26:H11 serotype, 18% with other serotypes. Forty six percent 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.

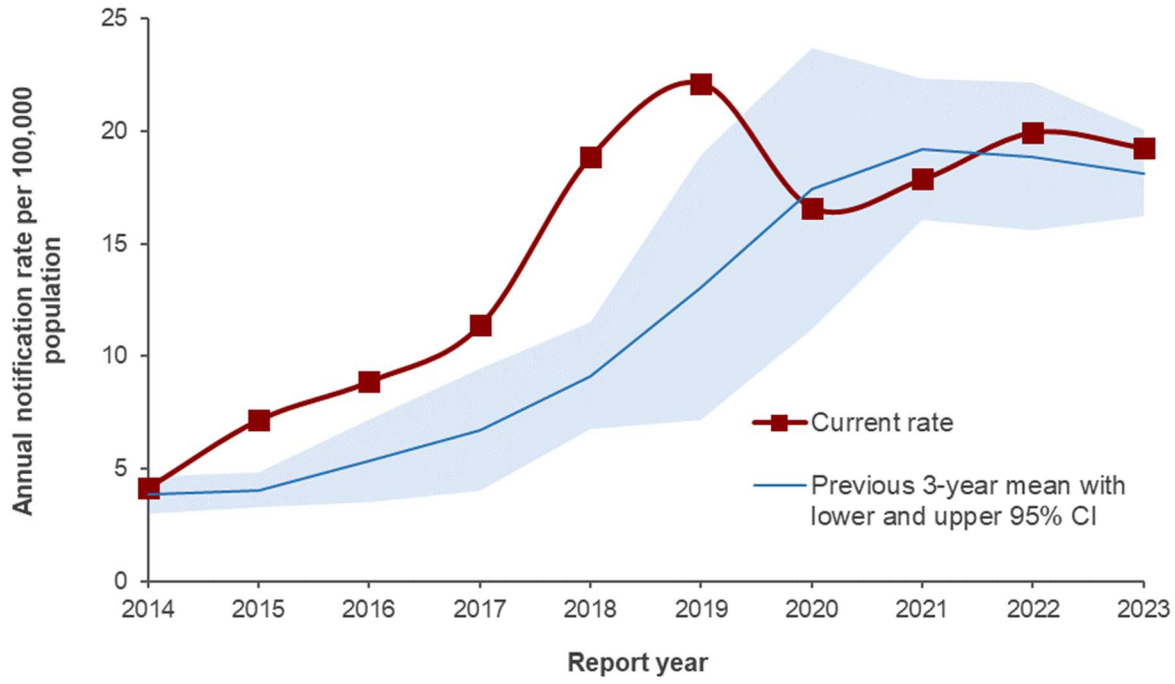
The frequency of overseas travel was lower in 2020 to 2023 compared to pre-COVID-19 years (see Introduction, page 9). In 2023, there were 72 STEC infection notifications in EpiSurv listing overseas travel as a risk factor, compared to 113 in the pre-COVID-19 year 2019, 18 in 2020, two in 2021 and 36 in 2022.

Figure 42. STEC infection EpiSurv notifications (line) and EpiSurv hospitalised cases (bar) by year, 2009–2023



Prior to 2015, notification rates for STEC infection were generally below five notifications per 100,000 population. Since 2015, increasing rates occurred every year until 2019 (22.1 cases per 100,000 population), followed by a drop attributed to the COVID-19 pandemic. The 2023 notification rate was 19.3 cases per 100,000 population, similar to the previous three-year mean (19.9 cases per 100,000 population) (Figure 43).

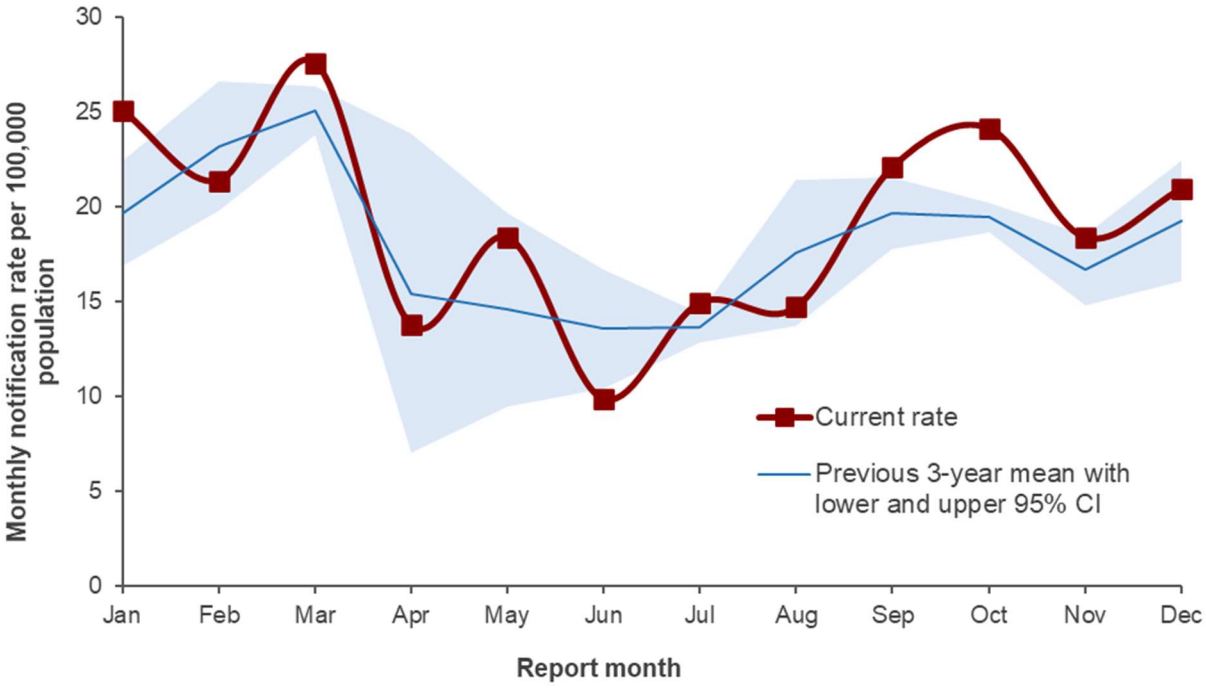
Figure 43. STEC infection notification rate by year, 2014–2023



Seasonal data

STEC infection notification rates per 100,000 population by month for 2023 are shown in Figure 44. 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 2023 ranged from 43 notifications in June (9.9 cases per 100,000 population) to 120 notifications in March (27.6 cases per 100,000 population).

Figure 44. STEC infection monthly notification rate (annualised), 2023



In the last five years, the monthly numbers of cases recorded as hospitalised in EpiSurv varied over the year (Table 48), with most hospitalised cases occurring in January to March/April and October. In 2022 there were more hospitalised cases in the winter months compared to the other years.

Table 48. STEC infection monthly EpiSurv cases recording hospitalisation, 2019-2023

Month	Hospital admissions recorded in EpiSurv				
	2019	2020	2021	2022	2023
January	31	21	18	26	36
February	22	22	21	19	21
March	35	25	26	33	26
April	26	9	14	30	14
May	13	9	9	17	23
June	12	3	14	12	14
July	12	11	9	20	14
August	17	15	12	23	11
September	14	17	7	19	21
October	18	21	13	17	24
November	13	11	12	17	19
December	11	19	13	21	12
Total	**224**	**183**	**168**	**254**	**235**

Demographics

In 2023, notification rates and hospitalised case rates were higher for females (19.6 cases and 4.7 hospitalised cases per 100,000 population) than for males (18.9 cases and 4.3 hospitalised cases per 100,000 population) (Table 49).

Table 49. STEC cases by sex, 2023

Sex	EpiSurv notified cases		Recorded as hospitalised in EpiSurv	
	No.	Rate[a]	No.	Rate[a]
Male	491	18.9	112	4.3
Female	515	19.6	123	4.7
Total	**1006**	**19.3**	**235**	**4.5**

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

In 2023, the STEC infection notification rate was highest for the <1 year age group followed by the 1 to 4 years age group (64.7 cases and 55.9 cases per 100,000 population, respectively). The hospitalised case rate was highest for the <1, 1 to 4 years and 70+ age groups (15.7, 14.3 and 12.7 EpiSurv hospitalised cases per 100,000 population) (Table 50).

Table 50. STEC cases by age group, 2023

Age group (years)	EpiSurv notified cases		Recorded as hospitalised in EpiSurv	
	No.	Rate[a]	No.	Rate[a]
<1	37	64.7	9	15.7
1 to 4	137	55.9	35	14.3
5 to 9	40	12.4	11	3.4
10 to 14	41	11.9	9	2.6
15 to 19	38	11.6	7	2.1
20 to 29	119	17.4	19	2.8
30 to 39	94	12.2	16	2.1
40 to 49	65	10.1	11	1.7
50 to 59	112	17.1	19	2.9
60 to 69	113	19.6	23	4.0
70+	209	34.8	76	12.7
Total	**1006**	**19.3**	**235**	**4.5**

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

Geographic distribution

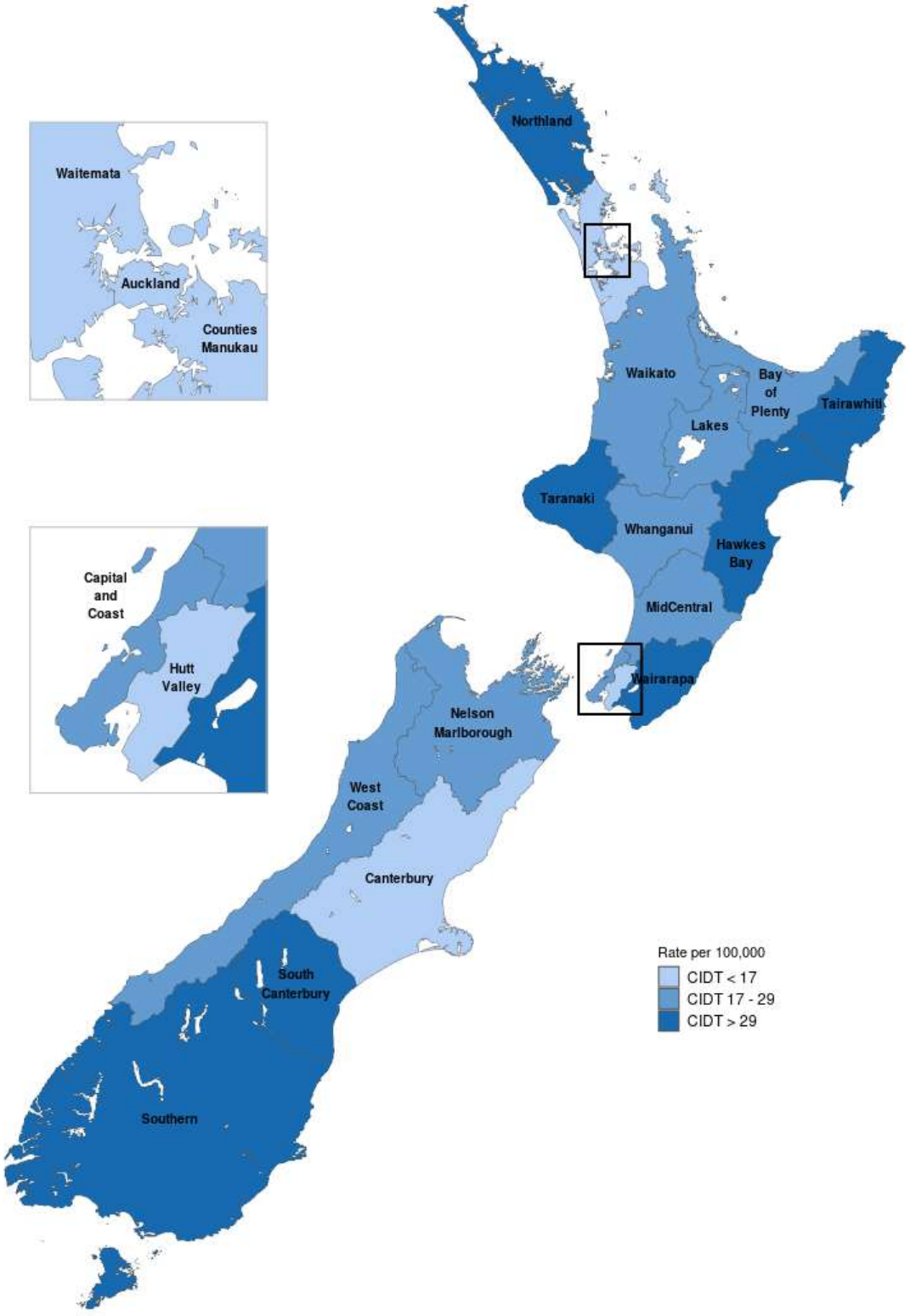
The notification rates by Health District calculated per 100,000 resident population are presented in Figure 45 (see also Table 80).

In 2023, the Health District notification rates of STEC infection ranged from 7.5 per 100,000 population in Counties Manukau (47 cases) to 60.5 per 100,000 population (31 cases) in Wairarapa. The Health Districts Wairarapa, Taranaki (44.3 per 100,000 population), Northland (41.7 per 100,000 population) and South Canterbury (41.3 per 100,000 population) had the highest notification rates.

For the last three 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 effected reporting rates (see also Changes to laboratory methods, page 91 and Appendix B, page 123).

