New Zealand Food Safety
Haumaru Kai Aotearoa

Annual report concerning Foodborne Diseases in New Zealand 2022

New Zealand Food Safety Technical Paper No: 2023/17

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eISSN No: 2624-022X (online)
ISSN No: 978-1991087-74-4

August 2023

Ministry for Primary Industries
Manatū Ahu Matua

New Zealand Government

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Cover Image: medical illustration of *Staphylococcus aureus*
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Scientific Interpretative Summary

This SIS is prepared by NZFS risk assessors to provide context to the following report for MPI risk managers and external readers.

Annual report concerning Foodborne Diseases in New Zealand 2022

ESR Report FW23005

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 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.

- 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.

Most cases of foodborne diseases in New Zealand are sporadic which makes attribution to a source or event difficult. In contrast, outbreaks offer a better opportunity to identify the source and most of the 27[1] outbreaks (253 cases) of potential foodborne disease in 2022 were associated with commercial food operators and only five outbreaks in 2022 were associated with food prepared in consumer's homes. Despite robust investigation, some outbreaks reported as "foodborne with an unidentified food source" could also be attributed to other routes of transmission, such as water, animal contact, or person to person contact. Listeriosis is perhaps the only disease fully attributable to consumption of contaminated food.

Campylobacteriosis, yersiniosis, infection by shiga toxin-producing *E. coli* (STEC), and salmonellosis remain the predominant notified foodborne illnesses. Notification rates per 100,000 population are generally stable being highest for very young children (0 to 4 years age group) and for elderly people (70+ years).

Campylobacteriosis

The reduction of human cases of foodborne campylobacteriosis is a strategic priority for New Zealand Food Safety with a performance target of a reduction in rates of foodborne campylobacteriosis by 20% from 88 to 70 per 100,000 population by the end of 2024. Progress toward this target is reported in the section entitled 'Reporting against targets. During the last several years both total numbers of human campylobacteriosis cases and rates per 100,000 population have been consistently, albeit slowly, decreasing. Despite a pronounced decrease in cases during the COVID-19 pandemic lock-down and travel

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[1] This number excludes a nationwide *V. parahaemolyticus* gastroenteritis outbreak (60 cases) which did not have a common location or supplier for the source of infection.

restriction periods (2020-2021), the number of notified cases is now similar to that of 2019 prior to the pandemic. While this indicates progress towards the target, the rate of notification during 2023 will provide a more robust indication of progress as social behaviour returns to normal after the pandemic. New Zealand Food Safety will continue to monitor this trend closely.

The significantly higher number of cases and rate of campylobacteriosis in rural areas compared with urban areas in 2022 suggests that risk factors other than food, including direct contacts with farm animals and exposure to potentially contaminated water may be assuming greater importance as a source of infection.

Listeriosis

Listeriosis, while low in total numbers, has a very high rate of hospitalisation and is associated with fatality in frail elderly, immune-compromised persons, and foetal loss in pregnancy. The listeriosis notification numbers and rate has been relatively stable for the past 20 years, although the number of notified cases was highest this year and New Zealand Food Safety will monitor the notification rate through 2023.

Hospitalisation

In the last two years there was a pronounced increase in hospital admissions (a significant burden on the health sector), especially so for campylobacteriosis, yersiniosis, and STEC infection; the latter associated with the serious sequelae haemolytic uraemic syndrome which often requires an extended stay in hospital and occasionally involves intensive care. Half of campylobacteriosis cases spent in hospitals not more than two nights, while some cases while reported as hospitalized were discharged on the day of admission.

Specific reasons for the increase in hospitalisation rates are unknown but could have resulted from delays in seeking medical attention during which the health of infected people deteriorated such that they then required hospitalisation. Although most of COVID-19 restrictions were not in place in 2022, the impact of pandemic remained. One in five people in a major COVID study[2] in New Zealand reported Long COVID symptoms after their initial infection. For these people, common foodborne infections may lead to more severe illness that required hospitalisation. Increased cost of living and shortage of GPs might have led to the situation where people go straight to the hospitals bypassing primary health care[3].

Demographics

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

For most foodborne illnesses, Māori and Pacific people have the lowest rate of notifications per 100,000 people in the relevant demographic group while hospitalisation rates are similar for different ethnic groups. The exceptions are for campylobacteriosis where Māori and Pacific people have the lowest rate of hospitalisation, and for *Vibrio parahaemolyticus* infection which disproportionally affects Māori people presumably due to their traditional consumption of raw seafood. The Asian population is more reflected in yersiniosis notifications.

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[2] Impacts of COVID-19in Aotearoa. MoH, January 2023 https://covidaotearoa.com/wp-content/uploads/2023/01/Nga-Kawekawe-o-Mate-Korona-Full-Report-2023-01-24.pdf

[3] https://rnz.co.nz/national/programmes/checkpoint/audio/2018845975/gp-shortage-people-travelling-hundreds-of-kms-to-see-doctor

While new research intends to bring more clarity on these issues, the observations suggest that dietary choices have a significant impact on risk of foodborne illness. New Zealand Food Safety has ongoing targeted consumer education campaigns to enable all New Zealanders to protect themselves from foodborne diseases.

Attributable foods

Poultry meat, alongside consumer behaviour, remains the focus for New Zealand Food Safety to achieve the performance target of a 20% reduction in rates of foodborne campylobacteriosis by the end of 2024.

In 2022, for the second consecutive year, there were no outbreaks of campylobacteriosis associated with consumption of raw milk. This indicates that the Raw Milk for Sale to Consumers Regulations (2015), with associated compliance actions, and consumer education campaigns have been effective in reducing food safety risks associated with consumption of raw milk.

New Zealand Food Safety activities

In addition to its *Campylobacter* Action Plan, New Zealand Food Safety has ongoing risk assessment and risk management activities underway to mitigate the risks of *Vibrio* infection from seafood, hepatitis A infection from frozen berries and salmonellosis from tahini. While STEC infection has only been attributed to consumption of raw drinking milk in New Zealand, further attribution studies are underway to identify, if any, other food sources.

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

ANNUAL REPORT CONCERNING FOODBORNE DISEASE IN NEW ZEALAND 2022

Prepared for New Zealand Food Safety under
Project 406850 – Systematic reporting of epidemiology of potentially
foodborne disease in New Zealand for year 2022

by

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August 2023

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

Client Report FW23005

ACKNOWLEDGEMENTS

Particular thanks to the staff in the public health services in New Zealand who provide data from their regions and Food Compliance Services, New Zealand Food Safety, for providing information on their outbreak investigations. Thanks also to ESR staff Joanne Hewitt, Jackie Wright, Ernest Williams, Briony Fanslow and Shevaun Paine for assistance with data and their interpretation, Maritza Marull for report formatting, Jacqui Ritchie for quality control and Rob Lake for the peer-review of this report.

The authors also wish to acknowledge the New Zealand Ministry of Health as funders of the surveillance of notifiable diseases in New Zealand.

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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 here 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.

This report for the calendar year 2022 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 115). Some notifiable illnesses may be caused by transmission of pathogens through foods[*], 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 these data as indicators, we are assuming that they are 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:
    - <u>Outbreak reports</u>: 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.
    - <u>Expert opinion</u>: 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.
    - <u>Overseas analyses and estimates</u>: 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 Organisation (WHO) project to estimate the global burden of foodborne diseases derived estimates for 14 international regions [11, 12]. The estimates for New Zealand, Australia, Canada, the Netherlands and the international WHO estimates are based on expert opinion, the estimates for England and Wales are based on outbreak analysis, while

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

the USA estimates are based on data from surveillance, risk factor studies and a literature review.

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 is considered to only contribute a small proportion of the total disease burden.

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, 13]	Canada (2015) [6]	Australia (2005, 2014) [7, 8]	England and Wales (2002) [9]	Netherlands[b] (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[e]	60[c]	61	56[d,e]	63	40
STEC non-O157	40	40–60[e]	50[c]	60	56[d,e]	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[c]	11	11
Norovirus	33	12–26	19[c]	18	18[c]	NE	17
Sapovirus	NE	NE	13[c]	17	NE	0	NE

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

[b] The Dutch 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 Dutch 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

[c] The 2021 study did not cover all organisms included in the 2011 study. Figures 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

[e] Estimate was derived for total STEC

[f] 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

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

NE = not estimated

This report considers information for the 2022 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 2022 becomes available in the future.

Conditions included in this report

The conditions that have been selected for inclusion in the 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 conditions included in this report are listed in Table 2. Data have been drawn from a number of sources including disease notification, hospitalisation, outbreak reports and laboratory surveillance databases.

Notifiable conditions were selected for inclusion in the 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 conditions were obtained from the Communicable Disease Control Manual, published by the Ministry of Health (MoH) [14] or the EpiSurv CRF Instructions website [15].

Table 2. Potentially foodborne conditions included in the report

Disease	Type	Source(s)	ICD-10 code[a]
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
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*

Data sources: EpiSurv notifications (N), EpiSurv outbreaks (O), Ministry of Health hospitalisations (H), ESR laboratory data (L)

STEC = Shiga toxin-producing *Escherichia coli*

[a] International statistical classification of diseases and related health problems, 10th revision [16]

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

Data Sources: Ministry of Health hospitalisations (H)

[a] International statistical classification of diseases and related health problems, 10th revision [16]

[b] 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 molecular techniques such as multiplex polymerase chain reaction (PCR). All faecal specimens in the affected district health boards (DHBs) are screened by multiplex PCR for *Campylobacter spp.*, *Salmonella spp.*, *Shigella spp.*, STEC, and *Yersinia enterocolitica*. In some of the affected DHBs all faecal specimens are also routinely screened for *Giardia* spp., *Cryptosporidium spp.*, *Yersinia pseudotuberculosis* and *Vibrio parahaemolyticus.* An overview of when laboratories servicing different DHBs moved to PCR detection methods and which pathogens are included in the respective PCR panels[*] is provided in Table 67 in Appendix B.

For the 2022 reporting year, nationally reported notification rates are a mixture of notifications based on PCR and non-PCR approaches. In October 2022, Hawke's Bay hospital moved to PCR-based methods; no other laboratory method changes have been recorded during the 2022 year.

Multiple different testing related factors (e.g., change in sensitivity of methods, proportion of faecal specimens being tested) affect the notification rates on top of any underlying changes to disease incidence happening in New Zealand. The impact of the move to using PCR 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 PCR-based culture independent diagnostic tests (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 *Campylobacter spp.*, *Salmonella spp.*, *Shigella spp.* and *Yersinia enterocolitica* [17]. Any observed trends in changes in STEC notification rates between 2015 and 2022 must be considered in the context of changes to testing approaches.

Changes in overseas travel

Some cases notified in New Zealand are due to exposure to a pathogen or toxin while they were 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 2022, the number of New Zealand residents returning from absences of less than 12 months and total passenger arrivals were approximately 40% of the numbers observed during the pre COVID-19 years of 2018 and 2019 (Table 4).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, 2018-2022

	2018	2019	2020	2021	2022
NZ resident travellers	3,020,007	3,101,427	681,893	142,879	1,327,126
Total passenger arrivals[a]	6,996,947	7,100,373	1,733,521	398,556	2,856,072

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 03 July 2023.

[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.

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

REPORTING

SUMMARY OF MAIN FOODBORNE DISEASES

The incidence of the main foodborne diseases is summarised for 2022 in Table 5 below.

Table 5. Estimated proportion and incidence of the main foodborne diseases for 2022

	Total notified[a]		Estimated foodborne transmission[b]		
	Cases	Rate[c]	Cases	Proportion (%)	Rate[c]
Campylobacteriosis	5878	114.7	4148	75	81.0
Cryptosporidiosis	612	11.9	NE	-	-
Giardiasis	707	13.8	NE	-	-
Hepatitis A	59	1.2	NE	-	-
Listeriosis	39	0.8	NE	-	-
Salmonellosis	750	14.6	371	62	7.2
Shigellosis	68	1.3	NE	-	-
STEC infection	1022	19.9	390	40[d]	7.6
Yersiniosis	1294	25.3	938	75	18.3

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

[a] The diseases included in this table are those that are individually specified in the New Zealand schedule of notifiable diseases [14]. Cases of disease due to other potentially foodborne organisms may be notified under 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.
Estimated foodborne transmission proportions were derived from two expert consultations in 2013 and 2020, respectively [2, 3]

[c] Rate per 100,000, 2022 mid-year estimated population

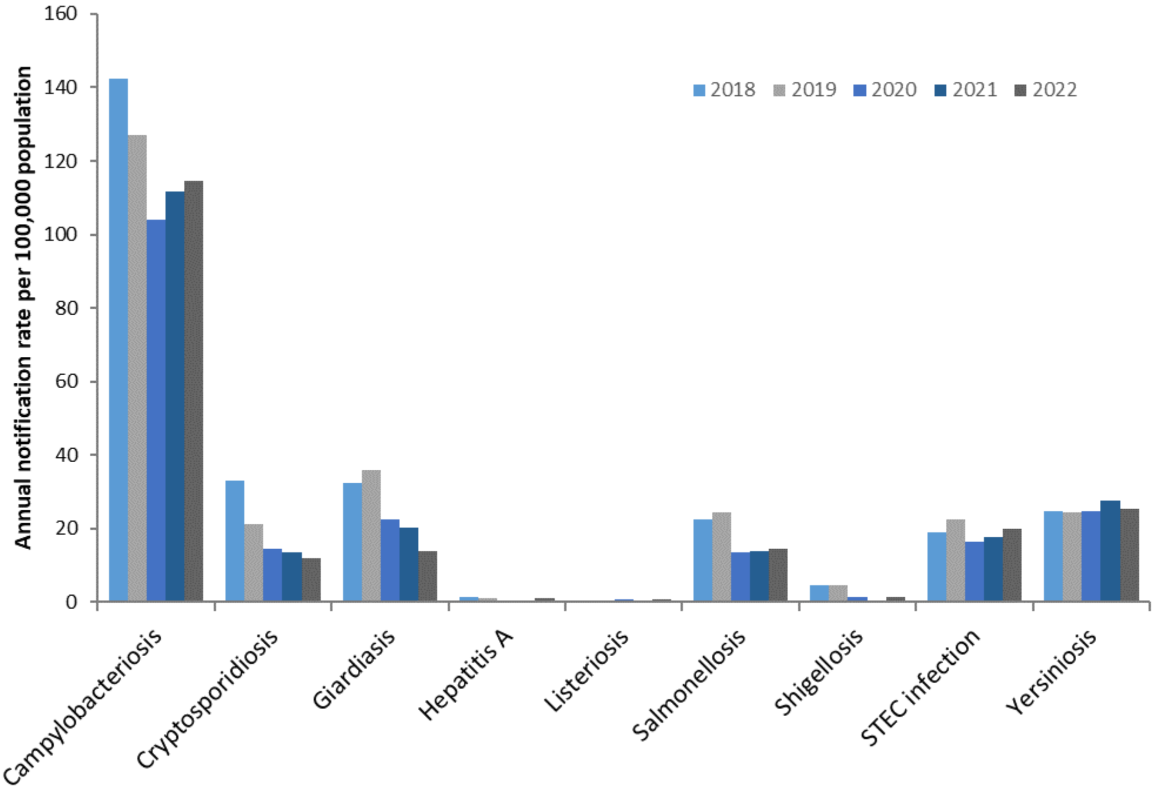
[d] The expert elicitation [3] derived separate estimates of the foodborne proportion for O157 STEC (20%) and non-O157 STEC (40%). The estimate for non-O157 STEC, the dominant set of serotypes, has been used to estimate the number of food-related cases

In 2022, notification rates for the main foodborne diseases showed distinct disease specific temporal patterns compared to preceding years (Figure 1). The campylobacteriosis notification rate increased from 112.1 cases per 100,000 population in 2021 to 114.7 in 2022 but remained below 2018 and 2019 rates. Notification rates for Hepatitis A, salmonellosis and shigellosis all increased slightly from 2021 to 2022 but were still below 2018 and 2019 rates. The changes in notification rates for these diseases reflect the changes in the number of passengers arriving from overseas. In 2019, the estimated proportion of cases travelling overseas within the incubation period was 59% for hepatitis A, 34% for salmonellosis and 61% for shigellosis [18].

Notification rates for cryptosporidiosis and giardiasis decreased from 2021 to 2022, following a downward trend from previous years. In 2022, the yersiniosis notification rate was lower than in 2021 but similar to each of the preceding three years (~25 cases per 100,000 population in 2018–2020). STEC notification rates increased from 2021 to 2022, following an upward trend again after a drop in 2020 considered due to COVID-19 restrictions.

Public health and social measures introduced in 2020 and 2021 to prevent the spread of COVID-19 in New Zealand have affected exposure behaviours and pathways, as well as changes in access to medical care and laboratory testing priorities. Thus, multiple factors may have 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* [19].

Figure 1. Notification rates of the main foodborne diseases, 2018–2022



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*. The target uses the estimate of the food attributable campylobacteriosis proportion (75%) from the latest expert elicitation process (2020) [3].

Rationale

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

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

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 MoH [21].

To assess reporting against targets, the annual number of notified cases is adjusted for the estimated proportion of cases having travelled overseas during the likely incubation period. The number of (non-travel) 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) [21]. This allows for demographic changes within the New Zealand population to be appropriately captured. The proportion of infections acquired overseas is estimated through data from the EpiSurv programme administered by ESR and MoH.

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 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 [19].

The estimated incidence of domestically acquired foodborne campylobacteriosis in 2022 is given in Table 6.

Table 6. Estimated proportion and incidence of foodborne campylobacteriosis for 2022

	Cases	Proportion of total notified cases (%)	Rate (per 100,000, mid-year estimated population)
Total notified	5878	-	114.7
Total estimated as not related to overseas travel[a]	5531	94.1	107.9
Estimated domestically acquired foodborne transmission[b]	4148	70.6	81.0

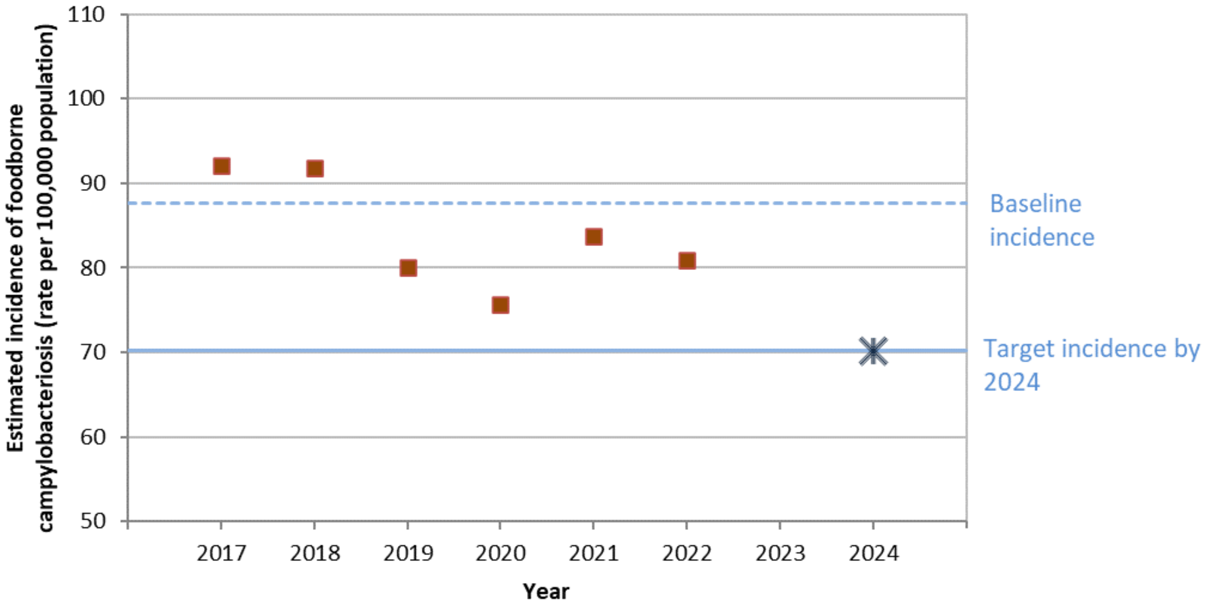
[a] The number of cases listing overseas travel as a risk factor in 2022 was 128, out of 2254 completed responses (5.9%). Thus, it was estimated 94.1% of all notified campylobacteriosis infections were domestically acquired.

[b] From expert consultation in 2020 [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 2022 are between the performance target baseline and 2024 target rates. The estimated rate for 2022 is slightly lower than the estimate for 2021 (83.8 cases per 100,000 population).

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



Notes:

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

The total number of campylobacteriosis notifications in 2022 (5878) was higher than in 2021 (5729). However, the estimated number of overseas travel associated cases was much higher in 2022 (347) than in 2021 (17), leading to a decrease in the estimated incidence of domestically acquired foodborne campylobacteriosis from 2021 to 2022.

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 or ESR's Enteric, Food and Environmental Virology/Norovirus Reference 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 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 DHB of the case 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 $\geq 10^3$/g *Bacillus cereus* from a clinical specimen or $\geq 10^4$ *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 2022 by data source

During 2022, no individual cases of *B. cereus* intoxication were reported in EpiSurv.

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

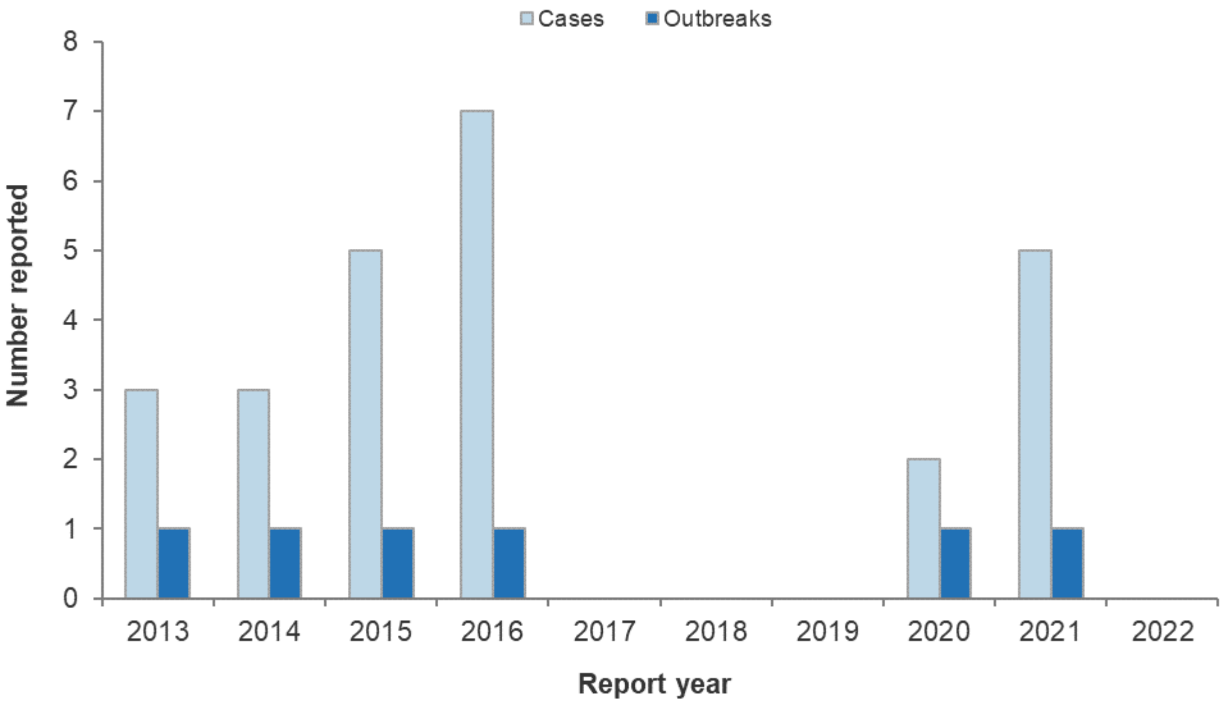
The international statistical classification of diseases and related health problems 10th revision (ICD-10) code A05.4 was used to extract foodborne *B. cereus* intoxication hospitalisation data from the MoH National Minimum Dataset (NMDS). Of the two hospital admissions (0.04 admissions per 100,000 population) recorded in 2022, one case was reported with *B. cereus* intoxication as the primary diagnosis and one with *B. cereus* intoxication as another relevant diagnosis.

Outbreaks reported as caused by *Bacillus cereus*

During 2022, there were no outbreaks reported in EpiSurv with *B. cereus* confirmed as the causative agent. NZFS Food Compliance Services recorded two investigations of possible *B. cereus* intoxication. These included three cases in Auckland Regional Public Health Service region and two cases in Regional Public Health region.

Outbreaks of *B. cereus* intoxication are rare, with only six outbreaks reported in EpiSurv since 2013. The number of cases associated with individual outbreaks ranged between two and seven cases (Figure 3).

Figure 3. *B. cereus* intoxication outbreaks reported in EpiSurv with food reported as a possible mode of transmission and associated cases reported by year, 2013–2022



Note: The 2021 outbreak information is from NZFS Food Compliance Services records and is not recorded in EpiSurv.

Other *Bacillus* species reported in 2022 for individual notified gastroenteritis cases

During 2022, one individual case was reported in EpiSurv with *B. lichenoformis* and *B. megaterium* infection. Vegetable samosa from a food service outlet was the suspected source due to food having an unpleasant odour. Laboratory testing of vegetable samosa was found to be positive for *Bacillus* spp..

Recent surveys

Nil.

Relevant New Zealand studies and publications

Nil.

Relevant regulatory developments

Nil.

Campylobacteriosis

Summary data for campylobacteriosis in 2022 are given in Table 7.

Table 7. Summary of surveillance data for campylobacteriosis, 2022

Parameter	Value in 2022	Source
Number of notified cases	5878	EpiSurv
Notification rate (per 100,000)	114.7	EpiSurv
Hospitalisations[a]	999	MoH NMDS
Deaths	0	EpiSurv
Travel-related cases[b, c]	128	EpiSurv
Estimated domestically acquired food-related cases (%)[d]	4148 (75%)	Expert consultation

NMDS = MoH 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. 2126 cases had not travelled overseas during the incubation period and for the remaining 3624 cases travel history is unknown.

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

[d] For estimation of food-related cases, the proportions derived from expert consultation [3] exclude travel-related cases (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).

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.

Changes to laboratory methods

Since 2015, laboratories across New Zealand have changed the methodology for testing faecal specimens (Appendix B, page 120). In 2022, community faecal specimens in all DHBs except for Canterbury, South Canterbury, and West Coast were screened by PCR methods for *Campylobacter* spp.

There is no evidence that campylobacteriosis notification rates have been affected by the introduction of PCR methods by diagnostic laboratories [3, 17].

Campylobacteriosis individual cases reported in 2022 by data source

During 2022, 5878 individual cases (114.7 per 100,000 population) of campylobacteriosis and no resulting deaths were reported in EpiSurv. Of the 5878 cases, the symptoms of 5410 cases (92%) were reported as fitting the clinical description for campylobacteriosis, the symptoms were unknown for 462 cases, and for 6 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 MoH NMDS database. Of the 999 hospital admissions (19.5 admissions per 100,000 population) recorded in 2022, 812 cases were reported with campylobacteriosis as the primary diagnosis and 187 were reported with campylobacteriosis as another relevant diagnosis.

It should be noted that EpiSurv and the MoH 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 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].

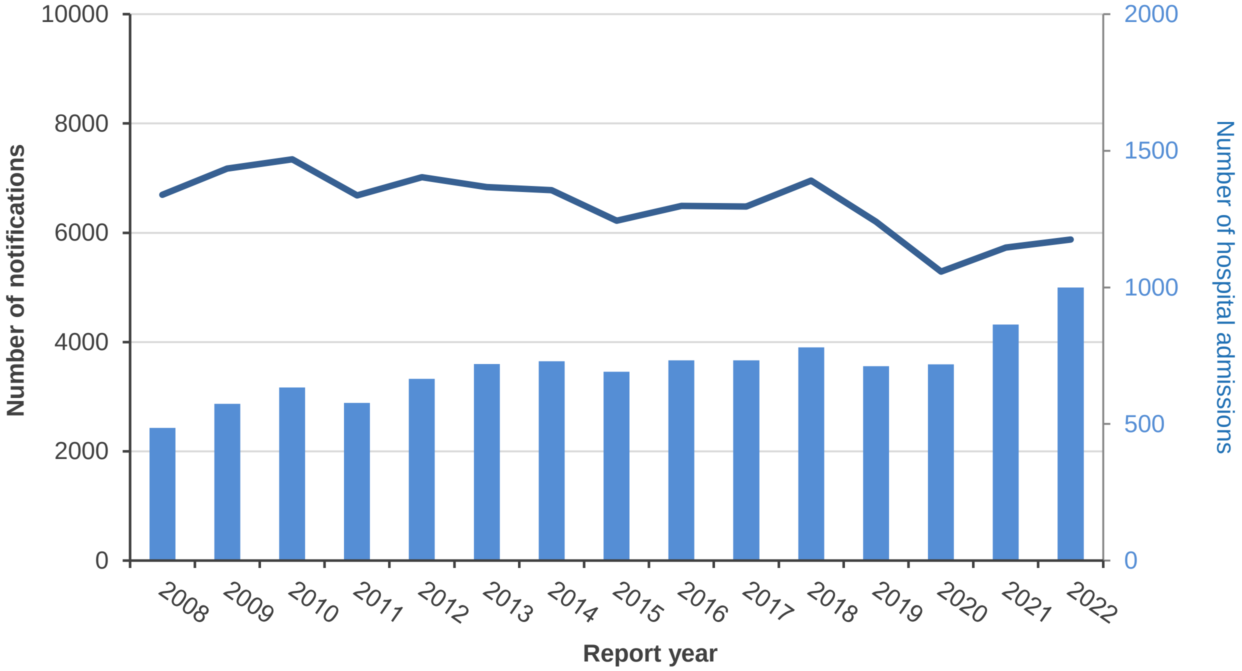
Annual data

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 due to restrictions related to the COVID-19 pandemic (Figure 4 and Figure 5) [19]. The number of hospital admissions with campylobacteriosis as a primary or secondary diagnosis has been increasing from 2008 (485 admissions, 6694 notifications) to 2022 (999 admissions, 5878 notifications) with a considerable increase in the last couple of years.

The frequency of overseas travel was lower in 2020 to 2022 compared to pre-COVID-19 years (see Introduction, page 5). This is reflected in the notifications; in 2022, there were 128 campylobacteriosis notifications in EpiSurv listing overseas travel as a risk factor, compared to 394 in 2019, 66 in 2020 and seven in 2021.

The number of cases listing overseas travel as a risk factor in 2022 was 128, out of 2254 completed responses (5.9%). Thus, it was estimated 94.1% of all notified campylobacteriosis infections were domestically acquired.

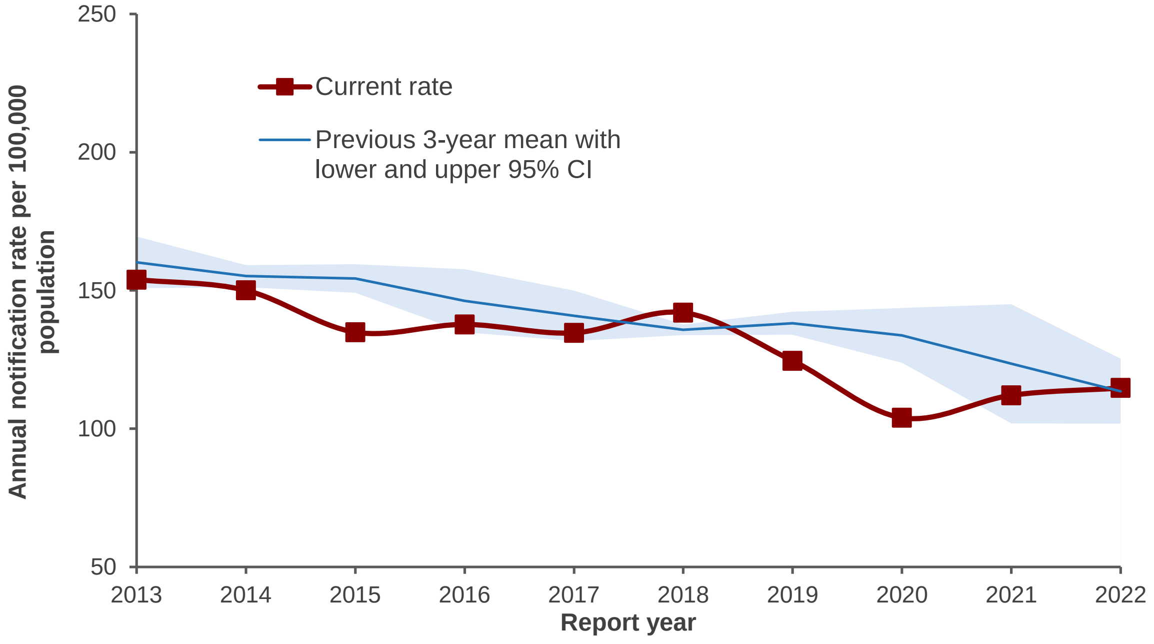
Figure 4. Campylobacteriosis EpiSurv notifications (line) and NMDS hospitalisations (bar) by year, 2008–2022



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

Between 2013 and 2019, the notification rate of campylobacteriosis was in the range of 124.6 to 153.9 notifications per 100,000 population (Figure 5). The trend for the previous three-year mean was generally downward over that period. In 2020, the campylobacteriosis notification rate (104.0 cases per 100,000 population) was much lower compared to the previous years, likely due to the impact of COVID-19. In 2022, the notification rate increased to 114.7 cases per 100,000 population.

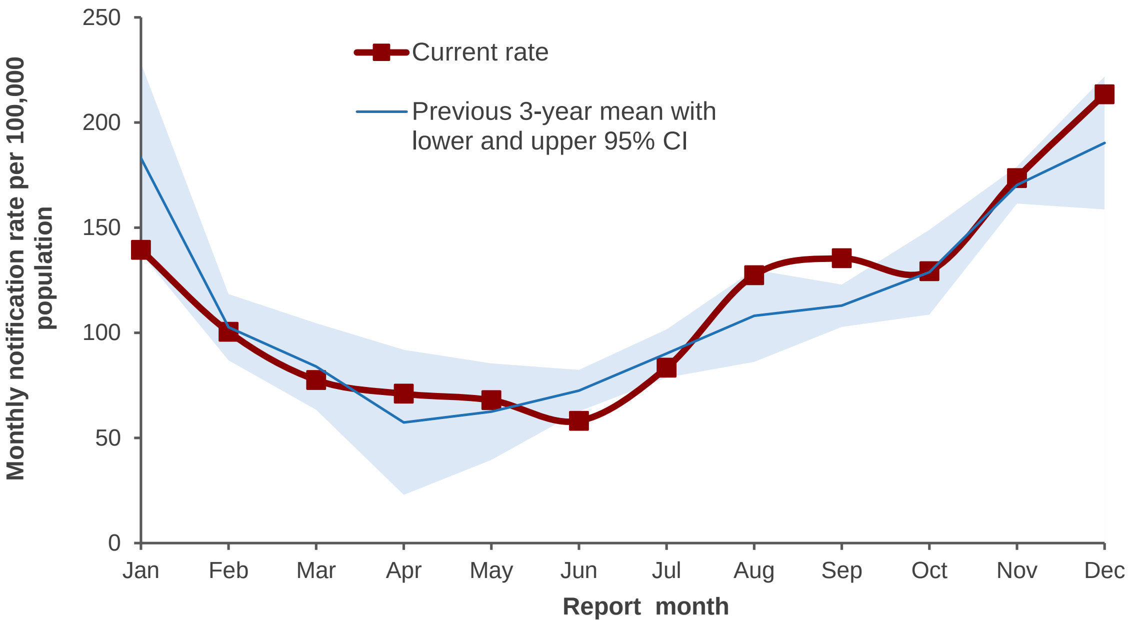
Figure 5. Campylobacteriosis notification rate by year, 2013–2022



Seasonal data

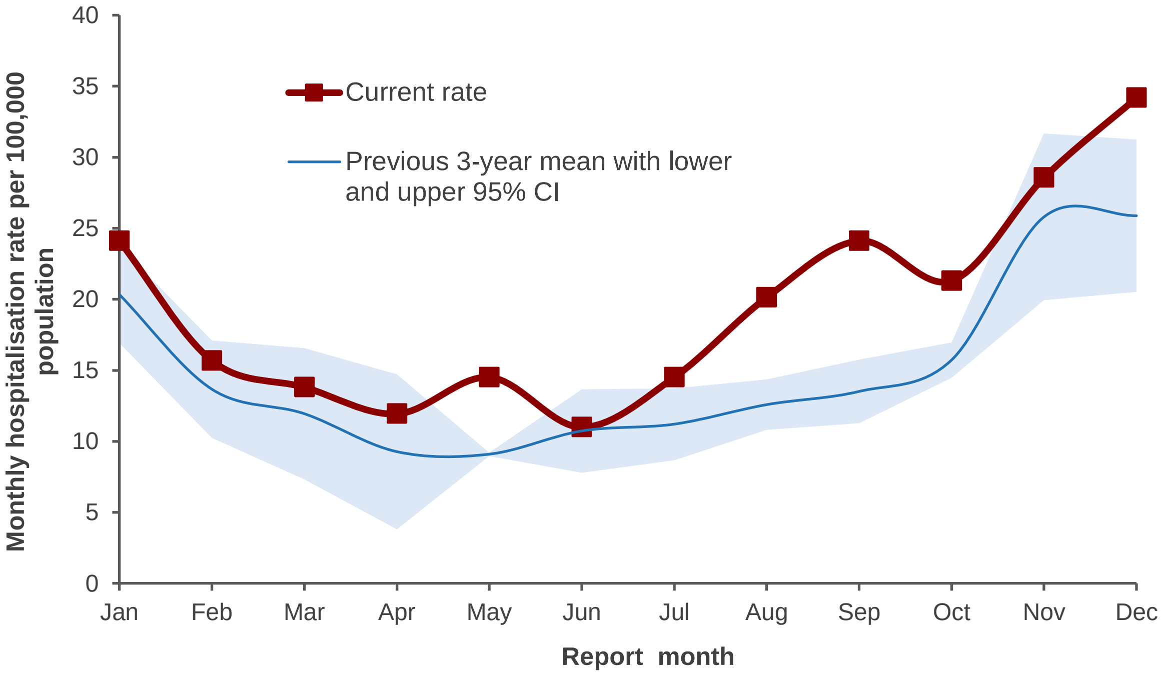
Campylobacteriosis notification rates per 100,000 population by month for 2022 are shown in Figure 6. In 2022, the monthly notification rates followed a trend similar to the mean of the previous three years. The monthly number of notifications in 2022 ranged from 248 notifications (June, 58 per 100,000 population) to 911 notifications (December, 213 per 100,000 population).

Figure 6. Campylobacteriosis monthly notification rate (annualised), 2022



In 2022, the monthly hospitalisation rates for the first four months of the year were similar to the previous three-year average, with higher rates in some other months (Figure 7).

Figure 7. Campylobacteriosis monthly hospitalisation rate (annualised), 2022



Demographics

In 2022, the rates of notifications and hospitalisations for campylobacteriosis were higher for males (127.6 and 20.5 per 100,000 population) compared with females (101.9 and 18.5 per 100,000 population) (Table 8).

Table 8. Campylobacteriosis cases by sex, 2022

Sex	EpiSurv notifications		Hospitalisations[a]	
	No.	Rate[b]	No.	Rate[b]
Male	3244	127.6	521	20.5
Female	2631	101.9	478	18.5
Total	**5878**	**114.7**	**999**	**19.5**

[a] MoH NMDS data for hospital admissions

[b] per 100,000 population in this sex group

The highest age-specific notification rate for campylobacteriosis in 2022 was reported for children aged 1 to 4 years (230.1 per 100,000 population, 559 cases). The highest hospitalisation rate was for the 70 years and over age group (51.0 admissions per 100,000 population, 292 cases) (Table 9).

Table 9. Campylobacteriosis cases by age group, 2022

Age group (years)	EpiSurv notifications		Hospitalisations[a]	
	No.	Rate[b]	No.	Rate[b]
<1	112	186.7	14	23.3
1 to 4	559	230.1	56	23.1
5 to 9	259	80.4	23	7.1
10 to 14	210	62.0	20	5.9
15 to 19	293	92.5	39	12.3
20 to 29	811	119.4	134	19.7
30 to 39	646	88.0	95	13.0
40 to 49	595	94.3	63	10.0
50 to 59	699	106.9	108	16.5
60 to 69	800	142.4	155	27.6
70+	893	153.3	292	50.1
Total[c]	**5878**	**114.7**	**999**	**19.5**

[a] MoH NMDS data for hospital admissions

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

[c] total includes notifications where age is unknown

Geographic distribution

The notification rates by DHB calculated per 100,000 resident population are presented in Figure 8 (see also Table 86). Blue shading is used in DHBs which are using CIDT community testing, the brown shading is used for DHBs using culture-based community testing.

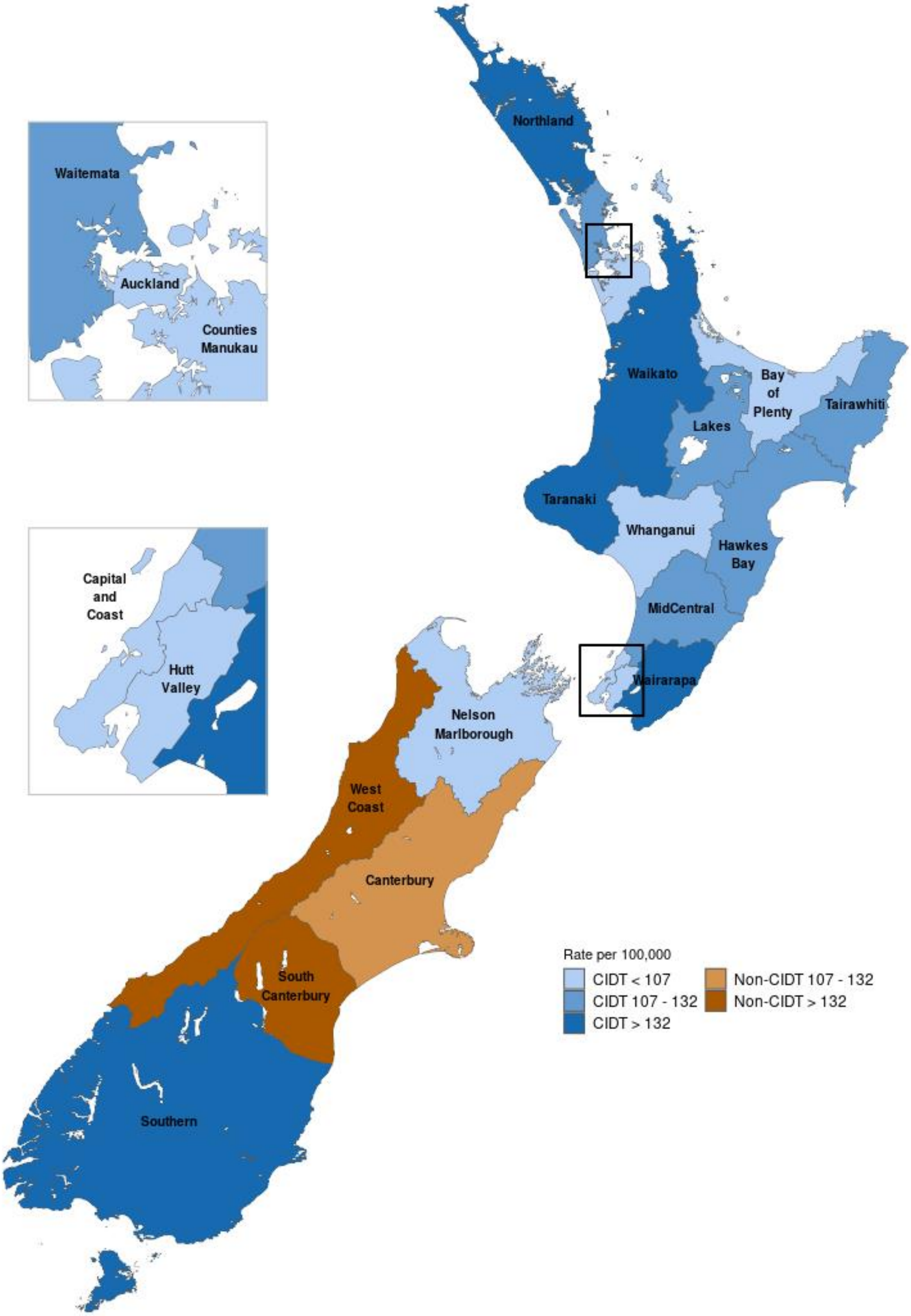
In 2022, the DHB notification rates of campylobacteriosis ranged from 85 per 100,000 population (513 cases) in Counties Manukau DHB to 230 per 100,000 population (143 cases) in South

Canterbury DHB. Wairarapa (169 per 100,000 population, 86 cases), West Coast (168 per 100,000 population, 55 cases), and Taranaki (169 per 100,000 population, 215 cases) DHBs had the joint second highest notification rates.

Historically, notification rates for campylobacteriosis have been variable across New Zealand with the South Canterbury, Wairarapa, and Taranaki DHBs consistently in the highest quartile of notification rates since 2016. Southern DHB had rates in the highest quartile between 2016 and 2021 but had a lower rate in 2022 (136 per 100,000 population, 475 cases), similar to Waikato (133 per 100,000 population, 599 cases) and Hawke’s Bay (131 per 100,000 population, 239 cases) DHBs.

Campylobacteriosis notification rates stratified by 2023 Urban Rural Classification [22] of the cases’ residential address monotonically increased with decreasing urbanisation (Appendix C, Table 87). Rates were lowest for ‘major urban areas’ (85 per 100,000 population, 2194 cases) and highest for ‘rural other’ (215 per 100,000 population, 1455 cases).

Figure 8. Geographic distribution of campylobacteriosis notifications, 2022



Outbreaks reported as caused by *Campylobacter* spp.

In 2022, there were 11 campylobacteriosis outbreak notifications in EpiSurv, three (27%) of which recorded food as a possible mode of transmission (Table 10). It is important to note that a single outbreak may have multiple pathogens, settings and possible modes of transmission.

Table 10. Campylobacteriosis outbreaks reported in EpiSurv, 2022

	Possible foodborne transmission with a suspected or confirmed source	Possible foodborne transmission but no suspected source	Total campylobacteriosis outbreaks
Outbreaks	3	0	11
Outbreak-associated cases	12	0	94
Hospitalised cases	1	0	1

Table 11 contains details of the three campylobacteriosis outbreaks reported in 2022 with food as a possible mode of transmission. The evidence for the source being the cause of the outbreak was weak for all three outbreaks, with no leftover food available for testing. In addition to the outbreaks recorded in EpiSurv at the cut-off date for this report (1 May 2023), NZFS investigated two further outbreaks (Table 11).

Table 11. Details of campylobacteriosis outbreaks reported in EpiSurv and/or investigated by NZFS Food Compliance Services with food reported as a possible mode of transmission, 2022

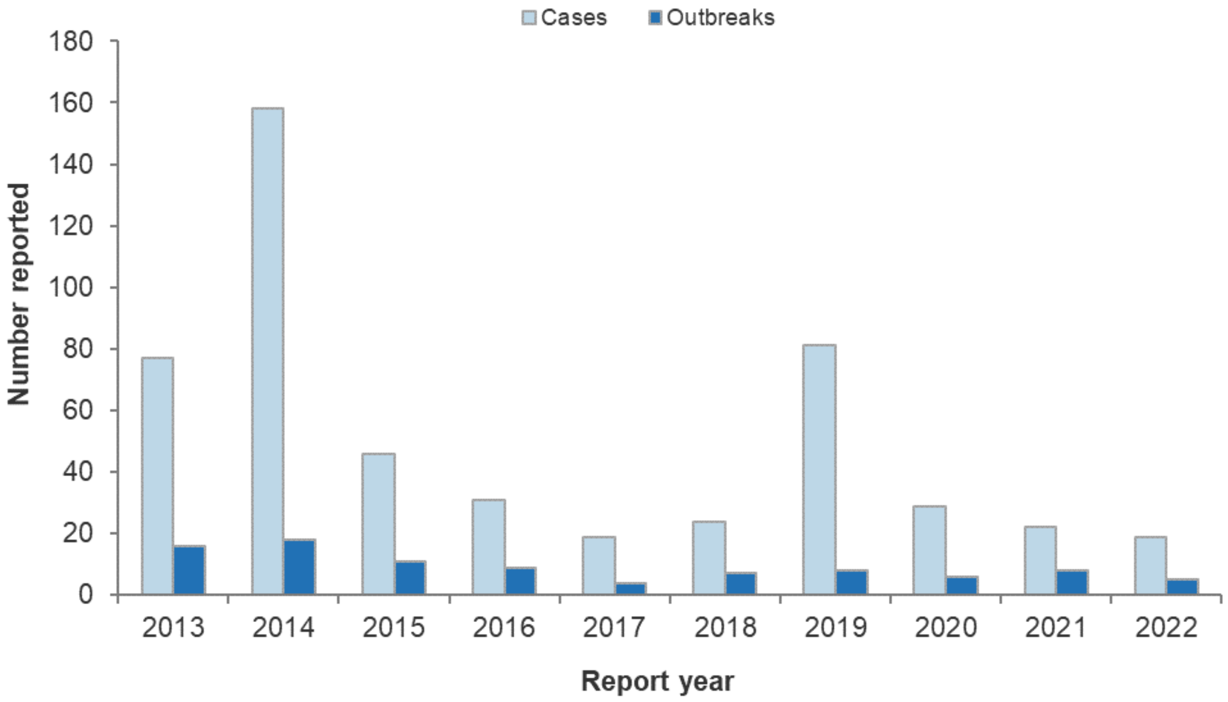
PHU	Report Month	Suspected source	Evidence	Setting	No. ill
C and PH	January	Any of smoked duck, spicy seaweed, smoke dried tofu, quail egg	Common event	Restaurant/cafe/bakery/food outlet	1C 5P
Regional PH	May	Liver and unpasteurised cheese	Common meal suspected	Unknown	1C 4P
Northland PHS	September	Chicken dishes from takeaway outlet	Common meal	Food outlet	1C 1P
Northland PHS	November	Shrimps	Common source and time	Restaurant/cafe/bakery	2C
PH South	December	Home cooked chicken	Common meal and observed as undercooked	Home	2C 2P

PHU: Public Health Unit, PH South: Public Health South, C and PH: Community and Public Health

Number ill: C: confirmed, P: probable

Over the 7-year period 2016 to 2022 the number of outbreaks of campylobacteriosis with food reported as a possible mode of transmission has ranged between four and nine outbreaks each year with between 19 (2017 and 2022) and 81 (2019) 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 reported in EpiSurv with food reported as a possible mode of transmission and associated cases reported by year, 2013–2022



Note: From 2021, the figure includes investigations of clusters of potentially foodborne disease by NZFS Food Compliance Services that where not recorded as a potentially foodborne outbreak in EpiSurv (2021: three outbreaks, seven cases; 2022: two outbreaks, seven cases).

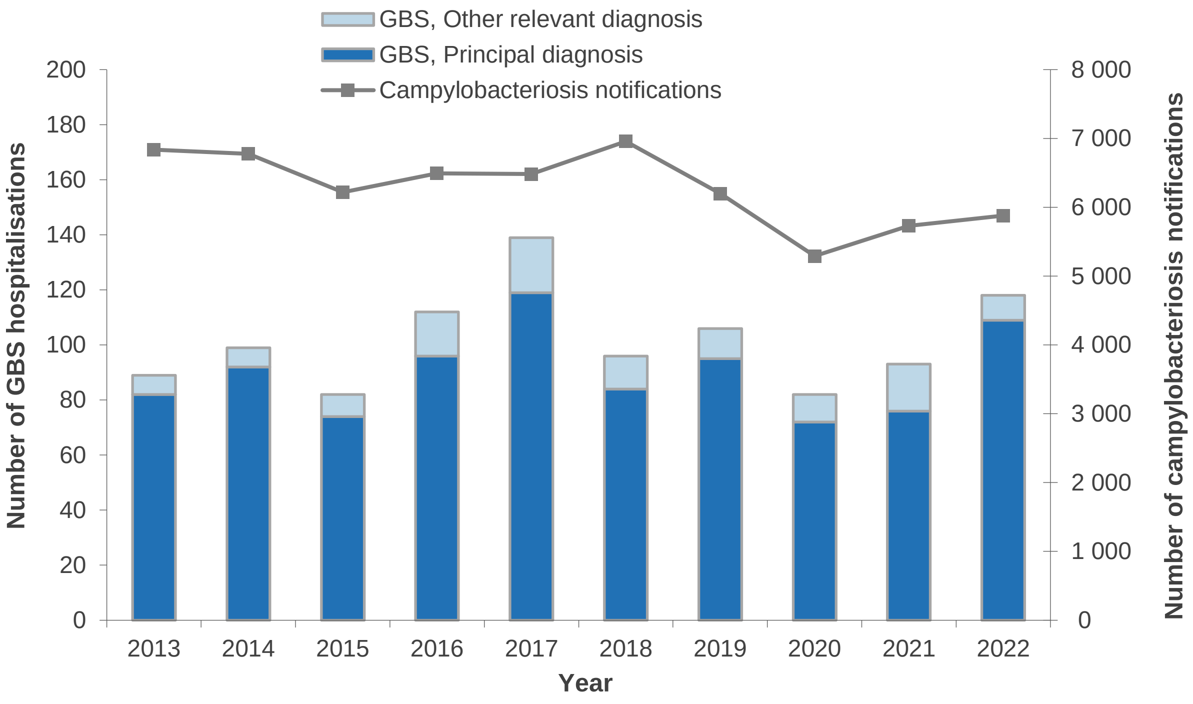
Disease sequelae - Guillain-Barré syndrome

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 [23].

The ICD-10 code G61.0 was used to extract GBS hospitalisation data from the MoH NMDS database. Only GBS cases that were incident in 2022 were considered, rather than all cases that were hospitalised in 2022. That is, if a GBS case hospitalised in 2022 had been hospitalised with GBS in a previous year, the 2022 admission was considered to be a readmission, rather than an incident case. There were 118 incident hospitalised cases recorded in 2022 (2.3 admissions per 100,000 population), 109 were reported with GBS as the primary diagnosis and nine with GBS as another relevant diagnosis.

Between 2013 and 2022, the annual number of incident hospitalised 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 hospitalisations had decreased by 13% {Baker, 2012 #14769}. 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 2013-2022 would be difficult to detect, although the decline in numbers of both conditions in 2020 is suggestive.

Figure 10. Guillain-Barré syndrome incident hospitalised cases, 2013–2022



In 2022, the number of incident hospitalised cases due to GBS was higher for males than for females (Table 12). 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 2022 (Table 8).

Table 12. Guillain-Barré syndrome incident hospitalised cases by sex, 2022

Sex	Hospitalised cases[a]	
	No.	Rate[b]
Male	75	2.9
Female	43	1.7
Total	**118**	**2.3**

[a] MoH NMDS data for hospital admissions

[b] per 100,000 population

In 2022, the highest rates of incident hospitalisation for GBS were in the 50-59 years age group, followed by the 70+ years age group (Table 13).

Table 13. Guillain-Barré syndrome incident hospitalised cases by age group, 2022

Age group (years)	Hospitalised cases[a]	
	No.	Rate[b]
<1	0	-
1 to 4	7	2.9
5 to 9	3	-
10 to 14	5	1.5
15 to 19	3	-
20 to 29	10	1.5
30 to 39	13	1.8
40 to 49	7	1.1
50 to 59	26	4.0
60 to 69	21	3.7
70+	23	3.9
Total	**118**	**2.3**

[a] MoH NMDS data for hospital admissions

[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

Evaluation of needle injection practices contributing to Campylobacter contamination in New Zealand chicken and chicken products – Al-Sakkaf 2022

Chicken marination with needle injection may introduce pathogenic bacteria from the surface into the interior muscle tissue [24]. Initial experiments in brine solutions demonstrated that *Campylobacter jejuni* could survive in 0.5 - 1.0% salt solution for 24 hours and in 6 - 7.5% salt solution for 6 hours, but not 24 hours. Chicken drumsticks, sterilised by irradiation, were injected with either of two marinades (low salt and high salt) as part of the normal operations of a poultry processing plant. Following injection with the low salt marinade, all drumsticks were contaminated with *C. jejuni*, with counts up to 3.5 log per drumstick. For drumsticks injected with the high salt marinade, only 30% of the injected drumsticks were contaminated with *C. jejuni* and only on the drumstick outer surface. Chicken products injected with the low salt marinade are sold frozen, while chicken products injected with high salt marinade are sold fresh. At retail, the contamination was very low or undetectable for both product types, with a highest detected contamination level of 900 CFU/portion.

Relevant regulatory developments

Nil.

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.

Terminology

A FAO/WHO expert meeting, carried out in 2018 and reported in 2020 [25], concluded that there was sufficiently good evidence for cases of ciguatoxicity from consumption of non-finfish marine species. The meeting proposed that the condition should be known as ciguatera poisoning, rather than ciguatera fish poisoning. Ciguatera poisoning is now the preferred term and will be used throughout this document.

Ciguatera poisoning individual cases reported in 2022 by data source

During 2022, 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 MoH NMDS database. Of the two hospital admissions (0.04 admissions per 100,000 population) recorded in 2022, both cases were reported with ciguatera poisoning as the primary diagnosis. No cases were reported with ciguatera poisoning as another relevant diagnosis.

It should be noted that EpiSurv and the MoH 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.

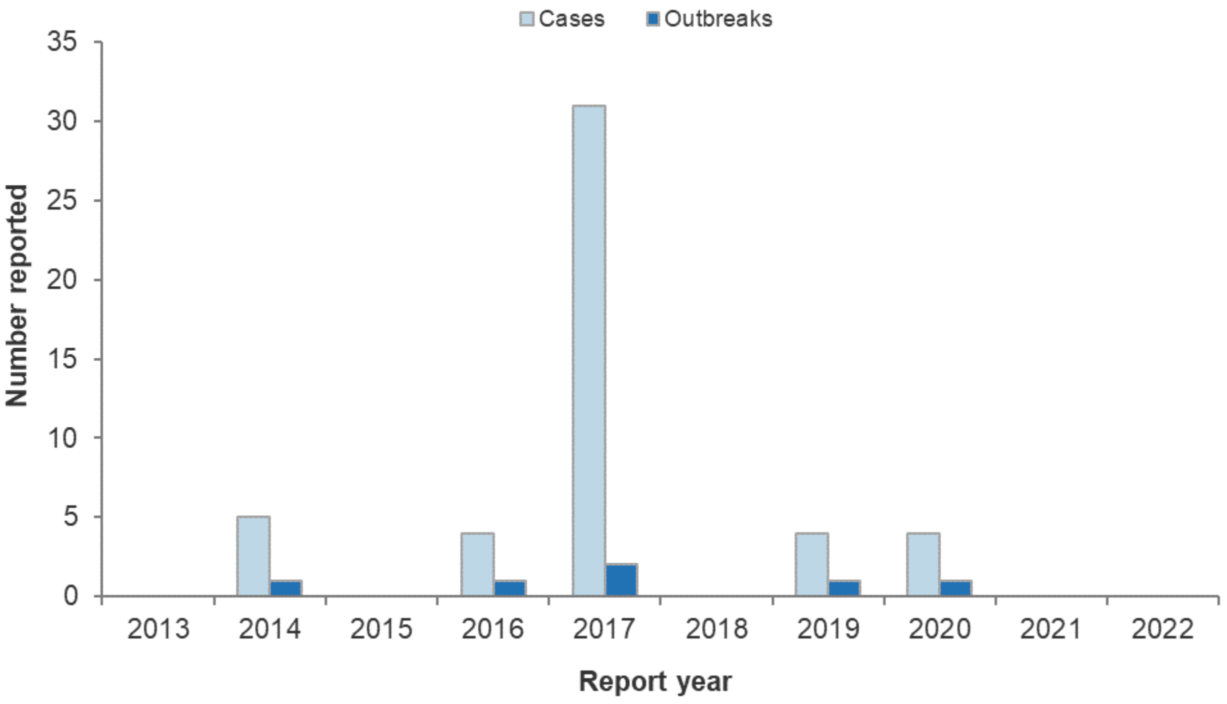
Outbreaks reported as caused by ciguatera poisoning

During 2022, 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 2013 to 2022, six 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, 2013–2022



Recent surveys

Nil.

Relevant New Zealand studies and publications

Nil.

Relevant regulatory developments

Nil.

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 $\geq 10^6$/g or isolation of $\geq 10^5$/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 2022 by data source

During 2022, 5 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 MoH NMDS database. Of the two hospital admissions (0.04 admissions per 100,000 population) recorded in 2022, one case was reported with *C. perfringens* intoxication as the primary diagnosis and one with *C. perfringens* intoxication as another relevant diagnosis.

Outbreaks reported as caused by *Clostridium perfringens*

In 2022, there was one *C. perfringens* intoxication outbreak (5 cases) reported in EpiSurv with food as a possible mode of transmission (Table 14).

Table 14. *C. perfringens* intoxication outbreaks reported in EpiSurv, 2022

	Possible foodborne transmission with a suspected source	Total *C. perfringens* intoxication outbreaks
Outbreaks	1	1
Outbreak-associated cases	5	5
Hospitalised cases	0	0

Table 15 contains details of the outbreak related to potentially undercooked chicken nuggets supplied to schools in the Regional Public Health region. The lunch provider advised schools of the potential for raw/uncooked chicken nugget consumption and for possible illness cases to be notified to PHU. Five students were notified as having symptoms, and one student tested positive for *C. perfringens* enterotoxin. The evidence linking the cases and the food source was weak. No testing of the product was conducted. It is estimated ~1150 people could have been exposed.

Table 15. Details of *C. perfringens* intoxication outbreak reported in EpiSurv with food reported as a possible mode of transmission, 2022

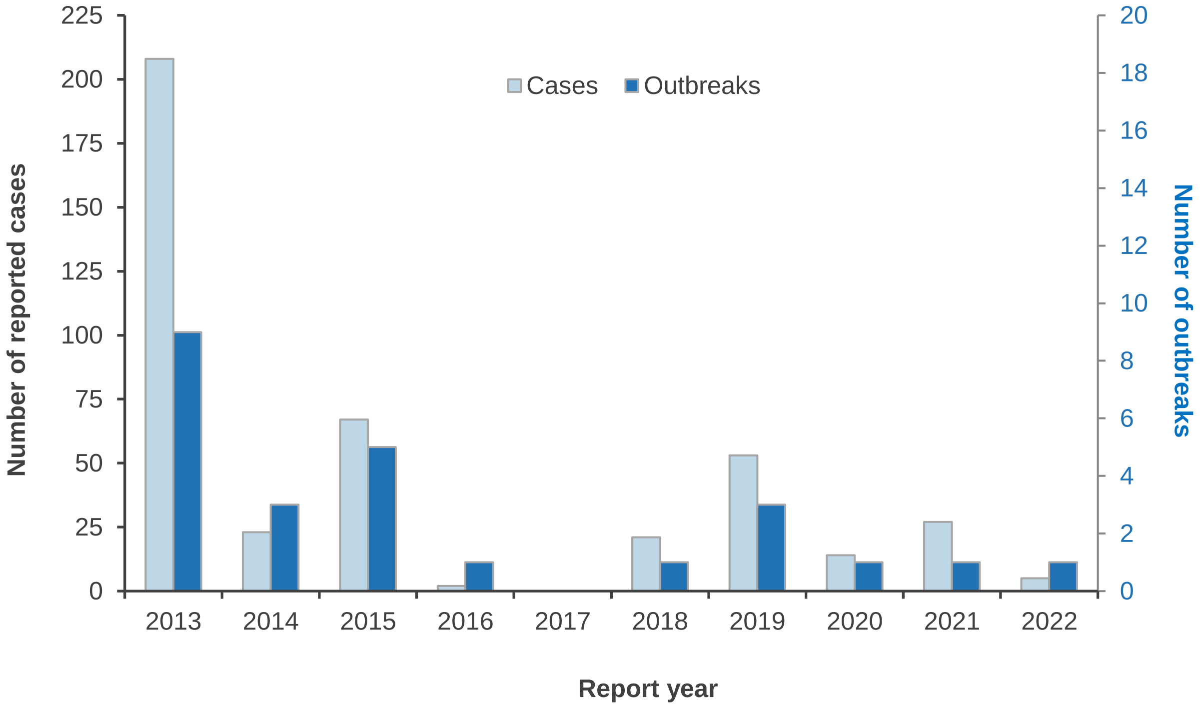
PHU	Month	Suspected source	Evidence	Setting	No. ill
Regional PH	March	Raw / undercooked chicken nuggets	Lunch provider advised of the possibility of uncooked product	School	1C 4P

PH: Public health,

Number ill: C: confirmed, P: probable

Over the 10-year period 2013-2022, the number of outbreaks of *C. perfringens* intoxication with food reported as a possible mode of transmission ranged from zero (2017) to nine outbreaks (in 2013) (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 2013 (208 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, 2013–2022



Recent surveys

Nil.

Relevant New Zealand studies and publications

Nil.

Relevant regulatory developments

Nil.

Cryptosporidiosis

Summary data for cryptosporidiosis in 2022 are given in Table 16.

Table 16. Summary of surveillance data for cryptosporidiosis, 2022

Parameter	Value in 2022	Source
Number of notified cases	612	EpiSurv
Notification rate (per 100,000)	11.9	EpiSurv
Hospitalisations[a]	70	MoH NMDS
Deaths	0	EpiSurv
Travel-related cases[b, c]	10	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 = MoH 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. 300 cases had not travelled overseas during the incubation period and for the remaining 302 cases travel history is unknown.

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

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.

Changes to laboratory methods

Since 2015, laboratories across New Zealand have changed the methodology for testing faecal specimens (Appendix B, page 120). In 2022, community faecal specimens in all DHBs except for Bay of Plenty, Canterbury, Lakes, South Canterbury, Waikato and West Coast were screened by PCR methods for a range of pathogens, including *Cryptosporidium* spp.. All community faecal specimens in these DHBs are now screened for *Cryptosporidium* spp., whereas previously only those specimens where parasite screening was requested were tested. The remainder of the DHBs (around 35% 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 PCR introduction) and PCR for the detection of *Cryptosporidium* spp. [26].

Cryptosporidiosis individual cases reported in 2022 by data source

During 2022, 612 individual cases (11.9 per 100,000 population) of cryptosporidiosis and no resulting deaths were reported in EpiSurv. Of the 612 cases, the symptoms of 591 cases (97%) were reported as fitting the clinical description for cryptosporidiosis, the symptoms were unknown for 20 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 MoH NMDS database. Of the 70 hospital admissions (1.4 admissions per 100,000 population) recorded in 2022, 47 cases were reported with cryptosporidiosis as the primary diagnosis and 23 were reported with cryptosporidiosis as another relevant diagnosis.

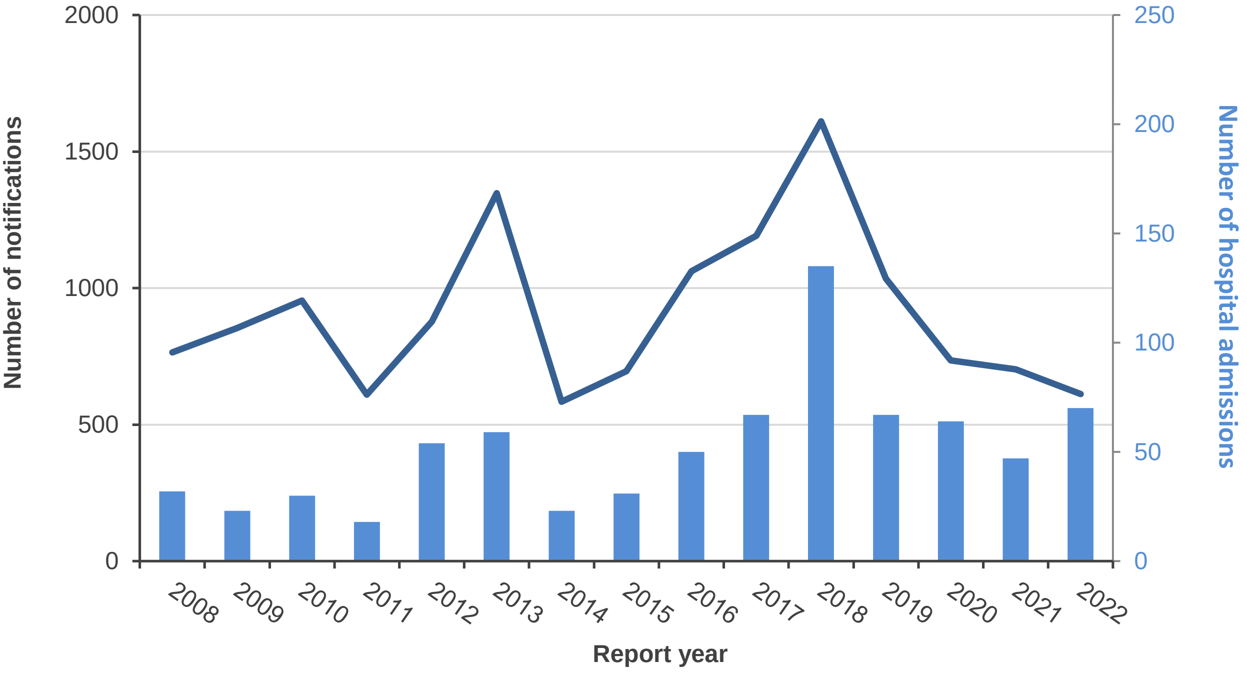
It should be noted that EpiSurv and the MoH NMDS database are separate systems and hospital admission can occur without cases being notified in EpiSurv.

Annual data

Over the last 15 years there were no clear trends regarding the number of cryptosporidiosis notifications (Figure 13). In 2022, the number of notifications was within the range seen in the previous 20 years (except for 2018). The number of hospital admissions with cryptosporidiosis as a primary or secondary diagnosis varied year by year and has ranged between 18 (2011) and 135 (2018).

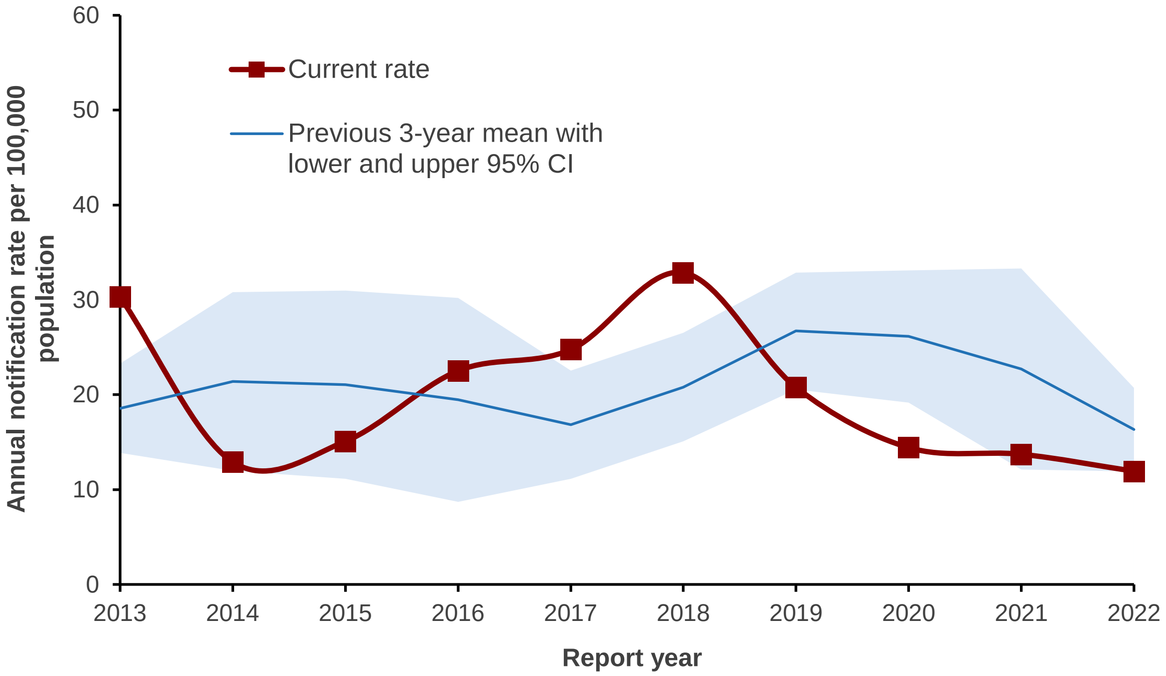
The frequency of overseas travel decreased in 2020 to 2022 compared to pre COVID-19 years (see Introduction, page 5). This is reflected in the notifications; in 2022, there were 10 cryptosporidiosis notifications in EpiSurv listing overseas travel as a risk factor, compared to 50 in 2019, seven in 2020 and none in 2021.

Figure 13. Cryptosporidiosis EpiSurv notifications (line) and NMDS hospitalisations (bar) by year, 2008–2022



In 2022, the notification rate for cryptosporidiosis (11.9 cases per 100,000 population) was lower than the previous three-year average (16.3 cases per 100,000 population) (Figure 14).

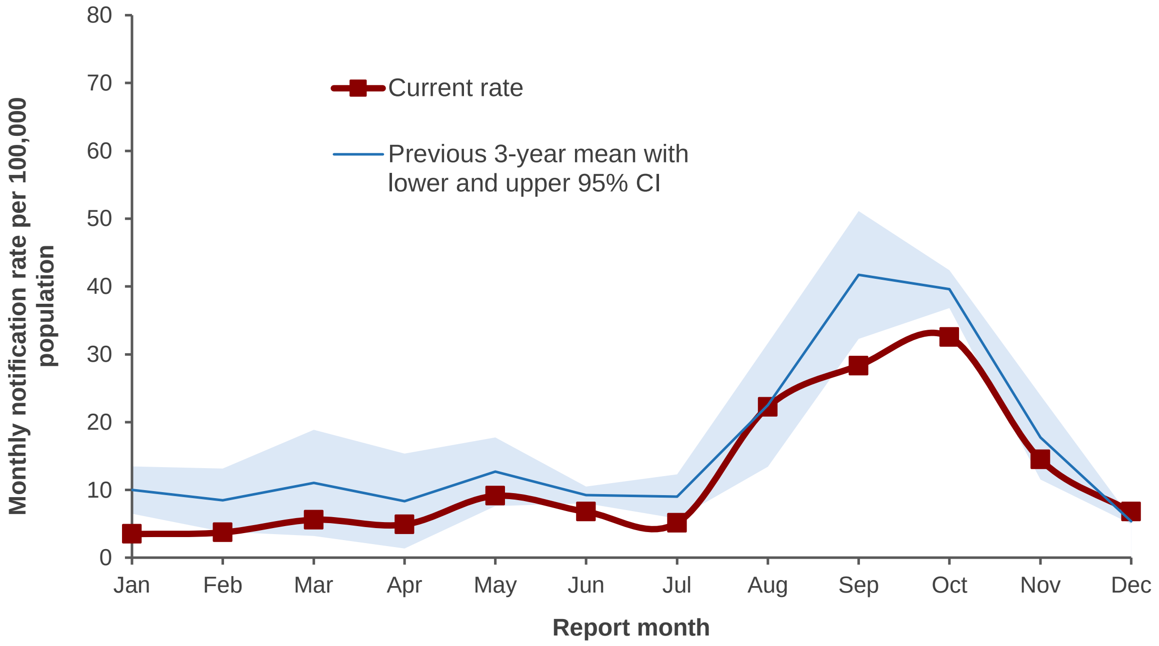
Figure 14. Cryptosporidiosis notification rate by year, 2013–2022



Seasonal data

Cryptosporidiosis notification rates per 100,000 population by month for 2022 are shown in Figure 15. In 2022, monthly notification rates followed the same trend but were mostly slightly lower than the mean of the previous three years. The monthly number of notifications in 2022 ranged from 15 notifications (January, 4 per 100,000 population) to 139 notifications (October, 33 per 100,000 population).

Figure 15. Cryptosporidiosis monthly notification rate (annualised), 2022



Demographics

In 2022, the rate of notifications for cryptosporidiosis was slightly higher for females (12.7 per 100,000 population) compared with males (11.2 per 100,000 population) whereas the rate of hospitalisations was the same (Table 17).

Table 17. Cryptosporidiosis cases by sex, 2022

Sex	EpiSurv notifications		Hospitalisations[a]	
	No.	Rate[b]	No.	Rate[b]
Male	285	11.2	35	1.4
Female	327	12.7	35	1.4
Total	**612**	**11.9**	**70**	**1.4**

[a] MoH NMDS data for hospital admissions

[b] per 100,000 population in this sex group

In 2022, the highest cryptosporidiosis age-specific notification rate and hospitalisation rate was reported for the 1 to 4 years age group (53.1 per 100,000 population, 129 cases and 4.9 admissions per 100,000 population, 12 cases) (Table 18).

Table 18. Cryptosporidiosis cases by age group, 2022

Age group (years)	EpiSurv notifications		Hospitalisations[a]	
	No.	Rate[b]	No.	Rate[b]
<1	7	11.7	0	-
1 to 4	129	53.1	12	4.9
5 to 9	65	20.2	14	4.3
10 to 14	33	9.7	2	-
15 to 19	46	14.5	5	1.6
20 to 29	136	20.0	16	2.4
30 to 39	82	11.2	8	1.1
40 to 49	49	7.8	3	-
50 to 59	24	3.7	1	-
60 to 69	27	4.8	4	-
70+	14	2.4	5	0.9
Total[c]	**612**	**11.9**	**70**	**1.4**

[a] MoH NMDS data for hospital admissions

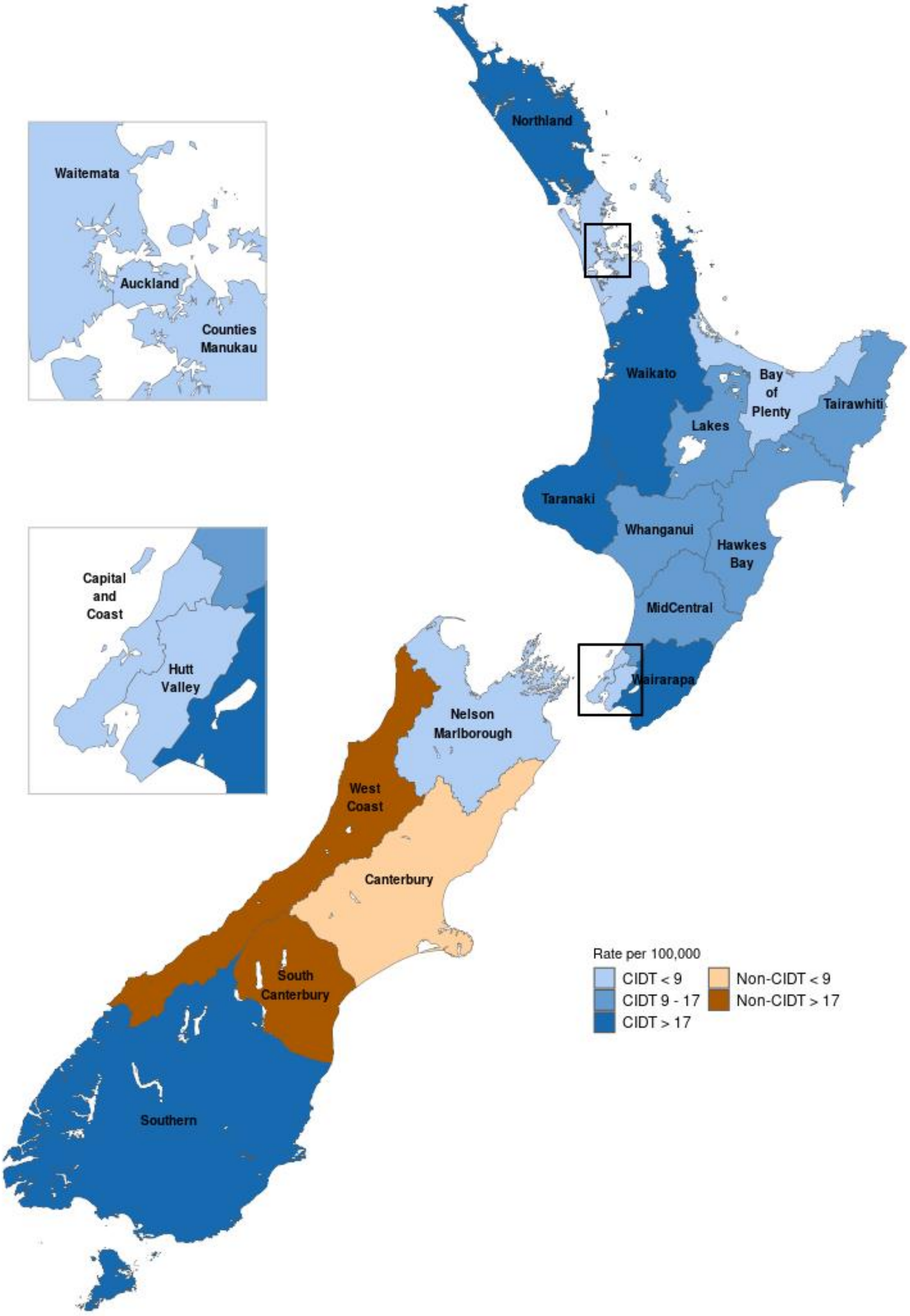
[b] per 100,000 population in this age group (rate not calculated when fewer than five cases reported)

[c] total includes notifications where age is unknown

Geographic distribution

The notification rates by DHB calculated per 100,000 resident population are presented in Figure 16 (see also Table 86). Blue shading is used in DHBs which are using CIDT community testing, the brown shading is used for DHBs using microscopy or EIA.

Figure 16. Geographic distribution of cryptosporidiosis notifications, 2022



In 2022, the DHB notification rates of cryptosporidiosis ranged from 7 per 100,000 population in Nelson Marlborough DHB (11 cases) and Counties Manukau DHB (41 cases) to 42 per 100,000 population (26 cases) in South Canterbury DHB. South Canterbury, Taranaki (31 per 100,000 population, 39 cases), Wairarapa (29 per 100,000 population, 15 cases), Waikato (20 per 100,000 population, 89 cases) DHBs had the highest notification rates.

Historically, notification rates for cryptosporidiosis have been variable across New Zealand with Waikato and Southern DHBs consistently in the highest quartile of notification rates since 2019. Taranaki and South Canterbury DHBs have rates consistently in the highest quartile since 2020.

Cryptosporidiosis notification rates stratified by 2023 Urban Rural Classification [22] of the cases' residential address monotonically increased with decreasing urbanisation (Appendix C, Table 87). Rates were lowest for 'major urban areas' (6 per 100,000 population, 155 cases) and highest for 'rural other' (31 per 100,000 population, 212 cases).

Outbreaks reported as caused by *Cryptosporidium* spp.

In 2022, there was a single cryptosporidiosis outbreak reported in EpiSurv, which was recorded as related to contact with a sick lamb (Table 19). One case was recorded in EpiSurv as being hospitalised.