STEC notification rates, stratified by 2023 Urban Rural Classification [20] of the cases' residential address and excluding cases associated with overseas travel, increased with decreasing urbanization (Appendix C, Table 81). Rates were lowest for 'major urban' areas (8.4 per 100,000 population) and highest for 'rural other' areas (45.8 per 100,000 population).

Figure 45. Geographic distribution of STEC infection notifications, 2023



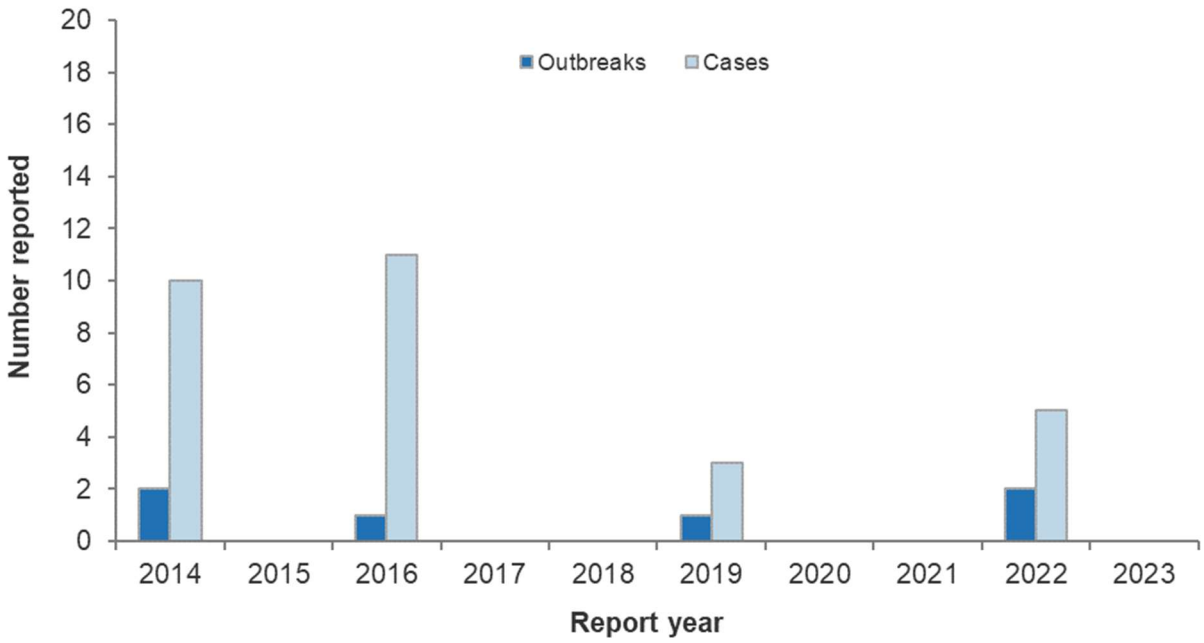
Note: Canterbury and South Canterbury Health Districts changed to community laboratory testing by CIDT methods in October 2023 and the West Coast Health District in June 2023. The plotted rates in these areas will not reflect a full year of CIDT testing in 2023.

Outbreaks reported as caused by STEC

In 2023, there were three outbreaks (14 cases, no hospitalisations) of STEC infection notified in EpiSurv, including a multi-disease outbreak of seven cases with strong evidence for cases becoming infected while overseas. Food consumed in New Zealand was not reported as a possible mode of transmission for these outbreaks. 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 2014 to 2023, the annual number of STEC outbreaks with food reported as a possible mode of transmission ranged from zero to four per year, with no outbreaks with food reported as a possible mode of transmission reported for four of the ten years (Figure 46). The total number of cases associated with outbreaks has varied over the same period with a peak in 2017 (157 cases). The 2017 outbreak took place on a cruise ship and no specific food was recorded as a suspected source for the 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, 2014–2023



Note: The figure includes data primarily from EpiSurv and includes a cluster of potentially foodborne disease referred to Food Compliance Services, NZFS, that was not recorded as potentially foodborne outbreak in EpiSurv (2022: one outbreak of two cases).

STEC types reported for notified cases

Isolates from 603 notified cases infected with STEC were typed by the ESR Enteric Reference Laboratory (ERL) in 2023. A single STEC serotype was confirmed from 591 cases; from eleven of the remaining twelve cases two different STEC serotypes were isolated and serotyped and for one case three different STEC serotypes were isolated. Of the 616 typed isolates, 134 (21.8%) were identified as STEC O157:H7 and 482 (78.2%) as non-O157:H7 STEC (Table 51). As in the previous three years, the most frequently typed non-O157:H7 STEC serotypes were O26:H11 and O128:H2.

Table 51. Annual number of case notifications with different STEC serotypes identified by the Enteric Reference Laboratory, 2019–2023

Serotype	2019	2020	2021	2022	2023
O157:H7 [a]	**196**	**167**	**183**	**259**	**134**
Non-O157	**417**	**388**	**444**	**448**	**482**
O26:H11	113	112	127	105	114
O38:H26	23	27	22	35	30
O64:H20	7	5	5	5	8
O84:H2	2	10	7	9	9
O88:H8	5	8	9	8	8
O91:H14	11	10	25	18	26
O103:H2	6	9	17	10	15
O104:H7	1	1	5	2	7
O112:H9	3	3	6	6	7
O117:H7	7	4	1	0	8
O123:H10	2	8	3	7	16
O128:H2	46	62	62	65	68
O146:H21	12	17	24	30	23
O153:H2	10	6	8	5	11
O174:H8	8	9	11	15	7
O176:H4	10	14	14	20	19
Other Types[b]	132	63	76	77	106
Cases without typing information	**499**	**291**	**291**	**328**	**403**

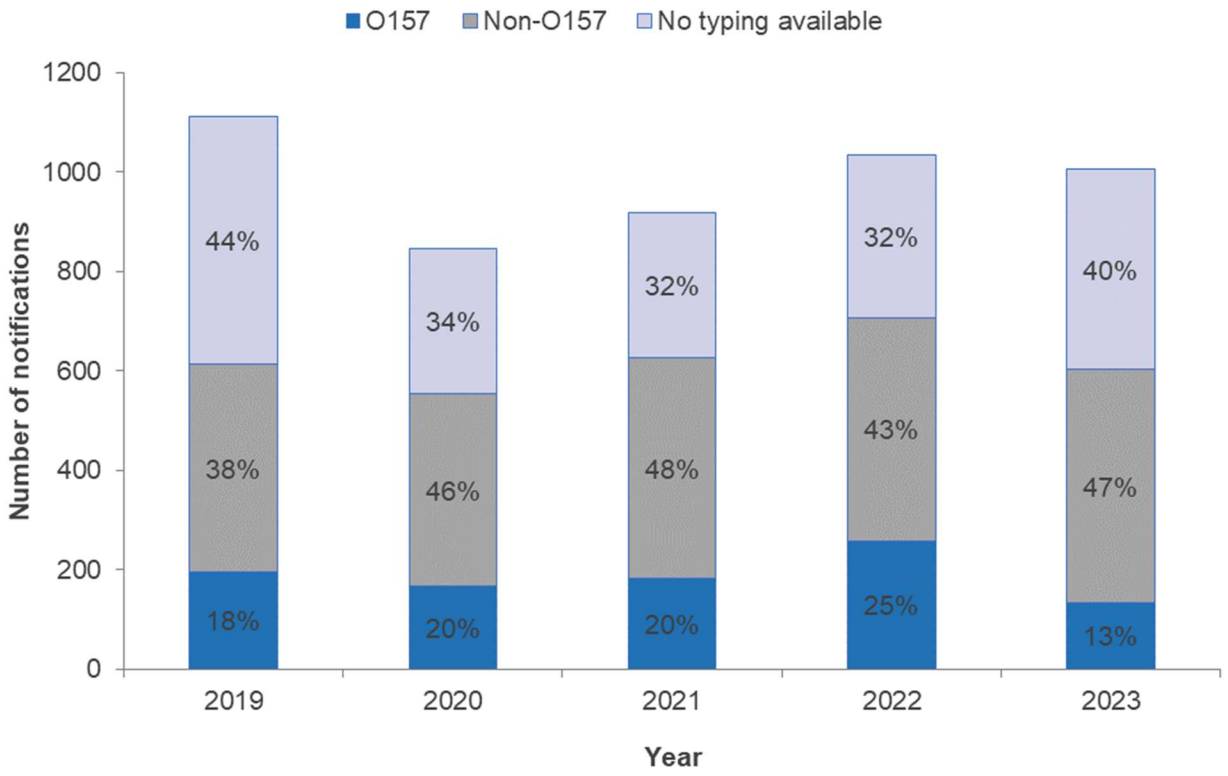
[a] Whole genome sequencing of human O157:H7 isolates from 2020 to 2023 revealed a wide diversity of genotypes present, with most of the isolates genomically distinct from each other.

[b] Other isolates with identifiable non-O157 serotypes, not listed in table. Full list available in the Appendix C, Table 90.

Note: Eleven cases have been identified with two serotypes in 2023, and one case with three serotypes. The sum of the total rows will not equal the number of notifications in a year.

For 403 (40%) of the 1006 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. Since August 2019, all isolates confirmed as STEC have been whole genome sequenced, which has increased the proportion of STEC isolates that can be assigned to a serotype.

Figure 47. STEC O157 and non-O157 associated notifications by year, 2019–2023



Investigation of the 2023 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 (39% of O157:H7 cases hospitalised, 2% no hospital information recorded). The proportion of cases hospitalised was lower for STEC O26:H11 (28% cases hospitalised, 2% no hospital information recorded) and STEC O128:H2 (13% cases hospitalised, 6% no hospital information recorded).

Other *E. coli* pathotypes reported in 2023 for gastroenteritis outbreaks

In 2023, there was one enterotoxigenic *Escherichia coli* and *Vibrio cholerae* outbreak (three cases) with food reported as a possible mode of transmission. Frozen Kina from an overseas source was identified as a possible source, but the evidence was weak.

Disease sequelae – haemolytic uraemic syndrome (HUS)

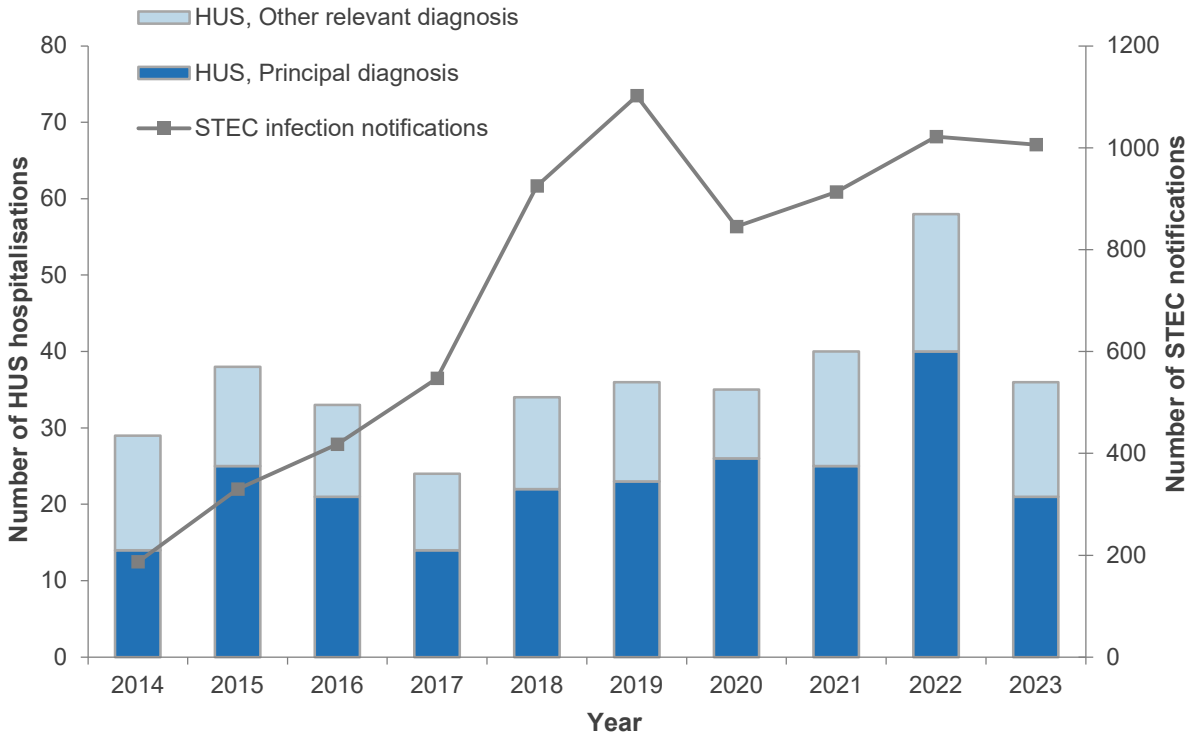
HUS is a serious sequela that may result from an STEC infection. HUS is usually preceded by an STEC infection [33]. It is not clear which STEC genotypes are most commonly associated with HUS cases. While it has been reported that two-thirds of HUS cases are associated with STEC O157:H7 infections [34], recent European data report that *STEC* O26:H11 was most frequently associated with HUS cases [35]. In 2023, 17 STEC cases notified in EpiSurv were reported to have developed HUS. The associated serotypes were O157:H7 (8), O26:H11 (4), O104:H7 (1), while for four 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 2023 year were considered, rather than all cases that were hospitalised in that year. That is, if an HUS case hospitalised in 2023 had been hospitalised with HUS in a previous year, the 2023 admission was considered as a re-admission, rather than an incident case. Of the 36 incident cases recorded in 2023 (0.7 per 100,000 population), 21 were reported with HUS as the principal diagnosis and 15 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 is likely to be an artefact of the reporting systems.