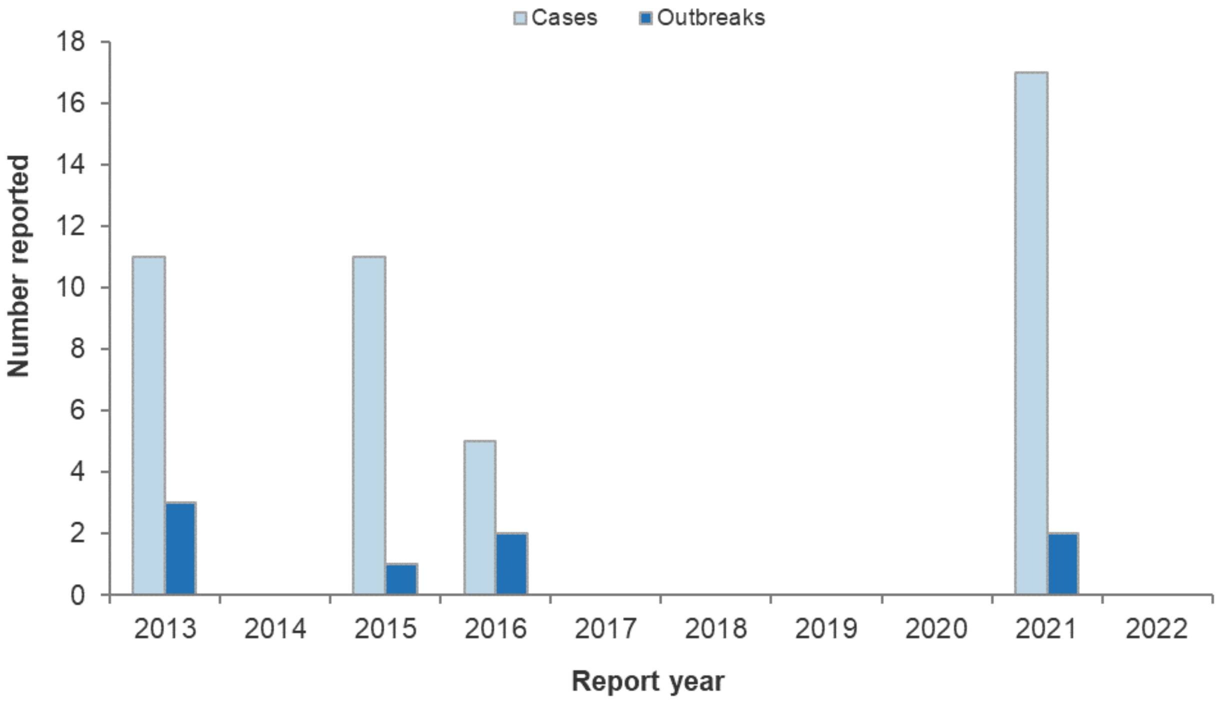
It is important to note that a single outbreak may have multiple pathogens, settings, and possible modes of transmission.

Table 19. Cryptosporidiosis outbreaks reported in EpiSurv, 2022

	Possible foodborne transmission	Total cryptosporidiosis outbreaks
Outbreaks	0	1
Outbreak-associated cases	0	4
Hospitalised cases	0	1

Between 2013 and 2022 there have been a total of eight outbreaks of potentially foodborne cryptosporidiosis (Figure 17), with no outbreaks recorded over the period 2017 to 2020. The number of cases associated with individual outbreaks ranged between five and 17.

Figure 17. Cryptosporidiosis outbreaks reported in EpiSurv with food reported as a possible mode of transmission and associated cases reported by year, 2013–2022



Recent surveys

Nil.

Relevant New Zealand studies and publications

Journal papers

Nil.

Relevant regulatory developments

Nil.

Giardiasis

Summary data for giardiasis in 2022 are given in Table 20.

Table 20. Summary of surveillance data for giardiasis, 2022

Parameter	Value in 2022	Source
Number of notified cases	707	EpiSurv
Notification rate (per 100,000)	13.8	EpiSurv
Hospitalisations[a]	46	MoH NMDS
Deaths	0	EpiSurv
Travel-related cases [b, c]	35	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 = MoH 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. 319 cases had not travelled overseas during the incubation period and for the remaining 353 cases travel history is unknown.

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

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.

Changes to laboratory methods

Since 2015, laboratories across New Zealand have changed the methodology for testing faecal specimens (Appendix B, page 120). In 2022, community faecal specimens in all DHBs except for Bay of Plenty, Canterbury, Lakes, South Canterbury, Waikato and West Coast were screened by PCR methods for a range of pathogens, including *Giardia* spp.. All community faecal specimens in these DHBs are now screened for *Giardia* spp., whereas previously only those specimens where parasite screening was requested were tested. The remainder of the DHBs (35% of the New Zealand population) are still serviced by community laboratories using microscopic methods or 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 gardiasis were generally well recognised leading to appropriate requests for testing.

Giardiasis individual cases reported in 2022 by data source

During 2022, 707 individual cases (13.8 per 100,000 population) of giardiasis and no resulting deaths were reported in EpiSurv. Of the 707 cases, the symptoms of 643 cases (91%) were reported as fitting the clinical description for giardiasis, the symptoms were unknown for 61 cases, and for three cases 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 MoH NMDS database. Of the 46 hospital admissions (0.9 admissions per 100,000 population) recorded in 2022, 22 cases were reported with giardiasis as the primary diagnosis and 24 were reported with giardiasis as another relevant diagnosis.

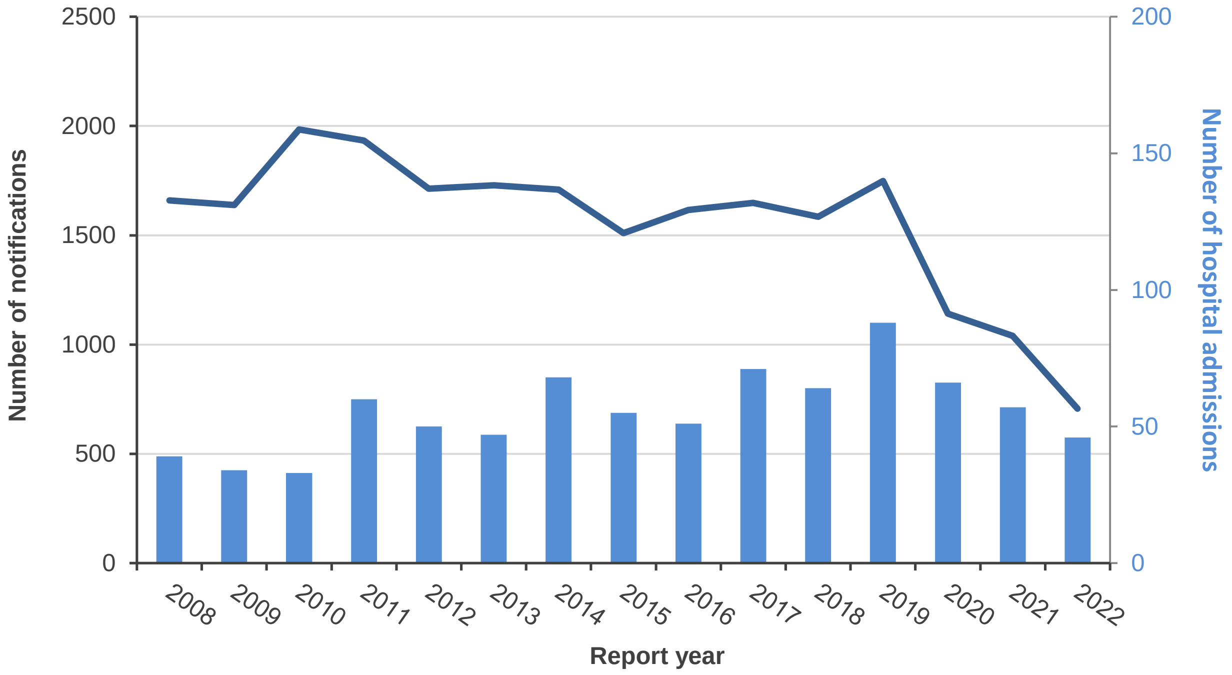
It should be noted that EpiSurv and the MoH NMDS database are separate systems and hospital admission can occur without cases being notified in EpiSurv.

Annual data

From 2008 to 2019, the number of giardiasis notifications reported each year ranged between 1510 (2015) and 1985 (2010) (Figure 18). There was a pronounced drop in notifications in the years 2020, 2021 and 2022. The number of hospital admissions with giardiasis as a primary or secondary diagnosis varied year by year and has ranged between 33 (2010) and 88 (2019).

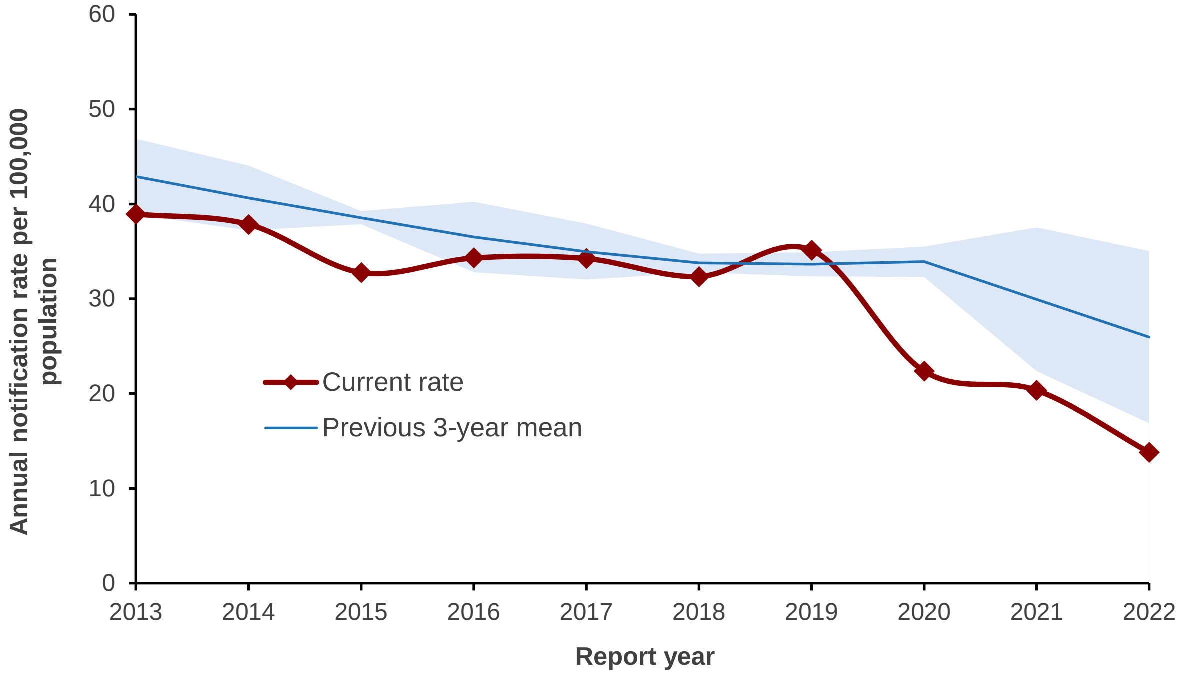
The frequency of overseas travel decreased in 2020 to 2022 compared to pre-COVID-19 years (see Introduction, page 5). This is reflected in the notifications; in 2022, there were 35 giardiasis notifications in EpiSurv listing overseas travel as a risk factor, compared to 179 in 2019, 59 in 2020 and six in 2021.

Figure 18. Giardiasis EpiSurv notifications (line) and NMDS hospitalisations (bar) by year, 2008–2022



In 2022, the notification rate for giardiasis (13.8 cases per 100,000 population) was much lower than the previous three-year average (25.9 cases per 100,000 population) (Figure 19). The drop in notification rates since 2020 can be attributed to the COVID-19 pandemic [19].

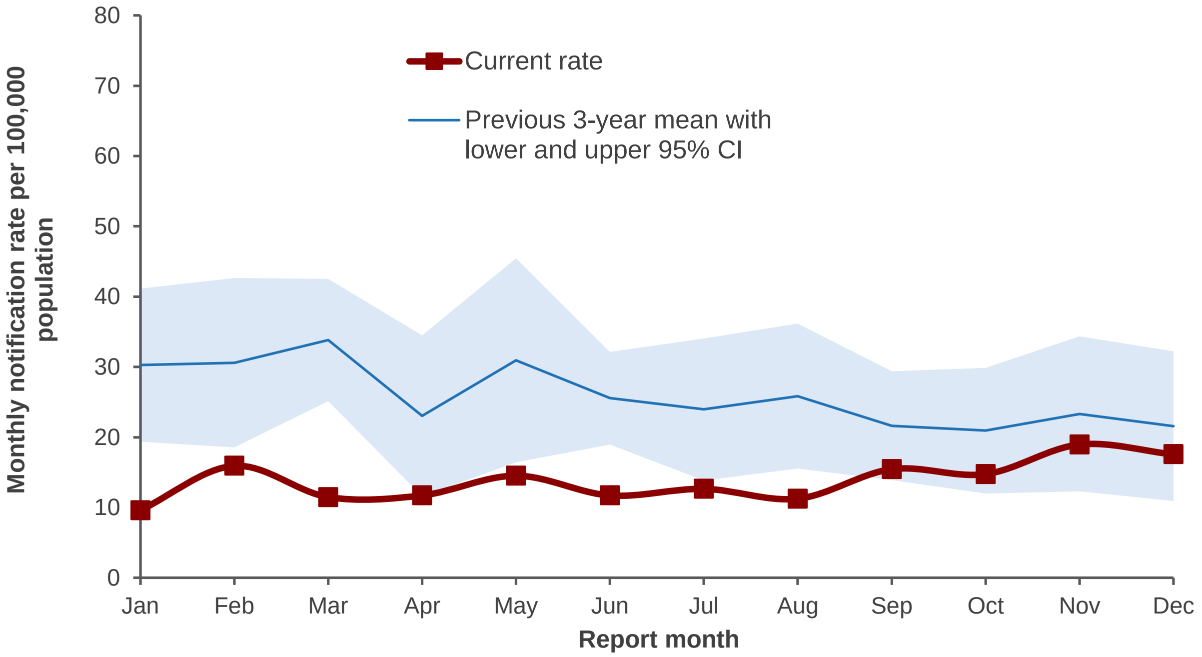
Figure 19. Giardiasis notification rate by year, 2013–2022



Seasonal data

Giardiasis notification rates per 100,000 population by month for 2022 are shown in Figure 20. In 2022, monthly notification rates followed a similar trend but were lower than the mean of the previous three years. The monthly number of notifications in 2022 ranged from 41 notifications (January, 10 per 100,000 population) to 81 notifications (November, 19 per 100,000 population).

Figure 20. Giardiasis monthly notification rate (annualised), 2022



Demographics

In 2022, the rate of notifications for giardiasis was higher for males (15.5 cases per 100,000 population) compared with females (12.1 cases per 100,000 population). Hospitalisation rates were the same for males and females (Table 21).

Table 21. Giardiasis cases by sex, 2022

Sex	EpiSurv notifications		Hospitalisations[a]	
	No.	Rate[b]	No.	Rate[b]
Male	394	15.5	24	0.9
Female	312	12.1	22	0.9
Total[c]	**707**	**13.8**	**46**	**0.9**

[a] MoH NMDS data for hospital admissions

[b] per 100,000 population in this sex group

[c] total includes notifications where sex is unknown

In 2022, the highest age-specific notification rate was for the 1 to 4 years age group (47.3 per 100,000 population, 115 cases), (Table 22). The highest hospitalisation rate was reported for the 60 to 69 years age group (2.1 admissions per 100,000 population, 12 cases).

Table 22. Giardiasis cases by age group, 2022

Age group (years)	EpiSurv notifications		Hospitalisations[a]	
	No.	Rate[b]	No.	Rate[b]
<1	10	16.7	1	-
1 to 4	115	47.3	4	-
5 to 9	45	14.0	1	-
10 to 14	15	4.4	0	-
15 to 19	12	3.8	0	-
20 to 29	73	10.7	4	-
30 to 39	154	21.0	5	0.7
40 to 49	89	14.1	7	1.1
50 to 59	70	10.7	4	-
60 to 69	79	14.1	12	2.1
70+	45	7.7	8	1.4
Total	**707**	**13.8**	**46**	**0.9**

[a] MoH NMDS data for hospital admissions

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

Geographic distribution

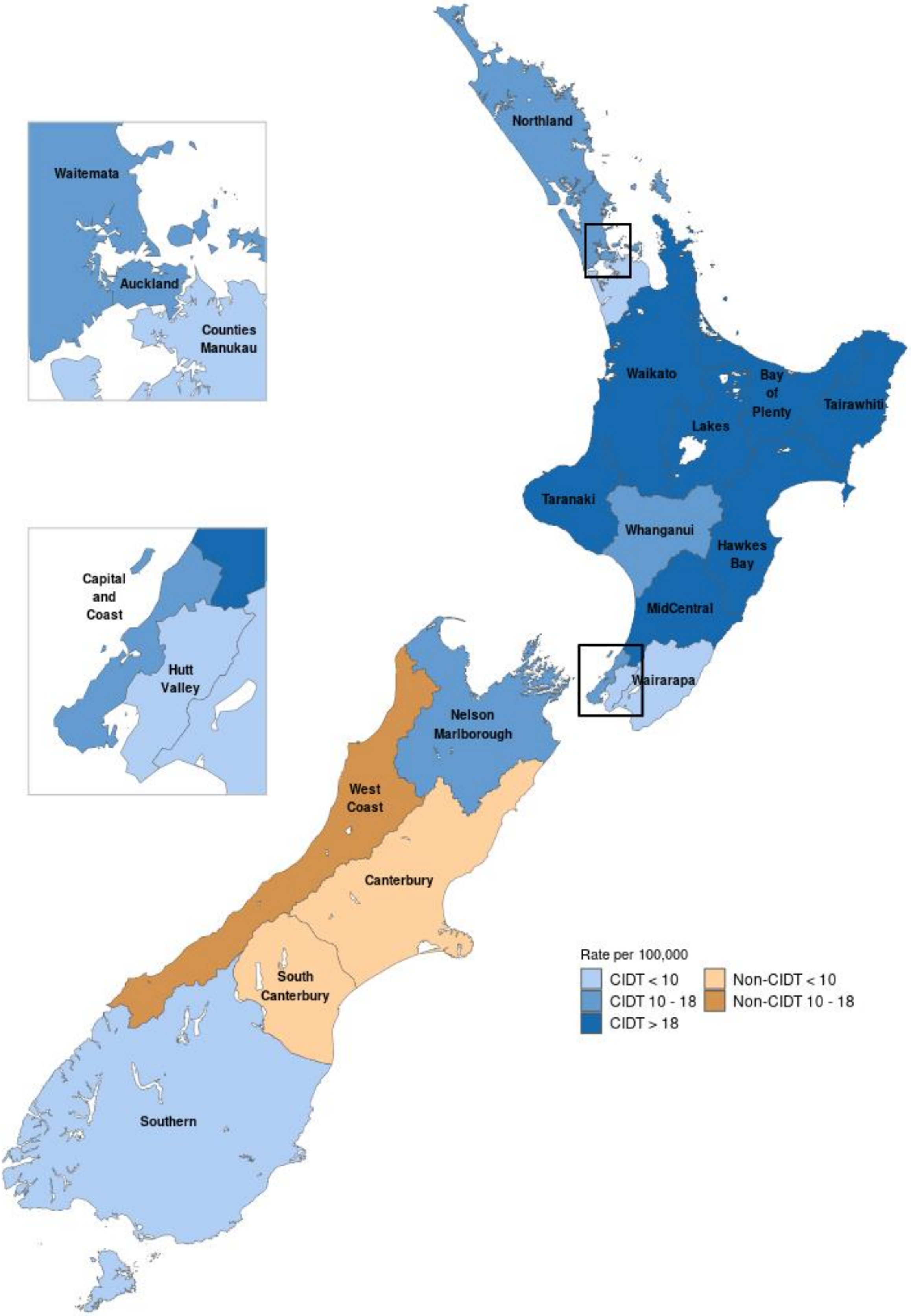
The notification rates by DHB calculated per 100,000 resident population are presented in Figure 21 (see also Table 86). Blue shading is used in DHBs which are using CIDT community testing, the brown shading is used for DHBs using microscopy or EIA.

In 2022, the DHB notification rates for giardiasis ranged from 7 per 100,000 population (11 cases) in Hutt Valley DHB and Canterbury (40 cases) to 42 per 100,000 population (22 cases) in Tairawhiti DHB. The Tairawhiti, Hawkes Bay (26 per 100,000 population, 47 cases) and Lakes (24 per 100,000 population, 28 cases) DHBs had the highest notification rates.

Historically, notification rates for giardiasis have been variable across New Zealand with Tairawhiti DHB consistently having the highest notification rate since 2016.

Giardiasis notification rates stratified by 2023 Urban Rural Classification [22] of the cases' residential address were higher in rural areas than urban rates (Appendix C, Table 87). Rates of cases residing in urban category areas ranged from 10 to 15 per 100,000 population. The highest rate was for the 'rural other' category (23 per 100,000 population).

Figure 21. Geographic distribution of giardiasis notifications, 2022



Outbreaks reported as caused by *Giardia spp.*

In 2022, there were four giardiasis outbreak notifications in EpiSurv, one of which reported food as a possible mode of transmission (Table 23). It is important to note that a single outbreak may have multiple pathogens, settings, and possible modes of transmission.

Table 23. Giardiasis outbreaks reported in EpiSurv, 2022

	Possible foodborne transmission with a suspected or confirmed source	Total giardiasis outbreaks
Outbreaks	1	4
Outbreak-associated cases	3	12
Hospitalised cases	0	0

The evidence linking the possibly foodborne outbreak (Table 24) to drinking raw milk was weak as no milk samples were taken. The cases also lived on a farm so other risk factors such as animal contact may have occurred.

Table 24. Details of giardiasis outbreak reported in EpiSurv with food reported as a possible mode of transmission, 2022

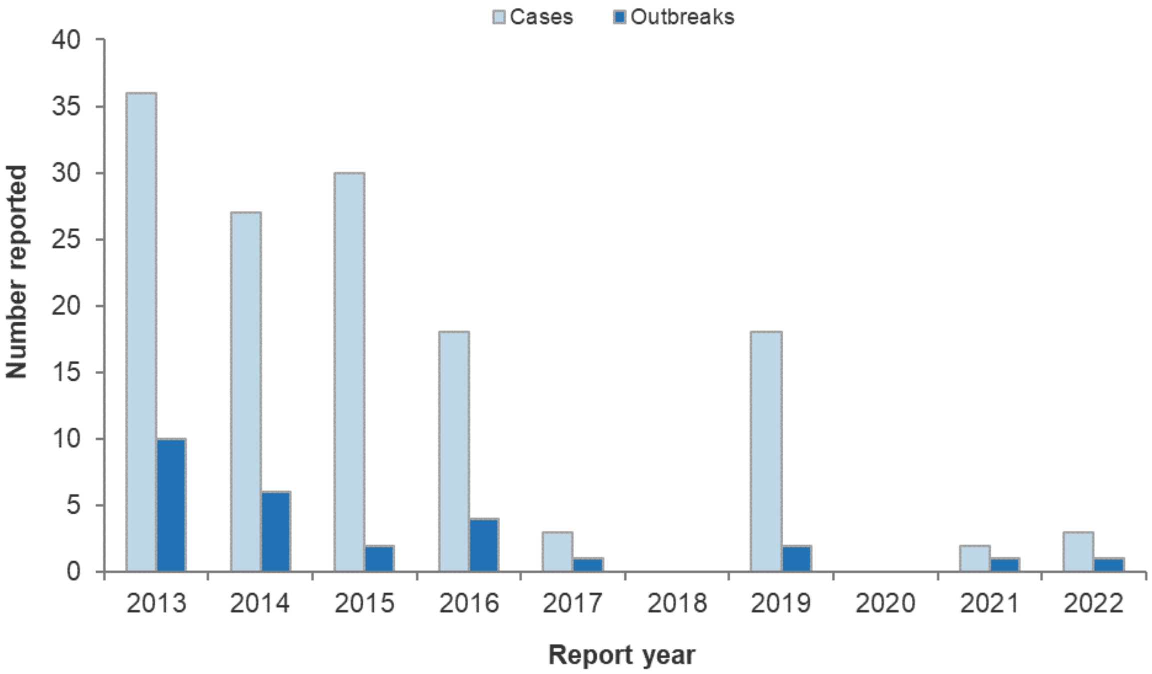
PHU	Month	Suspected source	Evidence	Setting	No. ill
PH Northland	March	Raw milk	None	Farm/home	2C 1P

PHU: Public health unit, PH Northland: Public Health Northland

Number ill: C: confirmed, P: probable

Over the 10-year period 2013 and 2022, between zero and 10 giardiasis outbreaks with food reported as a possible mode of transmission were notified each year with between two and 36 annual outbreak-associated cases (Figure 22).

Figure 22. Giardiasis outbreaks with food reported as a possible mode of transmission and associated cases reported by year, 2013–2022



Recent surveys

Nil.

Relevant New Zealand studies and publications

Nil.

Relevant regulatory developments

Nil.

Hepatitis A

Summary data for hepatitis A in 2022 are given in Table 25.

Table 25. Summary of surveillance data for hepatitis A, 2022

Parameter	Value in 2022	Source
Number of notified cases	59	EpiSurv
Notification rate (per 100,000)	1.2	EpiSurv
Hospitalisations[a]	36	MoH NMDS
Deaths	0	EpiSurv
Travel-related cases[b,c]	20	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 = MoH National Minimum Dataset of hospitalisations

[a] Hospitalisations with acute hepatitis A as the principal diagnosis. Another 43 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 (34%). 39 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 travel in 2022, overseas travel was still reduced compared to pre-COVID-19 years

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.

Hepatitis A individual cases reported in 2022 by data source

There were 79 hospital admissions (1.5 admissions per 100,000 population) recorded in 2022; 36 cases were reported with acute hepatitis A as the primary diagnosis and 43 cases with acute hepatitis A as another relevant diagnosis. The ICD-10 code B15 was used to extract acute hepatitis A hospitalisation data from the MoH NMDS database.

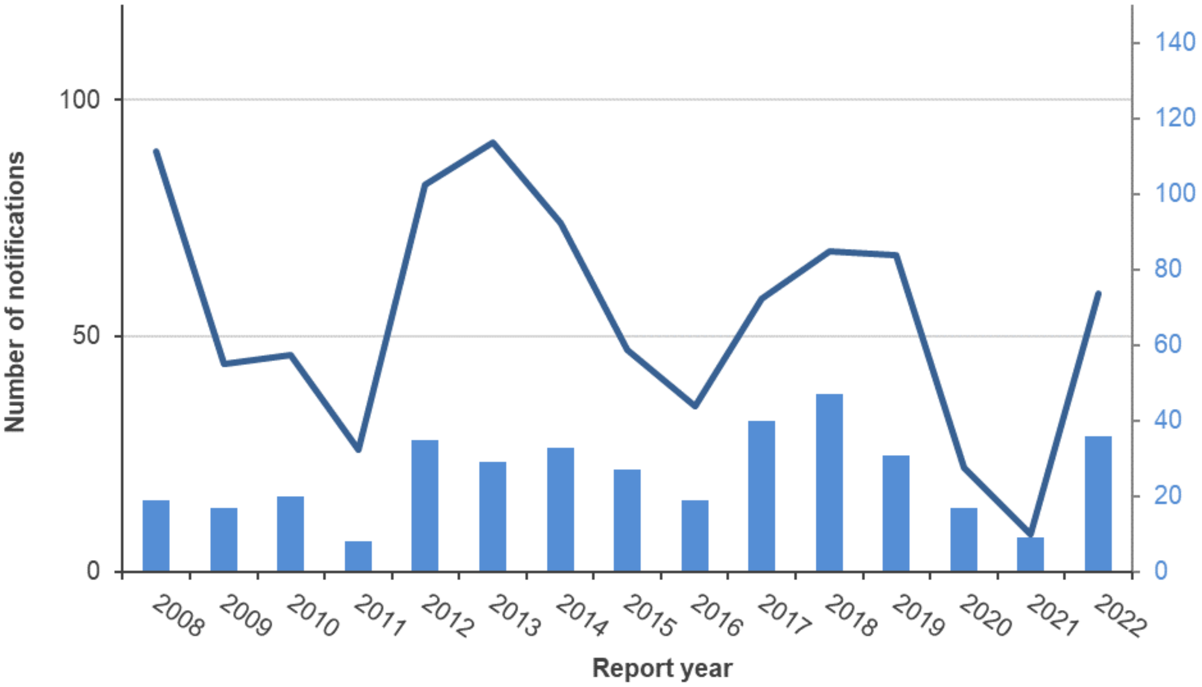
During 2022, 59 individual cases (1.2 per 100,000 population) of hepatitis A and no resulting deaths were reported in EpiSurv. Hospitalisation rates are usually high for hepatitis A with 61% of notified cases recorded in EpiSurv as hospitalised in 2022.

It should be noted that EpiSurv and the MoH 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 [16]. 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 2008 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) and an increase again in 2022. In 2022, 35 of the notified cases were related to a national hepatitis A outbreak linked to frozen berries. The frequency of overseas travel changed in the years 2020 to 2022 compared to pre COVID-19 years (see Introduction, page 5). This is reflected in the notifications; there were 20 hepatitis A notifications in EpiSurv listing overseas travel as a risk factor in 2022, compared to 33 in 2019, 16 in 2020 and two in 2021.

Figure 23. Hepatitis A EpiSurv notifications (line) and NMDS hospitalisations (bar) by year, 2008–2022



Note: Number of hospital admissions include only cases with hepatitis A as a primary 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 2022, notification and hospitalisation rates for hepatitis A were similar for females (1.1 notified cases and 0.7 admissions per 100,000 population) and males (1.2 notified cases and 0.7 admissions per 100,000 population) (Table 26).

Table 26. Hepatitis A cases by sex, 2022

Sex	EpiSurv notifications		Hospitalisations[a]	
	No.	Rate[b]	No.	Rate[b]
Male	31	1.2	18	0.7
Female	28	1.1	18	0.7
Total	**59**	**1.2**	**36**	**0.7**

[a] MoH NMDS data for hospital admissions with hepatitis A as a primary diagnosis

[b] per 100,000 population in this sex group

In 2022, the hepatitis A notified cases ranged in age from 5 to 70+ years old. The age range for hospital admissions was 5 to 69 years old (Table 27).

Table 27. Hepatitis A cases by age group, 2022

Age group (years)	EpiSurv notifications		Hospitalisations[a]	
	No.	Rate[b]	No.	Rate[b]
<1	0	-	0	-
1 to 4	0	-	0	-
5 to 9	4	-	6	1.9
10 to 14	1	-	0	-
15 to 19	4	-	2	-
20 to 29	18	2.6	15	2.2
30 to 39	14	1.9	6	0.8
40 to 49	2	-	0	
50 to 59	6	0.9	3	
60 to 69	7	1.2	4	
70+	3	-	0	
Total	**59**	**1.2**	**36**	**0.7**

[a] MoH NMDS data for hospital admissions with hepatitis A as a primary diagnosis

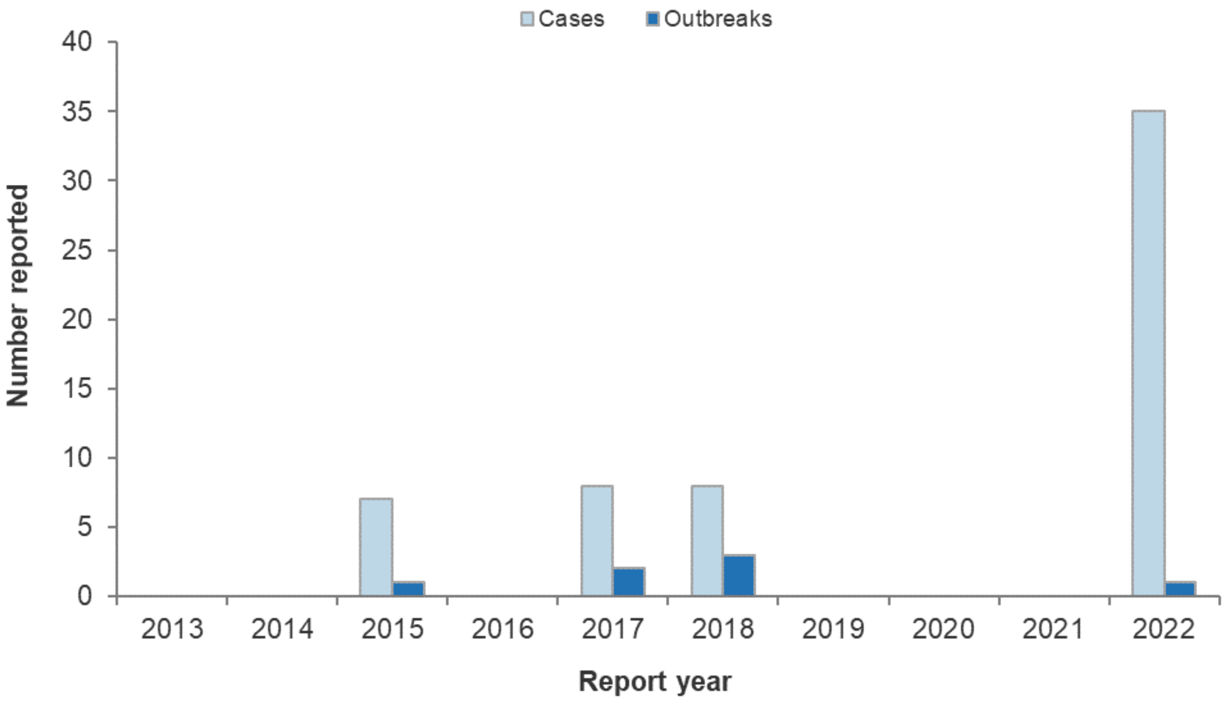
[b] per 100,000 population in this age group (rate not calculated when fewer than five cases reported)

Outbreaks reported as caused by hepatitis A virus

In 2022, there were a total of 35 reported cases in the national hepatitis A outbreak associated with imported frozen berries. This outbreak continued into the 2023 reporting year and has not been finalised. Of the 35 cases reported in 2022, there were seven cases that had no recollection of having eaten imported frozen berries and are likely due to secondary transmission. Hepatitis A virus was detected in one opened bag of frozen berries submitted from one of the cases. The genotype associated with this outbreak was Hepatitis A genotype IA.

Previously, from 2019 to 2021 there were no outbreaks of hepatitis A reported in EpiSurv (Figure 24). In the preceding four years (2015 to 2018) there were six outbreaks with a total of 23 associated cases.

Figure 24. Hepatitis A outbreaks reported in EpiSurv with food reported as a possible mode of transmission and associated cases reported by year, 2013–2022



Note: The outbreak in 2022 with 35 cases was still ongoing at the start of 2023.

Hepatitis A virus genotypes commonly reported

In 2022, faecal and/or serum/plasma specimens from 57 hepatitis A cases were submitted to ESR's Enteric, Environmental and Food Virology Laboratory for hepatitis A virus typing (Table 28). This compares to four hepatitis A cases in 2021. The data include those cases not associated with foodborne transmission.

Hepatitis A virus genotypes IA, IB and IIIA were identified in cases in 2022. Hepatitis A virus IA was the most commonly identified sub-genotype between 2018 and 2022.

Table 28. Hepatitis A virus genotypes identified by the Enteric, Environmental and Food Virology Laboratory, 2018–2022

Hepatitis A virus genotypes	2018	2019	2020	2021	2022
IA	20	24	10	2	35
IIIA	14	8	4	2	19
IB	0	1	2	0	2
Unable to genotype	3	1	0	0	1
Total	**37**	**34**	**16**	**4**	**57**

Recent surveys

Nil.

Relevant New Zealand studies and publications

Nil.

Relevant regulatory developments

In September 2022, NZFS advised consumers to consider extra precautions if eating frozen berries, to minimise the risk of hepatitis A [27]. NZFS advised people to be aware of the risks and, if eating frozen berries, to take the following precautions, if they are pregnant, elderly or with chronic liver damage:

- briefly boil frozen berries before eating them, or
- ensure cooking temperatures exceed 85°C for one minute.
- wash hands before eating and preparing food.

Consumer and trade level recalls were undertaken in response to this outbreak and imported food controls are being revised.

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 2022 by data source

During 2022, 2 outbreak-related cases and no 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 MoH NMDS database. Of the 14 hospital admissions (0.3 admissions per 100,000 population) recorded in 2022, all cases were reported with histamine (scombroid) fish poisoning as the primary diagnosis.

It should be noted that EpiSurv and the MoH 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

One histamine (scombroid) fish poisoning outbreak was reported in EpiSurv in 2022 involving two cases. None of the cases were reported as having been hospitalised (Table 29). It should be noted that all cases of histamine (scombroid) fish poisoning will be categorised as foodborne as consumption of contaminated fish is the only recognised transmission route for this disease.

Table 29. Histamine (scombroid) fish poisoning outbreaks reported in EpiSurv, 2022

	Histamine (scombroid) fish poisoning outbreaks
Outbreaks	1
Outbreak-associated cases	2
Hospitalised cases	0

Table 30 contains details of the histamine (scombroid) fish poisoning outbreak reported in 2022. No food was tested to confirm the source of the illness.

In addition to the outbreak recorded in EpiSurv at the cut-off date for this report (1 May 2023) (Table 30), NZFS carried out two further investigations of suspected histamine (scombroid) fish poisoning, including one investigation of three cases in the Taranaki Public Health region in February and one investigation of six cases in the Auckland Regional Public Health Service region in April.

Table 30. Details of histamine (scombroid) fish poisoning outbreak reported in EpiSurv, 2022

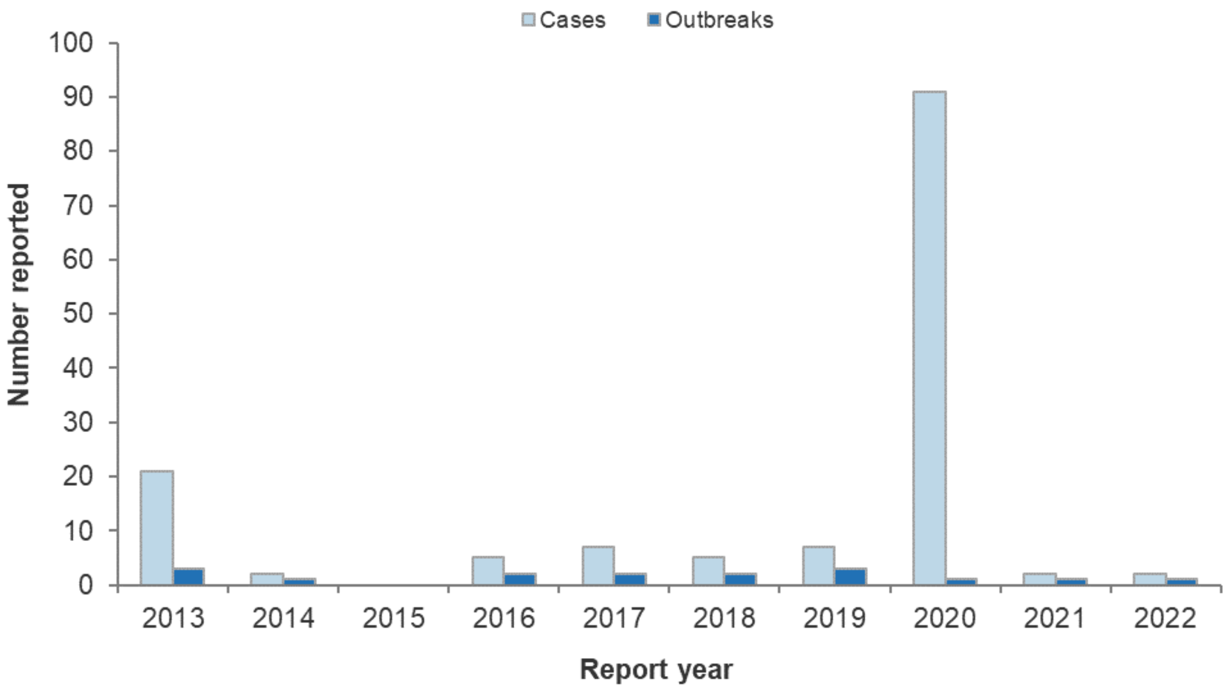
PHU	Report Month	Suspected source	Evidence	Setting	No. Ill
Auckland	November	Fish and chips meal	Common meal	Food premise	2P

PHU: Public health unit, Auckland: Auckland Regional Public Health Service

Number ill: P: probable. Histamine (scombroid) fish poisoning cases are classified as probable if no sample of suspect fish can be analysed

Over the 10-year period 2013 and 2022, the annual number of histamine (scombroid) fish poisoning outbreaks reported each year ranged from one to four, 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 reported in EpiSurv and associated cases reported by year, 2013–2022



Recent surveys

Nil.

Relevant New Zealand studies and publications

Nil.

Relevant regulatory developments

Nil.

Listeriosis

Summary data for listeriosis in 2022 are given in Table 31.

Table 31. Summary of surveillance data for listeriosis, 2022

Parameter	Value in 2022	Source
Number of notified cases[a]	39	EpiSurv
Notification rate (per 100,000)	0.8	EpiSurv
Hospitalisations[b]	40	MoH NMDS
Deaths	6[c]	EpiSurv
Travel-related cases[d]	2	EpiSurv
Estimated domestically acquired food-related cases	Sources other than food are unlikely	

NMDS = MoH National Minimum Dataset of hospitalisations

[a] Includes non-perinatal (32) and perinatal cases (7)

[b] Cases hospitalised may not be notified on EpiSurv

[c] Four non-perinatal cases and two perinatal cases died with listeriosis recorded as the primary cause of death. Two additional non-perinatal cases died with other causes recorded as the primary cause of death.

[d] Number of notified cases reporting overseas travel as risk factor. 33 cases had not travelled overseas during the incubation period and for the remaining four cases travel history is unknown. While New Zealand borders opened again for travel in 2022, overseas travel was still reduced compared to pre-COVID-19 years.