Between 2014 and 2023, the number of incident cases (any diagnosis code) of HUS each year ranged from 24 to 58 (Figure 48). In 2023, the number of incident cases (36) was at the mean for the 10-year period 2014 - 2023. 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, 2014–2023



In 2023, the number of female cases hospitalised due to HUS was greater than the number of male cases (Table 52). This is the predominant pattern seen in the last 10 years.

Table 52. Haemolytic uraemic syndrome incident cases by sex, 2023

Sex	Cases[a]	
	No.	Rate[b]
Male	13	0.5
Female	23	0.9
Total	**36**	**0.7**

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

[b] Per 100,000 population in group.

In 2023, 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 53).

Table 53. Haemolytic uraemic syndrome incident cases by age group, 2023

Age group (years)	Cases [a]	
	No.	Rate[b]
<1	5	8.7
1 to 4	21	8.6
5 to 9	1	-
10 to 14	1	-
15 to 19	2	-
20 to 29	-	-
30 to 39	-	-
40 to 49	1	-
50 to 59	2	-
60 to 69	1	-
70+	2	-
Total	**36**	**0.7**

[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

Nil.

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 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.

Neurotoxic 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 maximum permissible 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 2023 by data source

During 2023, no individual cases of toxic shellfish poisoning were 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. Of the seven hospitalised cases (0.13 hospitalised cases per 100,000 population) recorded in 2023, six cases were reported with 'other fish and shellfish poisoning' as the principal diagnosis and one case was reported with 'other fish and shellfish poisoning' as another relevant diagnosis. Note that this ICD-10 code includes shellfish and other fish.

It should be noted that EpiSurv and the NMDS database are separate systems and hospital admission can occur without cases being notified in EpiSurv. This means that not all cases diagnosed with toxic shellfish poisoning in hospital are reported in EpiSurv.

Outbreaks reported as caused by toxic shellfish poisoning

In 2023 no toxic shellfish poisoning outbreaks were reported in EpiSurv. 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.

In addition to EpiSurv records, two suspected shellfish poisoning outbreaks in the Auckland Public Health Service region were referred to NZFS. The two cases associated with the first outbreak had consumed steamed mussels from a food service outlet as the suspected source. The seven cases associated with the second outbreak had consumed oysters as the suspected source, however, case symptoms were more consistent with a bacterial or viral infection than shellfish poisoning. Cases consumed oysters just prior to a trade level recall of oysters due to the detection of paralytic shellfish poison in the growing area.

There have been no confirmed outbreaks of toxic shellfish poisoning in the last nine years. The last outbreaks were in 2014 (13 cases) and 2012 (29 cases).

Recent surveys

Nil.

Relevant New Zealand studies and publications

Nil.

Relevant regulatory developments

No shellfish toxin-specific regulatory developments.

Vibrio parahaemolyticus infection

Case definition

Clinical description:	Gastroenteritis with watery diarrhoea and abdominal cramps.
Laboratory test for diagnosis:	Isolation of Kanagawa-positive or pathogenic serotype of *Vibrio parahaemolyticus* from a faecal specimen or isolation of ≥10^5/gram *V. parahaemolyticus* 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.

Changes to laboratory methods

Since 2015, laboratories across New Zealand have changed the methodology for testing faecal specimens (Appendix B, page 123). Three of the four CIDT panels used across New Zealand include *Vibrio* species, in addition to other faecal pathogens. In 2023, community faecal specimens in the Health Districts: Auckland, Bay of Plenty, Counties Manukau, Lakes, Northland, Waikato, Waitematā and West Coast were screened by CIDT for a range of pathogens, including *Vibrio* species. Samples positive for the *Vibrio* species target are cultured in order to confirm *V. parahaemolyticus* infection.

It is unclear at this stage how laboratory changes have affected the notification rates for *V. parahaemolyticus* infection. The increased number of samples screened for *V. parahaemolyticus* may affect the number of positive results and increase notification rates.

Vibrio parahaemolyticus infection individual cases reported in 2023 by data source

During 2023, 21 individual cases (0.4 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 (0.06 hospitalised cases per 100,000 population) recorded in 2023 were reported with *V. parahaemolyticus* infection as the principal diagnosis. There were no hospital admissions reported with *V. parahaemolyticus* infection as another relevant diagnosis.

It should be noted that EpiSurv and the NMDS database are separate systems with different objectives and hospital admissions can occur without cases being notified in EpiSurv or vice versa. Cases of *V. parahaemolyticus* infection may also be notified as acute gastroenteritis without listing the causal pathogen and therefore may not be captured in the notifications listed above.

Seasonal data

The number of cases of *V. parahaemolyticus* infection notified in EpiSurv by reporting month are summarised in Table 54. Generally, notifications show no pronounced seasonal trends consistent over multiple years.

Table 54. *V. parahaemolyticus* infection monthly notified cases, 2019-2023

Month	*V. parahaemolyticus* infection cases notified in EpiSurv				
	2019	2020	2021	2022	2023
January	1	5	3	28 [b]	4
February	1	5	3	7 [b]	2
March	2	4	20 [a]	4 [b]	5
April	1	0	4	4 [b]	1
May	9 [a]	0	0	3 [b]	2
June	19 [a]	12 [a]	3	1	1
July	4	4	0	1	0
August	2	0	0	0	0
September	3	0	2	1	2
October	5	2	2	0	0
November	1	1	7 [b]	1	3
December	1	1	7 [b]	2	1
Total	**49**	**34**	**51**	**52**	**21**

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

[b] Period of elevated case numbers across the country in 2021 and 2022, which have been reported as a single outbreak in EpiSurv [36].

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 2023, 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.

Vibrio parahaemolyticus sequence types commonly reported

From 2019 onwards, the ESR 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 55). ST50 has been the most frequently isolated sequence type between 2020 and 2023.

Table 55. *V. parahaemolyticus* 7-gene multi locus sequence types of case isolates, identified by the Enteric Reference Laboratory, 2019–2023

Sequence type	2019	2020	2021	2022	2023
ST3	0	0	0	7	3
ST8	0	0	0	1	3
ST36	14	2	2	0	1
ST50	**2[a]**	**24**	**24**	**37**	**6**
ST55	0	0	1	1	1
ST69	0	0	0	2	0
ST199	0	0	5	1	2
ST217	0	0	0	1	0
ST265	1[a]	0	0	0	0
ST558	0	0	0	1	0
ST607	0	0	0	0	1
ST635	0	0	0	0	1
ST1165	0	0	0	0	2
ST1381	0	0	0	1	0
ST2058	0	0	0	1	0
ST2549	0	0	4	1	1
ST2650	0	0	0	0	1
ST2903	0	0	0	1	0
ST2904	0	0	0	1	1
ST3267	0	0	0	0	1
ST3329	0	0	0	0	1
ST3478	0	0	0	0	1
ST3572	0	0	0	0	1
No typing information	**26**	**18**	**0**	**1**	**1**
Total	**43**	**44**	**36**	**57**	**28**

Recent surveys

Nil.

Relevant New Zealand studies and publications

Nil.

Relevant regulatory developments

No *V. parahaemolyticus*-specific regulatory developments.

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[1].
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 2023 are given in Table 56.

Table 56. Summary of surveillance data for yersiniosis, 2023

Parameter	Value in 2023	Source
Number of notified cases	1408	EpiSurv
Notification rate (per 100,000)	27.0	EpiSurv
Hospitalised cases[a]	207	NMDS
Deaths[b]	0	EpiSurv
Travel-related cases[c,d]	56	EpiSurv
Estimated domestically acquired food-related cases[e]	976	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] One case of yersinosis was reported as having died in EpiSurv, the cause of death was unknown. No cases were reported as dying due to yersiniosis.

[c] Number of notified cases reporting overseas travel as risk factor. 685 cases had not travelled overseas during the incubation period and for the remaining 667 cases travel history is unknown.

[d] While New Zealand borders opened again for international travel in 2022, overseas travel in 2023 was still reduced compared to pre-COVID-19 years.

[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]. Estimate of cases acquired overseas calculated as *Total cases* X *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*.

[1] Note that presently PCR testing may not detect *Y. pseudotuberculosis* and the ability of the assays to adequately detect *Y. enterocolitica* biotype 1A is uncertain [12].

Changes to laboratory methods

Since 2015, laboratories across New Zealand have changed the methodology for testing faecal specimens (Appendix B, page 123). In 2023, laboratories servicing community faecal specimens for Canterbury (October 2023), South Canterbury (October 2023), and West Coast (June 2023) have changed to CIDT methods. Since these changes were implemented community faecal specimens in all Health Districts were screened by multiplex CIDT for a range of pathogens, including *Yersinia.*

Within the Health Districts that have moved to CIDT methods, all community faecal specimens in Canterbury, Capital and Coast, Hawke's Bay, Hutt Valley, MidCentral, Nelson Marlborough, South Canterbury, Southern, Tairāwhiti, Taranaki, Wairarapa, and Whanganui are routinely tested for *Y. enterocolitica and Y. pseudotuberculosis.* Community faecal specimens in the Health Districts Auckland, Bay of Plenty, Counties Manukau, Lakes, Northland, Waikato, Waitematā and Westcoast are only being screened for *Y. enterocolitica* [37]. This corresponds to 42% of the New Zealand population only being screened for *Y. enterocolitica*. 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 cultural methods identified isolates as belonging to the *Yersinia* genus, followed by additional testing to identify the species.

The introduction of CIDT methods has not significantly affected notifications for yersiniosis [16].

Yersiniosis cases reported in 2023 by data source

During 2023, 1408 individual cases (27.0 per 100,000 population) of yersiniosis were reported in EpiSurv. Of the 1408 cases, the symptoms of 1364 cases (97%) were reported as fitting the clinical description for yersiniosis infection, the symptoms were unknown for 42 cases, and for two cases the symptoms were reported as not fitting the clinical description. One case in the 70+ age group was recorded in EpiSurv as died from an unknown cause.

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 207 hospitalised cases (4.0 hospitalised cases per 100,000 population) recorded in 2023, 116 cases were reported with yersiniosis as the principal diagnosis and 91 were reported with yersiniosis as another relevant diagnosis. Some of the 207 hospitalised cases were admitted to hospital more than once resulting in a total of 218 hospital admissions.

It should be noted that EpiSurv and the NMDS database are separate systems and hospital admission can occur without cases being notified in EpiSurv.

Foodborne transmission

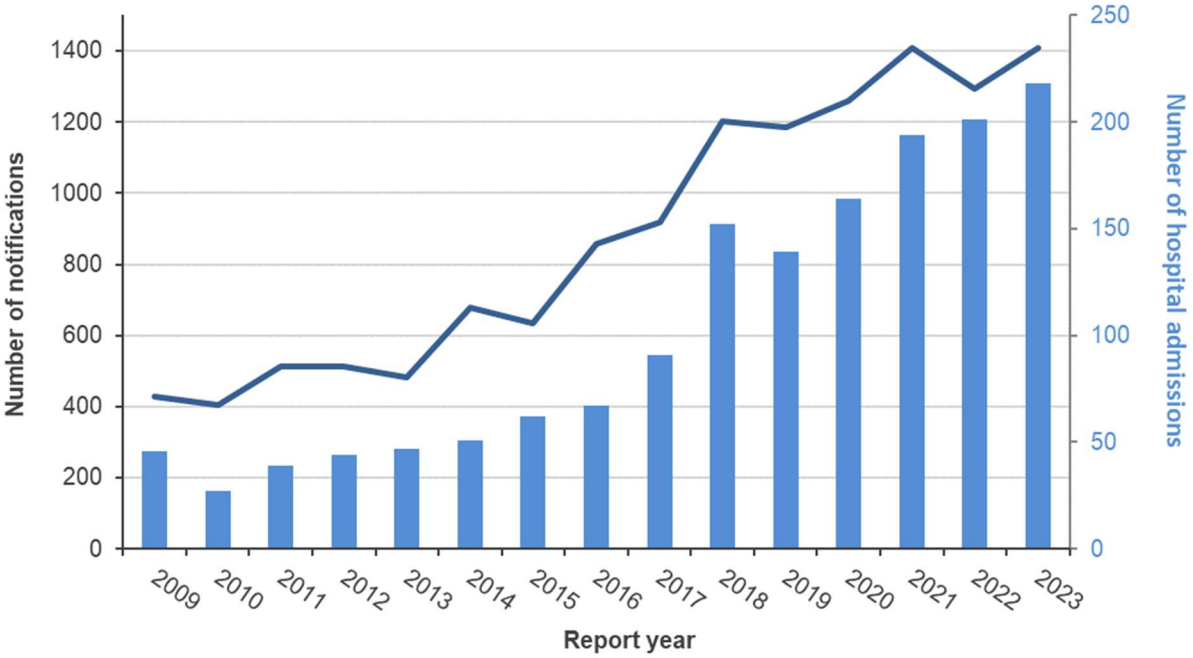
It has been estimated by expert consultation that 75% of yersiniosis incidence is due to foodborne transmission [3]. It was further estimated that approximately 71% of foodborne transmission was due to transmission via pork [2].

Annual data

Between 2009 and 2013 the annual number of notifications reported ranged between 406 and 514. Since 2013, the number of notifications for yersiniosis and the rate of yersiniosis notifications per 100,000 population has generally been generally increasing until 2021. With 1410 cases reported in 2021, 1294 cases in 2022 and 1408 cases in 2023 (Figure 49 and Figure 50). The number of hospital admissions with yersiniosis as a principal or other relevant diagnosis has increased in line with the number of notifications.

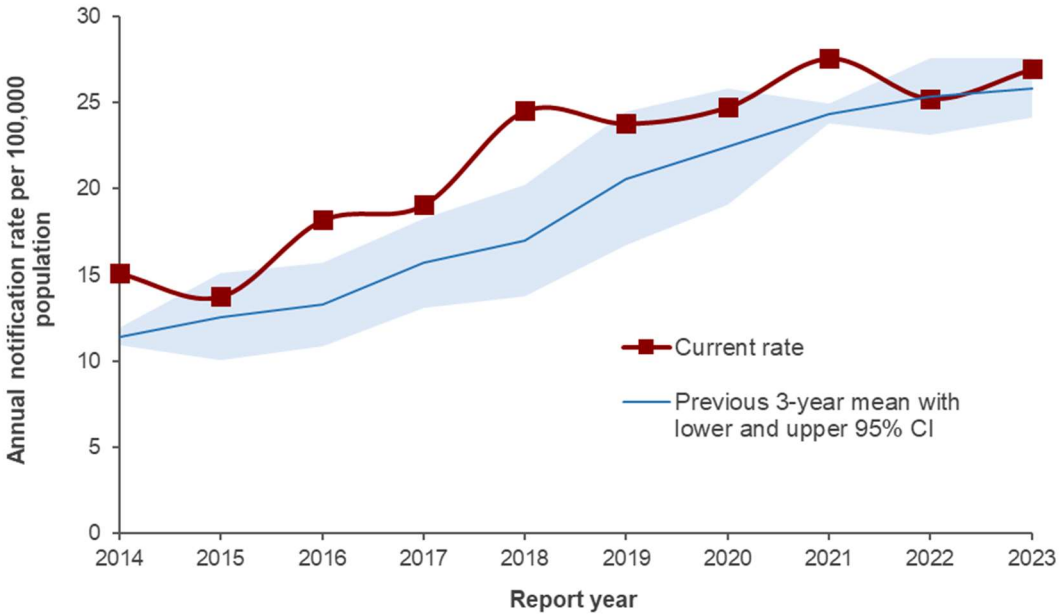
The frequency of overseas travel was lower in 2020 to 2023 compared to pre COVID-19 years (see Introduction, page 9). This is reflected in the notifications; in 2023, there were 56 yersiniosis notifications in EpiSurv listing overseas travel as a risk factor, compared to 58 in 2019, 11 in 2020, two in 2021 and 22 in 2022.

Figure 49. Yersiniosis EpiSurv notifications (line) and NMDS hospital admissions (bar) by year, 2009–2023



The yersiniosis annual notification rate has been generally increasing from 2014 to 2021 (Figure 50). The 2023 notification rate was 27.0 cases per 100,000 population, similar to the previous three-year mean (25.9 cases per 100,000 population).

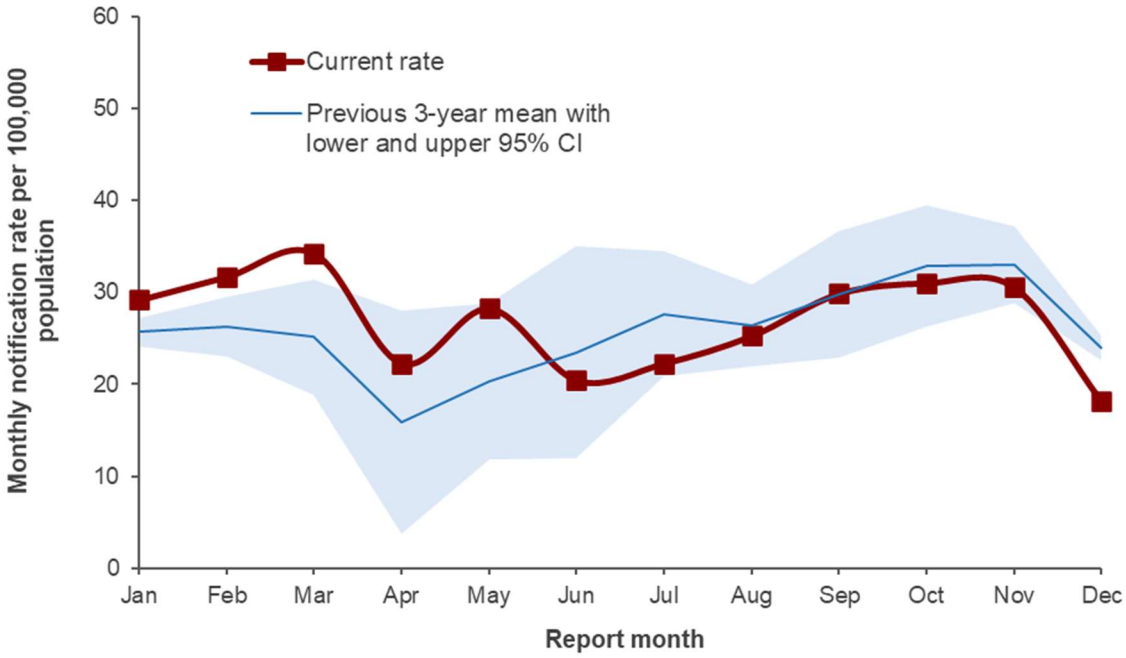
Figure 50. Yersiniosis notification rate by year, 2014–2023



Seasonal data

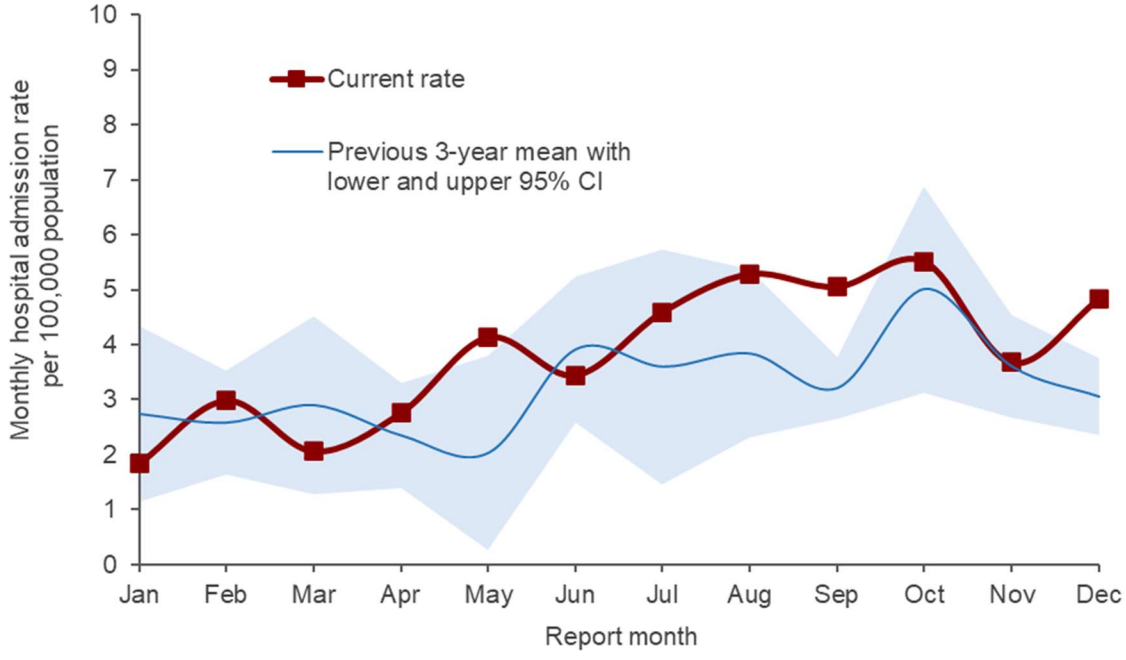
Yersiniosis notification rates per 100,000 population by month for 2023 are shown in Figure 51. For most of the year, the monthly notification rates were similar to the mean of the previous three years. The monthly number of notifications in 2023 ranged from 79 notifications (December, 18.2 cases per 100,000 population) to 149 notifications (March, 34.2 cases per 100,000 population).

Figure 51. Yersiniosis monthly notification rate (annualised), 2023



In 2023, the monthly hospital admission rates were higher in the second half of the year, in a similar trend to the previous three years (Figure 52).

Figure 52. Yersiniosis monthly hospital admissions (annualised), 2023



Demographics

In 2023, the yersiniosis notification and hospitalised case rates were slightly higher for females (27.2 cases and 4.4 hospitalised cases per 100,000 population) than males (26.6 cases and 3.5 hospitalised cases per 100,000 population) (Table 57).

Table 57. Yersiniosis cases by sex, 2023

Sex	EpiSurv notified cases		Hospitalised cases[a]	
	No.	Rate[b]	No.	Rate[b]
Male	691	26.6	91	3.5
Female	715	27.2	116	4.4
Total[c]	**1408**	**27.0**	**207**	**4.0**

[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 2023, the highest yersiniosis notification rates and hospitalised case rates were for the <1 year age group (134.7 cases and 22.7 hospitalised cases per 100,000 population) (Table 58).

Table 58. Yersiniosis cases by age group, 2023

Age group (years)	EpiSurv notified cases		Hospitalised cases[a]	
	No.	Rate[b]	No.	Rate[b]
<1	77	134.7	13	22.7
1 to 4	147	59.9	20	8.2
5 to 9	37	11.4	9	2.8
10 to 14	48	14.0	1	-
15 to 19	37	11.3	21	6.4
20 to 29	167	24.4	14	2.0
30 to 39	189	24.5	12	1.6
40 to 49	159	24.7	2	-
50 to 59	175	26.8	23	3.5
60 to 69	172	29.9	33	5.7
70+	200	33.3	59	9.8
Total	**1408**	**27.0**	**207**	**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).

Geographic distribution

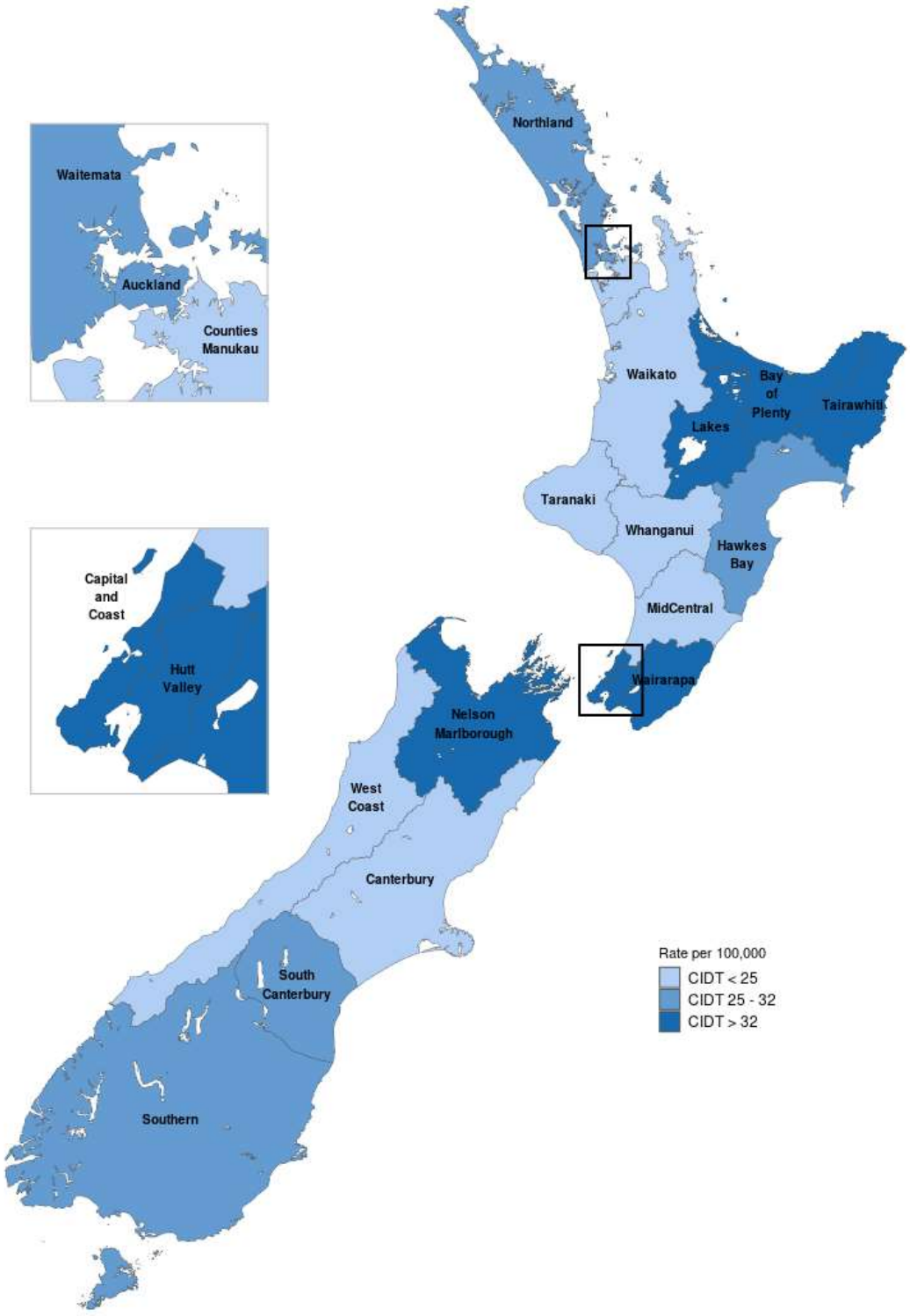
The notification rates by Health District calculated per 100,000 resident population are presented in Figure 53 (see also Table 80).