Case definition

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

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

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

Listeriosis individual cases reported in 2022 by data source

During 2022, 39 individual cases (0.8 per 100,000 population) of listeriosis (32 non-perinatal related cases and seven perinatal cases) were reported in EpiSurv, with four non-perinatal resulting deaths (all in the 70+ age group) and two deaths of pre-term foetuses. An additional two non-perinatal cases in the 70+ age group died with other causes recorded as the primary cause of death. Hospitalisation rates are usually very high for listeriosis with 37 notified cases recorded as hospitalised in 2022 (95%) in EpiSurv.

The ICD-10 code A32 was used to extract listeriosis hospitalisation data from the MoH NMDS database. Of the 40 hospital admissions (0.8 admissions per 100,000 population) recorded in 2022, 20 were reported with listeriosis as the principal diagnosis and 20 with listeriosis as another relevant diagnosis.

It should be noted that EpiSurv and the MoH 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 10th revision of the International Classification of Diseases (ICD10) coding system [16]. 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.

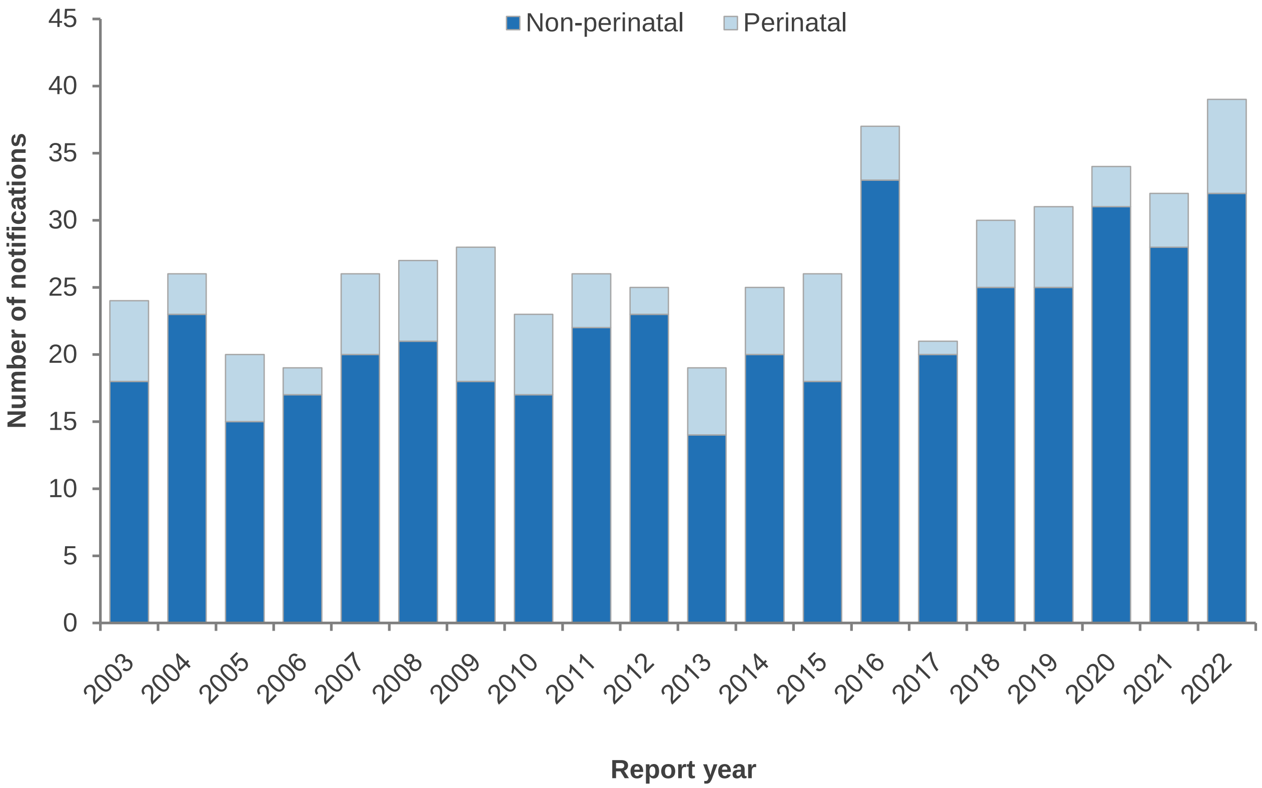
Foodborne transmission

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.

Notifiable disease data

Between 2003 and 2022, 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 per 100,000 population. In 2022, overseas travel was recorded as a risk factor for two cases.

Figure 26. Listeriosis EpiSurv non-perinatal and perinatal notifications by year, 2003–2022



Demographics

In 2022, the rate and number of notifications and hospitalisations for listeriosis was higher for females (1.0 per 100,000 population, 26 cases, 1.1 admissions per 100,000 population, 29 hospitalisations) than for males (0.5 per 100,000 population, 13 cases, 0.4 admissions per 100,000 population, 11 hospitalisations) (Table 32). It should be noted that notification case details for perinatal cases are those for the mother, so the female cases include the seven perinatal cases.

Table 32. Listeriosis cases by sex, 2022

Sex	EpiSurv notifications		Hospitalisations[a]	
	No.	Rate[b]	No.	Rate[b]
Male	13	0.5	11	0.4
Female	26	1.0	29	1.1
Total	**39**	**0.8**	**40**	**0.8**

[a] MoH NMDS data for hospital admissions. The total may include cases admitted on more than one occasion (readmissions)

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

In 2022, notification and hospitalisation rates for listeriosis were highest in the 70+ years age group (3.6 notified cases and 4.5 admissions per 100,000 population) (Table 33).

Table 33. Listeriosis cases by age group, 2022

Age group (years)	EpiSurv notifications		Hospitalisations[a]	
	No.[b]	Rate[c]	No.	Rate[c]
<1	2	-	1	-
1 to 4	0	-	0	-
5 to 9	0	-	0	-
10 to 14	0	-	0	-
15 to 19	1	-	1	-
20 to 29	4	-	2	-
30 to 39	3	-	4	-
40 to 49	2	-	2	-
50 to 59	2	-	1	-
60 to 69	4	-	3	-
70+	21	3.6	26	4.5
Total	**39**	**0.8**	**40**	**0.8**

[a] MoH NMDS data for hospital admissions (ICD-10 code A32). The total may include cases admitted on more than one occasion (readmissions)

[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.

There was one listeriosis outbreak which started in December 2021 but was reported in 2022. This outbreak had two confirmed cases and one associated perinatal death.

Table 34 contains details of the listeriosis outbreak reported in 2022 which was initially identified through occurrence of a rare listeria strain (Serotype O1/2, ST204) from cases' clinical samples. Investigation of the outbreak identified paneer cheese as a possible source of the outbreak. *Listeria* was subsequently detected in batches of the product, and a consumer recall was initiated (https://www.mpi.govt.nz/news/media-releases/gopals-paneer-cheese-recalled/).

Table 34. Details of listeriosis outbreak reported in EpiSurv, 2022

PHU	Report Month	Suspected source	Evidence	Setting	No. Ill
Auckland PHS and Toi Te Ora	January[a]	Paneer cheese	WGS showed close association between case isolates with product samples	Home consumption of supermarket bought product	2C

PHU: Public health unit, **PHS**: Public Health Service, Toi Te Ora: Toi Te Ora - Public Health, **WGS**: Whole genome sequencing

Number ill: C: confirmed.

[a] First case was identified in December 2021, but the outbreak was reported in January 2022.

Since 2006 there have been three other listeriosis outbreaks reported. There was an outbreak with two associated cases in 2009, an outbreak with food reported as the mode of transmission with six associated cases in 2012 and an outbreak associated with ready-to-eat meats with four associated cases in 2021. 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 40 human isolates of *L. monocytogenes* during 2022. Table 35 shows the number of isolates and percentage of *L. monocytogenes* serotypes reported by the Special Bacteriology Laboratory at ESR between 2018 and 2022. The annual number of isolates identified to be serotype O4 or serotype O1/2 has been in the range of 15 to 23 isolates and 11 to 16 isolates, respectively, over the 5-year period. The most common sequence types since 2018 were ST1 (50 cases in total) and ST4 (21 cases in total).

Table 35. *L. monocytogenes* serotypes and sequence types identified by the Special Bacteriology Laboratory, 2018–2022

Serotype / Sequence type (ST)	2018	2019	2020	2021	2022
Serotype O1/2	**11**	**15**	**13**	**11**	**16**
1	1	1	4	1	1
ST120	2	2	1	1	1
ST9	1	2	1	2	0
ST155	1	2	1	2	0
ST14	3	1	0	0	0
ST224	0	1	2	0	1
ST324	0	0	0	0	4
ST59	0	2	0	1	1
ST91	0	0	0	0	3
ST424	1	1	0	0	1
ST451	0	0	0	1	2
ST26	0	0	1	0	1
ST204	0	0	0	1	1
Other ST	2	3	3	2	0
Serotype O4	**20**	**15**	**18**	**21**	**23**
ST1	7	6	10	11	16
ST4	6	3	5	4	3
ST2	2	3	1	3	1
ST455	2	1	2	2	1
ST220	2	1	0	0	0
Other ST	1	1	0	1	2
Non-serotypable	**1**	**0**	**0**	**0**	**1**
Total	**32**	**30**	**31**	**32**	**40**

Recent surveys

Nil.

Relevant New Zealand studies and publications

Reports

Product testing for Listeria monocytogenes – Rivas and Horn 2022

Large products such as whole ready-to-eat (RTE) hams are often produced in small batches and have a high value for the processor [28]. Current test methods for *Listeria* involve obtaining a representative 25 g sample from five products per batch, and by its nature is destructive, resulting in a downgraded product, if it is even available for sale after sampling has occurred. Further, sending five whole RTE hams is not only cost prohibitive for the processor but also causes handling, storage, and disposal issues for the testing laboratories. This project evaluated the use of non-invasive and non-destructive and destructive sampling methods for the detection of the presence of *L.*

monocytogenes on large, whole RTE hams. A literature review of non-invasive sampling methods was undertaken, and this was followed by experimentation to assess the suitability of these methods to recover *L. monocytogenes* from ham portions. The second part of the project was to evaluate selected *L. monocytogenes* enumeration methods for recovery from three RTE products: baby leaf spinach, cold smoked salmon and hot smoked mussels.

Three different *Listeria* enumeration methods were examined: two plate-based methods – an International Standards Organisation (ISO) and a Health Canada method; and traditional 3- and 5-tube Most Probable Number (MPN) method. Method evaluation was performed using spiked baby spinach leaves, smoked salmon and hot smoked mussels. Data showed that both plate-based methods performed as well as each other with less intra-assay variation compared to the MPN methods. At the lower inoculum level range of 40 to 100 CFU/g *Listeria* there was more variability in the data; further work would need to be undertaken to assess this variability. No change to current enumeration methods was recommended.

Relevant regulatory developments

Nil.

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 2022 by data source

During 2022, 19 individual cases of norovirus infection were reported in EpiSurv of which nine were reported as also associated with outbreaks. 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 MoH NMDS database. Of the 374 hospital admissions (7.3 admissions per 100,000 population) recorded in 2022, 235 cases were reported with norovirus infection as the primary diagnosis and 139 were reported with norovirus infection as another relevant diagnosis. Of the 374 hospital admissions, 112 were in the 0 to 4 years age group and 63 were in the 70+ years age group.

It should be noted that EpiSurv and the MoH 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 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 2022, there were 127 notified outbreaks of norovirus infection recorded in EpiSurv, five (4%) of which reported food or a food handler as one of the possible modes of transmission (Table 36). There were no hospitalisations 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 36. Norovirus infection outbreaks reported in EpiSurv, 2022

	Possible foodborne transmission with a suspected or confirmed source	Possible foodborne transmission but no suspected source	Total norovirus infection outbreaks
Outbreaks	2	3	127
Outbreak-associated cases	11	12	2670[a]
Hospitalised cases	0	0	67

[a] One outbreak's records did not record number of cases

Table 37 contains details of the five norovirus infection outbreaks with food reported as a possible mode of transmission in 2022 and two clusters of cases investigated by NZFS Food Compliance Services (June Community and Public Health PHU and August Auckland PHU). The evidence for foodborne transmission was weak for all seven outbreaks. In the April outbreak, of the five people who ate a meal together, four cases ate the salad, while the fifth person did not. Similarly, in the October outbreak a group of 12 people ate a meal together and the seven people who ate the oysters became ill. Further investigation of these outbreaks was unable to conclude the cause of illness.

Table 37. Details of norovirus infection outbreaks in EpiSurv and/or investigated by NZFS Food Compliance Services with food or food handling reported as a possible mode of transmission, 2022

PHU	Month	Suspected source	Evidence	Setting	No. Ill	Norovirus genotype
Auckland	April	Salad	Common meal	Restaurant/café/bakery	2C 2P	GII.6[P7]
PH South	May	Unknown	Common location	Restaurant/café/bakery	3P	Not typed
Auckland	June	Unknown	Common location	Childcare centre	2C	GII.6[P7]
C and PH	June	Salad/ coleslaw	Common event	Restaurant/café/bakery	1C 10P	GII.4 Sydney[P31]
Auckland	August	Unknown	Common event but no common food apart from a fruit punch	Restaurant/café/bakery	2C 4P	GII.4 Sydney[P16]
Auckland	October	Oysters	Common meal	Restaurant/café/bakery	1C 6P	Not typed
Auckland	October	Unknown	Three separate groups eating at common location	Restaurant/café/bakery	3C 4P	GII.3[P12]

PHU: Public health unit, Auckland: Auckland Regional Public Health Service, C and PH: Community and Public Health, PH South: Public Health South

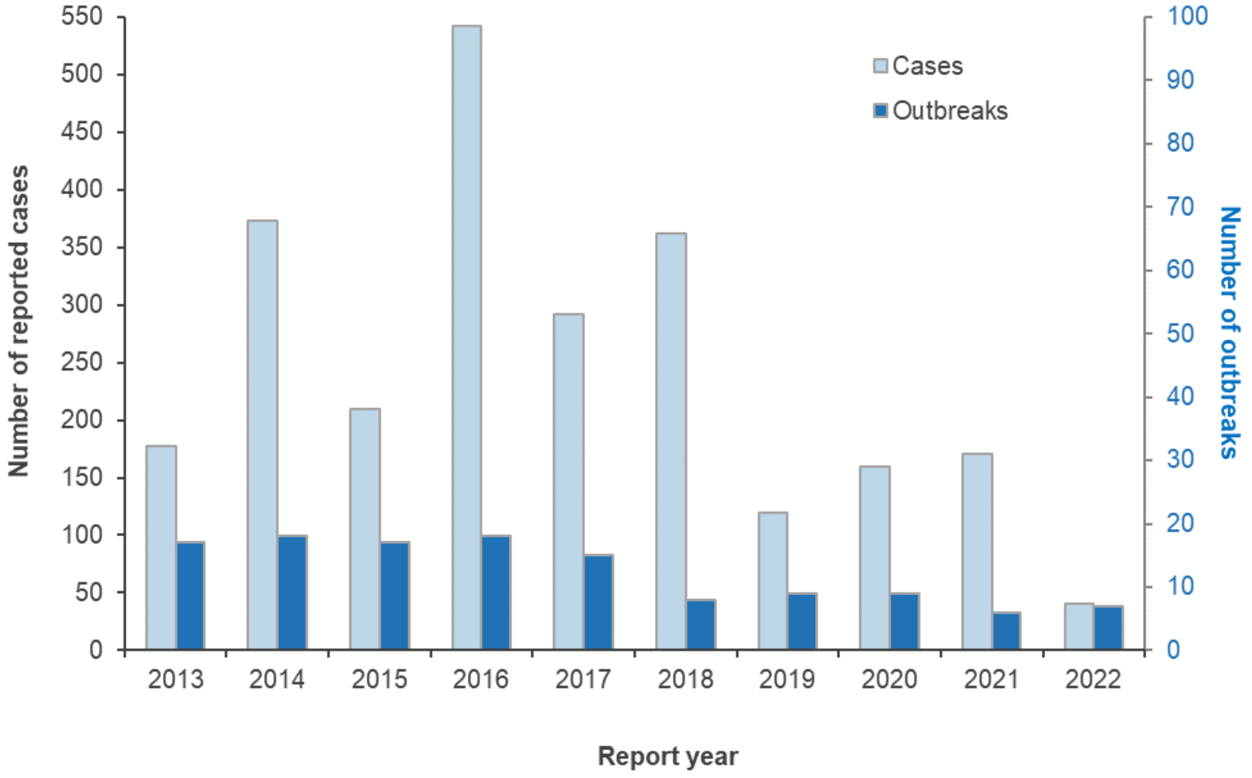
Number ill: C: confirmed, P: probable

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 five outbreaks (Table 37) were received for norovirus testing. Norovirus was detected in faecal samples from all of those outbreaks. The outbreaks were due to four genotypes, GII.3[P12], GII.4 Sydney[P16], GII.4 Sydney[P31] and GII.6[P7]. No samples were received from two other suspected foodborne illness outbreaks.

Over the 10-year period 2013 to 2022, 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 ranged from 40

(2022) to 542 cases (2016) each year. The number of cases associated with norovirus outbreaks which were recorded as potentially foodborne was much smaller in 2022 than in previous years.

Figure 27. Norovirus infection outbreaks reported in EpiSurv with food reported as a possible mode of transmission and associated cases reported by year, 2013–2022



Note: The figure includes investigations of clusters of potentially foodborne disease by NZFS Food Compliance Services that where not recorded as a potentially foodborne outbreak in EpiSurv (2022: two outbreaks, 17 cases).

Norovirus types commonly reported

Norovirus genotyping data from the NRL are shown in Table 38. 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 2022, 138 norovirus outbreaks were ESR laboratory-confirmed. Norovirus genogroup II (GII) was identified in 126/138 (91.3%) outbreaks. In the previous four years (2018-2021), GII was also the predominant norovirus genogroup being identified in between 77.3% (2021) and 90.8% (2018) of outbreaks.

The norovirus genotype was determined for 133/138 (96.4%) of ESR laboratory-confirmed norovirus outbreaks. GII.6[P7] was the most common (54/138, 40.6% of outbreaks) genotype identified.

Table 38. Norovirus genotypes identified in outbreaks by the Norovirus Reference Laboratory, 2018–2022

Norovirus genotypes[a]	2018	2019	2020	2021	2022
Genogroup I	**15**	**32**	**33**	**22**	**10**
GI untyped	-	1	2	2	-
GI.1[P1]	1	-	-	-	-
GI.2[P2]	1	1	-	-	5
GI.3[P3]	4	9	5	-	-
GI.3[P13]	2	4	8	14	2
GI.4[P4]	3	5	-	-	1
GI.5[P4]	2	5	14	1	-
GI.5[P5]	-	1	-	-	2
GI.5[P12]	-	-	1	-	-
GI.6[P6]	1	4	-	-	-
GI.6[P11]	-	1	3	5	-
GI.7[P7]	-	-	-	-	-
GI.8[P8]	-	-	-	-	-
GI.9[P9]	1	1	-	-	-
Genogroup II	**158**	**147**	**125**	**75**	**126**
GII.2[P16]	38	17	93	35	5
GII.3[P12]	8	20	5	-	11
GII.4 Sydney[P16][b]	70	49	6	-	18
GII.4 Sydney[P31][b]	3	21	-	34	28
GII.4 Sydney[P4 New Orleans][b]	2	13	1	-	-
GII.6[P7]	10	13	3	2	54
GII.9[P7]	-	2	-	-	-
GII.10[P16]	-	3	-	-	-
GII.14[P7]	7	2	1	-	-
GII.17[P17]	4	1	6	2	2
Other[c]	16	6	10	2	8
Mixed GI and GII	**1**	**3**	**2**	**-**	**1**
Genogroup GIX[d]	**-**	**-**	**1**	**-**	**1**
Total outbreaks[e]	**174**	**182**	**161**	**97**	**138**

[a] Classification of norovirus changed in 2019, previous year's genotypes have been re-classified accordingly.

[b] GII.4 variants.

[c] 'Other' includes GII untyped, GII.1[P16], GII.2[P2], GII.3[P3], GII.3[P13], GII.3[P16], GII.3[P21], GII.7[P7], GII.8[P8], GII12[P16], GII.13[P16], GII.13[P21].

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

[e] 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

Nil.

Salmonellosis

Summary data for salmonellosis in 2021 are given in Table 39. 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 39. Summary of surveillance data for salmonellosis, 2022

Parameter	Value in 2022	Source
Number of notified cases	750	EpiSurv
Notification rate (per 100,000)	14.6	EpiSurv
Hospitalisations[a]	212	MoH NMDS
Deaths	0	EpiSurv
Travel-related cases[b, c]	120	EpiSurv
Estimated domestically acquired food-related cases (%)[d]	371 (62%)	Expert consultation

NMDS = MoH 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. 476 cases had not travelled overseas during the incubation period and for the remaining 154 cases travel history is unknown.

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

[d] For estimation of food-related cases the proportions derived from expert consultation [2] exclude travel-related cases (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).

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.

Changes to laboratory methods

Since 2015, laboratories across New Zealand have changed the methodology for testing faecal specimens (Appendix B, page 120). In 2022, all community faecal specimens in all DHBs except for Canterbury, South Canterbury, and West Coast were screened by multiplex PCR for a range of pathogens, including *Salmonella* spp. Following the introduction of PCR methods there was no sustained increase in notification rates for salmonellosis [17].

Salmonellosis individual cases reported in 2022 by data source

During 2022, 750 individual cases (14.6 per 100,000 population) of salmonellosis and no resulting deaths were reported in EpiSurv. Of the 750 cases, the symptoms of 729 cases (97%) were reported as fitting the clinical description for salmonellosis, the symptoms were unknown for 19 cases, and for two cases the symptoms were reported as not fitting the clinical description.

The ICD-10 code A02.0 (*Salmonella* enteritis) was used to extract salmonellosis hospitalisation data from the MoH NMDS database. Of the 212 hospital admissions (4.1 admissions per 100,000 population) recorded in 2022, 173 cases were reported with salmonellosis as the primary diagnosis and 39 were reported with salmonellosis as another relevant diagnosis.

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

Foodborne transmission

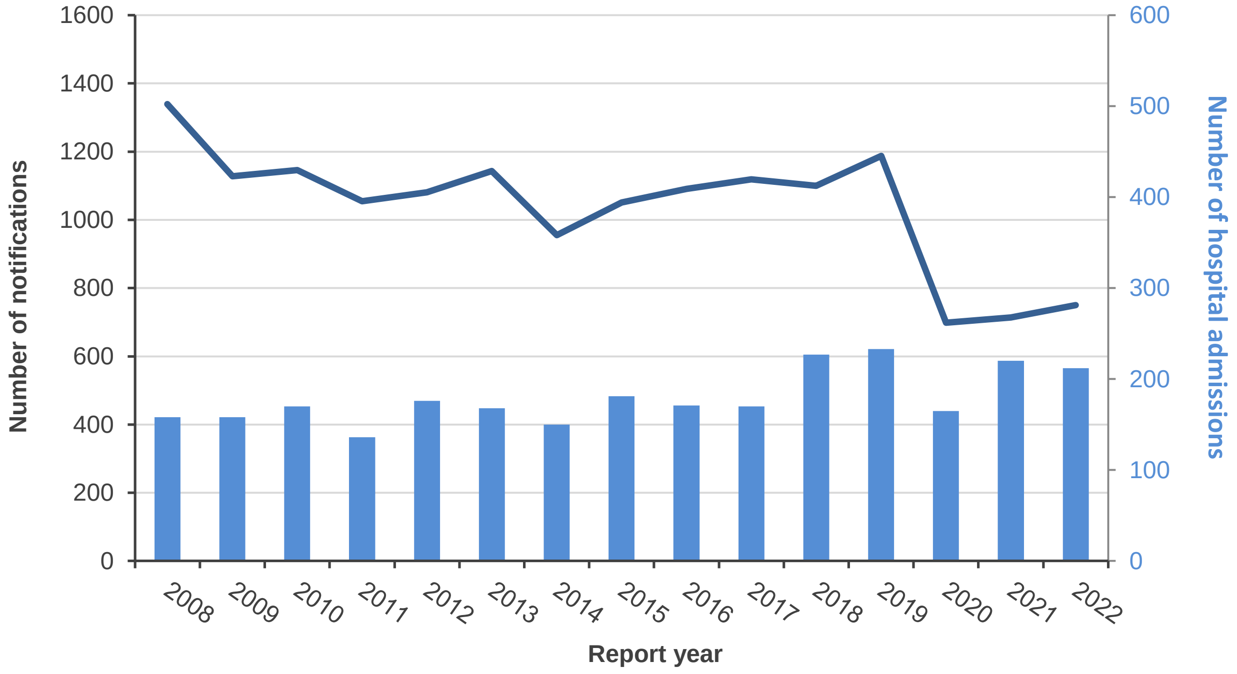
It has been estimated by expert consultation that 62.1% (95th percentile credible interval: 35.2% to 86.4%) of salmonellosis incidence is due to foodborne transmission. It was further estimated that approximately 19% of foodborne salmonellosis was due to transmission via poultry [2].

Annual data

Between 2008 and 2019 the number of salmonellosis notifications per year ranged between 955 (2014) and 1339 (2008) (Figure 28), with associated notification rates between 21.1 and 31.3 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 [19] and the reduction in overseas travel (see Introduction, page 5). In 2022, there were 120 salmonellosis notifications in EpiSurv listing overseas travel as a risk factor, compared to 349 in the pre-COVID-19 year 2019, 49 in 2020 and none in 2021.

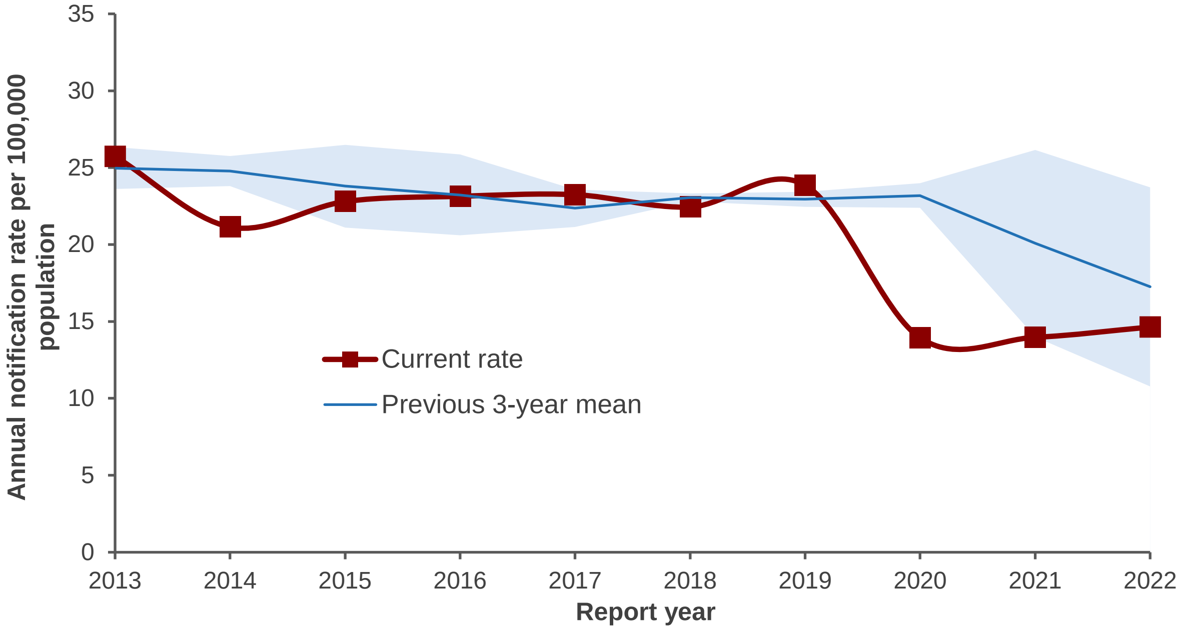
The number of hospital admissions with salmonellosis as a primary or secondary diagnosis varied slightly year by year but did not show the same pronounced reduction in the years 2020 to 2022 as the number of annual notifications.

Figure 28. Salmonellosis EpiSurv notifications (line) and NMDS hospitalisations (bar) by year, 2008–2022



The notification rate in 2022 (14.6 cases per 100,000 population) was lower than the previous three-year average (17.3 cases per 100,000 population) (Figure 29) and similar to the years 2020 and 2021.

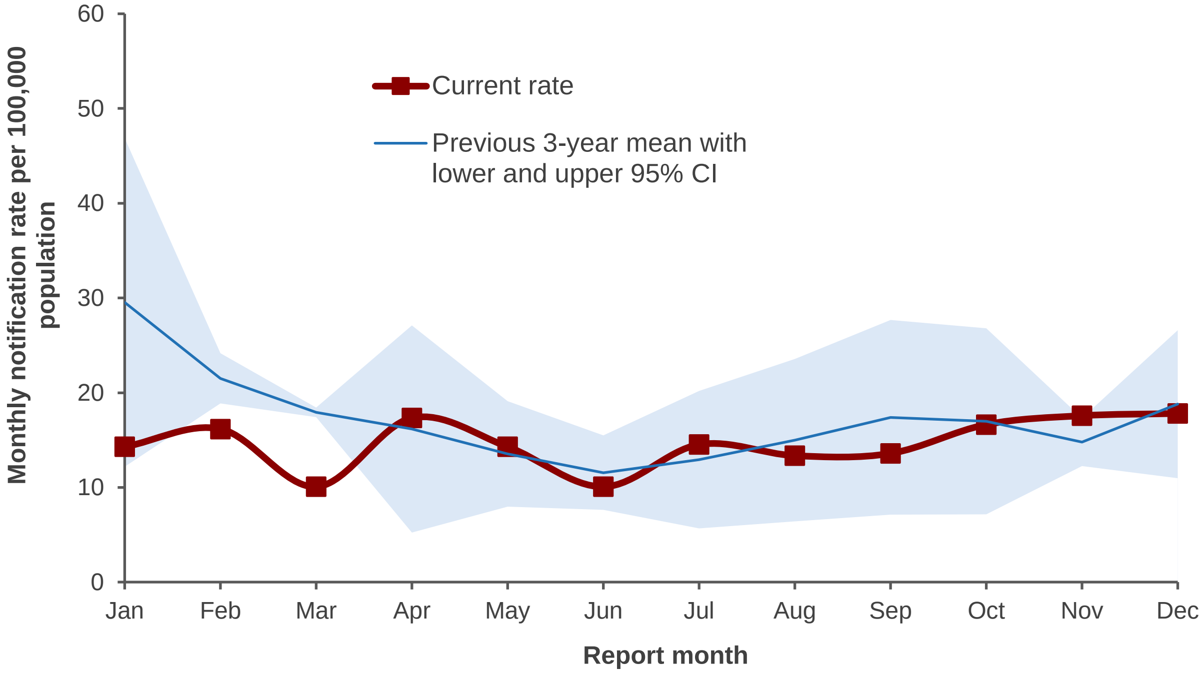
Figure 29. Salmonellosis notification rate by year, 2013–2022



Seasonal data

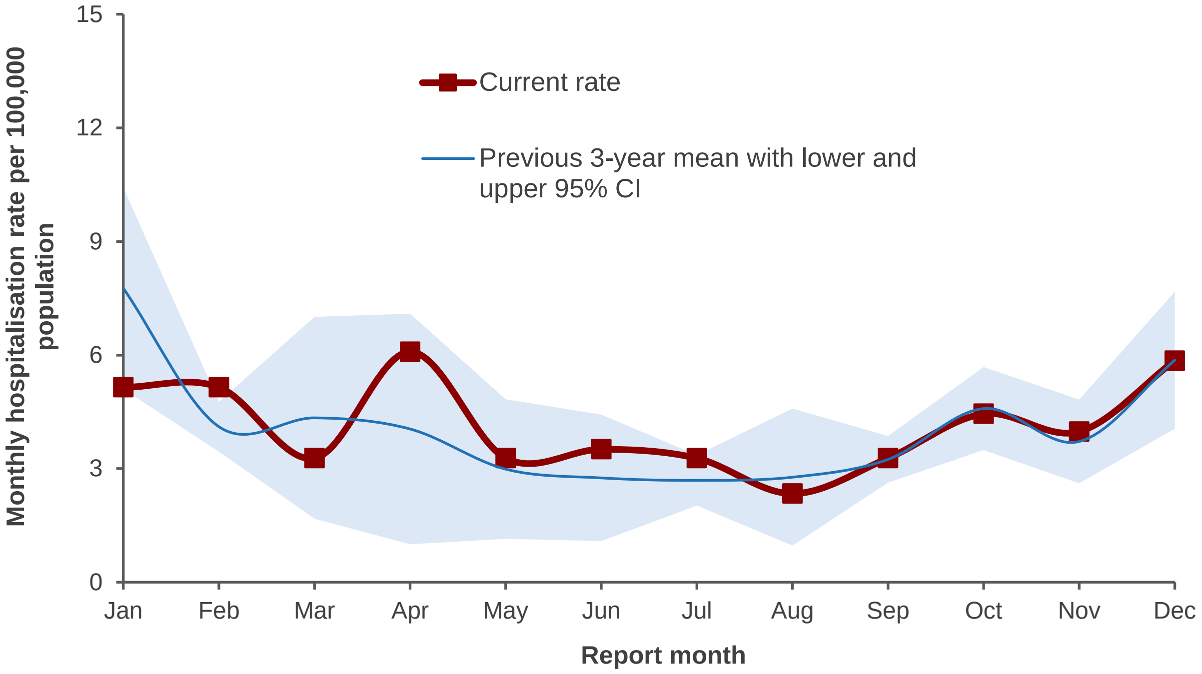
Salmonellosis notification rates per 100,000 population by month for 2022 are shown in Figure 30. In 2022, the monthly notification rates were similar to the mean of the previous three years with lower rates reported from January to March. The monthly number of notifications in 2022 ranged from 43 notifications (March and June, 10 per 100,000 population) to 76 notifications (December, 18 per 100,000 population).

Figure 30. Salmonellosis monthly notification rate (annualised), 2022



In 2022, the monthly hospitalisation rates varied slightly over the year and followed a similar pattern as the previous 3-year mean (Figure 31). The exception was the month of April which was higher (six admissions per 100,000 population, 26 hospitalised cases) compared to the previous 3-year mean (four admissions per 100,000 population) but still within the upper 95% convidence inerval and at a similar level to April 2019 (six admissions per 100,000 population, 27 hospitalsed cases). The lowest hospitalisation rate was for August 2022 (two admissions per 100,000 population, 10 hospitalised cases).

Figure 31. Salmonellosis monthly hospitalisation rate (annualised), 2022



Demographics

In 2022, the notification rate for females was higher (15.4 cases per 100,000 population, 397 cases) than for males (13.8 cases per 100,000 population, 352 cases). The rate of hospital admissions was also slightly higher for females (4.3 admissions per 100,000 population, 112 hospitalisations) compared to males (3.9 admissions per 100,000 population, 100 hospitalisations) (Table 40).

Table 40. Salmonellosis cases by sex, 2022

Sex	EpiSurv notifications		Hospitalisations[a]	
	No.	Rate[b]	No.	Rate[b]
Male	352	13.8	100	3.9
Female	397	15.4	112	4.3
Total[c]	**750**	**14.6**	**212**	**4.1**

[a] MoH NMDS data for hospital admissions

[b] per 100,000 population in this sex group

[c] total includes notifications where sex is unknown

In 2022, notification and hospital admission rates of salmonellosis were highest for children in the <1 years age group (83.3 cases and 23.3 admissions per 100,000 population) (Table 41).

Table 41. Salmonellosis cases by age group, 2022

Age group (years)	EpiSurv notifications		Hospitalisations[a]	
	No.	Rate[b]	No.	Rate[b]
< 1	50	83.3	14	23.3
1 to 4	105	43.2	28	11.5
5 to 9	56	17.4	14	4.3
10 to 14	21	6.2	4	-
15 to 19	42	13.3	7	2.2
20 to 29	82	12.1	16	2.4
30 to 39	78	10.6	25	3.4
40 to 49	61	9.7	20	3.2
50 to 59	85	13.0	24	3.7
60 to 69	89	15.8	30	5.3
70+	81	13.9	30	5.2
Total	**750**	**14.6**	**212**	**4.1**

[a] MoH NMDS data for hospital admissions

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

Geographic distribution

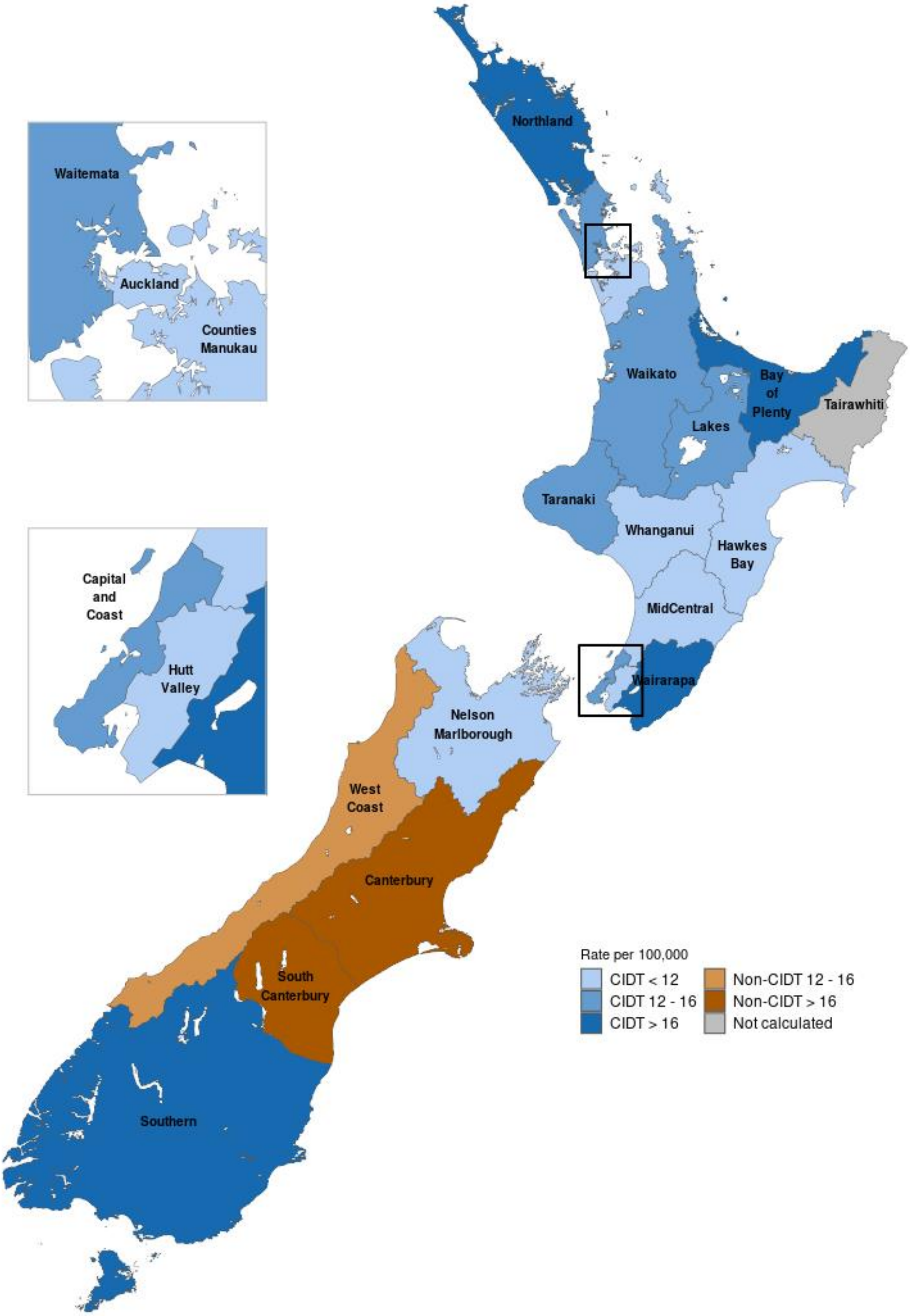
The notification rates by DHB calculated per 100,000 resident population are presented in Figure 32 (see also Table 86). Blue shading is used for DHBs which are using CIDT community testing, the brown shading is used for DHBs using culture-based community testing. The rate has not been calculated for DHBs with less than five cases (grey shading): Tairawhiti DHB (four cases).

In 2022, the DHB notification rates of salmonellosis ranged from 9 per 100,000 population in Whanganui DHB (six cases) and Hutt Valley DHB (14 cases) to 27 per 100,000 population (17 cases) in South Canterbury DHB. The South Canterbury, Wairarapa (26 per 100,000 population, 13 cases), Southern (22 per 100,000 population, 77 cases) and Canterbury (21 per 100,000 population, 121 cases) DHBs had the highest notification rates.

Historically, notification rates for salmonellosis have been highest in the lower half of the South Island. South Canterbury and Southern DHBs have rates in the highest quartile of notification rates since 2019. Canterbury DHB has been in the highest quartile of notification rates since 2020 and the West Coast DHB in 2018, 2019 and 2021.

Salmonellosis notification rates stratified by 2023 Urban Rural Classification [22] of the cases' residential address were lower for urban area categories compared to rural categories (Appendix C Table 87). Rates for urban categories ranged from 8 to 14 per 100,000 population, while rates for rural categories were 20 per 100,000 for 'rural settlement' areas and 23 per 100,000 for 'rural other' areas.

Figure 32. Geographic distribution of salmonellosis notifications, 2022



Outbreaks reported as caused by *Salmonella*

In 2022, there were five salmonellosis notified outbreaks in EpiSurv, three of which reported food as a possible mode of transmission (Table 42). One of these three outbreaks was related to overseas travel to Fiji. The two remaining outbreaks included 13 cases, of which eight cases were reported to have been hospitalised (four cases per outbreak).

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 42. Salmonellosis outbreaks reported in EpiSurv, 2022

	Possible foodborne transmission with a suspected or confirmed source	Possible foodborne transmission but no suspected source	Total salmonellosis outbreaks
Outbreaks	2	1	5
Outbreak-associated cases	13	25	44
Hospitalised cases	8	8	16

Table 43 contains details of the three salmonellosis outbreaks with food reported as a possible mode of transmission reported in EpiSurv in 2022. In addition to the outbreaks recorded in EpiSurv at the cut-off date for this report (1 May 2023), NZFS investigated two further clusters of salmonellosis cases (Table 43, March and April outbreaks).

The July-August outbreak was associated with imported seasame-based products bought or eaten in the Regional Public Health region. Sequencing of clinical isolates showed cases were the same sequence type and closely genomically related to an earlier European outbreak linked to seasame-based products from Syria. This outbreak resulted in a recall of specific batches of tahini and halvah products (https://www.mpi.govt.nz/food-safety-home/food-recalls-and-complaints/recalled-food-products/algota-brand-sesame-tahini/, accessed 10 July 2023).

Testing of associated products identified the presence of *S*. Kintambo, *S*. Amsterdam and *S.* Orion. One of the July-August outbreak seven cases was likely to be due to person to person contact.

The evidence linking an outbreak to a common suspected food source was weak for the other four outbreaks listed in Table 43.

Table 43. Details of salmonellosis outbreaks reported in EpiSurv and/or investigated by NZFS Food Compliance Services with food reported as a possible mode of transmission, 2022

PHU	Report Month	Suspected source	Evidence	Setting	No. Ill	Serotype[a]
Nelson Marlborough PHS	March	Chicken dishes	Common meal	Food service establishment	1C 1P	*S.* Infantis
ARPHS	April	Nachos (refried beans)	Common meal	Cafe	1C 2P	*S.* Enteritidis
Regional PH	July-August	Imported seasame-based products	Common source and matched typing between clinical and food samples	Home	7C	*S.* Kintambo
Toi Te Ora	Sept	Chickpea Curry on rice with yoghurt	Common meal	Institution	6C	*S.* Typhimurium
Multi PHU	October	Airport or aircraft food (Fiji)	Common meals	Overseas	25C	*S.* Typhimurium

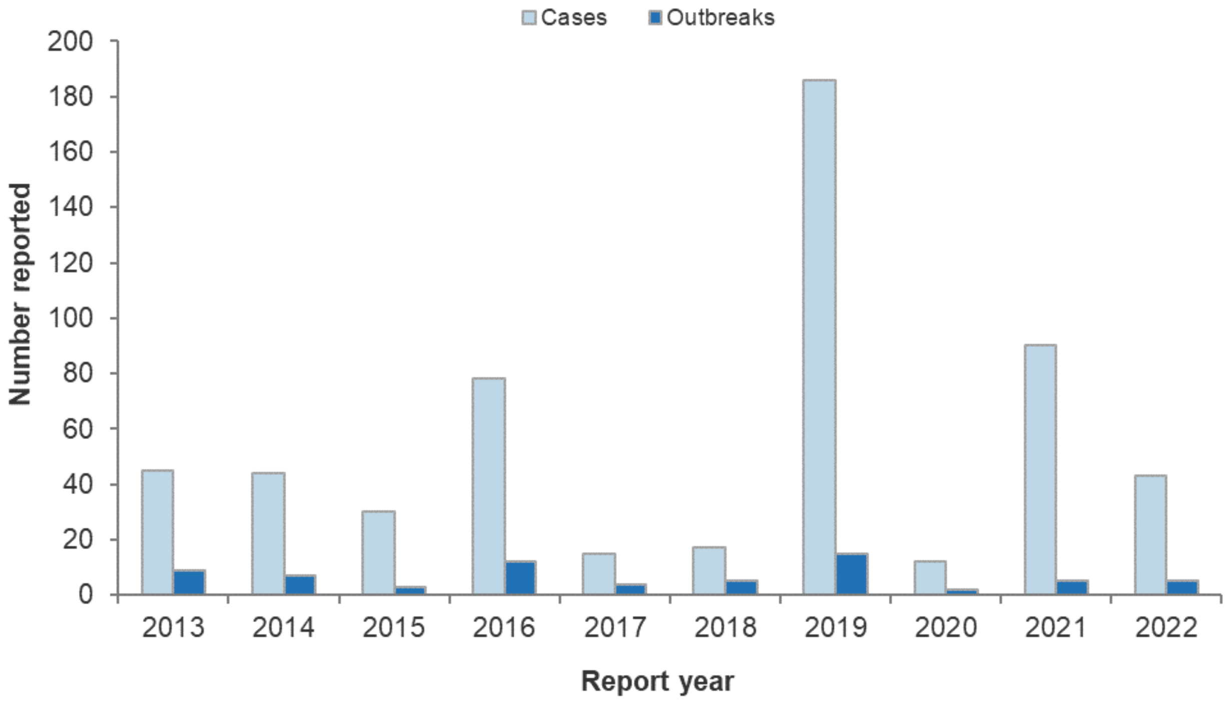
PHU: Public health unit, Regiona PH: Regional Public Health, Toi Te Ora: Toi Te Ora - Public Health, Nelson Marlborough PHS: Nelson Marlborough Public Health Service, ARPHS: Auckland Regional Public Health Seervice

Number ill: C: confirmed, P: probable

[a] Serotypes were identified in clinical samples from outbreak cases

Over the 10-year period 2012 to 2021, 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 total number of cases associated with the outbreaks over the same period ranged between 12 (2020) and 186 (2019).

Figure 33. Salmonellosis outbreaks reported in EpiSurv with food reported as a possible mode of transmission and associated cases reported by year, 2013–2022



Note: The 2022 outbreak information includes three outbreaks reported in EpiSurv plus two further outbreaks from NZFS Food Compliance Services records that were not recorded in EpiSurv as outbreaks at the cut off date for this report (five cases) (1 May 2023).

Salmonella types commonly reported

Human isolates

In 2022, isolates from 654 notified cases with non-typhoidal *Salmonella* infections were typed by the ESR Enteric Reference Laboratory (Table 44). *S.* Typhimurium (325 cases) and *S.* Enteritidis (69 cases) were the most common serotypes identified. Other serotypes commonly reported were *S.* Bovismorbificans (42 cases), *S.* Saintpaul (21 cases), *S*. Brandenburg (19 cases) and *S.* Stanley (18 cases).

Table 44. Annual number of notifications with different *Salmonella* serotypes identified by the Enteric Reference Laboratory, 2018–2022

Serotype[a]	2018	2019[b]	2020	2021	2022	% of cases with overseas travel history, 2022[b]	% of cases with unknown travel history, 2022[c]
S. Typhimurium[d]	332	440	312	291	325	11	20
Monophasic *S.* Typhimurium[d]	28	42	18	21	11	9	27
S. Enteritidis[d]	130	153	70	131	69[e]	17	16
S. Bovismorbificans	81	47	60	50	42	0	26
S. Saintpaul	37	22	26	30	21	5	62
S. Brandenburg	42	37	36	39	19	0	16
S. Stanley	34	41	11	9	18	50	22
S. Mississippi	16	15	17	7	14	21	21
S. Thompson	9	11	11	10	12	0	0
S. Agona	26	13	4	4	9	11	22
S. Give	2	1	5	2	9	0	33
S. Virchow	7	7	3	0	9	78	0
S. Javiana	5	5	2	1	8	63	13
S. Kintambo	0	0	0	0	7	0	0
S. Pensacola	9	6	1	8	6	17	33
S. Sandiego	1	2	0	0	6	50	33
S. Weltevreden	22	19	11	3	6	33	17
S. Bareilly	8	5	1	1	5	20	20
S. Infantis	15	27	7	9	5	0	20
S. Paratyphi B var. Java	30	26	9	3	5	20	0
S. Oranienburg	3	1	2	0	4	50	50
S. Hvittingfoss	5	5	1	6	2	50	50
S. Newport	9	10	3	1	2	50	0
Other[f]	186	161	49	39	42	43	19
Unknown[g]	89	113	63	54	96	16	18
Total Cases	1100	1188	709	714	750[h]		

[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 four or more associated cases in 2022 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 [29], 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] Some notified cases were still being linked to the 2021 outbreak via whole genome sequencing in 2022 (i.e., cases were infected by the outbreak strain *S.* Enteritidis ST11) but not necessarily to a common source.

[f] Serotypes where able to be determined, but there were three or less associated notified cases in 2022.

[g] Isolates unable to be typed by the Enteric Reference Laboratory.

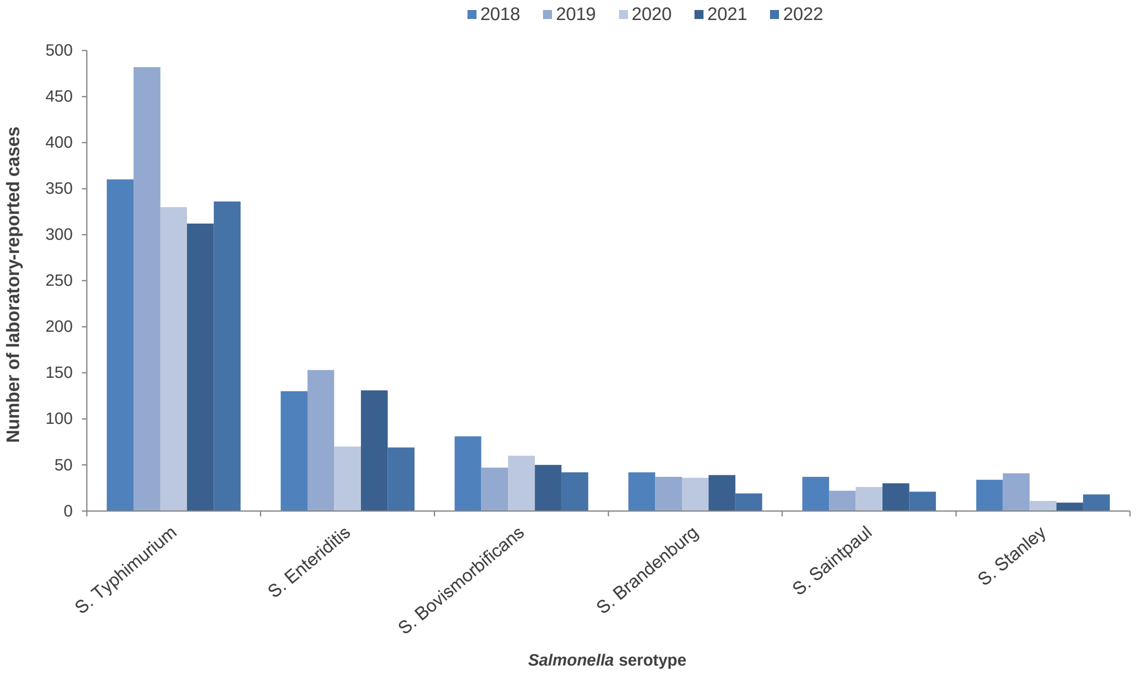
[h] Two cases in 2022 had a mixed infection, i.e., an individual case was represented by two *Salmonella* serotypes

EpiSurv records for 2022 indicate that 63% of cases infected with *S*. Brandenburg were hospitalised. *S*. Typhimurium, *S.* Enteritidis and *S.* Bovismorbificans records indicate between 29% and 34% of cases were hospitalised with hospitalisation status reported for most (99-100%) of cases infected with these serotypes. In contrast, hospitalisation rates for cases infected with *S*. Stanley and *S*. Saintpaul were lower (22% and 14%, respectively, with hospitalisation status reported for ~95% of cases infected with these serotypes).

Figure 34 shows the annual trend for selected *Salmonella* serotypes from 2018 to 2022. For the types shown, there is within-type variation year to year. *S*. Typhimurium was the most prevalent serotype isolated from notified cases in the years shown. The high number of cases of *S*. Typhimurium in 2019 compared to 2018 and 2020 to 2022, is due to a large number of outbreak cases reported in 2019.

There was a drop in *S*. Enteritidis cases in 2020 and 2022 compared to 2018, 2019 and 2021. The drop in *S*. Enteritidis cases in 2020 may be due to COVID-19 overseas travel restrictions. In 2019 overseas travel was a risk factor in 38% of *S*. Enteritidis cases compared to 10% of *S*. Typhimurium cases. While the travel restrictions continued in 2021, there were two *S*. Enteritidis outbreaks (74 cases) in 2021 accounting for the increase in *S*. Enteritidis cases compared to 2020. There were no *S*. Enteritidis cases in 2022 which recorded overseas travel.

Figure 34. Number of laboratory-reported case related isolates for selected *Salmonella* serotypes by year, 2018–2022



Non-human isolates

A total of 785 non-human *Salmonella* isolates were serotyped by the Enteric Reference Laboratory during 2022. *S.* Typhimurium (248 isolates) was the most common serotype in non-human samples in 2022. The next most common serotypes were *S*. Give (102 isolates), *S.* Enteritidis (101 isolates) and *S*. Bovismorbificans (100 isolates) (Table 45). In 2021, 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 is 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 45. *Salmonella* serotypes from non-human sources recorded by the Enteric Reference Laboratory, 2018–2022

Serotype	2018	2019	2020	2021	2022	Major sources, 2022
***S.* Typhimurium**	**282**	**320**	**336**	**330**	**248**	Bovine (153), equine (18), feline (18), poultry miscellaneous[b] (15), poultry environmental (12), canine (10) and avian (9)
***S.* Enteritidis**	**5**	**8**	**5**	**188**[a]	**101**[c]	Poultry environmental[b] (62) and poultry miscellaneous (35)
Other serotypes	**561**	**598**	**492**	**497**	**436**	-
S. Agona	18	9	9	7	30	Canine (15), bovine (6), poultry miscellaneous[b] (5)
S. Bovismorbificans	297	309	247	127	100	Bovine (70), canine (10), feline (6) and ovine (6)
S. Brandenburg	106	133	91	89	23	Bovine (12)
S. Give	0	12	78	88	102	Bovine (50), poultry miscellaneous[b] (29) and canine (15)
S. Hindmarsh	26	28	8	23	17	Ovine (15)
S. Infantis	8	3	3	17	14	Poultry environmental (11)
S. Livingston	1	0	0	1	24	Canine (23)
S. Mbandaka	4	16	7	39	19	Poultry environmental (10), poultry miscellaneous[b] (5)
S. Saintpaul	12	14	8	9	15	Avian (6)
S. Senftenberg	8	8	2	7	19	Poultry miscellaneous[b] (8) and bovine (6)
Other or unknown serotypes	89	68	40	52	73	-
Total	**848**	**926**	**833**	**1015**	**785**	**-**

[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] Including product.

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

Recent surveys

Nil.

Relevant New Zealand studies and publications

Nil.

Relevant regulatory developments

Nil.

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 2022 by data source

During 2022, four individual cases of sapovirus infection were reported in EpiSurv. Two of the four cases also reported with norovirus infection. 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).

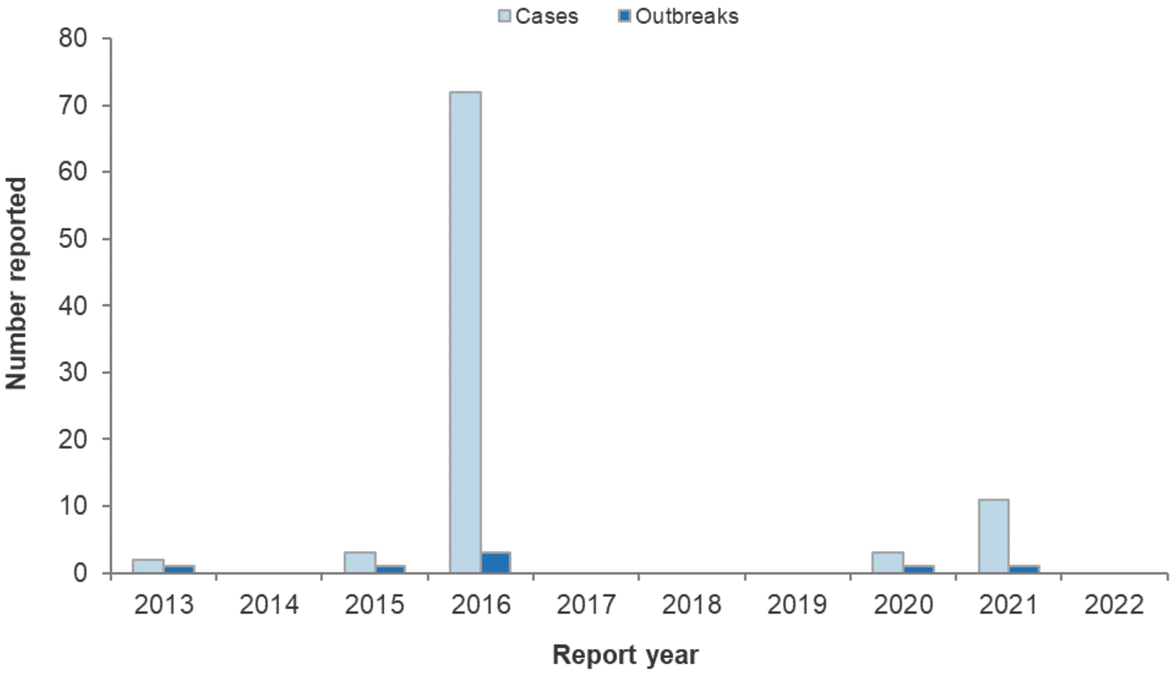
Outbreaks reported as caused by sapovirus

In 2022, ten sapovirus infection outbreaks were notified in EpiSurv. None of the outbreaks reported food as a possible mode 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.

In the last 10 years there have been four years with a single potentially foodborne sapovirus outbreak recorded, with between two and 11 cases being associated with an outbreak. In 2016, the largest number of potentially foodborne outbreak related cases were recorded, a total of 72 cases from three outbreaks (Figure 35).

Figure 35. Sapovirus infection outbreaks reported in EpiSurv with food reported as a possible mode of transmission and associated cases reported by year, 2013–2022



Recent surveys

Nil.

Relevant New Zealand studies and publications

Nil.

Relevant regulatory developments

Nil.

Shigellosis

Summary data for shigellosis in 2022 are given in Table 46.

Table 46. Summary of surveillance data for shigellosis, 2022

Parameter	Value in 2022	Source
Number of notified cases	68	EpiSurv
Notification rate (per 100,000)	1.3	EpiSurv
Hospitalisations[a]	70	MoH NMDS
Deaths	0	EpiSurv
Travel-related cases [b, c]	43	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 = MoH 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. 23 cases had not travelled overseas during the incubation period and for the remaining two cases travel history is unknown.

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

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.

Changes to laboratory methods

Since 2015, laboratories across New Zealand have changed the methodology for testing faecal specimens (Appendix B, page 120). In 2022, all community faecal specimens in all DHBs except for Canterbury, South Canterbury, and West Coast were screened by culture-independent diagnostic tests (CIDT) for a range of pathogens, including *Shigella* spp. Following the introduction of CIDT there was no sustained increase in notification rates for shigellosis [17].

Shigellosis individual cases reported in 2022 by data source

In 2022, 68 individual cases (1.3 per 100,000 population) of shigellosis and no resulting deaths were reported in EpiSurv. Of the 68 cases, the symptoms of 66 cases (97%) were reported as fitting the clinical description for shigellosis while for the two 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 MoH NMDS database. Of the 70 hospital admissions (1.4 admissions per 100,000 population) recorded in 2022, 27 were reported with shigellosis as the principal diagnosis and 43 with shigellosis as another relevant diagnosis.

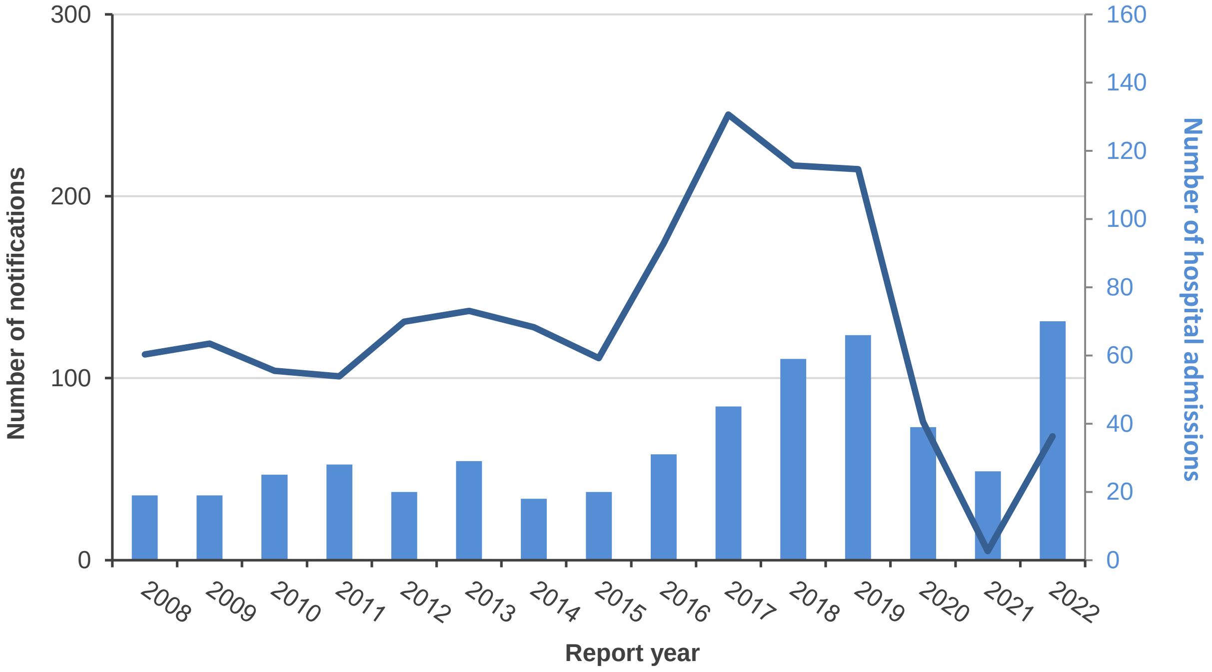
It should be noted that EpiSurv and the MoH NMDS database are separate systems and hospital admission can occur without cases being notified in EpiSurv.

Annual data

Between 2008 and 2015 the number of shigellosis notifications has been in the range of 101 to 137 cases per year. From 2016 to 2019 there was an increase in notifications and the notification rate per 100,000 population, followed by much lower numbers in the years 2020 to 2022 (ranging between five cases (2021) and 76 cases (2020)) (Figure 36 and Figure 37). The drop in notifications between 2020 and 2022 can be attributed to a decrease in the frequency of overseas travel (see Introduction, page 5). In 2022, there were 43 shigellosis notifications in EpiSurv listing overseas travel as a risk factor, compared to 82 in the pre-COVID-19 year 2019, 26 in 2020 and none in 2021.

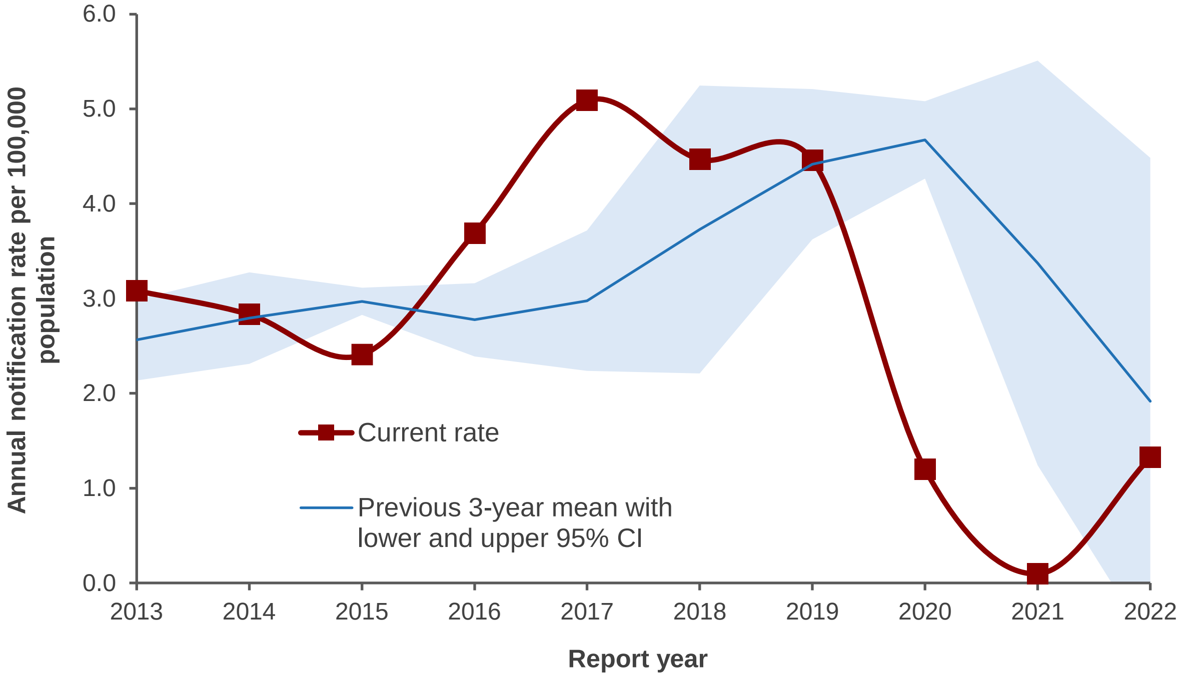
The number of hospital admissions with shigellosis as a primary or secondary diagnosis varied year by year, following a similar pattern to the number of annual notifications. The number of hospitalisations in 2022 was similar to that in 2019 (70 hospitalisations and 66 hospitalisations, respectively).

Figure 36. Shigellosis EpiSurv notifications (line) and NMDS hospitalisations (bar) by year, 2008–2022



The notification rate in 2022 (1.3 cases per 100,000 population) was lower than the previous three-year average (1.9 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.

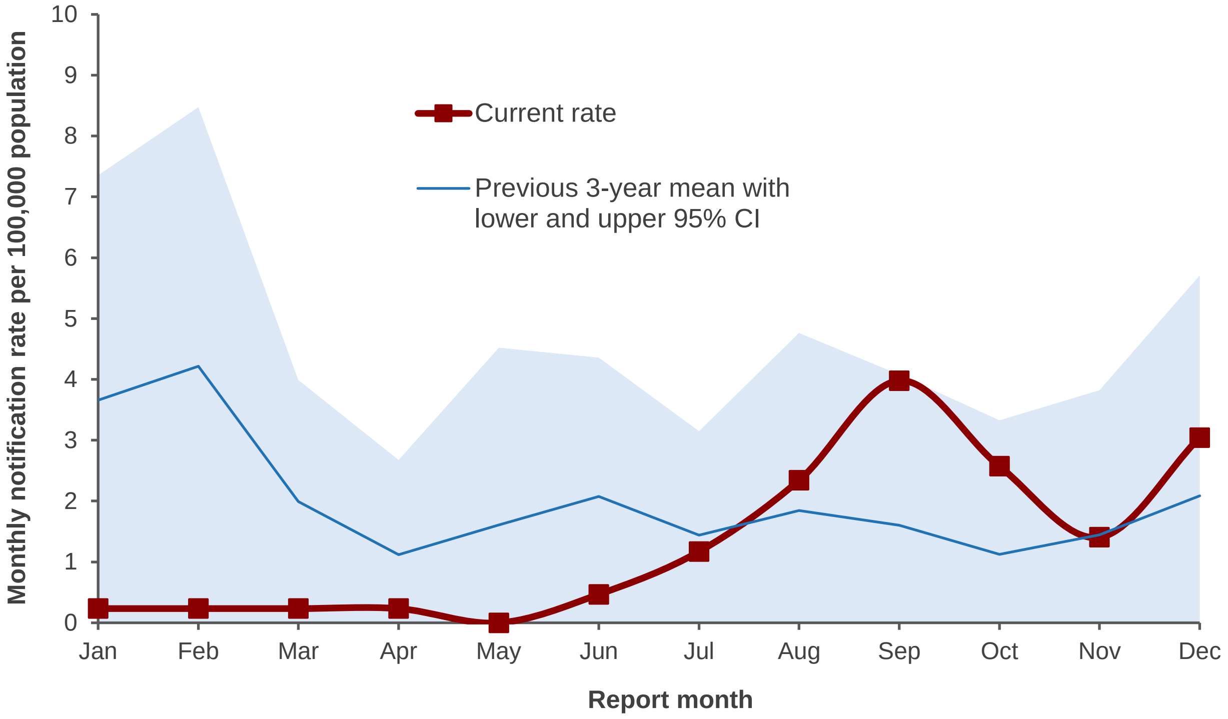
Figure 37. Shigellosis notification rate by year, 2013–2022



Seasonal data

Shigellosis notification rates per 100,000 population by month for 2022 are shown in Figure 38. The number of notifications per month for the first six months of the year was much lower than the previous three-year average (ranging between zero and two notifications per month). Increasing travel in the second half of the year has led to an increase in shigellosis notifications, ranging from five notifications (July, one per 100,000 population) to 17 notifications (September, four per 100,000 population).

Figure 38. Shigellosis monthly notification rate (annualised), 2022



Demographics

In 2022, notification and hospitalisation rates were slightly higher for males (1.7 cases and 1.7 admissions per 100,000 population) compared to females (1.0 cases and 1.0 admissions per 100,000 population) (Table 47).

Table 47. Shigellosis cases by sex, 2022

Sex	EpiSurv notifications		Hospitalisations[a]	
	No.	Rate[b]	No.	Rate[b]
Male	42	1.7	44	1.7
Female	26	1.0	26	1.0
Total	**68**	**1.3**	**70**	**1.4**

[a] MoH NMDS data for hospital admissions

[b] per 100,000 population in this sex group

In 2022, shigellosis notification rates were highest for the 1 to 4 years age group (3.3 cases per 100,000 population) (Table 48). Hospitalisations rates were highest for the 1 to 4 years and 70+ years age groups (3.3 admissions per 100,000 population).

Table 48. Shigellosis cases by age group, 2022

Age group (years)	EpiSurv notifications		Hospitalisations[a]	
	No.	Rate[b]	No.	Rate[b]
<1	0	-	3	-
1 to 4	8	3.3	8	3.3
5 to 9	3	-	3	-
10 to 14	1	-	0	-
15 to 19	1	-	3	-
20 to 29	7	1.0	8	1.2
30 to 39	11	1.5	5	0.7
40 to 49	12	1.9	8	1.3
50 to 59	11	1.7	6	0.9
60 to 69	8	1.4	7	1.2
70+	6	1.0	19	3.3
Total	**68**	**1.3**	**70**	**1.4**

[a] MoH NMDS data for hospital admissions

[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 2022, there were three shigellosis outbreaks reported in EpiSurv (Table 49). None were reported as foodborne, but one outbreak recorded dried Tuna from the Pacific Islands as a possible source of infection. The two outbreak cases were from two different households, but both consumed the fish. It is important to note that an outbreak may have multiple pathogens, modes of transmission, settings where exposure occurred, or settings where preparation of food was conducted.

Table 49. Shigellosis outbreaks reported in EpiSurv, 2022

	Possible foodborne transmission with suspected source	Total shigellosis outbreaks
Outbreaks	1	3
Outbreak-associated cases	2	26
Hospitalised cases	0	0

Table 50 contains details of the shigellosis outbreak with dried tuna reported as a possible mode of transmission. No food sample was available for testing.

Table 50. Details of shigellosis outbreak reported in EpiSurv with food reported as a possible mode of transmission, 2022

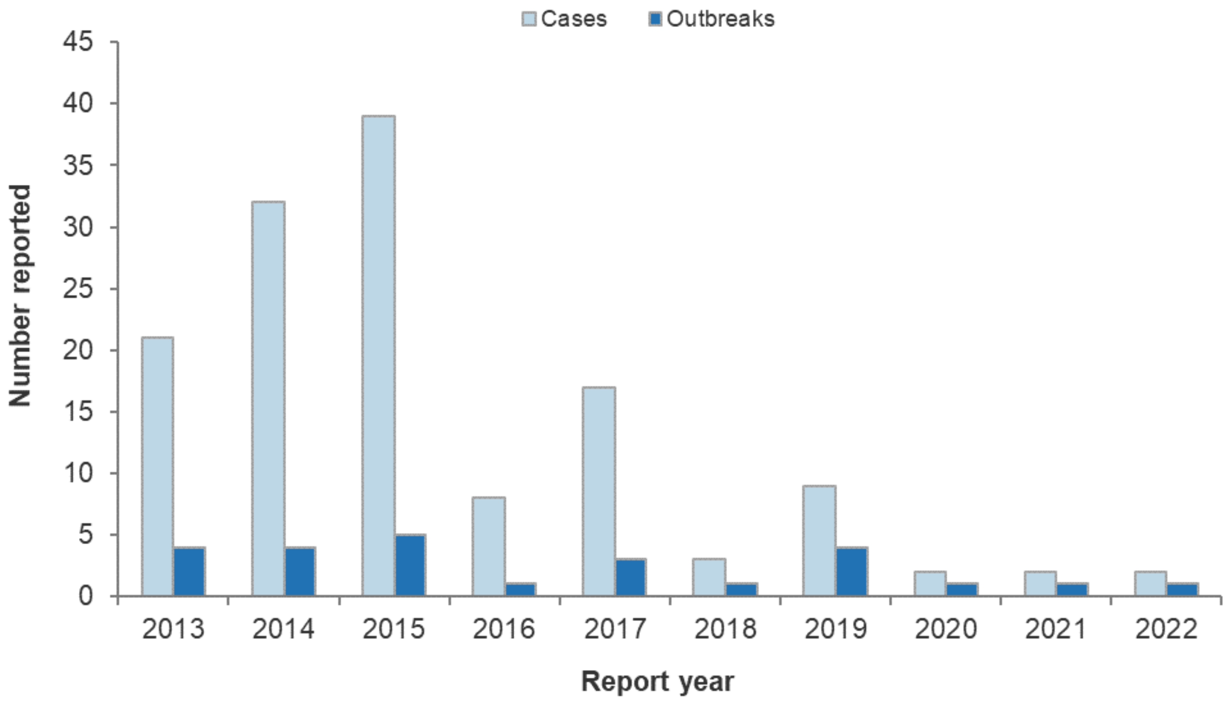
PHU	Report Month	Suspected source	Evidence	Setting	No. Ill
Auckland	October	Dried tuna from Pacific Islands	Common food	Home	2C

PHU: Public health unit, Auckland: Auckland Regional Public Health Service

Number ill: C: confirmed

Over the 10-year period 2013–2021, the annual number of shigellosis outbreaks with food reported as a possible mode of transmission has ranged between one and five outbreaks each year, with between two and 39 associated cases (Figure 39). For each of the last three years there has been a single outbreak of two cases.

Figure 39. Shigellosis outbreaks reported in EpiSurv with food reported as a possible mode of transmission and associated cases reported by year, 2013–2022



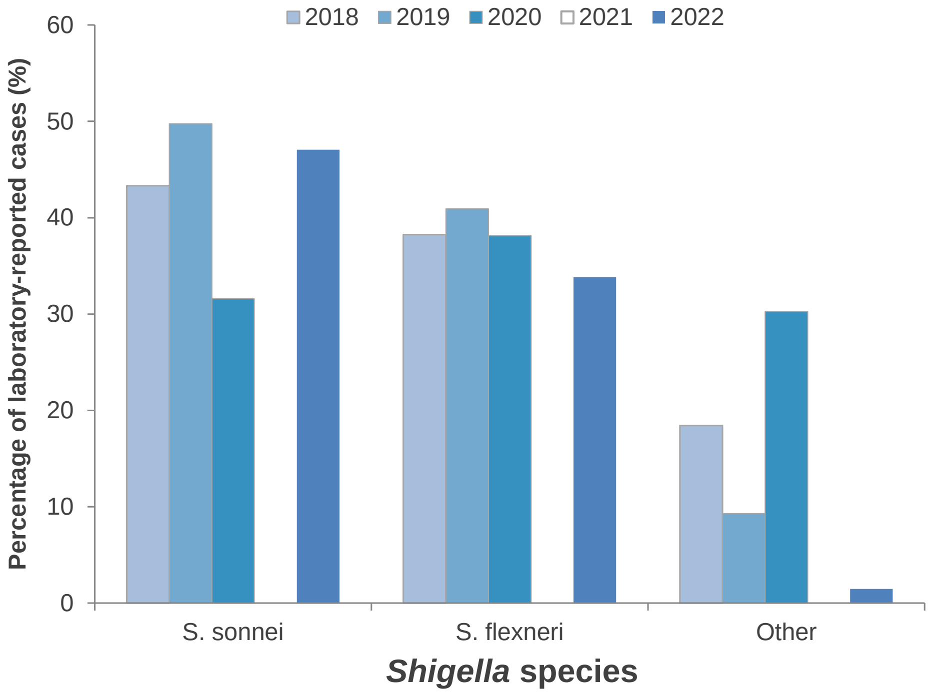
Shigella species commonly reported

In 2022, isolates from 56 out of the 68 notified cases infected with *Shigella* spp. (82%) were typed by the Enteric Reference Laboratory at ESR. *S. sonnei* was isolated most frequently (32 cases) followed by *S. flexneri* (23 cases), which is similar in relative proportions to 2018 and 2019 (Table 51, Figure 40).

Table 51. *Shigella* species and subtypes identified by the Enteric Reference Laboratory, for notified cases of shigellosis, 2018–2022

Species	2018	2019	2020	2021	2022
S. sonnei	**99**	**107**	**28**	**0**	**32**
biotype a	37	33	9	0	17
biotype f	1	1	2	0	2
biotype g	61	73	17	0	13
S. flexneri	**84**	**84**	**34**	**3**	**23**
1b	36	14	2	0	1
1c	0	0	0	1	3
2a	15	19	12	0	5
6 biotype Boyd 88	13	12	1	0	4
Other	20	39	19	1	10
Other	**14**	**8**	**2**	**1**	**1**
S. boydii	10	3	2	1	0
S. dysenteriae	4	4	0	0	1
Shigella species not identified	0	1	0	0	0
Total	**197**	**199**	**64**	**4**	**56**

Figure 40. Percentage of notified shigellosis cases by species by year, 2018-2022



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

Nil.

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 2022 by data source

In 2022, 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 MoH NMDS database. One hospital admission was recorded in 2022 with *S. aureus* intoxication as the primary diagnosis and no cases were reported with *S. aureus* intoxication as another relevant diagnosis.

It should be noted that EpiSurv and the MoH 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.

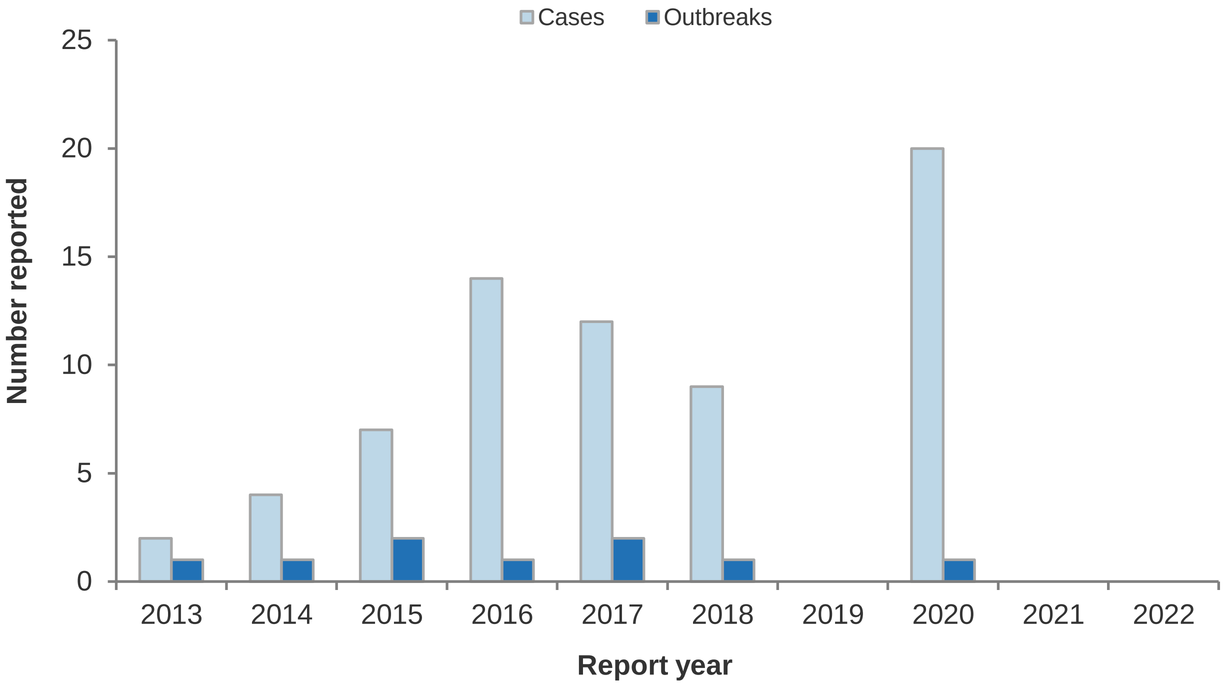
Outbreaks reported as caused by *Staphylococcus aureus*

During 2022, 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.

NZFS carried out two further investigations of suspected *S. aureus* intoxication. These were, one investigation of two cases in the Nelson and Marlborough Public Health Service region in March and one investigation of three cases in Public Health South region in October.

Over the 10-year period 2013 to 2022, the annual number of *S. aureus* intoxication outbreaks with food reported as a possible mode of transmission ranged from zero to two, with between two and 20 associated cases in years when outbreaks were reported (Figure 41).

Figure 41. *S. aureus* intoxication outbreaks reported in EpiSurv with food reported as a possible mode of transmission and associated cases reported by year, 2013–2022



Recent surveys

Nil.