In 2023, the Health District notification rates of yersiniosis ranged from 8.6 per 100,000 population (six cases) for Whanganui to 44.4 per 100,000 population for Hutt Valley (72 cases). The Health Districts Hutt Valley, Wairarapa (43.0 cases per 100,000 population, 22 cases), and Nelson Marlborough (41.9 cases per 100,000 population, 70 cases) had the highest rates.

Historically, notification rates for yersiniosis have been variable across New Zealand, with the lower North Island Health Districts Wairarapa, Capital and Coast and Hutt Valley consistently in the highest quartile of notification rates since 2017.

Yersiniosis notification rates, stratified by 2023 Urban Rural Classification [20] of the cases' residential address and excluding cases associated with overseas travel varied across the different urban and rural areas (Appendix C, Table 81). Notification rates were highest in major urban (26.2 cases per 100,000 population), large urban (28.3 cases per 100,000 population) and other rural areas (29.4 per 100,000 population). The lowest rate was 20.8 cases per 100,000 population in small urban areas.

Figure 53. Geographic distribution of yersiniosis notifications, 2023



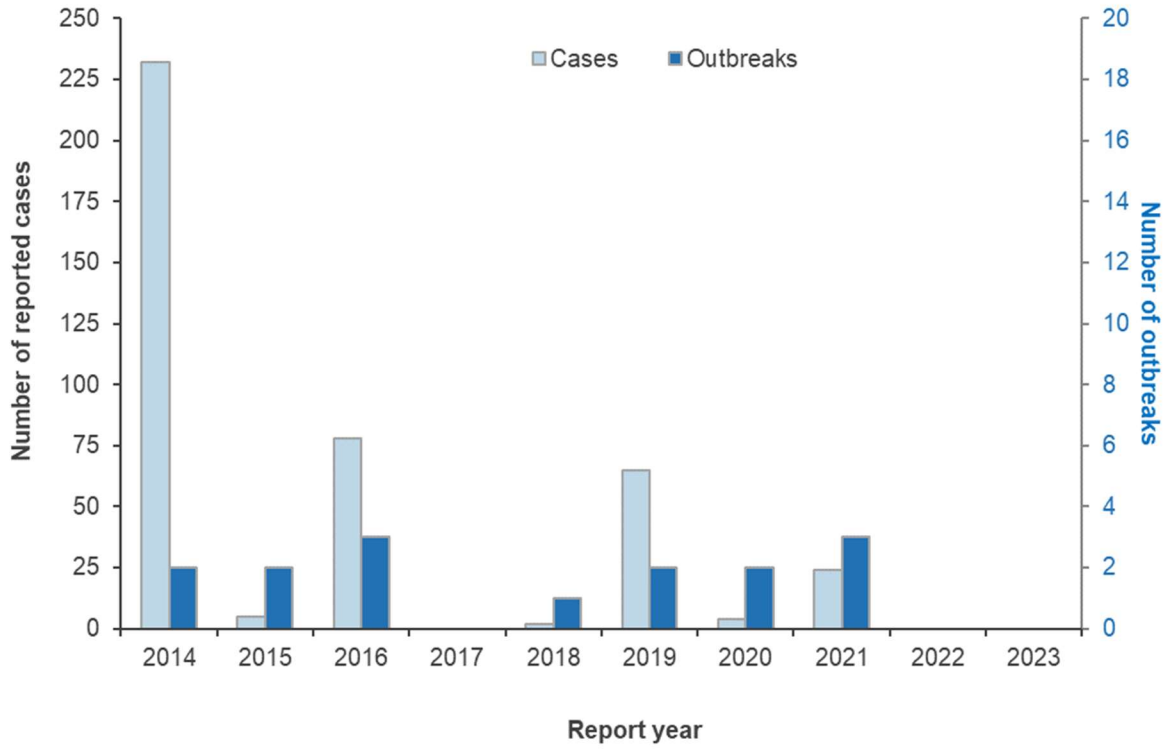
Note: Canterbury and South Canterbury Health Districts changed to community laboratory testing by CIDT methods in October 2023 and the West Coast Health District in June 2023. The plotted rates in these areas will not reflect a full year of CIDT testing in 2023.

Outbreaks reported as caused by *Yersinia* spp.

In 2023, there were four multi-disease outbreaks including yersiniosis notified in EpiSurv, with a total of 24 associated cases. Food consumption in New Zealand was not reported as a possible mode of transmission for these outbreaks. 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 2014 to 2023, three or fewer yersiniosis outbreaks with food reported as a possible mode of transmission were notified annually in EpiSurv. The number of annual outbreak associated cases ranged from two to 232 (Figure 54). The number of outbreaks in 2014 was not unusual, but the number of cases involved (232) was higher than recorded in New Zealand previously or since. The suspected source of this outbreak was raw salad vegetables from a supermarket. The suspected source of an outbreak of 51 cases in 2016 was sprouts.

Figure 54. Yersiniosis outbreaks reported in EpiSurv with food reported as a possible mode of transmission and associated cases reported by year, 2014-2023



Yersinia species commonly reported

In 2023, isolates from 969 out of 1408 cases (69%) of notified yersiniosis were typed by the Enteric Reference Laboratory (ERL). Table 59 shows the number of isolates typed by the Enteric Reference Laboratory at ESR 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 69% in 2023,
- 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, but >50% of New Zealand samples are no longer being tested for *Yersinia pseudotuberculosis* as the organism is not targeted by the commercial CIDT panels some diagnostic laboratories have chosen to use.
- Some CIDT positive samples do not provide an isolate that can be typed.

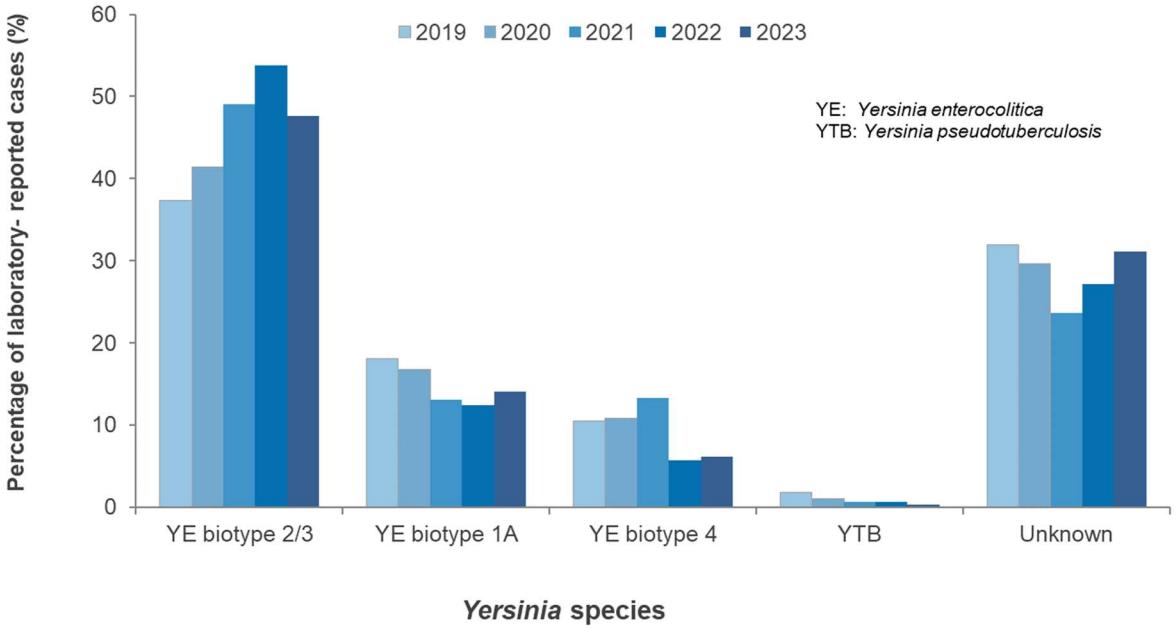
Between 2019 and 2023, each year the largest proportion of yersiniosis cases was due to *Y. enterocolitica* (Table 59 and Figure 55). *Yersinia* isolates from two cases were identified as *Y. hibernica* and *Y. frederiksenii*, respectively. The most prevalent type of *Y. enterocolitica* has been biotype 2/3, serotype O:9 in each year since 2019. This type was associated with almost 50% of the notified cases in 2023. In the same time period (2019 to 2023), *Y. enterocolitica* biotype 1A accounted for between 12% and 18% of yersiniosis notifications and biotype 4 accounted for between 6% and 13% of annual yersiniosis notified cases.

Table 59. Annual number of case notifications of different *Yersinia* spp. biotypes and serotypes identified by the Enteric Reference Laboratory, 2019–2023

Species	2019	2020	2021	2022	2023[a]
Yersinia enterocolitica	**785**	**877**	**1080**	**933**	**961**
biotype 1A	**215**	**213**	**191**	**161**	**199**
serotype O:5	18	38	19	19	23
serotype O:8	18	39	37	39	20
biotype 2/3	**443**	**523**	**705**	**695**	**670**
serotype O:5, 27	16	40	27	24	20
serotype O:9	425	483	678	670	647
biotype 4	**125**	**137**	**184**	**75**	**87**
serotype O:3	125	137	184	75	87
biotype not identified	**2**	**4**	**1**	**2**	**5**
Yersinia pseudotuberculosis	**21**	**13**	**10**	**9**	**5**
Cases without typing information	**379**	**373**	**319**	**348**	**439**

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

Figure 55. Percentage of notified yersiniosis cases by species and biotype by year, 2019–2023



Recent surveys

Nil.

Relevant New Zealand studies and publications

Nil.

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 quality of data, including known limitations.

The report uses the calendar year, 1 January to 31 December 2023, 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 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* [18].

Laboratory-based surveillance

For a number of organisms (e.g., *Salmonella*, *Escherichia coli*), clinical laboratory isolates are forwarded to reference laboratories at ESR 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 [15]. 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.

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)

ESR 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* [38]. 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.

Laboratory investigation of outbreaks

PHSs may submit clinical, food or environmental samples associated with single cases or outbreaks of suspected food poisoning to ESR’s Public Health Laboratory (PHL). While faeces are the most common human clinical sample, on occasions other clinical samples, such as vomit, urine or breast milk, may be submitted. Wherever possible, samples are linked to associated EpiSurv records. Samples are analysed for possible causative agents, based on information on symptoms and incubation period. In this report, laboratory investigations are reported only for outbreaks classified as foodborne in EpiSurv.

The present report only includes information on samples submitted to ESR’s PHL. It should be noted that human faecal samples associated with outbreaks and sporadic cases may be tested by community laboratories, following submission by general practitioners or PHSs. If the pathogen identified is a notifiable disease, a notification will be generated, and a case reported in EpiSurv. No information is available from community laboratories on the number of samples submitted for which no pathogen is detected.

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 [20] 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 2013 index mapping files were sourced from The University of Otago, Department of Public Health (https://www.otago.ac.nz/wellington/departments/publichealth/research/hirp/otago020194.html).

NZFS project reports and other publications

NZFS project reports, prepared by ESR 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 7 March 2024. Outbreak data contained in this report are based on information recorded as an outbreak in EpiSurv as at 24 April 2024. Disease numbers are reported according to the date of notification. Hospitalisation data was extracted from the NMDS on the 23 April 2024.

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.

Case status for notifications

All notifications recorded in EpiSurv that meet the case definitions [39] 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.

Data used for calculating rates of disease

All population rates use Statistics New Zealand 2023 mid-year population estimates and are crude rates unless otherwise stated. At 30 June 2023, the New Zealand population was estimated to be 5,223,100. The population estimates for 2014 to 2021 have been revised by Statistics New Zealand, considering new migration measures and 2018 Census distributions. Any cases rates given in this report for 2014 to 2021 will be based on the revised population estimates.

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 2023 this report reports on Health New Zealand Te Whatu Ora districts (Health Districts) which have the same boundaries as the corresponding previous DHBs.

Urban rural classification

The urban rural classification of area of usual residence of notified EpiSurv cases and hospitalised cases was via mapping the residence 2013 Meshblock to urban rural categories [20]. Where a meshblock 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 (2020−2022).

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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

Table 60 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 2023 there were four different commercial panels used across New Zealand.

Table 60. Dates of the change to CIDT methods for enteric pathogens by Health District (X: not yet changed, NS: not screened for)

Health District		*Campylobacter*	*Salmonella*	*Shigella*	STEC	*Yersinia enterocolitica*	*Yersinia pseudotuberculosis*	*Giardia*	*Cryptosporidium*	*Vibrio parahaemolyticus*
Auckland Te Toka Tumai	Hospital	Jul 2017	Jul 2017	Jul 2017	Jul 2017	Jul 2017	X	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	X	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	Hospital	Jan 2018	Jan 2018	Jan 2018	Jan 2018	Jan 2018	Jan 2018	Jan 2018	Jan 2018	X
Capital & Coast	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	X	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	X	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[a]	Dec 2014[a]	X
Hutt Valley	Hospital	Jan 2018	Jan 2018	Jan 2018	Jan 2018	Jan 2018	Jan 2018	Jan 2018	Jan 2018	X
Hutt Valley	Community	Jan 2018	Jan 2018	Jan 2018	Jan 2018	Jan 2018	Jan 2018	Jan 2018	Jan 2018	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

Health District		*Campylobacter*	*Salmonella*	*Shigella*	STEC	*Yersinia enterocolitica*	*Yersinia pseudotuberculosis*	*Giardia*	*Cryptosporidium*	*Vibrio parahaemolyticus*
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
Nelson Marlborough	Hospital	Jan 2018	Jan 2018	Jan 2018	Jan 2018	Apr 2019	Apr 2019	Dec 2014[a]	Dec 2014[a]	X
Nelson Marlborough	Community	Jan 2018	Jan 2018	Jan 2018	Jan 2018	Apr 2019	Apr 2019	Dec 2014[a]	Dec 2014[a]	X
Northland Te Tai Tokerau	Hospital	Dec 2022	Dec 2022	Dec 2022	Dec 2022	Dec 2022	X	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[a]	Dec 2014[a]	X
Southern	Community	Jan 2017	Jan 2017	Jan 2017	Jan 2017	Apr 2019	Apr 2019	Dec 2014[a]	Dec 2014[a]	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	X	X	X	X	X	X	X	X	X
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	X	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	X	X	X	Jun 2023
West Coast To Tai o Poutini	Community	Jun 2023	Jun 2023	Jun 2023	Jun 2023	Jun 2023	X	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, February 2024.

[a] 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 community laboratory covering faecal specimens 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 the community 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 61. Number of cases notified in EpiSurv and rate per 100,000 population of selected notifiable diseases in New Zealand, 2022–2023

Disease	2022		2023	
	Cases	Rate	Cases	Rate
Acute gastroenteritis[a]	331	6.5	461	8.8
Campylobacteriosis	5878	114.9	6089	116.6
Hepatitis A	58	1.1	34	0.7
Listeriosis	39	0.8	37	0.7
Salmonellosis	749	14.6	827	15.8
STEC infection	1022	20.0	1006	19.3
Yersiniosis	1294	25.3	1408	27.0

[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*, *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 [13]. Please note that other publications or reports may report botulism and toxic shellfish poisoning separately, resulting in differing case numbers for acute gastroenteritis.

Table 62. 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 (2023)	Australia[a] (2023)	USA[b,c] (2022)	Canada[d] (2021)	UK[e] (2019)	EU Total[e,g] (2022)	Other high
Campylobacteriosis	116.6	155.4	19.2	20.4	88.1	43.1	141.3 (Luxembourg)[f] 137.0 (Czechia)[f]
Hepatitis A	0.7	0.80	1.7[c]	0.46	0.6[g]	1.0[g]	5.5 (Hungary)[g] 5.3 (Croatia)[g]
Listeriosis	0.7	0.32	0.3	0.41	0.23	0.62	1.5 (Denmark)[f] 1.3 (Finland)[f]
Salmonellosis	15.8	42.6	16.3	8.7	14.6	15.3	71.9 (Czechia)[f] 67.5 (Slovakia)[f]
STEC infection	19.3	3.2	5.7	2.0	2.4	2.1	17.6 (Ireland)[f] 15.0 (Malta)[f]
Yersiniosis	27.0	NN	2.0	NN	0.2	2.2	12.7 (Denmark)[f] 7.4 (Finland)[f]

NN: Not notifiable

[a] The Australian National Notifiable Diseases Surveillance System (NNDSS, https://nindss.health.gov.au/pbi-dashboard/) currently only reports notifiable disease rates for states and territories and case numbers for states and territories and total. These data were used to estimate total disease rates for Australia.

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

[c] Centers for Disease Control and Prevention. Summary of notifiable disease https://wonder.cdc.gov/nndss/nndss_annual_tables_menu.asp (CDC data presented here relate to the 2021 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 2022. While UK case numbers are reported on a weekly basis, no annual summary was located and figures presented here for the UK relate to 2019 or earlier years.

[f] European Food Safety Authority and European Centre for Disease Prevention and Control (ECDC). The European Union One Health 2022 Zoonoses Report https://www.efsa.europa.eu/en/efsajournal/pub/8442.

[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 63. Number of cases of selected notifiable diseases recorded in EpiSurv by year, 1994–2023

Disease	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008
Acute gastroenteritis[a]	-	-	555	316	493	608	730	942	1088	1030	1362	559	926	617	676
Campylobacteriosis	7714	7442	7635	8924	11,572	8161	8418	10,146	12,493	14,788	12,215	13,836	15,873	12,778	6692
Hepatitis A	179	338	311	347	144	119	107	61	106	70	49	51	123	42	89
Listeriosis	8	13	10	35	17	19	22	18	19	24	26	20	19	26	27
Salmonellosis	1522	1334	1141	1177	2069	2077	1795	2417	1880	1401	1081	1382	1335	1275	1337
STEC infection [a,b]	3	6	7	13	48	64	67	76	73	104	89	92	87	100	122
Yersiniosis[a]	-	-	330	488	546	503	396	429	472	436	407	383	453	502	508

Disease	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023
Acute gastroenteritis	713	502	570	765	558	775	506	513	324	231	486	357	244	331	461
Campylobacteriosis	7177	7346	6686	7016	6837	6782	6218	7457	6482	6957	6203	5292	5729	5878	6089
Hepatitis A	44	46	26	82	91	74	47	35	58	68	67	21	8	58	34
Listeriosis	28	23	26	25	19	25	26	36	21	30	31	35	32	39	37
Salmonellosis	1128	1146	1055	1081	1143	955	1051	1091	1127	1100	1190	709	714	749	827
STEC infection	143	138	153	147	205	187	330	417	547	925	1103	845	912	1022	1006
Yersiniosis	430	406	513	514	483	680	634	858	917	1201	1185	1260	1410	1294	1408

[a] Acute gastroenteritis, STEC infection and yersiniosis were added to the Health Act 1956 notification schedule in June 1996.

[b] The first case of STEC infection confirmed in New Zealand was reported in October 1993 [40].

Note: cell marked "-" where data are unavailable.

Table 64. Deaths due to selected notifiable diseases recorded in EpiSurv[a], 2004–2023

Disease	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023
Acute gastroenteritis[b]	0	0	0	0	0	0	0	0	0	0	2	0	1	0	0	0	0	0	0	0
Campylobacteriosis	0	1	1	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0[c]
Listeriosis- non perinatal	3	1	0	2	3	2	3	1	4	2	3	1	0	0	2	0	1	3	4	5[d]
Listeriosis- perinatal	2	4	1	2	2	2	4	0	2	3	2	3	2	0	0	4	1	1	2	2
Salmonellosis	0	1	1	1	1	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0[e]
STEC infection	0	0	0	0	0	1	0	0	0	0	1	0	0	0	2	1	0	0	1	0[f]
Yersiniosis	1	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 [13]. 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 2023, there were four deaths of campylobacteriosis cases recorded in EpiSurv; one case died from a cause other than campylobacteriosis and the cause of death was not recorded for the other three cases.

[d] In 2023, there were four additional deaths of listeriosis cases recorded in EpiSurv. One case died from a cause other than listeriosis, but the listeriosis was recorded as contributing to the condition. The cause of death was not recorded for the three other listeriosis cases who died.

[e] In 2023, one salmonellosis case was recorded in EpiSurv as died from a cause other than salmonellosis.

[f] In 2023, there were two deaths of STEC infection cases recorded in EpiSurv; one case died from a cause other than STEC infection and the cause of death was not recorded for the other case.

[g] In 2023, one yersiniosis case was recorded in EpiSurv as died. The cause of death was not recorded.

Table 65. Hospitalised cases of selected notifiable diseases, 2022–2023

Disease	Source	ICD-10 Codes	2022			2023		
			Principal diagnosis	Other relevant diagnosis	Total	Principal diagnosis	Other relevant diagnosis	Total
Campylobacteriosis	NMDS[a]	A04.5	784	167	**951**	803	186	**989**
Hepatitis A	NMDS	B15	31	38	**69**	32	28	**60**
Listeriosis	NMDS	A32	19	15	**34**	21	19	**40**
Salmonellosis[b]	NMDS	A02.0	163	35	**198**	161	57	**218**
STEC infection[c]	NMDS	A04.3	34	31	**65**	23	19	**42**
	EpiSurv	NA	NA	NA	**254**	NA	NA	**235**
Yersiniosis	NMDS	A04.6	103	92	**195**	116	91	**207**

[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] *Salmonella* enterocolitis.

[c] 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 [30] has shown that ICD-10 code A04.3 alone does not capture all the cases hospitalised due to STEC infection. In 2023, 235 cases were listed as hospitalised in EpiSurv, compared to 42 cases identified using the A04.3 code.

NA: Not applicable.

Table 66. Hospitalisation and duration in hospital or intensive care unit (ICU) for cases of selected notifiable diseases, reported in NMDS, 2023

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	989	347	519	123	13 (1.3%)	94 [6 to 366]
Hepatitis A	B15	60	23	26	11	5 (8.3%)	93 [20 to 427]
Listeriosis	A32	40	5	9	26	2 (5.0%)	96 and 192
Salmonellosis[d]	A02.0	218	65	108	45	8 (3.7%)	85 [8 to 1026]
STEC infection	A04.3	42 (235)[e]	8	22	12	4 (9.5%)	118 [9 to 143]
Yersiniosis	A04.6	207	53	93	61	8 (3.9%)	56 [24 to 441]

[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 in 2023.

[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] *Salmonella* enterocolitis.

[e] 42 is the number of cases admitted to hospital, with an associated ICD-10 diagnosis code of A04.3 (enterohaemorrhagic *Escherichia coli* infection). A new 2024 study [30] has shown that ICD-10 code A04.3 alone does not capture all the cases hospitalised due to STEC infection. 235 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.

Table 67. Number of cases notified in EpiSurv and rate per 100,000 population of selected notifiable diseases by ethnic group[a], 2023

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]	84	11	32	8	313	**461**	9.7	3.1	4.0	10.5	10.0	**8.8**
Campylobacteriosis	608	177	537	82	4319	**6089**	69.9	50.3	67.7	107.8	137.9	**116.6**
Hepatitis A	4	1	17	4	8	**34**	-	-	2.1	-	0.3	**0.7**
Listeriosis	4	4	8	1	20	**37**	-	-	1.0	-	0.6	**0.7**
Salmonellosis	107	49	128	9	533	**827**	12.3	13.9	16.1	11.8	17.0	**15.8**
STEC infection	130	30	57	12	767	**1006**	14.9	8.5	7.2	15.8	24.5	**19.3**
Yersiniosis	173	53	268	28	821	**1408**	19.9	15.0	33.8	36.8	26.2	**27.0**

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 [39]. Please note that other publications or reports may report botulism and toxic shellfish poisoning separately, resulting in differing case numbers for acute gastroenteritis.

Table 68. Hospitalised cases[a] and rate per 100,000 population of selected notifiable diseases by ethnic group[b], 2023

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	120	63	88	14	701	**989**	13.8	17.9	11.1	18.4	22.4	**18.9**
Hepatitis A	NMDS	9	8	20	3	20	**60**	1.0	2.3	2.5	-	0.6	**1.1**
Listeriosis	NMDS	6	5	7	1	21	**40**	0.7	1.4	0.9	-	0.7	**0.8**
Salmonellosis	NMDS	38	24	38	4	114	**218**	4.4	6.8	4.8	-	3.6	**4.2**
STEC infection	EpiSurv[a]	37	9	13	1	173	**235**	4.3	2.6	1.6	-	5.5	**4.5**
Yersiniosis	NMDS	32	15	39	7	114	**207**	3.7	4.3	4.9	9.2	3.6	**4.0**

[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 '-'.

A new 2024 study [30] 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.

[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.

Table 69. NMDS[a] length of hospital stay of cases of selected notifiable diseases by ethnic group[b], 2023

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	54	58	8	23	31	9	39	43	6	9	5	0	219	382	100
Hepatitis A	B15	0	0	9	0	0	8	0	1	19	1	0	2	0	0	20
Listeriosis	A32	0	0	6	0	0	5	0	0	7	0	0	1	0	0	21
Salmonellosis[e]	A02.0	13	18	7	3	15	6	14	14	10	1	3	0	34	58	22
STEC infection[f]	A04.3	2	3	3	1	0	0	1	1	0	0	0	0	4	18	9
Yersiniosis	A04.6	7	16	9	2	7	6	14	15	10	2	4	1	28	51	35

[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 new 2024 study [30] 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 70. NMDS ICU admissions and duration of stay of selected notifiable diseases by ethnic group[a], 2023

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	1	1	0	0	11	13	113	100	-	-	91 [6 to 366]
Hepatitis A	1	2	2	0	0	5	125	20 and 427	23 and 93	-	-
Listeriosis	0	0	1	0	1	2	-	-	96	-	192
Salmonellosis[d]	2	0	1	1	4	8	61 and 84	-	404	8	270 [68 to 1026]
STEC infection[e]	1	0	0	0	3	4	143	-	-	-	94 [9 to 142]
Yersiniosis	1	1	0	1	5	8	365	45	-	77	25 [24 to 441]

[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 new 2024 study [30] 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.

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Sex tables

Table 71. Number of EpiSurv cases and rate per 100,000 population of selected notifiable diseases by sex, 2023

Disease	Sex					
	Male		Female		Total[a]	
	Cases	Rate	Cases	Rate	Cases	Rate
Acute gastroenteritis[b]	217	8.4	243	9.3	461	8.8
Campylobacteriosis	3370	129.7	2716	103.5	6089	116.6
Hepatitis A	16	0.6	18	0.7	34	0.7
Listeriosis[c]	24	0.9	13	0.5	37	0.7
Salmonellosis	424	16.3	401	15.3	827	15.8
STEC infection	491	18.9	515	19.6	1006	19.3
Yersiniosis	691	26.6	715	27.2	1408	27.0

[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 [39]. 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 three perinatal cases are those for the mother.