Relevant New Zealand studies and publications

Nil.

Relevant regulatory developments

Nil.

STEC infection

Important 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.

Summary data for STEC infection in 2022 are given in Table 52.

Table 52. Summary of surveillance data for STEC infection, 2022

Parameter	Value in 2022	Source
Number of notified cases	1022	EpiSurv
Notification rate (per 100,000)	19.9	EpiSurv
Hospitalisations[a]	67	MoH NMDS
Deaths	1	EpiSurv
Travel-related cases[b,c]	36	EpiSurv
Estimated domestically acquired food-related cases (%)[b,d]	390 (40%)	Expert consultation

NMDS = MoH 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. 742 cases had not travelled overseas during the incubation period and for the remaining 244 cases travel history is unknown.

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

[d] For estimation of food-related cases the proportions derived from expert consultation [3] exclude travel-related cases (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). 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.

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.

Changes to laboratory methods

Since 2015, laboratories across New Zealand have changed the methodology for testing faecal specimens (Appendix B, page 120). In 2022, community faecal specimens in all DHBs apart from Canterbury, South Canterbury, and West Coast were screened by multiplex PCR for a range of pathogens, including STEC.

Prior to the changes in methodology, only specimens from patients meeting certain epidemiological or clinical criteria (e.g., aged less than 5 years, presence of haemolytic uraemic syndrome (HUS), or bloody diarrhoea) were tested for STEC infection, particularly O157. With multiplex PCR testing, all faecal samples are screened for all STEC serotypes, approximately doubling the number of samples tested for O157 (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 screening PCR, cultures are referred to the Enteric Reference Laboratory at ESR to obtain a STEC isolate for serotyping. In 2022, isolates were recovered for approximately two-thirds of notified cases.

The community laboratory covering Canterbury, South Canterbury and part of the West Coast DHB has not changed to PCR testing but altered their culture-based testing approach for STEC infection to include more non-O157 STEC serotypes. Since September 2018, all faecal samples submitted to the community laboratory are tested for STEC with this new, still culture-based, approach (plating to CHROMagar STEC, followed up with EIA *stx* testing), which will identify some non-O157 serotypes but not as many as PCR. As yet unpublished ESR data have shown CHROMagar STEC is inhibitory to a number of STEC and ESR therefore recommends that it is used in combination with the less inhibitory selective medium blood agar supplemented with vancomycin, cefixime and cefsulodin to maximise STEC yield.

STEC individual cases reported in 2022 by data source

During 2022, 1022 individual cases (19.9 cases per 100,000 population) of STEC infection and one resulting death were reported in EpiSurv. Of the 1022 cases, the symptoms of 1017 cases (99%) were reported as fitting the clinical description for STEC infection while for the remaining 5 cases the symptoms were unknown.

The ICD-10 code A04.3 was used to extract enterohaemorrhagic *E*. *coli* (EHEC) infection hospitalisation data from the MoH NMDS database. EHEC and STEC are synonymous [30], but ICD-10 uses EHEC rather than STEC. Of the 67 hospital admissions (1.3 admissions per 100,000 population) recorded in 2022, 35 cases were reported with enterohaemorrhagic *E*. *coli* infection as the primary diagnosis and 32 were reported with enterohaemorrhagic *E*. *coli* infection as another relevant diagnosis.

It should be noted that EpiSurv and the MoH 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 20% of O157 STEC (20%) and 40% of non-O157 STEC (40%) incidence is due to foodborne transmission [3]. It was further estimated that approximately 34% of foodborne O157 STEC infections and 27% of foodborne non-O157 STEC infections were due to transmission via red meat [2].

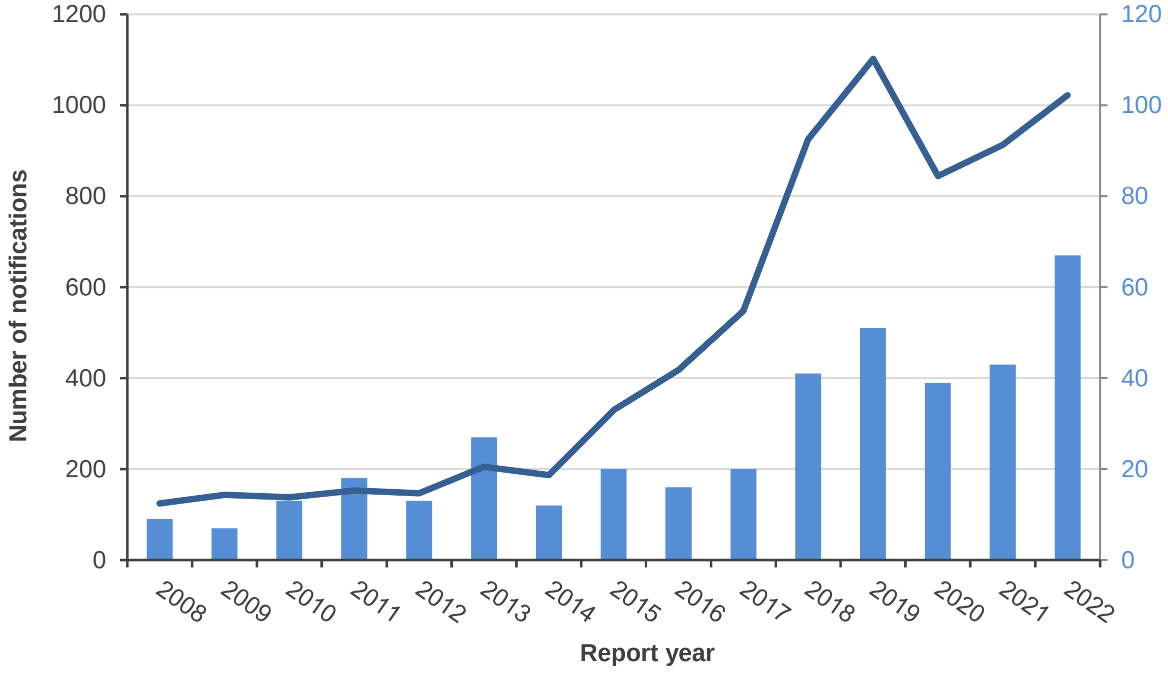
Annual data

Until 2014, the number of STEC notifications was below 210 cases per year. From 2015 there was a steady increase in notifications until 2019, followed by a small drop in 2020 and increases again in 2021 and 2022 (Figure 42). The decrease in 2020 compared to 2019 data is related to the reduction in reported cases during months with COVID-19 Alert Level restrictions [19].

The number of hospital admissions with STEC infection as a primary or secondary diagnosis varies year to year. The last five years (2018-2022) have seen hospital admission numbers consistently higher than the previous 10 years. Of the hospitalisations recorded in EpiSurv in 2022, ~40% were identified with the O157:H7 serotype, ~30% with non-O157 serotypes and ~30% of cases did not have samples typed. Before the introduction of CIDT, non-O157 hospital admissions with gastrointestinal infection symptoms may not have been diagnosed with an STEC infection.

The frequency of overseas travel decreased in 2020 to 2022 compared to pre COVID-19 years (see Introduction, page 5). In 2022, there were 36 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 and two in 2021.

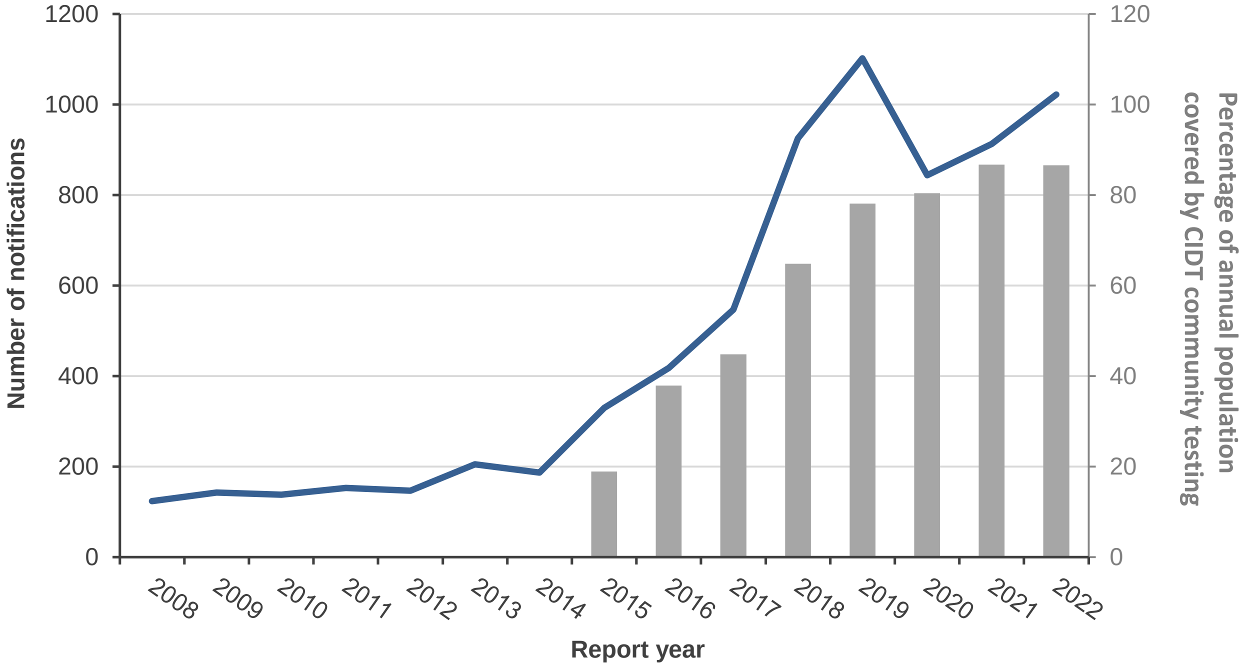
Figure 42. STEC infection EpiSurv notifications (line) and NMDS hospitalisations (bar) by year, 2008–2022



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 120) (Figure 43). The increased sensitivity of CIDT to detect non-O157 STEC serotypes (Table 58) 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 [17].

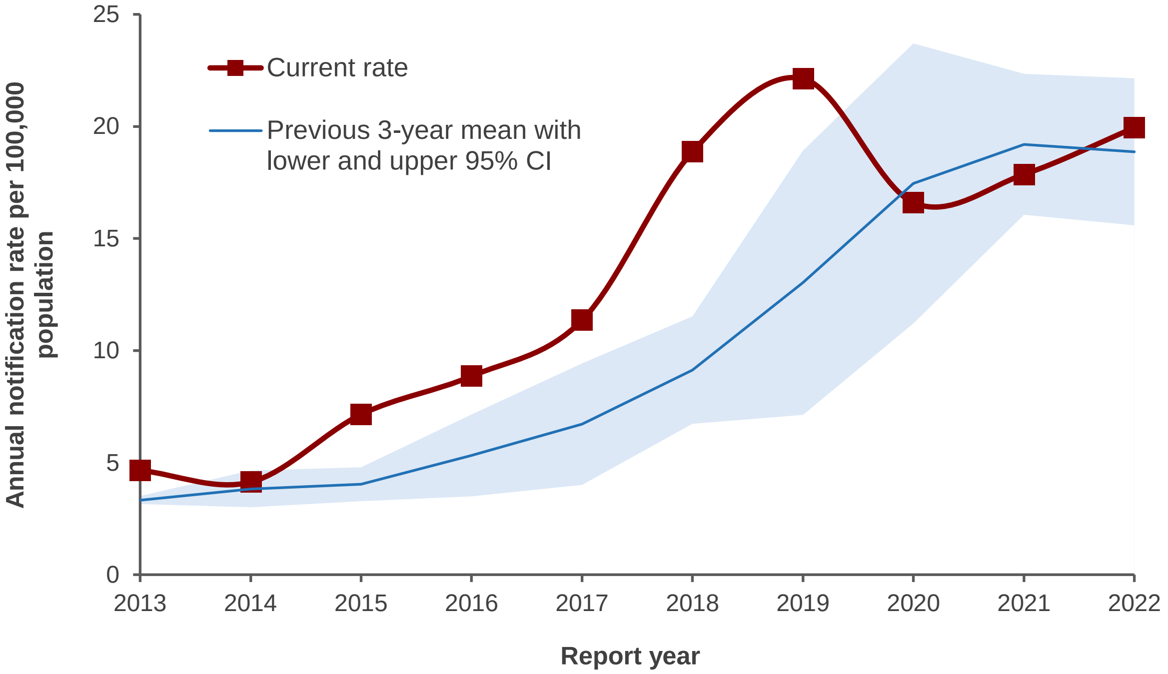
In 2022, approximately 87% of the New Zealand population was covered by community laboratories using CIDT for STEC testing.

Figure 43. STEC infection EpiSurv notifications (line) and proportion of the NZ population covered by community CIDT (bar) by year, 2008–2022



In the past, notification rates for STEC infection were generally below five notifications per 100,000 population. Since 2015, increasing rates have been noted every year until 2019 (22.1 cases per 100,000 population), with a drop in 2020, attributed to the COVID-19 pandemic, followed by increases in 2021 and 2022 (19.9 cases per 100,000 population) (Figure 44). The previous three-year average was 18.9 cases per 100,000 population.

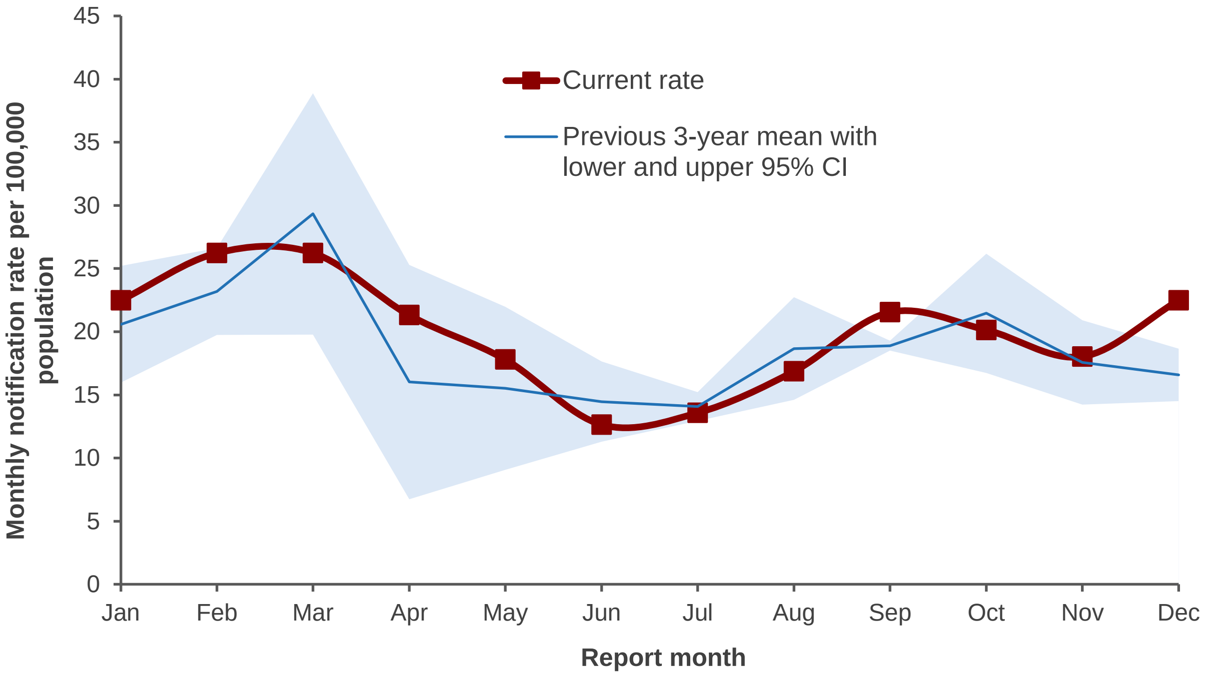
Figure 44. STEC infection notification rate by year, 2013–2022



Seasonal data

STEC infection notification rates per 100,000 population by month for 2022 are shown in Figure 45. In 2022, monthly notification rates were similar to the mean of the previous three years. The monthly number of notifications in 2022 ranged from 54 notifications in June (13 per 100,000 population) to 112 notifications in February and March (26 per 100,000 population).

Figure 45. STEC infection monthly notification rate (annualised), 2022



In 2022, the monthly numbers of hospitalised cases varied over the year, with monthly hospitalised case numbers generally within the range observed in the previous four years (Table 53), with slightly higher numbers in March 2022 (13 hospitalisations).

Table 53. STEC infection monthly NMDS hospitalisation admissions 2018-2022

Month	Hospital admissions with a primary or secondary diagnosis of STEC infection				
	2018	2019	2020	2021	2022
January	4	9	3	3	6
February	7	4	8	4	8
March	5	9	3	4	13
April	3	9	0	9	8
May	4	1	3	4	2
June	0	1	2	5	2
July	3	3	2	1	4
August	1	6	1	2	5
September	5	5	3	2	5
October	2	0	4	4	7
November	1	3	3	1	3
December	6	1	7	4	4
Total	**41**	**51**	**39**	**43**	**67**

Demographics

In 2022, notification rates and hospitalisation rates were higher for females (22.2 cases and 1.5 admissions per 100,000 population) than for males (17.7 cases and 1.1 admissions per 100,000 population) (Table 54).

Table 54. STEC cases by sex, 2022

Sex	EpiSurv notifications		Hospitalisations[a]	
	No.	Rate[b]	No.	Rate[b]
Male	450	17.7	28	1.1
Female	572	22.2	39	1.5
Total	**1022**	**19.9**	**67**	**1.3**

[a] MoH NMDS data for hospital admissions

[b] per 100,000 population in this sex group

In 2022, the STEC infection notification rate was highest for the 1 to 4 years age group followed by the <1 years age group (68.3 cases and 58.3 cases per 100,000 population, respectively). The hospital admission rate was also highest for the 1 to 4 years age group (5.8 hospital admissions per 100,000 population) (Table 55).

Table 55. STEC cases by age group, 2022

Age group (years)	EpiSurv notifications		Hospitalisations[a]	
	No.	Rate[b]	No.	Rate[b]
<1	35	58.3	2	-
1 to 4	166	68.3	14	5.8
5 to 9	61	18.9	8	2.5
10 to 14	51	15.1	2	-
15 to 19	47	14.8	1	-
20 to 29	103	15.2	4	-
30 to 39	77	10.5	4	-
40 to 49	69	10.9	2	-
50 to 59	105	16.1	6	0.9
60 to 69	118	21.0	7	1.3
70+	190	32.6	17	2.9
Total	**1022**	**19.9**	**67**	**1.3**

[a] MoH NMDS data for hospital admissions

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

Geographic distribution

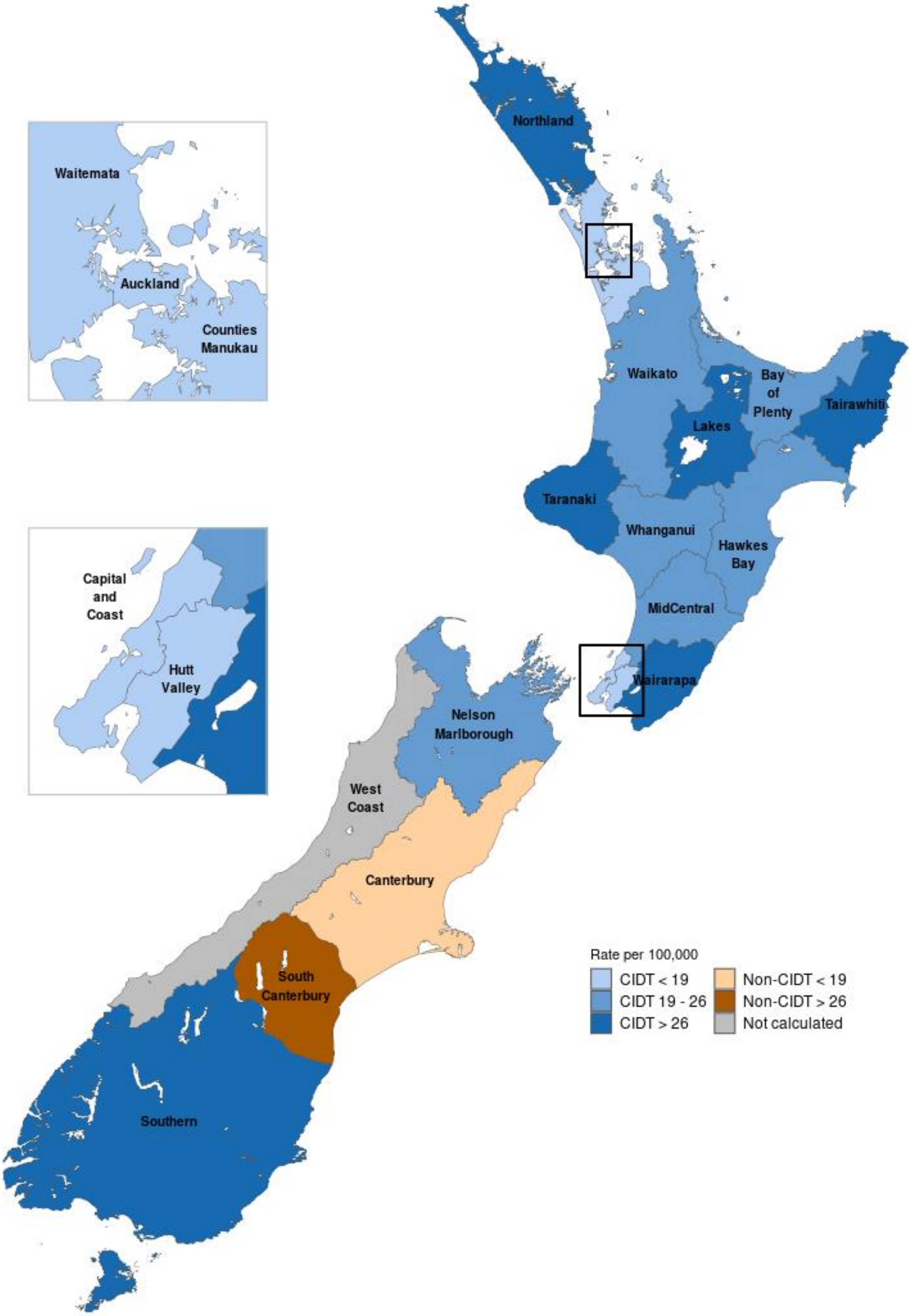
The notification rates by DHB calculated per 100,000 resident population are presented in Figure 46 (see also Table 86). Blue shading is used for DHBs which are using CIDT community testing, the brown shading is used for DHBs using culture-based community testing. The rate has not been calculated for DHBs with less than five cases (grey shading): West Coast DHB (no cases). The West Coast DHB used culture-based testing for STEC during the reporting period.

In 2022, the DHB notification rates of STEC infection ranged from 8 per 100,000 population (13 cases) in Hutt Valley DHB to 73 per 100,000 (37 cases) in Wairarapa DHB. The Wairarapa, Taranaki (48 per 100,000 population, 61 cases) and Southern (45 per 100,000 population, 156 cases) DHBs had the highest notification rates.

Note, the changes in laboratory methods in different parts of the country at different times most likely affected historical reporting rates (see also Changes to laboratory methods, page 85 and Appendix B, page 120).

STEC notification rates stratified by 2023 Urban Rural Classification [22] of the cases' residential address steadily increased with decreasing urbanisation (Appendix C, Table 87). Rates were lowest for 'major urban' areas (10 per 100,000 population, 268 cases) and highest for 'rural other' areas (48 per 100,000 population, 324 cases).

Figure 46. Geographic distribution of STEC infection notifications, 2022



Outbreaks reported as caused by STEC

In 2022, there were five outbreaks (19 cases) of STEC infection notified in EpiSurv. One outbreak (3 cases) reported food as a possible mode of transmission (Table 56). It is important to note that an outbreak may have multiple pathogens, modes of transmission, settings where exposure occurred, or settings where preparation of food was conducted.

Table 56. STEC infection outbreaks reported in EpiSurv, 2022

	Possible foodborne transmission	Total STEC infection outbreaks
Outbreaks	1	5
Outbreak-associated cases	3	19
Hospitalised Cases	0	0

Table 57 contains details of the STEC infection outbreak reported in EpiSurv with a pizza meal as a possible mode of transmission. The potential for person to person transmission was also identified. In addition to the outbreak recorded in EpiSurv at the cut-off date for this report (1 May 2023), NZFS investigated one further outbreak (two confirmed cases in May) (Table 57). The evidence for food as a source was weak for both outbreaks.

Table 57. Details of STEC infection outbreaks reported in EpiSurv and/or investigated by NZFS Food Compliance Services with food reported as a possible mode of transmission, 2022

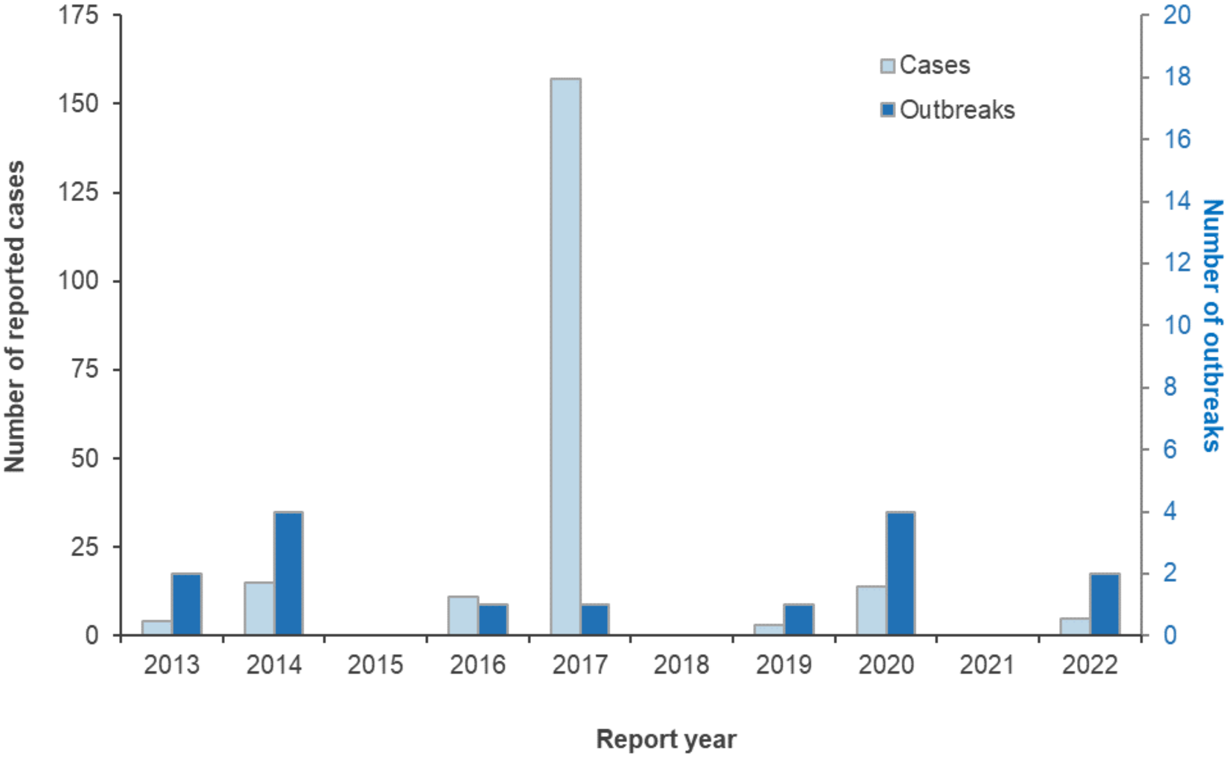
PHU	Report Month	Suspected source	Evidence	Setting	No. Ill
C and PH	May	Unknown	Common food	Rest home	2C
Public Health South	June	Proscuitto or meat pizza	Common food	Mobile food service outlet	1C 2P

PHU: Public health unit, C and PH: Community and Public Health

Number ill: C: confirmed, P: probable

Over the 10-year period 2013 to 2022, 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 three of the ten years (Figure 47). 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 47. STEC infection outbreaks reported in EpiSurv with food reported as a possible mode of transmission and associated cases reported by year, 2013–2022



Note: The 2022 outbreak information includes one outbreak reported in EpiSurv plus one further outbreak from NZFS Food Compliance Services records that were not recorded in EpiSurv at the cut off date for this report (1 May 2023).

STEC types reported for notified cases

Isolates from 694 notified cases infected with STEC were able to be typed by the ESR Enteric Reference Laboratory (ERL) in 2022. A single STEC serotype was confirmed from 681 cases; from each of the remaining thirteen cases two different STEC serotypes were isolated and serotyped. Of the 707 typed isolates, 259 (36.6%) were identified as *E. coli* O157 and 448 (63.4%) as non-O157 (Table 58). As in the previous three years, the most frequently typed non-O157 serotypes were *E. coli* O26:H11 and *E. coli* O128:H2.

Table 58. Annual number of notifications with different STEC serotypes identified by the Enteric Reference Laboratory, 2018–2022

Serotype	2018	2019	2020	2021	2022
O157 [a]	**190**	**196**	**167**	**183**	**259**
Non-O157	**281**	**417**	**388**	**444**	**448**
O26:H11	70	113	112	127	105
O128:H2	17	46	62	62	65
O38:H26	18	23	27	22	35
O146:H21	12	12	17	24	30
O176:H4	0	10	14	14	20
O91:H14	0	11	10	25	18
O174:H8	1	8	9	11	15
O103:H2	7	6	9	17	10
O103:H25	3	11	6	4	9
O5:HNT	0	6	12	12	9
O84:H2	0	2	10	7	9
O123:H10	0	2	8	3	7
O88:H8	0	5	8	9	8
O112:H9	0	3	3	6	6
O183:H18	0	2	0	1	6
O153:H2	4	10	6	8	5
O130:H11	1	6	7	7	5
O177:H25	0	2	2	4	4
O64:H20	3	7	5	5	5
Other Types[c]	145	132	63	76	77
Cases without typing information	**459**	**499**	**291**	**291**	**328**

[a] Whole genome sequencing of human O157 isolates from 2020 to 2022 revealed a wide diversity of genotypes present, with most of the isolates quite distinct to each other

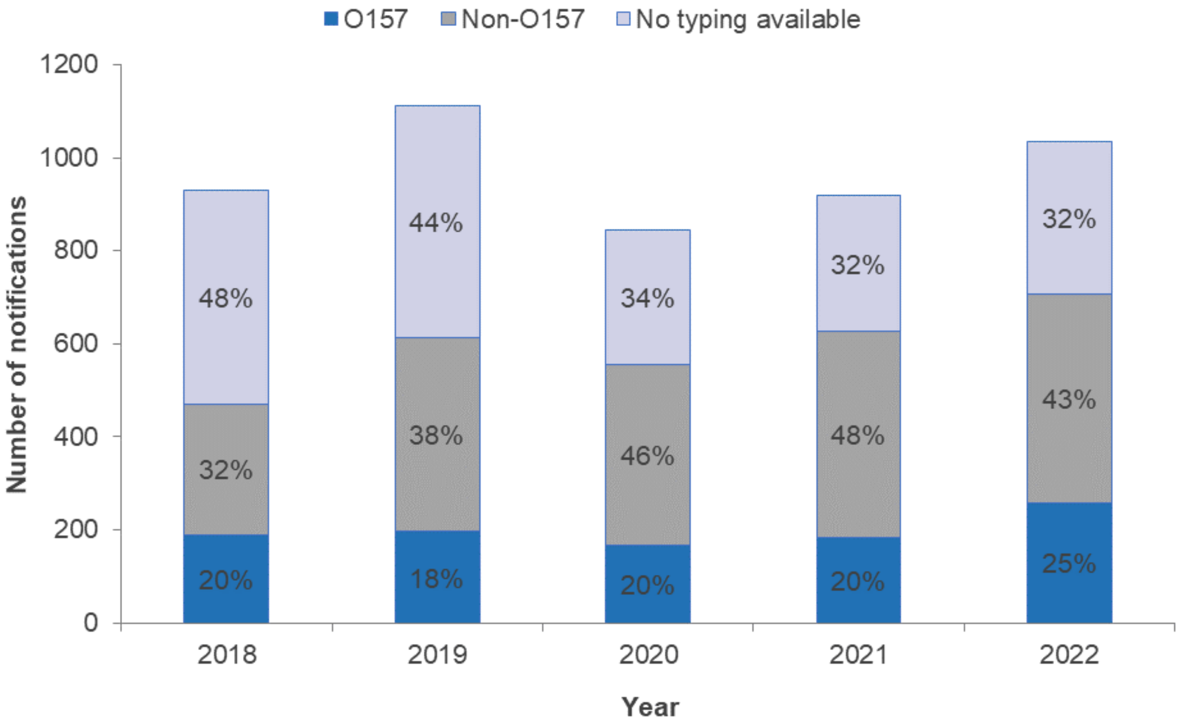
[b] HNT: Non-typable

[c] Other isolates with identifiable non-O157 serotypes, not listed in table. Full list available in the Appendix C, Table 96.

Note: Thirteen cases have been identified with dual serotypes in 2022. The sum of the total rows will not equal the number of notifications in a year.

For 328 (32%) of the 1022 STEC notifications in 2022, no typing information was available (Figure 48), due to ERL not receiving culture samples from diagnostic laboratories or due to the culture no longer being viable. All isolates confirmed as STEC have been whole genome sequenced since 2020, which has increased the proportion of STEC isolates that can be assigned to a serotype.

Figure 48. *E. coli* O157 and non-O157 associated notifications by year, 2018–2022



Investigation of the 2022 EpiSurv-recorded hospitalisation status for the three most commonly identified serotypes found that *E. coli* O157-infected cases were most frequently reported to have been hospitalised (38% of cases hospitalised, 3% no hospitalisation information recorded). The proportion of cases hospitalised was lower for *E. coli* O26:H11 (28% cases hospitalised, 8% no hospital data recorded) and *E. coli* O128:H2 (11% cases hospitalised, 13% no hospital data recorded).

Other *E. coli* pathotypes reported in 2022 for individual notified gastroenteritis cases

During 2022, one individual case was reported in EpiSurv with enterotoxigenic *E. coli* infection and one individual case with enteropathogenic *E. coli* infection. Neither of these was suspected to have become ill from a food source. The case with enterotoxigenic *E. coli* infection worked with sick calves, and the infant case with enteropathogenic *E. coli* infection had recreational water contact and contact with a parent's farm working clothes.

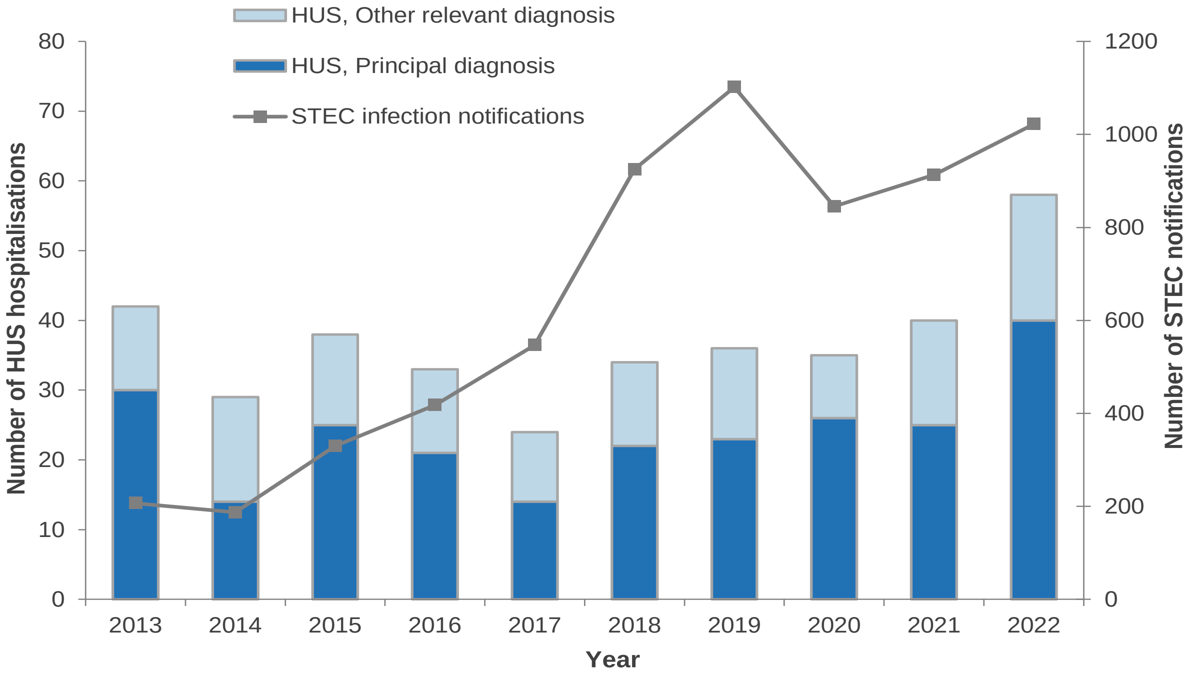
Disease sequelae – haemolytic uraemic syndrome (HUS)

HUS is a serious sequela that may result from an STEC infection. HUS is usually preceded by an STEC infection [32]. 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 *E. coli* O157 infections [33], the most recent European data report that *E. coli* O26 was most frequently associated with HUS cases [34]. In 2022, 19 STEC cases notified in EpiSurv were reported to have developed HUS. The associated serotypes were O157:H7 (9), O26:H11 (7), O130:H11 (1), while for two cases the serotype was not reported. However, this information was only reported for 631 of 1022 (62%) notified cases.

The ICD-10 code D59.3 was used to extract HUS hospitalisation data from the MoH NMDS database. Only HUS cases that were incident in the 2022 year were considered, rather than all cases that were hospitalised in that year. That is, if an HUS case hospitalised in 2022 had been hospitalised with HUS in a previous year, the 2022 admission was considered as a re-admission, rather than an incident case. Of the 58 incident hospital admissions recorded in 2022 (1.1 per 100,000 population), 40 were reported with HUS as the primary diagnosis and 18 with HUS as another relevant diagnosis. It should be noted that the number of incident hospitalised 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 2013 and 2022, the number of incident hospitalised cases (any diagnosis code) of HUS each year ranged from 24 to 58 (Figure 49). In 2022, the number of incident hospitalised cases (58) was the highest reported in the 10-year period 2013 - 2022. STEC notifications have increased steadily over this period. However annual numbers of HUS cases have remained largely similar over the last decade, with the exception of the 2022 year.

Figure 49. Haemolytic uraemic syndrome (HUS) incident hospitalised cases, 2013–2022



In 2022, the number of female cases hospitalised due to HUS was slightly less than the number of male cases (Table 59). This is the same pattern as seen in 2021, but the opposite of the pattern seen in most years other than 2017, with more females usually hospitalised with HUS than males.

Table 59. Haemolytic uraemic syndrome incident hospitalised cases by sex, 2022

Sex	Hospitalised cases[a]	
	No.	Rate[b]
Male	30	1.2
Female	28	1.1
Total	**58**	**1.1**

[a] MoH NMDS data for hospital admissions

[b] per 100,000 population.

In 2022, the highest age-specific rates of incident hospitalised cases due to HUS were for children in the <1 and 1 to 4 years age groups (Table 60).

Table 60. Haemolytic uraemic syndrome incident hospitalised cases by age group, 2022

Age group (years)	Hospitalised cases [a]	
	No.	Rate[b]
<1	9	15.0
1 to 4	26	10.7
5 to 9	6	1.9
10 to 14	2	-
15 to 19	-	-
20 to 29	2	-
30 to 39	4	-
40 to 49	2	-
50 to 59	1	-
60 to 69	2	-
70+	4	-
Total	**58**	**1.1**

[a] MoH NMDS data for hospital admissions

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

Haemolytic uraemic syndrome cases reported to the New Zealand Paediatric Surveillance Unit (NZPSU)

The surveillance data gathering for HUS cases by the NZPSU ended in December 2020. Data will not be available from this source for 2021 onwards. NZPSU Annual Reports for previous years are available from https://www.otago.ac.nz/nzpsu/reports/index.html.

Recent surveys

Nil.

Relevant New Zealand studies and publications

Reports

Prevalence of top 6 STEC and E. coli O157 in beef in New Zealand and genetic analysis of E. coli O157 (2018) – Wright et al. (2022)

In 2018, 276 primary laboratory screen-positive adult beef enrichments underwent Top 7 STEC culture confirmation procedures [35]. Among these, 227 were for Top 6 STEC confirmation, 22 were referred for O157 confirmation only, and 27 were for Top 7 STEC (Top 6 plus O157) confirmation. In addition to the beef enrichments, six presumptive *E. coli* O157 pure cultures were submitted for confirmation. Fifty of the submitted samples were confirmed by ESR as being culture positive for one of the Top 7 serogroups. The most common STEC serogroup identified was O26 (n = 26), followed by O157 (n = 19), O103 (n = 4), and O46 (n = 1).

Among 17 primary laboratory screen-positive very young calves veal enrichments received from the 2018 bobby calf season, one was cultured for *E. coli* O157 at the request of MPI. STEC O157 was cultured from this sample. All STEC O157:H7 isolates were sequence type (ST) 11, with three isolates possessing one single nucleotide polymorphism (SNP) in the adk allele.

One of the 2018 bovine isolates was within five SNP differences from a cluster of two human isolates from 2018.

Bovine *E. coli* O157:H7 from 2018 separated into three separate clades corresponding with the type of stx gene present (stx1a, stx2a, and stx2c). All bovine STEC O157 isolates from 2018 were found to have the mdf(A), an acquired macrolide–lincosamide–streptogramin B resistance gene, which is also common in New Zealand clinical STEC isolates. No other resistance genes were identified by WGS of STEC O157 isolates.

Prevalence of top 6 STEC and E. coli O157 in beef in New Zealand and genetic analysis of E. coli O157 (2019) – Wright et al. (2022)

In 2019, 272 primary laboratory screen-positive adult beef enrichments underwent Top 7 STEC culture confirmation procedures [36]. Among these, 215 were for Top 6 STEC confirmation, 29 were referred for O157 confirmation only, and 28 were for Top 7 STEC (Top 6 plus O157) confirmation. As well as beef enrichments, three presumptive *E. coli* O157 pure cultures were submitted for confirmation. Thirty-two of the submitted samples were confirmed by ESR as being culture positive for one of the Top 7 serogroups. The most common STEC serotype identified was O157:H7 (*n* = 16), followed by O26 (*n* = 12) and O103 (*n* = 4).

Among 81 primary laboratory screen-positive bobby veal enrichments received over the 2019 bobby calf season, 11 were cultured for *E. coli* O157 at the request of MPI. Nine *E. coli* O157 isolates were confirmed, five were STEC O157, four were non-toxigenic and H7 negative specifically, *E. coli* O157:H12 (*n* = 3); and *E. coli* O157:H19 (*n* = 1). The majority of the STEC O157:H7 isolates (20 of 21) were sequence type (ST) 11 with one isolate being the newly conferred ST10084. All three *E. coli* O157:H12 isolates were ST10 and the *E. coli* O157:H19 isolate was ST763.

There were two clusters of isolates (one of two isolates, one of three isolates) that differed by fewer than five single nucleotide polymorphisms (SNPs). A single 2019 bovine isolate clustered with a single human isolate from 2017. No strong epidemiological link was identified to explain this finding.

Bovine *E. coli* O157:H7 from 2019 separated into three separate clades broadly depending on the type of stx gene present (stx1a, stx2a, and stx2c). All bovine STEC O157 isolates from 2019 were found to have the mdf(A), an acquired macrolide–lincosamide–streptogramin B resistance gene, which is also common in New Zealand clinical STEC isolates. No other resistance genes were identified in this group.

Prevalence of top 6 STEC and E. coli O157 in beef in New Zealand and genetic analysis of E. coli O157 (2020) – Wright et al. (2022)

In 2020, 237 beef enrichments underwent Top 7 STEC culture confirmation procedures along with 3 presumptive *E. coli* O157 isolates submitted directly to ESR [37]. Of these, 169 were serogroup-positive for at least one of the Top 7, and of these only 34 were confirmed as culture-positive. As with previous years, the most common STEC serotype identified was O26, followed by O157 and O103.

In addition to the isolates from bovine enrichments, MPI requested that culture isolation for the serotype O157 from two veal enrichment samples be performed. One isolate was confirmed as *E. coli* O157:H7.

In total 10 *E. coli* O157:H7 isolates were whole genome sequenced (nine from bovine and one from veal). Sequence Type (ST) 11 was the only sequence type identified in 2020, however none of these isolates were genetically related to each other, nor were they closely related to any clinical isolates obtained between 2015 and 2020.

Whole genome multi-locus sequence type analysis (wg-MLST) demonstrated that STEC O157:H7 isolates from 2016 to 2020 separated into three separate clades depending on the type of stx gene present (stx 1a, 2a and 2c). All bovine STEC O157 isolates from 2020 were found to have the mdf(A) gene, an acquired macrolide–lincosamide–streptogramin B resistance gene, which is also common in New Zealand clinical STEC isolates. No other resistance genes were identified in this group.

Prevalence of top 7 STEC in beef in New Zealand and genetic analysis of E. coli O157 (2021) – Wright et al. (2022)

In 2021, 239 beef enrichments underwent Top 7 STEC culture confirmation procedures [38]. Of these, 182 were serogroup positive for at least one of the Top 7, and of these only 39 were confirmed as culture positive. As with previous years, the most common STEC serotype identified was O26, followed by O157 and O103.

In addition, MPI requested culture isolation for the serotype O157 for 17 veal samples. In total 31 *E. coli* O157:H7 isolates were sequenced; 25 of which were confirmed as STEC isolates (17 from bovine and six from veal) and six were O157 serotype positive but classed as nonpathogenic. Sequencing Type (ST) 11 was the dominant sequence type identified (24 of 25) with one being ST10084.

None of the beef isolates were genetically related but it was noted that two beef isolates were related (within five single nucleotide polymorphisms (SNP) difference) to three clinical isolates from 2021. No strong epidemiological link was identified to explain this finding.

Comparison of the non-STEC with STEC serogroup O157, as defined by the presence or absence of H7 revealed that there were significant differences in the core genome with H7-positive O157 clustering as a distinct group. Further STEC O157:H7 separated into three separate clades depending on the type of *stx* gene present (*stx* 1a, 2a and 2c). All bovine STEC O157 isolates from 2021 were found to have the mdf(A) gene, an acquired macrolide–lincosamide–streptogramin B resistance gene, which is also common in NZ clinical STEC isolates. No other resistance genes were identified in this group.

Relevant regulatory developments

Nil.

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
PSP: 10 MU/kg body weight (≅ 2µg/kg body weight)
(MU = mouse units)

Toxic shellfish poisoning cases reported in 2022 by data source

During 2022, two suspected individual cases of toxic shellfish poisoning were reported in EpiSurv. One case consumed raw recreationally gathered kina, and the other case was listed as consuming prawns, clams and scampi, but no other information was provided.

The ICD-10 code T61.2 was used to extract hospitalisation data for ‘other fish and shellfish poisoning’ from the MoH NMDS database. Of the four hospital admissions (0.1 admissions per 100,000 population) recorded in 2022, three cases were reported with ‘other fish and shellfish poisoning’ as the primary 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 MoH 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 2022 no toxic shellfish poisoning outbreaks were reproted 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.

There have been no outbreaks of toxic shellfish poisoning in the last eight 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

Nil.

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 $\geq 10^5$/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 120). Three of the four PCR panels used across New Zealand include *Vibrio* species, in addition to other faecal pathogens. In 2022, community faecal specimens in the Auckland, Bay of Plenty, Counties Manukau, Lakes, Northland, Waikato and Waitemata DHBs were screened by multiplex PCR 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 2022 by data source

During 2022, 52 individual cases (1.0 per 100,000 population) of *V. parahaemolyticus* infection were reported in EpiSurv. One of the cases was related to overseas travel to the Philipines.

The ICD-10 code A05.3 was used to extract foodborne *V. parahaemolyticus* infection hospitalisation data from the MoH NMDS database. Of the three hospital admissions (0.1 admissions per 100,000 population) recorded in 2022, two cases were reported with *V. parahaemolyticus* infection as the primary diagnosis. and one case was reported with *V. parahaemolyticus* infection as another relevant diagnosis.

It should be noted that EpiSurv and the MoH 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 shows no seasonal trend during 2019 to 2021 (Table 61). In the summer months November 2021 to February 2022 the number of notifications were higher than seen in other non-outbreak months during 2019 to 2022.

Table 61. *V. parahaemolyticus* infection monthly notified cases, 2019-2022

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

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

[b] Period of elevated case numbers across the country which have been captured as an outbreak in EpiSurv (see outbreak section below)

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*

No common source outbreaks of *V. parahaemolyticus* infection were reported in EpiSurv for 2022. In the last 10 years there were three years with common source potentially foodborne *V. parahaemolyticus* outbreaks recorded (2019, 2020 and 2021), with between two and 24 outbreak-associated cases per year.

In November 2021 an outbreak was initiated in EpiSurv due to higher than expected numbers of notifications around New Zealand of gastroenteritis due to *V. parahaemolyticus* infection. The final definition of an outbreak case was "*Any person with symptoms of acute gastroenteritis reported in New Zealand from 15 November 2021 to 31 May 2022 AND has laboratory confirmed Vibrio parahaemolyticus infection acquired in New Zealand associated with exposure to NZ sourced seafood*".

In total 60 cases were linked to this outbreak, with cases predominantly exposed via a range of recreationally caught seafood from around New Zealand coastal waters. Fifty three of the 60 cases reported how the seafood they consumed was prepared, and 40 of these cases reported eating raw or partially cooked seafood.

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 62). ST50 has been the most frequently isolated sequence type between 2000 and 2022.

Table 62. *V. parahaemolyticus* 7-gene multi locus sequence types identified by the Enteric Reference Laboratory, 2019–2022

Sequence type	2019	2020	2021	2022
ST50	2[a]	24	24	37
ST3	0	0	0	7
ST69	0	0	0	2
ST8	0	0	0	1
ST36	14	2	2	0
ST55	0	0	1	1
ST199	0	0	5	1
ST217	0	0	0	1
ST558	0	0	0	1
ST265	1[a]	0	0	0
ST1381	0	0	0	1
ST2058	0	0	0	1
ST2549	0	0	4	1
ST2903	0	0	0	1
ST2904	0	0	0	1
No typing information	**26**	**18**		**1**
Total	**43**	**44**	**36**	**57**

Recent surveys

Nil.

Relevant New Zealand studies and publications

Nil.

Relevant regulatory developments

In response to increased reporting of *V. parahaemolyticus* infections, NZFS issued consumer advice on safe consumption of shellfish [39]. Advice included:

- Don't eat shellfish raw or undercooked. Cook shellfish thoroughly (until they open and are firm to the touch) or so they get to at least 65°C for one minute.
- Avoid gathering shellfish after heavy rainfall or if the water is unusually dirty.
- Keep shellfish alive and cool.
- Refrigerate your shellfish as soon as possible and, ideally, eat it on the day of collection or within two days.
- To avoid cross-contamination, keep hands and utensils clean to prepare raw shellfish, and keep raw shellfish separated from cooked or ready-to-eat products.

This followed earlier advice to thoroughly cook mussels before eating, to manage risks due to *V. parahaemolyticus* [40].

Yersiniosis

Summary data for yersiniosis in 2022 are given in Table 63.

Table 63. Summary of surveillance data for yersiniosis, 2022

Parameter	Value in 2022	Source
Number of notified cases	1294	EpiSurv
Notification rate (per 100,000)	25.3	EpiSurv
Hospitalisations[a]	201	MoH NMDS
Deaths	0	EpiSurv
Travel-related cases[b,c]	22	EpiSurv
Estimated domestically acquired food-related cases (%)[d]	938 (75%)	Expert consultation

NMDS = MoH 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. 629 cases had not travelled overseas during the incubation period and for the remaining 643 cases travel history is unknown.

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

[d] For estimation of food-related cases the proportions derived from expert consultation [3] exclude travel-related cases (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).

Case definition

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

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* 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 120). In 2022, community faecal specimens in all DHBs except for Canterbury, South Canterbury, and West Coast were screened by culture-independent diagnostic tests (CIDT) for a range of pathogens, including *Yersinia.*

Within the DHBs that have moved to CIDT, all community faecal specimens in the Capital & Coast, Hawke's Bay, Hutt Valley, MidCentral, Nelson Marlborough, Southern, Tairawhiti, Taranaki, Wairarapa, and Whanganui DHBs are routinely tested for *Y. enterocolitica and Y. pseudotuberculosis.* Faecal specimens in Auckland, Bay of Plenty, Counties Manukau, Lakes, Northland, Waikato, and Waitemata DHBs are only being screened for *Y. enterocolitica* [41]. This corresponds to 54% of the New Zealand population only being screened for *Y. enterocolitica*. Cases of *Y. pseudotuberculosis* in these DHBs 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 impacted on notifications for yersiniosis [17].

Yersiniosis cases reported in 2022 by data source

During 2022, 1294 individual cases (25.3 per 100,000 population) of yersiniosis and no resulting deaths were reported in EpiSurv. Of the 1294 cases, the symptoms of 1266 cases (98%) were reported as fitting the clinical description for yersiniosis infection, the symptoms were unknown for 26 cases, and for two cases the symptoms were reported as not fitting the clinical description.

The ICD-10 code A04.6 was used to extract yersiniosis (enteritis due to *Y. enterocolitica)* hospitalisation data from the MoH NMDS database. Of the 201 hospital admissions (3.9 admissions per 100,000 population) recorded in 2022, 107 cases were reported with yersiniosis as the primary diagnosis and 94 were reported with yersiniosis as another relevant diagnosis.

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

Foodborne transmission

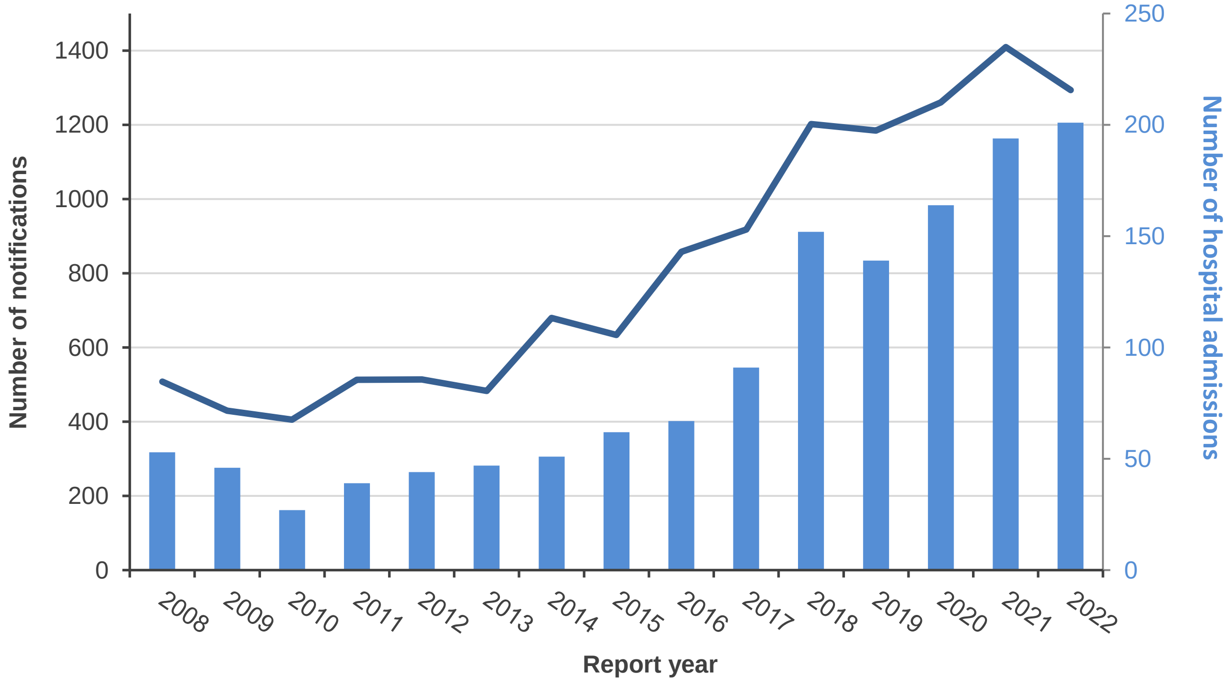
It has been estimated by expert consultation that 75% of yersiniosis incidence is due to foodborne transmission [3]. It was further estimated that approximately 71% of foodborne transmission was due to transmission via pork [2].

Annual data

Between 2008 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 been increasing, with 1410 cases reported in 2021 and 1294 cases in 2022 (Figure 50 and Figure 51). The number of hospital admissions with yersiniosis as a primary or secondary diagnosis has also increased in line with the number of notifications.

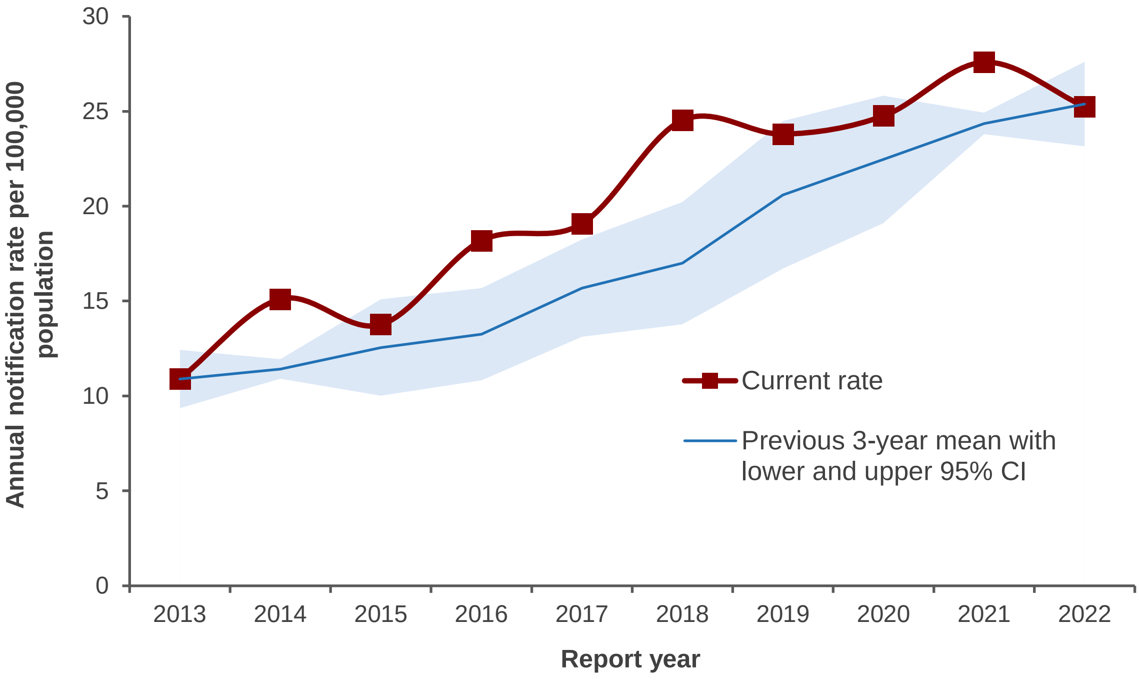
The frequency of overseas travel decreased in 2020 to 2022 compared to pre-COVID-19 years (see Introduction, page 5). This is reflected in the notifications; in 2022, there were 22 yersiniosis notifications in EpiSurv listing overseas travel as a risk factor, compared to 58 in 2019, 11 in 2020 and two in 2021.

Figure 50. Yersiniosis EpiSurv notifications (line) and NMDS hospitalisations (bar) by year, 2008–2022



The yersiniosis annual notification rate has been generally increasing since 2013 (Figure 51). The 2022 notification rate was 25.3 per 100,000 population, comparable to the previous three-year average (25.4 cases per 100,000 population).

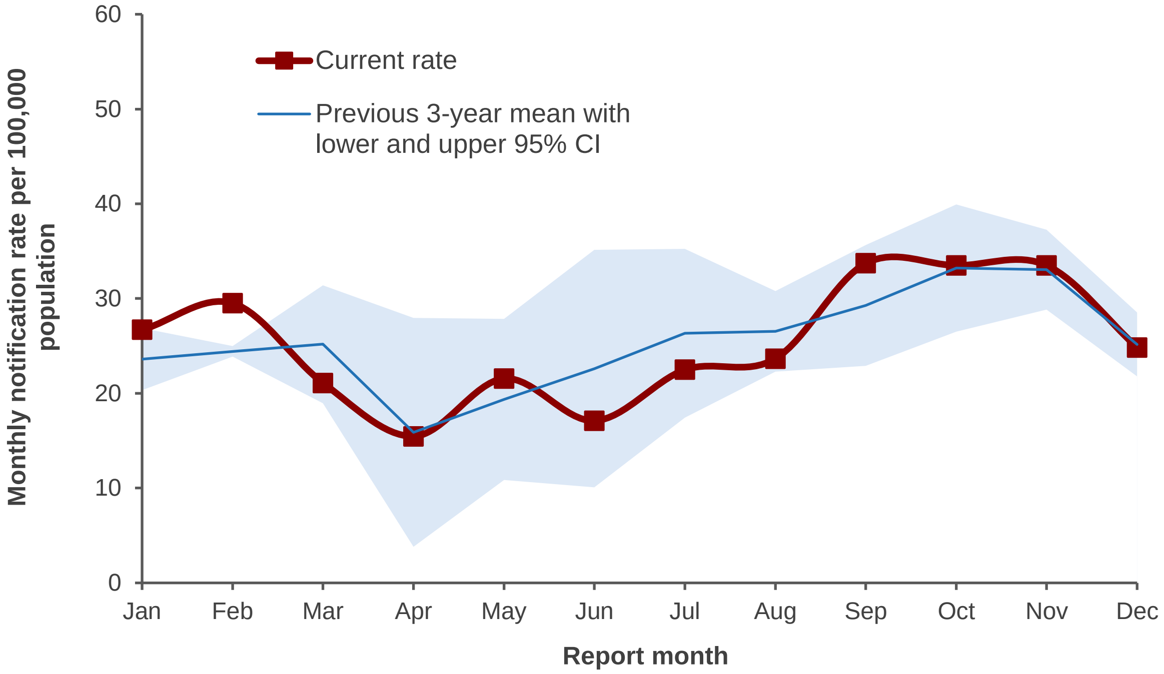
Figure 51. Yersiniosis notification rate by year, 2013–2022



Seasonal data

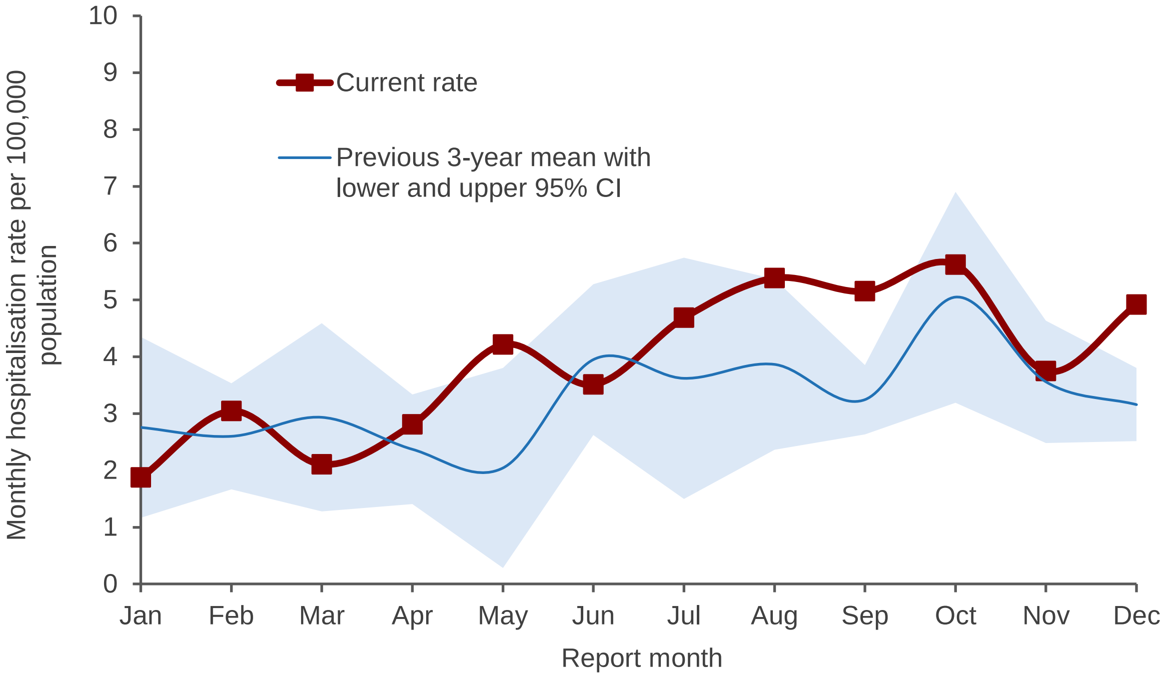
Yersiniosis notification rates per 100,000 population by month for 2022 are shown in Figure 52. In 2022, the monthly notification rates were similar to the mean of the previous three years. The monthly number of notifications in 2022 ranged from 66 notifications (April, 15 per 100,000 population) to a peak of 144 notifications (September, 34 per 100,000 population).

Figure 52. Yersiniosis monthly notification rate (annualised), 2022



In 2022, the monthly hospitalisation rates ranged between 1.9 (January) and 5.6 (October) hospitalisations per 100,000 population and varied over the year (Figure 53). The seasonal trend in monthly hospitalisation rates followed the seasonal trend in monthly notification rates (Figure 52).

Figure 53. Yersiniosis monthly hospitalisation rate (annualised), 2022



Demographics

In 2022, the yersiniosis notification and hospitalisation rates were slightly higher for females (26.0 cases and 4.1 admissions per 100,000 population) than males (24.5 cases and 3.7 admissions per 100,000 population) (Table 64).

Table 64. Yersiniosis cases by sex, 2022

Sex	EpiSurv notifications		Hospitalisations[a]	
	No.	Rate[b]	No.	Rate[b]
Male	622	24.5	94	3.7
Female	672	26.0	107	4.1
Total	**1294**	**25.3**	**201**	**3.9**

[a] MoH NMDS data for hospital admissions

[b] per 100,000 population in this sex group

In 2022, the highest yersiniosis notification rates and hospitalisation rates were for the <1 years age group (143.4 cases and 23.3 admissions per 100,000 population) (Table 65).

Table 65. Yersiniosis cases by age group, 2022

Age group (years)	EpiSurv notifications		Hospitalisations[a]	
	No.	Rate[b]	No.	Rate[b]
<1	86	143.4	14	23.3
1 to 4	156	64.2	8	3.3
5 to 9	36	11.2	3	-
10 to 14	35	10.3	7	2.1
15 to 19	46	14.5	1	-
20 to 29	148	21.8	20	2.9
30 to 39	175	23.8	27	3.7
40 to 49	137	21.7	16	2.5
50 to 59	135	20.6	23	3.5
60 to 69	170	30.3	26	4.6
70+	170	29.2	56	9.6
Total	**1294**	**25.3**	**201**	**3.9**

[a] MoH NMDS data for hospital admissions

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

Geographic distribution

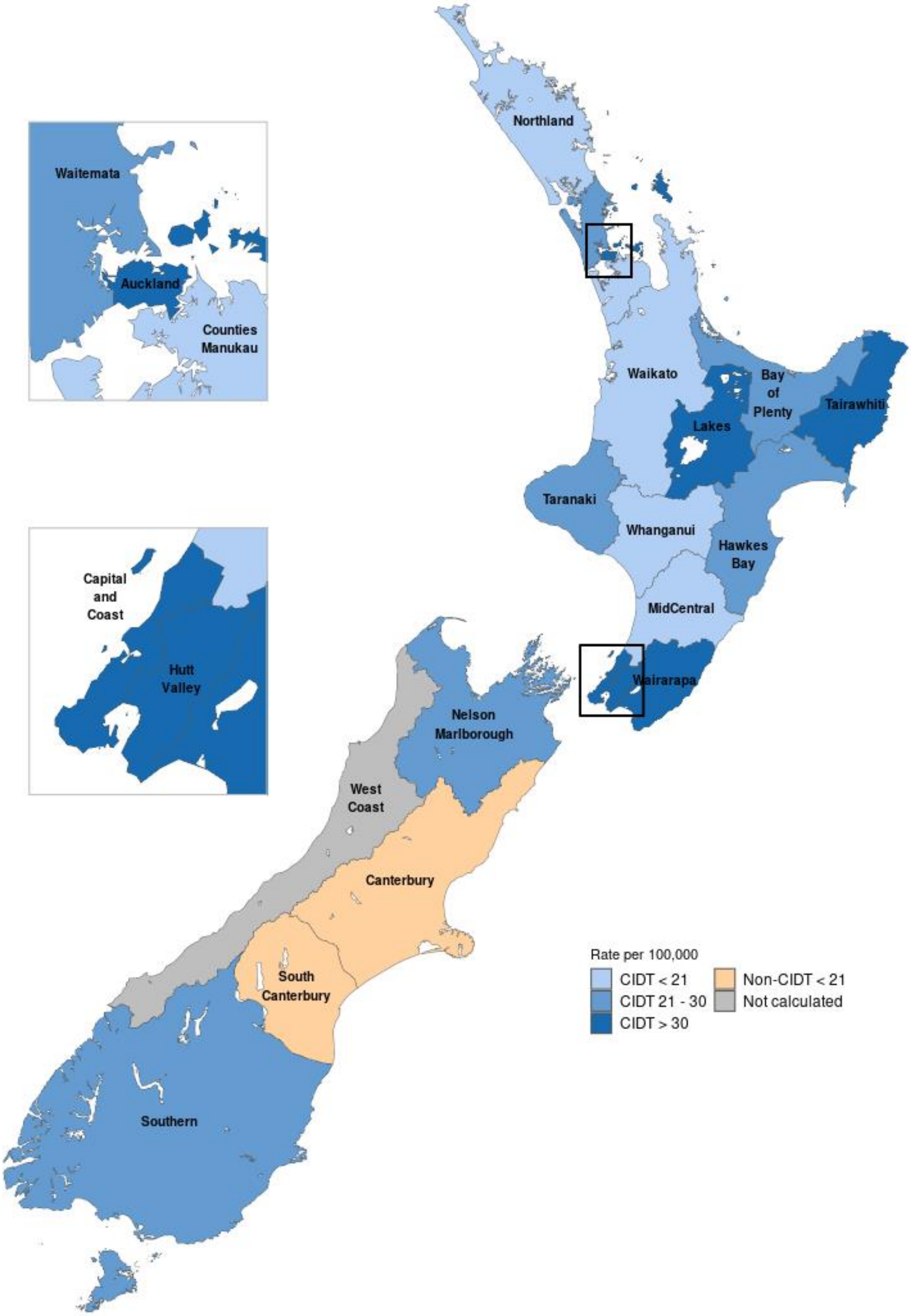
The notification rates by DHB calculated per 100,000 resident population are presented in Figure 54 (see also Table 86). Blue shading is used for DHBs which are using CIDT community testing, the brown shading is used for DHBs using culture-based community testing. The rate has not been calculated for DHBs with less than five cases (grey shading): West Coast DHB (three cases).

In 2022, the DHB notification rates of yersiniosis ranged from 10 per 100,000 population (seven cases) in Whanganui DHB to 61 per 100,000 population for Tairawhiti DHB (32 cases). The Tairawhiti, Wairarapa (51 per 100,000 population, 26 cases), Hutt Valley (39 per 100,000, 63 cases) and Capital and Coast (39 per 100,000 population, 124 cases) DHBs had the highest rates.

Historically, notification rates for yersiniosis have been variable across New Zealand, but with lower North Island DHBs 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 [22] of the cases' residential address varied across the different urban and rural areas (Appendix C, Table 87) with no clear trends related to urbanisation. Notification rates ranged between 18 cases per 100,000 population ('small urban area', 98 cases) and 29 cases per 100,000 population ('large urban area', 207 cases).

Figure 54. Geographic distribution of yersiniosis notifications, 2022



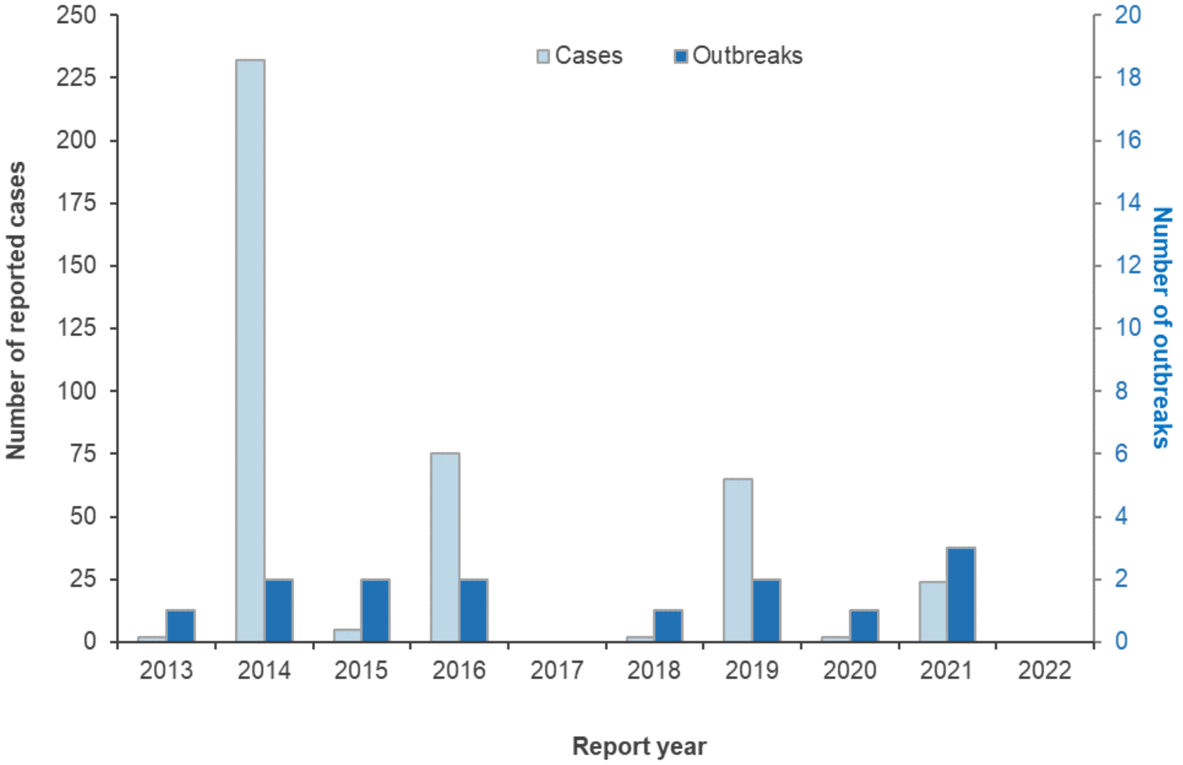
Outbreaks reported as caused by *Yersinia* spp.

In 2022, there were no yersiniosis outbreaks 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 2013 to 2022, three or fewer yersiniosis outbreaks with food reported as a possible mode of transmission were notified annually in EpiSurv; with a total number of annual outbreak-associated cases ranging from zero to 232 (Figure 55). The number of outbreaks in 2014 and 2016 (two outbreaks) was not unusual, but the number of cases involved (232 and 75, respectively) was higher than has been seen in New Zealand previously or since. In 2014 there was an outbreak of 220 cases suspected to be associated with lettuce or carrot and in 2016 there was an outbreak of 51 cases strongly associated with bean sprouts. The increased number of outbreak cases in 2019 was due to an outbreak in a prison setting.

Figure 55. Yersiniosis outbreaks reported in EpiSurv with food reported as a possible mode of transmission and associated cases reported by year, 2013-2022



Yersinia species commonly reported

In 2022, isolates from 942 out of 1294 cases (73%) of notified yersiniosis were typed by the Enteric Reference Laboratory (ERL).

Table 66 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 56. The table and figure need to be interpreted with some caution as:

a) not all clinical laboratories forward all *Yersinia* isolates to ERL for confirmation and typing,

b) 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 73% in 2022, and

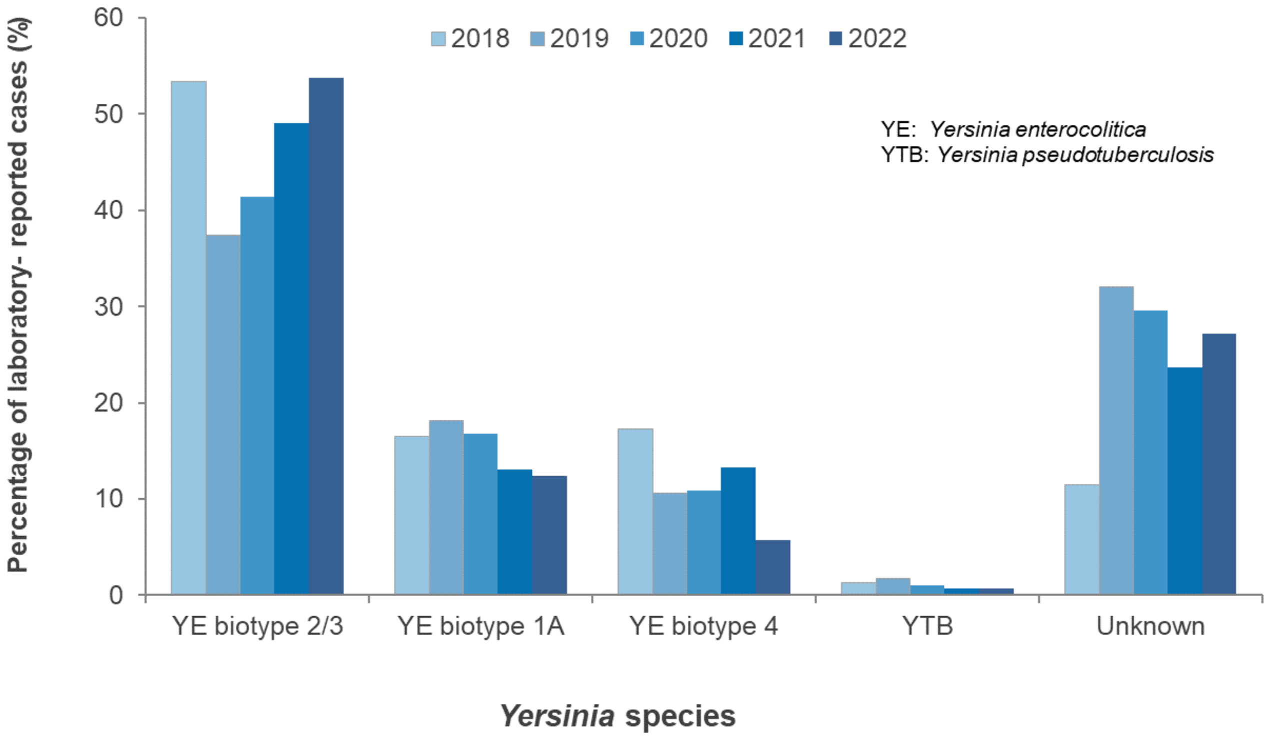
c) successful detection and identification of *Yersinia* spp. is influenced by the methods used by the laboratories. Newer nucleic acid-based (PCR) methods have not been shown to be more sensitive than the historical culture-based methods, but >50% of New Zealand samples are no longer being tested for *Yersinia pseudotuberculosis* as the organism is not targeted by the commercial PCR panels some diagnostic laboratories have chosen to use.

Between 2018 and 2022, each year the largest proportion of yersiniosis cases was due to *Y. enterocolitica* (Table 66 and Figure 56). The most prevalent type of *Y. enterocolitica* has been biotype 2/3, serotype O:9 in each year since 2018. This type was associated with over 50% of the notified cases in 2022. In the same time period (2018 to 2022), *Y. enterocolitica* biotype 1A accounted for between 12% and 18% of yersiniosis notifications and biotype 4 accounted for between 10% and 17% of annual yersiniosis notified cases.

Table 66. Annual number of notifications of different *Yersinia* spp. biotypes and serotypes identified by the Enteric Reference Laboratory, 2018–2022

Species	2018	2019	2020	2021	2022
Yersinia enterocolitica	**1048**	**785**	**877**	**1080**	**933**
biotype 1A	**198**	**215**	**213**	**191**	**160**
serotype O:5	-	18	38	19	19
serotype O:8	-	18	39	37	39
biotype 2/3	**641**	**443**	**523**	**705**	**696**
serotype O:5, 27	43	16	40	27	24
serotype O:9	598	425	483	678	671
biotype 4	**207**	**125**	**137**	**184**	**74**
serotype O:3	207	125	137	184	74
biotype not identified	**2**	**2**	**4**	**1**	**2**
Yersinia pseudotuberculosis	**15**	**21**	**13**	**10**	**9**
Cases without typing information	**138**	**379**	**373**	**319**	**352**

Figure 56. Percentage of notified yersiniosis cases by species and biotype by year, 2018–2022



Recent surveys

Nil.

Relevant New Zealand studies and publications

Nil.

Relevant regulatory developments

Nil.

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 2022, 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 each of the 12 PHUs 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 (MoH).

Data collected by PHUs 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* [21].

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 district health board (DHB) and organism (e.g., almost all isolates are forwarded for *Salmonella* typing but not all *Yersinia* isolates are forwarded). However, the advent of CIDT has resulted in a decrease in the number of isolates forwarded for typing as a proportion of the notifications.

Ministry of Health

The Ministry of Health collates national data on patients admitted and discharged from publicly funded 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) coding system [16]. Up to 99 diagnostic, procedure, and accident codes may be assigned to each admission. The first of these is the principal or primary diagnosis, which is the condition that led to admission. This may differ from the underlying diagnosis.

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 include 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 all hospitalisations, including re-admissions, have been reported for all primary diseases. For the disease sequelae (GBS and HUS) re-admissions of cases within the calendar year were removed. For GBS and HUS reported case numbers represent unique cases that have been hospitalised during the calendar year, not the total number of admissions due to the sequelae.

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

ESR has operated an outbreak surveillance system as an additional module in EpiSurv since mid-1997. This enables PHUs 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* [42]. There is considerable variability in the amount of information provided in reports from different outbreaks.

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

Laboratory investigation of outbreaks

PHUs 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 PHUs. 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 the 2023 urban rural geographies and mapping files [22] to allow assignment of urban areas, rural settlements, other rural areas and water areas to residence of EpiSurv notified or hospitalised cases.

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 8 March 2023. Outbreak data contained in this report are based on information recorded as an outbreak in EpiSurv as at 1 May 2023. Disease numbers are reported according to the date of notification. Hospitalisation data was extracted from the NMDS on the 23 March 2023.

Changes made to EpiSurv data by PHU 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 [14] 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 2022 mid-year population estimates and are crude rates unless otherwise stated. At 30 June 2022, the New Zealand population was estimated to be 5,124,100. 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 Te Whatu Ora. For 2022 this report continues to provide case numbers and rates for the 2022 DHB boundaries. The DHB populations have been derived from the Statistics New Zealand mid-year population estimates for territorial authorities in New Zealand incorporating the Census 2018 base data.

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 [22]. 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 the DHB 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). DHB populations covered by CIDT community testing for a pathogen are shown by a blue colour scale and DHBs where the community diagnostic testing is culture based are shown by a brown colour scale.

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 (2019−2021).