Table 72. NMDS hospital data[a] of selected notifiable diseases by sex, 2023

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	541	{ 187, 283, 71 }	7	66 [6 to 366]	448	{ 160, 236, 52 }	6	107 [9 to 363]
Hepatitis A	36	{ 13, 16, 7 }	5	93 [20 to 427]	24	{ 10, 10, 4 }	0	-
Listeriosis[d]	23	{ 0, 5, 18 }	2	96 and 192	17	{ 5, 4, 8 }	0	-
Salmonellosis[e]	102	{ 28, 55, 19 }	3	454 [85 to 1026]	116	{ 37, 53, 26 }	5	68 [8 to 404]
STEC infection[f]	20 (112)[g]	{ 5, 10, 5 }	2	94 and 143	22 (123)[g]	{ 3, 12, 7 }	2	9 and 142
Yersiniosis	91	{ 23, 42, 26 }	4	56 [25 to 441]	116	{30, 51, 35}	4	51 [24 to 365]

[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 three perinatal cases are those for the mother.

[e] *Salmonella* enterocolitis.

[f] Enterohaemorrhagic *Escherichia coli* infection ICD-10 code A04.3.

[g] X (Y): X is the number of cases admitted to hospital, with an associated ICD-10 diagnosis code of A04.3 for male or females. All the severity information is for cases hospitalised associated with code A04.3. A new 2024 study [30] 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 73. Number of Episurv cases of selected notifiable diseases by age group, 2023

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	35	10	7	13	63	68	53	68	62	67	**461**
Campylobacteriosis	97	506	197	187	318	847	747	585	779	822	1003	**6089**
Hepatitis A	0	1	4	0	4	9	7	2	1	3	3	**34**
Listeriosis[c]	0	2	0	0	0	3	1	3	2	5	21	**37**
Salmonellosis	42	114	48	28	38	74	88	78	105	107	104	**827**
STEC infection	37	137	40	41	38	119	94	65	112	113	209	**1006**
Yersiniosis	77	147	37	48	37	167	189	159	175	172	200	**1408**

[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 [13]. 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 three perinatal cases are those for the mother (two in the 20 to 29 age group, and one in the 30 to 39 age group).

Table 74. Rate per 100,000 population of selected notifiable diseases by age group, 2023

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]	21.0	14.3	3.1	2.0	4.0	9.2	8.8	8.2	10.4	10.8	11.2	**8.8**
Campylobacteriosis	169.7	206.4	60.9	54.5	97.2	123.9	96.9	90.8	119.1	142.8	167.2	**116.6**
Hepatitis A	-	-	-	-	-	1.3	0.9	-	-	-	-	**0.7**
Listeriosis[c]	-	-	-	-	-	-	-	-	-	0.9	3.5	**0.7**
Salmonellosis	73.5	46.5	14.8	8.2	11.6	10.8	11.4	12.1	16.1	18.6	17.3	**15.8**
STEC infection	64.7	55.9	12.4	11.9	11.6	17.4	12.2	10.1	17.1	19.6	34.8	**19.3**
Yersiniosis	134.7	59.9	11.4	14.0	11.3	24.4	24.5	24.7	26.8	29.9	33.3	**27.0**

[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 [13]. 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 three 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 75. Hospitalised cases[a] of selected notifiable diseases by age group, 2023

Disease	Source	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[a]	15	44	14	17	50	111	102	77	100	134	325	**989**
Hepatitis A	NMDS	0	2	2	0	5	7	10	5	7	7	15	**60**
Listeriosis[b]	NMDS	0	2	0	0	1	4	3	3	1	5	21	**40**
Salmonellosis	NMDS	11	20	7	4	6	20	23	18	25	38	46	**218**
STEC infection	EpiSurv[a]	9	35	11	9	7	19	16	11	19	23	76	**235**
Yersiniosis	NMDS	13	20	2	9	1	21	14	12	23	33	59	**207**

[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 new 2024 study [30] 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 three perinatal cases are those for the mother (two in the 20 to 29 age group, and one in the 30 to 39 age group).

Table 76. NMDS hospitalised cases[a] of selected notifiable diseases by nights admitted and age group[b], 2023

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	10	26	8	8	21	64	54	34	29	37	56	**347**
	Hepatitis A	0	0	1	0	1	5	2	2	3	4	5	**23**
	Listeriosis	0	0	0	0	1	1	3	0	0	0	0	**5**
	Salmonellosis	8	12	5	1	1	8	8	6	6	6	4	**65**
	STEC infection	1	0	0	0	0	2	1	0	2	1	1	**8**
	Yersiniosis	6	10	0	3	1	8	2	3	10	5	5	**53**
2 to 6	Campylobacteriosis	4	17	4	8	27	44	43	38	59	77	198	**519**
	Hepatitis A	0	2	1	0	4	2	4	2	2	2	7	**26**
	Listeriosis	0	0	0	0	0	3	0	0	0	1	5	**9**
	Salmonellosis	1	7	2	2	4	10	10	8	13	24	27	**108**
	STEC infection	1	5	1	1	1	0	4	1	1	2	5	**22**
	Yersiniosis	7	7	0	6	0	9	9	6	5	16	28	**93**
7+	Campylobacteriosis	1	1	1	2	3	5	5	2	12	20	71	**123**
	Hepatitis A	0	0	0	0	0	4	1	0	2	1	3	**11**
	Listeriosis	0	2	0	0	0	0	3	0	1	4	16	**26**
	Salmonellosis	2	1	1	1	2	5	4	0	6	8	15	**45**
	STEC infection	1	4	1	0	0	0	0	1	0	0	5	**12**
	Yersiniosis	0	3	0	0	4	3	3	2	8	12	26	**61**

[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 three perinatal cases are those for the mother (two in the 20 to 29 age group, and one in the 30 to 39 age group).

Table 77. NMDS hospitalised cases[a] admitted to an intensive care unit (ICU)[b] of selected notifiable disease by age group, 2023

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	1	0	0	2	0	1	4	4	**13**
Hepatitis A	0	0	0	0	0	0	2	0	1	2	0	**5**
Listeriosis	0	0	0	0	0	0	0	0	0	1	1	**2**
Salmonellosis	0	0	0	0	1	0	0	1	3	2	1	**8**
STEC infection	1	2	0	0	0	0	0	0	0	0	1	**4**
Yersiniosis	0	0	0	0	0	0	1	0	1	4	2	**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 78. NMDS ICU[a] duration (hours, median [range] or values)[b] of selected notifiable diseases by age group, 2023

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	-	9	-	100	-	-	66 and 363	-	113	62 [6 to 146]	97 [55 to 366]
Hepatitis A	-	-	-	-	-	-	93 and 427	-	20	23 and 125	-
Listeriosis	-	-	-	-	-	-	-	-	-	192	96
Salmonellosis	-	-	-	-	8	-	-	1026	68 [61-85]	404 and 454	84
STEC infection	142	9 and 143	-	-	-	-	-	-	-	-	94
Yersiniosis	-	-	-	-	-	-	24	-	45	221 [25 to 441]	24 and 66

[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 79. Number of EpiSurv cases of selected notifiable diseases by Health District, 2023

Disease	Northern Region				Te Manawa Taki Region					Central Region						Te Waipounamu Region					Total
	Northland Te Tai Tokerau	Waitematā	Auckland Te Toka Tumai	Counties Manukau	Waikato	Lakes	Bay of Plenty Hauora a Toi	Tairāwhiti	Taranaki	Hawkes Bay Te Marau a Māui	Whanganui	MidCentral Te Pae Hauora o Ruahine o Tararua	Hutt Valley	Capital and Coast	Wairarapa	Nelson Marlborough	West Coast Te Tai o Poutini	Canterbury Waitaha	South Canterbury	Southern	
Acute gastroenteritis[a]	55	5	4	6	85	30	64	1	1	6	12	0	10	21	3	4	0	72	2	80	**461**
Campylobacteriosis	266	834	572	535	590	148	280	65	233	294	61	224	134	294	85	146	57	687	122	462	**6089**
Hepatitis A	0	3	4	8	1	1	1	0	0	4	0	5	1	2	0	0	1	1	1	1	**34**
Listeriosis	1	3	6	7	5	2	2	0	0	1	0	0	3	3	0	1	0	2	0	1	**37**
Salmonellosis	37	71	94	80	52	11	61	6	29	19	7	18	29	37	7	27	5	135	24	78	**827**
STEC infection	85	75	53	47	79	28	54	17	57	58	16	33	23	58	31	44	6	88	26	128	**1006**
Yersiniosis	52	184	128	115	95	39	96	20	28	51	6	30	72	118	22	70	6	149	16	111	**1408**

[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 [13]. 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 80. Rate per 100,000 population of selected notifiable diseases by health district area, 2023

Disease	Northern Region				Te Manawa Taki Region					Central Region						Te Waipounamu Region					
	Northland Te Tai Tokerau	Waitematā	Auckland Te Toka Tumai	Counties Manukau	Waikato	Lakes	Bay of Plenty Hauora a Toi	Tairāwhiti	Taranaki	Hawkes Bay Te Marau a Māui	Whanganui	MidCentral Te Pae Hauora o Ruahine o Tararua	Hutt Valley	Capital and Coast	Wairarapa	Nelson Marlborough	West Coast Te Tai o Poutini	Canterbury Waitaha	South Canterbury	Southern	Total
Acute gastroenteritis[a]	27.0	0.8	-	1.0	18.5	25.0	22.9	-	-	3.2	17.1	-	6.2	6.4	-	-	-	12.0	-	22.2	**8.8**
Campylobacteriosis	130.5	128.5	116.2	85.7	128.7	123.2	100.1	123.6	180.9	159.2	87.1	116.2	82.6	90.0	166.0	87.3	173.3	114.1	193.7	128.1	**116.6**
Hepatitis A	-	-	-	1.3	-	-	-	-	-	-	-	2.6	-	-	-	-	-	-	-	-	**0.7**
Listeriosis	-	-	1.2	1.1	1.1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	**0.7**
Salmonellosis	18.1	10.9	19.1	12.8	11.3	9.2	21.8	11.4	22.5	10.3	10.0	9.3	17.9	11.3	13.7	16.1	15.2	22.4	38.1	21.6	**15.8**
STEC infection	41.7	11.6	10.8	7.5	17.2	23.3	19.3	32.3	44.3	31.4	22.9	17.1	14.2	17.8	60.5	26.3	18.2	14.6	41.3	35.5	**19.3**
Yersiniosis	25.5	28.4	26.0	18.4	20.7	32.5	34.3	38.0	21.7	27.6	8.6	15.6	44.4	36.1	43.0	41.9	18.2	24.8	25.4	30.8	**27.0**

[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[13]. 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 81. Number of EpiSurv cases and rate per 100,000 population of selected notifiable diseases by prioritised urban rural residence group[a] (excluding notifications with overseas travel as a risk factor), 2023

Disease	Cases							Rate per 100,000 population[b]						
	Major urban area	Large urban area	Medium urban area	Small urban area	Rural settlement	Rural other	Total[c]	Major urban area	Large urban area	Medium urban area	Small urban area	Rural settlement	Rural other	Total
Acute gastroenteritis[d]	126	57	54	43	15	58	**353**	4.8	7.8	11.4	7.9	9.5	8.7	**6.8**
Campylobacteriosis	2348	712	471	635	254	1354	**5774**	88.8	97.5	99.6	116.1	161.4	202.1	**110.5**
Hepatitis A	1	5	1	1	1	1	**10**	-	0.7	-	-	-	-	**0.2**
Listeriosis	22	5	4	1	0	5	**37**	0.8	0.7	-	-	-	0.7	**0.7**
Salmonellosis	230	68	56	62	22	133	**571**	8.7	9.3	11.8	11.3	14.0	19.8	**10.9**
STEC infection	222	141	101	115	48	307	**934**	8.4	19.3	21.4	21.0	30.5	45.8	**17.9**
Yersiniosis	693	207	104	114	37	197	**1352**	26.2	28.3	22.0	20.8	23.5	29.4	**25.9**

[a] Mapping to 2023 Urban Rural Classification is via 2013 meshblocks. Some of the meshblocks 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.

[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.

[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[13]. Please note that other publications or reports may report botulism and toxic shellfish poisoning separately, resulting in differing case numbers for acute gastroenteritis.

Table 82. Hospitalised cases[a] and rate per 100,000 population of selected notifiable diseases by urban rural residence group[b], 2023

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	Total	Major urban area	Large urban area	Medium urban area	Small urban area	Rural settlement	Rural other	Total
Campylobacteriosis	NMDS	450	151	97	165	72	54	989	17.0	20.7	20.5	30.2	45.7	8.1	**18.9**
Hepatitis A	NMDS	37	7	4	8	3	1	60	1.4	1.0	-	1.5	-	-	**1.1**
Listeriosis	NMDS	24	5	4	5	0	2	40	0.9	0.7	-	0.9	-	-	**0.8**
Salmonellosis	NMDS	117	27	17	30	12	15	218	4.4	3.7	3.6	5.5	7.6	2.2	**4.2**
STEC infection	EpiSurv	69	46	15	25	11	69	235	2.6	6.3	3.2	4.6	7.0	10.3	**4.5**
Yersiniosis	NMDS	113	33	13	32	12	4	207	4.3	4.5	2.7	5.9	7.6	-	**4.0**

[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 new 2024 study [30] 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 83. Number of cases of selected notifiable diseases by the 2013 Deprivation Index of area of residence[a] (excluding notifications with overseas travel as a risk factor), 2023

Disease	2013 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]	47	63	65	52	54	72	**353**
Campylobacteriosis	411	1371	1235	1123	935	699	**5774**
Hepatitis A	1	5	0	0	3	1	**10**
Listeriosis	2	3	8	5	6	13	**37**
Salmonellosis	39	102	130	109	88	103	**571**
STEC infection	69	192	214	195	146	118	**934**
Yersiniosis	80	342	282	233	233	182	**1352**

[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, bedroom occupancy, people living in single parent family, access to a car [41].

[b] Total cases notified in EpiSurv which did not record the person being overseas during the incubation period for the disease.

[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 [13]. Please note that other publications or reports may report botulism and toxic shellfish poisoning separately, resulting in differing case numbers for acute gastroenteritis.

Table 84. Percentage of total cases of selected notifiable diseases by 2013 Deprivation Index of area of residence[a] (excluding notifications with overseas travel as a risk factor), 2023

Disease	2013 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]	13.3	17.8	18.4	14.7	15.3	20.4
Campylobacteriosis	7.1	23.7	21.4	19.4	16.2	12.1
Salmonellosis	6.8	17.9	22.8	19.1	15.4	18
STEC infection	7.4	20.6	22.9	20.9	15.6	12.6
Yersiniosis	5.9	25.3	20.9	17.2	17.2	13.5

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, bedroom occupancy, people living in single parent family, access to a car [41].

[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 [13]. 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] of selected notifiable diseases by the 2013 Deprivation Index of area of residence[b], 2023

Disease	Source[a]	2013 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	7	213	203	179	194	193	**989**
Hepatitis A	NMDS	0	8	11	14	13	14	**60**
Listeriosis	NMDS	0	4	9	6	10	11	**40**
Salmonellosis	NMDS	3	33	39	31	54	58	**218**
STEC infection	EpiSurv	23	42	51	42	40	37	**235**
Yersiniosis	NMDS	0	29	35	45	49	49	**207**

[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 new 2024 study [30] 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 85 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, bedroom occupancy, people living in single parent family, access to a car [41].

Table 86. Percentage of hospitalised cases of selected notifiable diseases by the 2013 Deprivation Index of area of residence, 2023

Disease	2013 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	0.7	21.5	20.5	18.1	19.6	19.5
Salmonellosis	1.4	15.1	17.9	14.2	24.8	26.6
STEC infection[b]	9.8	17.9	21.7	17.9	17.0	15.7
Yersiniosis	0	14	16.9	21.7	23.7	23.7

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, bedroom occupancy, people living in single parent family, access to a car [41].

[b] A new 2024 study [30] 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 87. Potential foodborne outbreaks with a common source and associated cases by pathogen/condition as reported in EpiSurv, 2023

Pathogen/Condition	Outbreaks (n = 35)		Cases (n = 386)	
	No.	%[a]	No.	%[b]
Norovirus infection	6	17.1	137	35.5
Campylobacteriosis	5	14.3	36	9.3
Clostridium perfringens intoxication	2	5.7	15	3.9
Bacillus cereus and *Clostridium perfringens* intoxication	1	2.9	12	3.1
Enterotoxigenic *Escherichia coli* and *Vibrio cholerae* infection	1	2.9	3	0.8
Vibrio parahaemolyticus infection	1	2.9	4	1.0
Pathogen not identified [c]	19	54.3	179	46.4

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 (35).

[b] Percentage of cases for each pathogen/condition, calculated using the total number of associated cases (386).

[c] All enteric outbreaks with no pathogen identified in 2023 were recorded as gastroenteritis.

Table 88. Potential foodborne outbreaks with a common source and associated cases by exposure setting as reported in EpiSurv, 2023

Exposure setting	Outbreaks (n = 35)		Cases (n = 386)	
	No.	%[a]	No.	%[b]
Commercial food operators	**20**	**57.1**	**134**	**34.7**
Restaurant/cafe/bakery	10	28.6	102	26.4
Takeaway	8	22.9	25	6.5
Temporary or mobile service	2	5.7	7	1.8
Institutions	**4**	**11.4**	**144**	**37.3**
School	1	2.9	100	25.9
Workplace	1	2.9	23	6.0
Childcare Centre	1	2.9	12	3.1
Long term care facility	1	2.9	9	2.3
Other	**11**	**31.4**	**108**	**28.0**
Home	9	25.7	92	23.8
Community Event	1	2.9	12	3.1
Campsite	1	2.9	4	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 (35).

[b] Percentage of cases for each exposure setting, calculated using the total number of associated cases (386).

Table 89. Potential foodborne outbreaks with a common source and associated cases by preparation setting as reported in EpiSurv, 2023

Preparation setting	Outbreaks (n = 35)		Cases (n = 386)	
	No.	%[a]	No.	%[b]
Commercial food operators	**25**	**71.4**	**187**	**48.4**
Restaurant/cafe/bakery	10	28.6	102	26.4
Caterers	4	11.4	51	13.2
Takeaway	9	25.7	28	7.3
Supermarket	1	2.9	3	0.8
Imported food	1	2.9	3	0.8
Institutions	**3**	**8.6**	**121**	**31.3**
School	1	2.9	100	25.9
Childcare centre	1	2.9	12	3.1
Long term care facility	1	2.9	9	2.3
Other	**7**	**20.0**	**78**	**20.3**
Home	5	14.3	73	18.9
Farm	2	5.7	5	1.3

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 exposure setting, calculated using the total number of foodborne outbreaks (35).

[b] Percentage of cases for each exposure setting, calculated using the total number of associated cases (386).

Table 90. All non-O157 STEC serotypes identified from human isolates by the Enteric Reference Laboratory, 2019–2023

Note: This table gives the frequency of types from all human isolates typed by the Enteric Reference Laboratory (ESR) in a calendar year. These frequencies may be different to the frequency of types only associated with notified cases (Table 51), 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	2019	2020	2021	2022	2023
O1:H7	0	0	2	0	0
O2:H6	0	1	0	3	1
O2:H29	0	0	1	0	0
O3:H12	0	0	0	1	0
O3:H21	1	0	0	0	0
O5:H19	0	3	1	2	4
O5:HNT	8	13	12	9	6
O6:H10	0	1	0	0	1
O6:H34	1	0	0	0	0
O7:H14	0	0	1	1	3
O8:H8	0	0	0	1	4
O8:H9	0	1	1	1	1
O8:H16	0	2	1	3	1
O8/O30:H25	0	0	3	2	0
O8:H19	0	0	0	0	1
O8:H21	0	0	0	0	1
O9:H30	0	0	1	1	0
O11:H25	0	1	0	0	0
O15:H2	2	3	2	1	0
O15:H4	0	0	0	2	0
O15:H16	1	0	0	0	1
O15:H18	0	0	0	0	1
O15:H27	1	1	0	2	0
O17:H18	2	1	1	1	0
O17/O106:H45	0	1	0	0	0
O18:H5	0	0	1	0	0
O18:H7	0	0	1	0	0
O21:H2	0	0	1	0	0
O21:H21	0	0	0	1	0
O22:H16	1	0	1	0	0
O23:H8	1	0	0	0	0

Serotype	2019	2020	2021	2022	2023
O25:H4	1	0	0	0	0
O26:H8	1	0	0	0	0
O26:H11	119	121	131	109	120
O26:HNT	7	0	0	0	0
O38:H26	27	33	27	38	35
O38:HNT	2	0	0	0	0
O41:H21	2	0	0	0	0
O42/O28ac:H20	0	0	0	0	1
O43:H2	1	0	1	1	0
O45:H2	0	1	0	0	0
O45:H19	0	0	1	0	0
O51:H24	1	2	0	0	0
O53:H45	0	1	0	0	0
O54:H4	0	0	0	0	1
O54:H45	0	0	0	0	1
O55:H12	1	2	4	3	2
O61:H2	1	0	0	0	0
O64:H20	7	5	5	5	8
O65:H2	1	0	0	0	1
O66:H25	0	0	1	1	1
O69:H11	1	0	0	0	0
O71:H2	1	0	0	0	0
O74:H20	1	1	0	0	0
O75:H5	0	1	0	0	0
O75:H7	0	2	0	0	0
O75:H8	1	0	3	1	3
O76:H19	1	0	2	0	0
O78:H4	0	1	1	0	0
O80:H2	0	0	0	1	0
O82:H8	1	0	0	0	0
O83:H27	0	1	0	0	0

Serotype	2019	2020	2021	2022	2023
O84:H2	4	10	10	10	13
O84:HNT	3	0	0	0	0
O85:H49	2	1	1	3	1
O87:H16	0	0	1	1	2
O88:H8	7	7	11	8	10
O88:HNT	2	0	0	0	0
O91:H14	12	12	28	19	30
O91:H21	1	1	0	2	2
O91:HNT	1	0	0	1	0
O93:H28	0	0	1	1	0
O93:H46	0	1	0	0	0
O98:H21	0	0	0	0	1
O99:H11, H35	1	0	0	0	0
O100:H20	1	0	0	1	0
O103:H2	11	0	20	11	15
O103:H8	0	0	0	1	1
O103:H25	12	1	5	10	3
O103:HNT	1	0	0	0	0
O104:H7	1	1	5	2	7
O107/O117:H7	0	0	1	0	0
O108:H9	1	0	0	0	0
O108:H21	0	0	0	1	0
O108:H25	0	0	0	0	2
O100/O154:H25	0	0	0	3	1
O111:H2	0	1	0	1	1
O111:H8	0	0	0	2	5
O111:H11	0	0	0	0	1
O112:H2	0	0	0	0	1
O112:H8	1	0	0	0	0
O112:H9	4	5	7	7	8
O112:H19	1	0	0	1	1
O113:H4	1	1	0	0	0
O113:H21	1	1	0	4	4
O114:HNT	1	0	0	0	0
O117:H4	3	1	1	0	1
O117:H7	7	4	1	0	10

Serotype	2019	2020	2021	2022	2023
O117:H21	0	0	0	1	0
O118:H2	1	0	0	0	0
O120:H56	0	0	0	0	1
O121:H19	1	0	1	0	0
O123:H2	3	1	1	2	2
O123:H10	2	11	4	9	16
O123:H11	0	0	0	1	0
O124,O8:H19	0	0	1	0	0
O127:H40	0	0	0	0	1
O128:H2	55	79	82	82	91
O128:H8	1	0	0	0	0
O128:HNT	3	0	0	0	0
O129:H21	0	0	1	0	1
O130:H11	4	11	8	6	6
O134:H31	0	0	0	0	1
O136:H20	0	1	0	0	1
O141:H2	1	0	0	0	0
O141:HNT	1	0	0	0	0
O144:H2	1	0	0	0	0
O145:H2	0	0	3	1	0
O145:HNT	0	0	1	3	1
O146:H21	15	28	27	44	27
O146:H28	1	4	3	2	9
O148:H7	1	0	0	0	0
O149:H2	2	0	0	0	0
O150:H8	0	0	0	1	0
O151/O118:H2	0	0	0	0	1
O152:H7	0	0	0	1	0
O153:H2	10	8	8	6	10
O153:H7	0	1	0	0	0
O153:H21	0	1	1	0	0
O153:H25	0	0	0	0	1
O153:HNT	1	0	0	0	0
O153/O178:H7	0	0	1	2	1
O153/O178:H23	0	1	0	0	0
O156:H25	2	0	1	0	1

Serotype	2019	2020	2021	2022	2023
O159:H4	0	0	2	0	1
O159:HNT	1	0	0	0	0
O162/O101:H33	0	0	0	0	1
O163:H19	7	1	11	2	3
O165:H7	0	2	2	0	0
O165:H25	0	1	2	3	1
O165:HNT	2	0	0	0	0
O166:H15	1	0	0	1	0
O171:H2	1	1	0	0	0
O172:H25	0	1	0	0	0
O174:H8	10	10	14	16	9
O174:H21	5	7	1	3	2
O174:HNT	1	0	0	0	0
O176:H4	12	16	14	24	19
O176:HNT	4	0	0	0	0
O177:H2	0	1	0	0	0
O177:H25	2	3	4	4	4
O177:HNT	1	0	0	0	0
O179:H8	0	0	2	0	0
O179:H26	1	0	0	0	0
O181:H16	1	0	0	0	0
O182:H25	3	7	5	5	5
O183:H18	3	1	1	6	5
O186:H10	2	0	0	0	0
O186:HNT	4	0	0	0	0
O187:H52	0	0	2	0	1
ONT:H1	1	0	0	0	0
ONT:H2	11	0	0	0	0
ONT:H6	1	0	0	0	0
ONT:H7	6	0	0	0	0
ONT:H8	4	0	0	0	0
ONT:H9	1	0	0	0	0
ONT:H10	2	0	0	0	0

Serotype	2019	2020	2021	2022	2023
ONT:H14	1	0	0	0	0
ONT:H18	2	0	0	0	0
ONT:H19	1	0	0	0	1
ONT:H20	0	0	0	0	1
ONT:H21	5	0	0	0	0
ONT:H25	4	1	0	0	0
ONT:H45	0	0	1	0	0
ONT:H49	1	0	1	1	1
Onovel1:H16	0	1	0	0	0
Onovel1:H27	0	0	0	0	1
Onovel2:H49	0	0	1	2	0
Onovel5:H21	0	1	1	0	0
Onovel8:H21	0	0	0	0	1
Onovel21:H14	2	0	4	4	3
Onovel27:H16	0	1	0	0	0
Onovel27:H21	1	0	0	0	0
Onovel32:H10	1	0	0	0	1

NM: Non-Motile. NT: Non-typable

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