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APPENDIX B - LABORATORIES CHANGING DETECTION METHODS FOR ENTERIC PATHOGENS

Timeline of laboratories changing to PCR-based detection of enteric pathogens

Table 67 below summarises when laboratories across New Zealand moved to PCR-based detection methods and which pathogens are included in the respective PCR panels. In 2022 there were four different commercial panels used across New Zealand.

Table 67. Timeline when DHBs changed to PCR detection methods for enteric pathogens (X: no change to PCR-based methods, NS: Not screened for)

District Health Board		*Campylobacter*	*Salmonella*	*Shigella*	STEC	*Yersinia enterocolitica*	*Yersinia pseudotuberculosis*	*Giardia*	*Cryptosporidium*	*Vibrio parahaemolyticus*
Auckland	Hospital	Jul 2017	Jul 2017	Jul 2017	Jul 2017	Jul 2017	X	Jul 2017	Jul 2017	Jul 2017
Auckland	Community	Jul 2015	Jul 2015	Jul 2015	Jul 2015	Jun 2017	NS	Jul 2015	Jul 2015	Jun 2017
Bay of Plenty	Hospital	Nov 2018	Nov 2018	Nov 2018	Nov 2018	Nov 2018	NS	X	X	Nov 2018
Bay of Plenty	Community	Nov 2018	Nov 2018	Nov 2018	Nov 2018	Nov 2018	NS	X	X	Nov 2018
Canterbury	Hospital	X	X	X	X	X	X	X	X	X
Canterbury	Community	X	X	X	X	X	X	X	X	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	Hospital	Oct 2022	Oct 2022	Oct 2022	Oct 2022	Oct 2022	X	X	X	Oct 2022
Hawke's Bay	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	Hospital	May 2021	May 2021	May 2021	May 2021	May 2021	May 2021	May 2021	May 2021	X
MidCentral	Community	May 2021	May 2021	May 2021	May 2021	May 2021	May 2021	May 2021	May 2021	X

District Health Board		*Campylobacter*	*Salmonella*	*Shigella*	STEC	*Yersinia enterocolitica*	*Yersinia pseudotuberculosis*	*Giardia*	*Cryptosporidium*	*Vibrio parahaemolyticus*
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	Hospital	X	X	X	X	X	X	X	X	X
Northland	Community	Jul 2015	Jul 2015	Jul 2015	Jul 2015	Jun 2017	NS	Jul 2015	Jul 2015	Jun 2017
South Canterbury	Hospital	X	X	X	X	X	X	X	X	X
South Canterbury	Community	X	X	X	X	X	X	X	X	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
Tairawhiti	Hospital	May 2021	May 2021	May 2021	May 2021	May 2021	May 2021	May 2021	May 2021	X
Tairawhiti	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
Waitemata	Hospital	Jun 2022	Jun 2022	Jun 2022	Dec 2016	Jun 2022	X	X	X	Jun 2022
Waitemata	Community	Jul 2015	Jul 2015	Jul 2015	Jul 2015	Jun 2017	NS	Jul 2015	Jul 2015	Jun 2017
West Coast	Hospital	X	X	X	X	X	X	X	X	X
West Coast	Community	X	X	X	X	X	X	X	X	X
Whanganui	Hospital	May 2021	May 2021	May 2021	May 2021	May 2021	May 2021	May 2021	May 2021	X
Whanganui	Community	May 2021	May 2021	May 2021	May 2021	May 2021	May 2021	May 2021	May 2021	X

Data source: New Zealand Microbiology Network CIDT testing database, personal communication, March 2023

[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 testing most of Canterbury, South Canterbury and some West Coast DHB samples has not changed to PCR testing but changed their culture-based testing approach for STEC infections to include more non-O157 STEC serotypes. Since September 2018, all faecal samples are tested for STEC with this new, still culture-based, approach (plating to CHROMagar STEC, followed up with EIA *stx* testing) which will identify some non-O157 serotypes but not as many as PCR.

APPENDIX C - SUMMARY TABLES

Appendix C brings together data from EpiSurv, the NMDS and international data as summary tables to facilitate comparisons between conditions.

National tables

Table 68. Number of cases and rate per 100,000 population of selected notifiable diseases in New Zealand, 2021–2022

Disease	2021		2022	
	Cases	Rate	Cases	Rate
Campylobacteriosis	5729	112.1	5878	114.7
Cryptosporidiosis	702	13.7	612	11.9
Gastroenteritis[a]	244	4.8	331	6.5
Giardiasis	1041	20.4	707	13.8
Hepatitis A	8	0.2	59	1.2
Listeriosis	32	0.6	39	0.8
Salmonellosis	714	14.0	750	14.6
Shigellosis	4	-	68	1.3
STEC infection	911	17.8	1022	19.9
Yersiniosis	1410	27.6	1294	25.3

[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) single cases of chemical or toxic food poisoning such as botulism, histamine (scombroid) poisoning and any type of toxic shellfish poisoning [14]. Please note that other publications or reports may report botulism and toxic shellfish poisoning separately, resulting in differing case numbers for acute gastroenteritis.

Note: Where fewer than five cases have been notified, a rate has not been calculated.

Table 69. 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 (2022)	Australia[a] (2022)	USA[b,c] (2021)	Canada[d] (2020)	UK[e] (2019)	EU Total[e,g] (2021)	Other high
Campylobacteriosis	114.7	161.4	17.8	20.0	88.1	41.1	152.4 (Czechia)[f] 111.7 (Slovakia)[f]
Cryptosporidiosis	11.9	7.8	4.3[c]	2.5	8.8[g]	4.4[g]	20.0 (Netherlands)[g] 12.8 (Ireland)[g]
Giardiasis	13.8	NN	5.8[c]	6.5	7.9[g]	5.2[g]	18.0 (Belgium)[g] 16.3 (Bulgaria)[g]
Hepatitis A	1.2	0.5	5.7[c]	0.4	0.8[g]	0.9[g]	10.5 (Bulgaria)[g] 5.1 (Liechtenstein)[g]
Listeriosis	0.8	0.3	0.3	0.4	0.23	0.49	1.4 (Iceland)[f] 1.3 (Finland)[f]
Salmonellosis	14.6	39.8	14.2	12.3	14.6	15.7	93.7 (Czechia)[f] 81.3 (Slovakia)[f]
Shigellosis	1.3	5.4	3.4	1.2	3.1[g]	0.7[g]	2.1 (Luxembourg)[g] 1.9 (France/Slovakia)[g]
STEC infection	19.9	3.2	5.0	1.7	2.4	2.1	17.5 (Ireland)[f] 15.9 (Denmark)[f]
Yersiniosis	25.3	NN	1.4	NN	0.2	1.9	7.8 (Denmark)[f] 6.0 (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 case numbers. These have been converted to rates using a mid-year 2021 estimate of the Australian population of 25,996,144 (https://www.abs.gov.au/)

[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 2019 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 2020. 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 2021 Zoonoses Report https://www.efsa.europa.eu/en/efsajournal/pub/7666

[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 2021 year for hepatitis A, 2020 for shigellosis, 2019 for giardiasis, and 2018 for cryptosporidiosis

Table 70. Number of cases of selected notifiable diseases by year, 1993–2022

Disease	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007
Campylobacteriosis	8101	7714	7442	7635	8924	11,572	8161	8418	10,146	12,493	14,788	12,215	13,836	15,873	12,778
Cryptosporidiosis[a]	-	-	-	119	357	866	977	775	1208	975	817	611	888	737	924
Gastroenteritis[a, b]	-	-	-	555	316	493	608	730	942	1088	1030	1362	559	926	617
Giardiasis[a]	-	-	-	1235	2127	2183	1792	1688	1604	1547	1570	1514	1231	1214	1402
Hepatitis A	257	179	338	311	347	144	119	107	61	106	70	49	51	123	42
Listeriosis	11	8	13	10	35	17	19	22	18	19	24	26	20	19	26
Salmonellosis	1340	1522	1334	1141	1177	2069	2077	1795	2417	1880	1401	1081	1382	1335	1275
Shigellosis	128	185	191	167	117	122	147	115	157	112	87	140	183	102	129
STEC infection [a, b]	3	3	6	7	13	48	64	67	76	73	104	89	92	87	100
Yersiniosis[a]	-	-	-	330	488	546	503	396	429	472	436	407	383	453	502

Disease	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022
Campylobacteriosis	6692	7177	7346	6686	7016	6837	6782	6218	7457	6482	6957	6203	5292	5729	5878
Cryptosporidiosis	765	854	954	610	877	1348	584	696	1062	1192	1613	1035	735	702	612
Gastroenteritis	676	713	502	570	765	558	775	506	513	324	231	486	357	244	331
Giardiasis	1660	1639	1985	1934	1714	1729	1709	1510	1616	1648	1585	1749	1139	1041	707
Hepatitis A	89	44	46	26	82	91	74	47	35	58	68	67	22	8	59
Listeriosis	27	28	23	26	25	19	25	26	36	21	30	31	35	32	39
Salmonellosis	1337	1128	1146	1055	1081	1143	955	1051	1091	1127	1100	1190	709	714	750
Shigellosis	113	119	104	101	131	137	128	111	174	244	217	215	61	4	68
STEC infection	122	143	138	153	147	205	187	330	417	547	925	1103	845	911	1022
Yersiniosis	508	430	406	513	514	483	680	634	858	917	1201	1185	1260	1410	1294

[a] Acute gastroenteritis, cryptosporidiosis, giardiasis, 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 [43].

Note: cell marked "-" where data are unavailable

Table 71. Deaths due to selected notifiable diseases recorded in EpiSurv, 2003–2022

Disease	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022
Campylobacteriosis	0	0	1	1	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0
Cryptosporidiosis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Gastroenteritis[a]	0	0	0	0	0	0	0	0	0	0	0	2	0	1	0	0	0	0	0	0
Giardiasis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Listeriosis- non perinatal	2	3	1	0	2	3	2	3	1	4	2	3	1	0	0	2	0	1	3	4
Listeriosis- perinatal	2	2	4	1	2	2	2	4	0	2	3	2	3	2	0	0	4	1	1	2
Salmonellosis	0	0	1	1	1	1	1	0	0	0	0	0	0	0	1	0	0	0	0	0
Shigellosis	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
STEC infection	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0	2	1	0	0	1
Yersiniosis	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	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) single cases of chemical or toxic food poisoning such as botulism, histamine (scombroid) poisoning and any type of toxic shellfish poisoning [14]. Please note that other publications or reports may report botulism and toxic shellfish poisoning separately, resulting in differing case numbers for acute gastroenteritis.

Note: The numbers in this table are those recorded in EpiSurv where the notifiable disease was recorded as the primary cause of death.

Table 72. Ministry of Health hospital admissions data of selected notifiable diseases, 2020–2022

Disease	ICD 10 Codes	2020		2021		2022	
		Principal diagnosis	Other relevant diagnosis	Principal diagnosis	Other relevant diagnosis	Principal diagnosis	Other relevant diagnosis
Campylobacteriosis	A04.5	609	110	721	143	812	187
Cryptosporidiosis	A07.2	49	15	33	14	47	23
Giardiasis	A07.1	40	27	31	26	22	24
Hepatitis A	B15	17	40	9	31	36	43
Listeriosis	A32	19	19	20	19	20	20
Salmonellosis[a]	A02.0	138	27	185	35	173	39
Shigellosis	A03	15	24	7	19	27	43
STEC infection[b]	A04.3	17	22	24	19	35	32
Yersiniosis	A04.6	98	66	121	73	107	94

Note: Hospital admission data may include multiple admissions (to the same or different hospitals) for the same case and admissions may relate to cases first diagnosed in previous years. The data includes cases who are admitted with the disease as a primary or other diagnosis.

[a] *Salmonella* enterocolitis

[b] Enterohaemorrhagic *Escherichia coli* infection

Table 73. Ministry of Health hospital admissions and duration of hospital or intensive care unit (ICU) stay of selected notifiable diseases, 2022

Disease	ICD 10 Codes	Admissions to hospital	Nights in hospital per admission[a] Median [Range]	Admissions to ICU (% of admissions)[b]	Hours in ICU[b] Median [Range] or values
Campylobacteriosis	A04.5	999	2 [0 to 62]	15 (1.5)	43 [2 to 267]
Cryptosporidiosis	A07.2	70	2 [0 to 19]	1 (1.4)	39
Giardiasis	A07.1	46	3 [0 to 160]	1 (2.2)	327
Hepatitis A	B15	79	2 [0 to 73]	2 (2.5)	117 and 186
Listeriosis	A32	40	10 [1 to 38]	2 (5.0)	20 and 252
Salmonellosis[c]	A02.0	212	3 [0 to 30]	4 (1.9)	72 [20 to 249]
Shigellosis	A03	70	4 [0 to 48]	1 (1.4)	133
STEC infection[d]	A04.3	67	4 [0 to 32]	11 (16.4)	94 [4 to 282]
Yersiniosis	A04.6	201	3 [0 to 57]	7 (3.5)	57 [24 to 426]

Note: Hospital admission data may include multiple admissions (to the same or different hospitals) for the same case and admissions may relate to cases first diagnosed in previous years. The data includes cases who are admitted with the disease as a primary or other diagnosis.

[a] Nights admitted equates to the number of midnights spent in hospital by an individual during a single admission.

[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 during the hospital admission event, 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.

[c] *Salmonella* enterocolitis

[d] Enterohaemorrhagic *Escherichia coli* infection.

Ethnicity tables

Table 74. Number of cases and rate per 100,000 population of selected notifiable diseases by ethnic group[a], 2022

Disease	Notified Cases						Rates					
	Māori	Pacific peoples	Asian	MELAA[b]	European or Other	Total[c]	Māori	Pacific peoples	Asian	MELAA[b]	European or Other	Total[c]
Campylobacteriosis	596	162	410	76	4165	**5878**	69.8	46.9	52.7	101.9	135.6	**114.7**
Cryptosporidiosis	94	9	26	5	453	**612**	11.0	2.6	3.3	6.7	14.7	**11.9**
Gastroenteritis[d]	58	24	27	3	210	**331**	6.8	6.9	3.5	-	6.8	**6.5**
Giardiasis	88	9	49	11	514	**707**	10.3	2.6	6.3	14.7	16.7	**13.8**
Hepatitis A	5	1	18	1	33	**59**	0.6	-	2.3	-	1.1	**1.2**
Listeriosis	9	3	8	1	17	**39**	1.1	-	1.0	-	0.6	**0.8**
Salmonellosis	105	32	103	4	495	**750**	12.3	9.3	13.2	-	16.1	**14.6**
Shigellosis	4	5	14	1	43	**68**	-	1.4	1.8	-	1.4	**1.3**
STEC infection	112	24	62	14	794	**1022**	13.1	6.9	8.0	18.8	25.8	**19.9**
Yersiniosis	147	60	272	19	721	**1294**	17.2	17.4	34.9	25.5	23.5	**25.3**

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) single cases of chemical or toxic food poisoning such as botulism, histamine (scombroid) poisoning and any type of toxic shellfish poisoning [14]. Please note that other publications or reports may report botulism and toxic shellfish poisoning separately, resulting in differing case numbers for acute gastroenteritis.

Table 75. Ministry of Health hospital admissions and rate per 100,000 population of selected notifiable diseases by ethnic group[a], 2022

Disease	Hospital Admissions						Rate					
	Māori	Pacific peoples	Asian	MELAA[b]	European or Other	Total[c]	Māori	Pacific peoples	Asian	MELAA[b]	European or Other	Total[c]
Campylobacteriosis	140	57	78	21	700	**999**	16.4	16.5	10.0	28.1	22.8	**19.5**
Cryptosporidiosis	15	2	4	0	48	**70**	1.8	-	-	-	1.6	**1.4**
Giardiasis	10	2	6	1	27	**46**	1.2	-	0.8	-	0.9	**0.9**
Hepatitis A	8	6	23	4	37	**79**	0.9	1.7	3.0	-	1.2	**1.5**
Listeriosis	8	1	7	1	23	**40**	0.9	-	0.9	-	0.7	**0.8**
Salmonellosis	30	17	33	4	128	**212**	3.5	4.9	4.2	-	4.2	**4.1**
Shigellosis	11	8	18	0	33	**70**	1.3	2.3	2.3	-	1.1	**1.4**
STEC infection	12	1	4	0	50	**67**	1.4	-	-	-	1.6	**1.3**
Yersiniosis	29	21	47	5	99	**201**	3.4	6.1	6.0	6.7	3.2	**3.9**

Note: Where fewer than five cases have been notified, a rate has not been calculated (-).

Hospital admission data may include multiple admissions (to the same or different hospitals) for the same case and admissions may relate to cases first diagnosed in previous years. The data includes cases who are admitted with the disease as a primary or other diagnosis.

[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 (three campylobacteriosis cases, one cryptosporidosis case and 1 hepatitis A case)

Table 76. Ministry of Health hospitalisation duration of selected notifiable diseases by ethnic group[a], 2022

Disease	ICD 10 Codes	Nights in hospital per individual admission[b] Median [Range] or values if 1 or 2 admissions					
		Māori	Pacific peoples	Asian	MELAA[c]	European or Other	Total[c]
Campylobacteriosis	A04.5	2 [0 to 37]	2 [0 to 52]	2 [0 to 25]	1 [0 to 8]	2 [0 to 62]	**2 [0 to 62]**
Cryptosporidiosis	A07.2	2 [0 to 7]	0 and 8	3 [2 to 9]	-	2 [0 to 19]	**2 [0 to 19]**
Giardiasis	A07.1	4 [0 to 160]	3 and 9	3 [2 to 13]	1	2 [0 to 16]	**3 [0 to 160]**
Hepatitis A	B15	5 [1 to 34]	7 [0 to 40]	2 [0 to 10]	4 [0 to 4]	2 [0 to 73]	**2 [0 to 73]**
Listeriosis	A32	13 [2 to 24]	5	10 [3 to 22]	25	13 [1 to 38]	**10 [1 to 38]**
Salmonellosis[d]	A02.0	3 [0 to 8]	3 [0 to 7]	3 [0 to 10]	3 [0 to 17]	2 [0 to 30]	**3 [0 to 30]**
Shigellosis	A03	3 [0 to 48]	5 [0 to 28]	2 [0 to 39]	-	5 [0 to 45]	**4 [0 to 48]**
STEC infection[e]	A04.3	4 [0 to 23]	12	4 [2 to 32]	-	4 [0 to 28]	**4 [0 to 32]**
Yersiniosis	A04.6	3 [0 to 34]	4 [0 to 44]	2 [0 to 34]	2 [0 to 5]	5 [0 to 57]	**3 [0 to 57]**

Note: Hospital admission data may include multiple admissions (to the same or different hospitals) for the same case and admissions may relate to cases first diagnosed in previous years. The data includes cases who are admitted with the disease as a primary or other diagnosis.

[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] Nights admitted equates to the number of midnights spent in hospital by an individual during a single admission. - : No admissions recorded.

[c] MELAA: Middle Eastern, Latin American and African

[d] *Salmonella* enterocolitis

[e] Enterohaemorrhagic *Escherichia coli* infection

Table 77. Ministry of Health intensive care unit admissions and duration of selected notifiable diseases by ethnic group, 2022

Disease	ICU Admission[b] during hospitalisation						Hours admitted to ICU[b] Median [Range] or values if 1 or 2 admissions				
	Māori	Pacific peoples	Asian	MELAA[b]	European or Other	Total	Māori	Pacific peoples	Asian	MELAA[b]	European or Other
Campylobacteriosis	3	0	1	0	11	15	41 [2 to 114]	-	119	-	43 [28 to 267]
Cryptosporidiosis	0	1	0	0	0	1	-	39	-	-	-
Giardiasis	1	0	0	0	0	1	327	-	-	-	-
Hepatitis A	0	1	0	0	1	2	-	117	-	-	186
Listeriosis	1	0	0	0	1	2	20	-	-	-	252
Salmonellosis[d]	0	1	1	0	2	4	-	46	97	-	20 and 249
Shigellosis	1	0	0	0	0	1	133	-	-	-	-
STEC infection[e]	2	0	1	0	8	11	133 and 162	-	140	-	87 [4 to 282]
Yersiniosis	3	2	0	0	2	7	98 [24 to 108]	47 and 426	-	-	36 and 57

Note: Hospital admission data may include multiple admissions (to the same or different hospitals) for the same case and admissions may relate to cases first diagnosed in previous years. The data includes cases who are admitted with the disease as a primary or other diagnosis.

[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 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 admissions to ICU.

[c] MELAA: Middle Eastern, Latin American and African

[d] *Salmonella* enterocolitis

[e] Enterohaemorrhagic *Escherichia coli* infection

Sex tables

Table 78. Number of cases and rate per 100,000 population of selected notifiable diseases by sex, 2022

Disease	Sex					
	Male		Female		Total[a]	
	Cases	Rate	Cases	Rate	Cases	Rate
Campylobacteriosis	3244	127.6	2631	101.9	**5878**	**114.7**
Cryptosporidiosis	285	11.2	327	12.7	**612**	**11.9**
Gastroenteritis[b]	159	6.3	171	6.6	**331**	**6.5**
Giardiasis	394	15.5	312	12.1	**707**	**13.8**
Hepatitis A	31	1.2	28	1.1	**59**	**1.2**
Listeriosis[c]	13	0.5	26	1.0	**39**	**0.8**
Salmonellosis	352	13.8	397	15.4	**750**	**14.6**
Shigellosis	42	1.7	26	1.0	**68**	**1.3**
STEC infection	450	17.7	572	22.2	**1022**	**19.9**
Yersiniosis	622	24.5	672	26.0	**1294**	**25.3**

Note: Rate is not calculated for fewer than five cases

[a] Total includes cases where sex 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) single cases of chemical or toxic food poisoning such as botulism, histamine (scombroid) poisoning and any type of toxic shellfish poisoning [14]. 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 seven perinatal cases are those for the mother.

Table 79. Ministry of Health hospitalisations and duration of hospital or intensive care unit (ICU) stay of selected notifiable diseases by sex, 2022

Disease	Sex							
	Male				Female			
	Hospital Admissions[a]	Nights per hospital admission[b] Median [Range]	Admission to ICU[c]	ICU hours[c] Median [Range] or values	Hospital Admissions[a]	Nights per hospital admission[b] Median [Range]	Admission to ICU[c]	ICU hours[c] Median [Range] or values
Campylobacteriosis	521	2 [0 to 44]	9	59 [30 to 237]	478	2 [0 to 62]	6	38 [2 to 267]
Cryptosporidiosis	35	1 [0 to 12]	0	-	35	2 [0 to 19]	1	39
Giardiasis	24	4.5 [0 to 13]	0	-	22	2 [0 to 160]	1	327
Hepatitis A	40	2 [0 to 73]	2	117 and 186	39	2 [0 to 40]	0	-
Listeriosis[d]	11	15 [3 to 35]	2	20 and 252	29	9 [1 to 38]	0	-
Salmonellosis[e]	100	2 [0 to 30]	2	20 and 97	112	3 [0 to 27]	2	46 and 249
Shigellosis	44	4 [0 to 39]	1	133	26	3 [0 to 48]	0	-
STEC infection[f]	28	2 [0 to 23]	4	109 [43 to 282]	39	4 [0 to 32]	7	94 [4 to 162]
Yersiniosis	94	3 [0 to 57]	3	98 [47 to 426]	107	3 [0 to 49]	4	47[24 to 108]

[a] Hospital admission data may include multiple admissions (to the same or different hospitals) for the same case and admissions may relate to cases first diagnosed in previous years. The data includes cases who are admitted with the disease as a primary or other diagnosis.

[b] Nights admitted equates to the number of midnights spent in hospital by an individual during a single admission.

[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 admissions to ICU

[d] Case details for the seven perinatal cases are those for the mother.

[e] *Salmonella* enterocolitis

[f] Enterohaemorrhagic *Escherichia coli* infection

Age group tables

Table 80. Number of cases of selected notifiable diseases by age group, 2022

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]
Campylobacteriosis	112	559	259	210	293	811	646	595	699	800	893	**5878**
Cryptosporidiosis	7	129	65	33	46	136	82	49	24	27	14	**612**
Gastroenteritis[b]	4	24	15	7	9	53	45	49	37	43	40	**331**
Giardiasis	10	115	45	15	12	73	154	89	70	79	45	**707**
Hepatitis A	0	0	4	1	4	18	14	2	6	7	3	**59**
Listeriosis[c]	2	0	0	0	1	4	3	2	2	4	21	**39**
Salmonellosis	50	105	56	21	42	82	78	61	85	89	81	**750**
Shigellosis	0	8	3	1	1	7	11	12	11	8	6	**68**
STEC infection	35	166	61	51	47	103	77	69	105	118	190	**1022**
Yersiniosis	86	156	36	35	46	148	175	137	135	170	170	**1294**

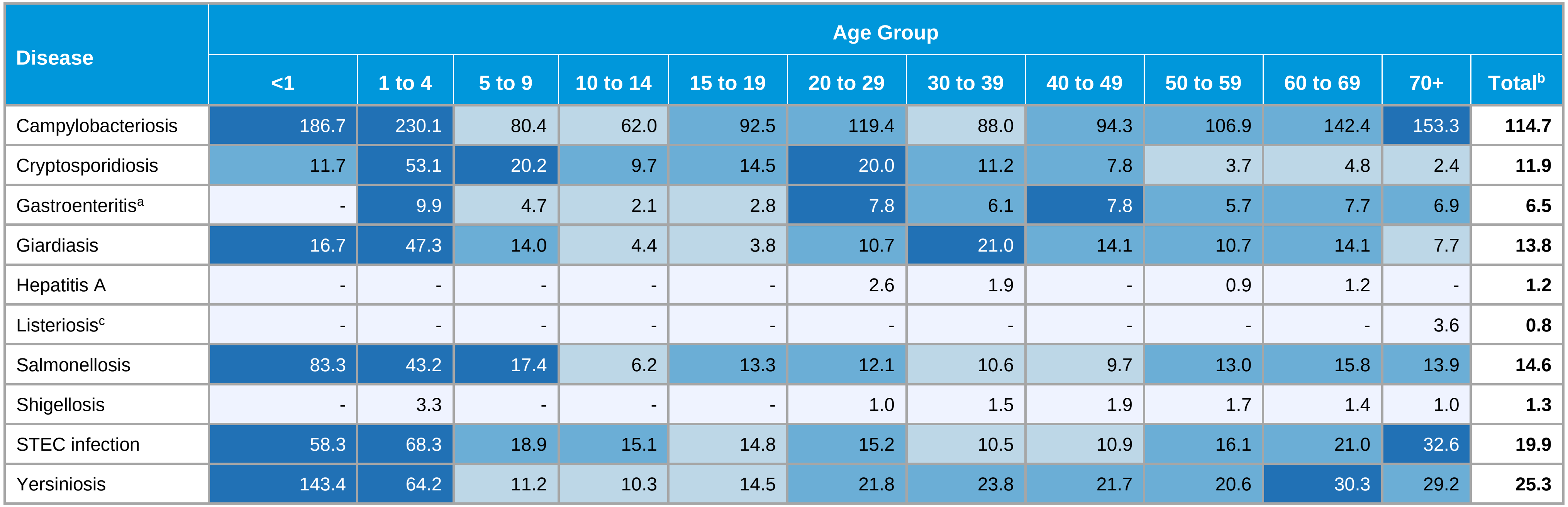
[a] Total includes cases where age was unknown

[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) single cases of chemical or toxic food poisoning such as botulism, histamine (scombroid) poisoning and any type of toxic shellfish poisoning [14]. 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 seven perinatal cases are those for the mother.

Table 81. Rate per 100,000 population of selected notifiable diseases by age group, 2022



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[b]
Campylobacteriosis	186.7	230.1	80.4	62.0	92.5	119.4	88.0	94.3	106.9	142.4	153.3	**114.7**
Cryptosporidiosis	11.7	53.1	20.2	9.7	14.5	20.0	11.2	7.8	3.7	4.8	2.4	**11.9**
Gastroenteritis[a]	-	9.9	4.7	2.1	2.8	7.8	6.1	7.8	5.7	7.7	6.9	**6.5**
Giardiasis	16.7	47.3	14.0	4.4	3.8	10.7	21.0	14.1	10.7	14.1	7.7	**13.8**
Hepatitis A	-	-	-	-	-	2.6	1.9	-	0.9	1.2	-	**1.2**
Listeriosis[c]	-	-	-	-	-	-	-	-	-	-	3.6	**0.8**
Salmonellosis	83.3	43.2	17.4	6.2	13.3	12.1	10.6	9.7	13.0	15.8	13.9	**14.6**
Shigellosis	-	3.3	-	-	-	1.0	1.5	1.9	1.7	1.4	1.0	**1.3**
STEC infection	58.3	68.3	18.9	15.1	14.8	15.2	10.5	10.9	16.1	21.0	32.6	**19.9**
Yersiniosis	143.4	64.2	11.2	10.3	14.5	21.8	23.8	21.7	20.6	30.3	29.2	**25.3**

[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) single cases of chemical or toxic food poisoning such as botulism, histamine (scombroid) poisoning and any type of toxic shellfish poisoning [14]. Please note that other publications or reports may report botulism and toxic shellfish poisoning separately, resulting in differing case numbers for acute gastroenteritis. Please note that other publications or reports may report botulism and toxic shellfish poisoning separately, resulting in differing case numbers for acute gastroenteritis.

[b] Total includes cases where age was unknown

[c] Case details for the seven perinatal cases are those for the mother

⬜	Fewer than five cases in a cell or less than a national total of 100 cases for the year
░	First band (lower than 25th percentile)
▒	Second (middle) band
▓	Third band (above 75th percentile)

Table 82. Ministry of Health duration of hospital admissions of selected notifiable diseases by age group (nights in hospital per admission, median [range])[a], 2022

Disease	Age group (years)					
	<1	1 to 4	5 to 9	10 to 14	15 to 19	20 to 29
Campylobacteriosis	1 [0 to 4]	1 [0 to 12]	1 [0 to 6]	1 [0 to 5]	1 [0 to 6]	1 [0 to 44]
Cryptosporidiosis	-	2 [1 to 5]	1 [0 to 12]	5 and 6	4 [0 to 11]	1 [0 to 5]
Giardiasis	160	1.5 [1 to 8]	0	-	-	2 [0 to 4]
Hepatitis A	-	3	2 [0 to 4]	1	1 and 2	1 [0 to 34]
Listeriosis[b]	25	-	-	0	5	5 and 7
Salmonellosis	3 [0 to 5]	1 [0 to 9]	2 [0 to 5]	2 [0 to 3]	1 [0 to 2]	1 [0 to 9]
Shigellosis	3 [0 to 23]	2 [0 to 4]	3 [3 to 6]	-	2 [2 to 7]	6 [1 to 48]
STEC infection	4 and 23	3 [0 to 32]	2 [0 to 28]	2 and 13	0	3 [0 to 5]
Yersiniosis	1 [0 to 4]	1 [0 to 3]	1 [1 to 6]	1 [0 to 9]	2	2 [0 to 7]

Disease	Age group (years)				
	30 to 39	40 to 49	50 to 59	60 to 69	70+
Campylobacteriosis	2 [0 to 37]	2 [0 to 29]	2 [0 to 21]	3 [0 to 25]	3 [0 to 62]
Cryptosporidiosis	2 [0 to 19]	5 [0 to 6]	5	3 [1 to 4]	5 [2 to 9]
Giardiasis	3 [0 to 5]	2 [0 to 9]	2 [1 to 8]	2 [0 to 30]	6 [5 to 16]
Hepatitis A	1 [0 to 7]	4 [0 to 31]	4 [0 to 73]	2 [0 to 10]	4 [0 to 48]
Listeriosis[b]	5 [1 to 18]	6 and 11	9	22 [10 to 30]	13 [2 to 38]
Salmonellosis	2 [0 to 8]	4 [0 to 13]	5 [0 to 10]	3 [0 to 19]	4 [0 to 30]
Shigellosis	2 [0 to 5]	3 [1 to 29]	4 [0 to 5]	4 [0 to 8]	9 [1 to 45]
STEC infection	2 [1 to 13]	3 and 3	7 [2 to 17]	9 [0 to 23]	5 [1 to 14]
Yersiniosis	2 [0 to 23]	3 [1 to 27]	4 [0 to 31]	4 [0 to 44]	7 [0 to 57]

Note: Hospital admission data may include multiple admissions (to the same or different hospitals) for the same case and admissions may relate to cases first diagnosed in previous years. The data includes cases who are admitted with the disease as a primary or other diagnosis. The duration of hospital admissions represents the number of midnights a case was admitted to hospital.

a 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 admissions to hospital.

b Case details for the seven perinatal cases are those for the mother.

Table 83. Ministry of Health hospital admissions which included time in an intensive care unit (ICU) of selected notifiable diseases by age group, 2022

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[a]
Campylobacteriosis	0	2	0	0	0	0	1	0	0	6	6	**15**
Cryptosporidiosis	0	0	0	0	0	0	0	0	0	0	1	**1**
Giardiasis	1	0	0	0	0	0	0	0	0	0	0	**1**
Hepatitis A	0	0	0	0	0	1	0	1	0	0	0	**2**
Listeriosis[b]	0	0	0	0	0	0	0	0	1	0	1	**2**
Salmonellosis	0	0	0	0	0	1	0	2	0	0	1	**4**
Shigellosis	1	0	0	0	0	0	0	0	0	0	0	**1**
STEC infection	1	1	1	0	0	0	1	0	0	2	5	**11**
Yersiniosis	0	0	0	0	0	0	0	3	2	1	1	**7**

Note: Hospital admission data may include multiple admissions (to the same or different hospitals) for the same case and admissions may relate to cases first diagnosed in previous years. The data includes cases who are admitted with the disease as a primary or other 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.

[a] Total includes cases where age was unknown

[b] Case details for the seven perinatal cases are those for the mother.

Table 84. Ministry of Health ICU duration (hours, median [range] or values)[a] of selected notifiable diseases by age group, 2022

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	-	41 and 114	-	-	-	-	119	-	-	37 [2 to 84]	86 [30 to 267]
Cryptosporidiosis	-	-	-	-	-	-	-	-	-	-	39
Giardiasis	327	-	-	-	-	-	-	-	-	-	-
Hepatitis A	-	-	-	-	-	117	-	186	-	-	-
Listeriosis[b]	-	-	-	-	-	-	-	-	20	-	252
Salmonellosis	-	-	-	-	-	46	-	20 and 97	-	-	249
Shigellosis	133	-	-	-	-	-	-	-	-	-	-
STEC infection	133	140	4	-	-	-	156	-	-	84 and 282	90 [43 to 162]
Yersiniosis	-	-	-	-	-	-	-	47 [24 to 426]	57 and 98	108	36

Note: Hospital admission data may include multiple admissions (to the same or different hospitals) for the same case and admissions may relate to cases first diagnosed in previous years. The data includes cases who are admitted with the disease as a primary or other diagnosis. The duration of hospital admissions represents the number of midnights a case was admitted to hospital.

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 admissions to ICU

[a] 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.

[b] Case details for the seven perinatal cases are those for the mother

Table 85. Number of cases of selected notifiable diseases by District Health Board area, 2022

Disease	District Health Board																				
	Northland	**Waitemata**	**Auckland**	**Counties Manukau**	**Waikato**	**Lakes**	**Bay of Plenty**	**Tairawhiti**	**Taranaki**	**Hawkes Bay**	**Whanganui**	**MidCentral**	**Hutt Valley**	**Capital and Coast**	**Wairarapa**	**Nelson Marlborough**	**West Coast**	**Canterbury**	**South Canterbury**	**Southern**	**Total**
Campylobacteriosis	300	703	509	513	599	140	292	60	215	239	66	229	146	298	86	173	55	637	143	475	**5878**
Cryptosporidiosis	39	57	37	41	89	15	22	6	39	17	7	30	9	29	15	11	6	49	26	68	**612**
Gastroenteritis[a]	27	4	6	7	55	21	27	0	2	2	3	0	23	19	5	10	4	89	2	25	**331**
Giardiasis	28	71	81	58	84	28	53	22	25	47	7	36	11	51	5	20	5	40	5	30	**707**
Hepatitis A	1	5	8	8	6	0	3	1	0	5	2	0	1	3	0	0	2	9	2	3	**59**
Listeriosis	3	2	5	4	2	2	6	0	1	1	0	1	2	2	0	2	0	4	0	2	**39**
Salmonellosis	37	77	58	70	71	17	46	4	20	20	6	18	14	41	13	18	5	121	17	77	**750**
Shigellosis	5	10	15	9	5	0	4	1	3	3	0	2	0	1	0	3	0	5	0	2	**68**
STEC infection	60	68	61	58	107	31	55	20	61	35	17	46	13	58	37	38	0	82	19	156	**1022**
Yersiniosis	25	169	155	98	93	40	82	32	38	42	7	31	63	124	26	48	3	124	11	83	**1294**

[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) single cases of chemical or toxic food poisoning such as botulism, histamine (scombroid) poisoning and any type of toxic shellfish poisoning [14]. 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 86. Rate per 100,000 population of selected notifiable diseases by District Health Board area, 2022

Disease	District Health Board																				
	Northland	Waitemata	Auckland	Counties Manukau	Waikato	Lakes	Bay of Plenty	Tairawhiti	Taranaki	Hawke's Bay	Whanganui	MidCentral	Hutt Valley	Capital & Coast	Wairarapa	Nelson Marlborough	West Coast	Canterbury	South Canterbury	Southern	Total
Campylobacteriosis	148.9	111.0	105.7	84.8	132.6	118.4	106.3	115.2	168.6	130.9	95.0	120.3	91.1	92.5	168.6	104.8	168.2	107.7	229.5	135.5	**114.7**
Cryptosporidiosis	19.4	9.0	7.7	6.8	19.7	12.7	8.0	11.5	30.6	9.3	10.1	15.8	5.6	9.0	29.4	6.7	18.3	8.3	41.7	19.4	**11.9**
Gastroenteritis[a]	13.4	-	1.2	1.2	12.2	17.8	9.8	-	-	-	-	-	14.4	5.9	9.8	6.1	-	15.0	-	7.1	**6.5**
Giardiasis	13.9	11.2	16.8	9.6	18.6	23.7	19.3	42.2	19.6	25.7	10.1	18.9	6.9	15.8	9.8	12.1	15.3	6.8	8.0	8.6	**13.8**
Hepatitis A	-	0.8	1.7	1.3	1.3	-	-	-	-	2.7	-	-	-	-	-	-	-	1.5	-	-	**1.2**
Listeriosis	-	-	1.0	-	-	-	2.2	-	-	-	-	-	-	-	-	-	-	-	-	-	**0.8**
Salmonellosis	18.4	12.2	12.0	11.6	15.7	14.4	16.7	-	15.7	11.0	8.6	9.5	8.7	12.7	25.5	10.9	15.3	20.5	27.3	22.0	**14.6**
Shigellosis	2.5	1.6	3.1	1.5	1.1	-	-	-	-	-	-	-	-	-	-	-	-	0.8	-	-	**1.3**
STEC infection	29.8	10.7	12.7	9.6	23.7	26.2	20.0	38.4	47.8	19.2	24.5	24.2	8.1	18.0	72.5	23.0	-	13.9	30.5	44.5	**19.9**
Yersiniosis	12.4	26.7	32.2	16.2	20.6	33.8	29.9	61.4	29.8	23.0	10.1	16.3	39.3	38.5	51.0	29.1	-	21.0	17.7	23.7	**25.3**

[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) single cases of chemical or toxic food poisoning such as botulism, histamine (scombroid) poisoning and any type of toxic shellfish poisoning [14]. 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

First band (lower than 25th percentile)

Second (middle) band

Third band (above 75th percentile)

Table 87. Number of cases and rate per 100,000 population of selected notifiable diseases by prioritised urban rural residence group, 2022

Disease	Cases (excluding those with overseas travel as a risk factor)							Rate per 100,000 population						
	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	2194	699	483	685	234	1455	**5750**	85.0	97.7	109.8	125.9	142.1	214.9	**112.2**
Cryptosporidiosis	155	74	52	80	29	212	**602**	6.0	10.3	11.8	14.7	17.6	31.3	**11.7**
Gastroenteritis[a]	135	30	28	36	7	43	**277**	5.2	4.2	6.4	6.6	4.3	6.4	**5.4**
Giardiasis	262	106	49	73	26	156	**672**	10.1	14.8	11.1	13.4	15.8	23.0	**13.1**
Hepatitis A	15	5	1	9	1	8	**39**	0.6	0.7	-	1.7	-	1.2	**0.8**
Listeriosis	19	4	2	6	2	4	**37**	0.7	-	-	1.1	-	-	**0.7**
Salmonellosis	258	60	47	74	33	158	**630**	10.0	8.4	10.7	13.6	20.0	23.3	**12.3**
Shigellosis	19	0	0	2	3	1	**25**	0.7	-	-	-	-	-	**0.5**
STEC infection	268	134	94	112	54	324	**986**	10.4	18.7	21.4	20.6	32.8	47.9	**19.2**
Yersiniosis	662	207	101	98	40	164	**1272**	25.6	28.9	23.0	18.0	24.3	24.2	**24.8**

Note: Where fewer than five cases have been notified, a rate has not been calculated.

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.

[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) single cases of chemical or toxic food poisoning such as botulism, histamine (scombroid) poisoning and any type of toxic shellfish poisoning [14]. Please note that other publications or reports may report botulism and toxic shellfish poisoning separately, resulting in differing case numbers for acute gastroenteritis

Table 88. Ministry of Health hospital admissions and rate per 100,000 population of selected notifiable diseases by urban rural residence group, 2022

Disease	Hospital admissions							Hospital admissions per 100,000 population						
	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	472	126	103	184	71	43	**999**	18.3	17.6	23.4	33.8	43.1	6.4	19.5
Cryptosporidiosis	17	6	10	20	12	5	**70**	0.7	0.8	2.3	3.7	7.3	0.7	1.4
Giardiasis	20	5	1	15	2	3	**46**	0.8	0.7	-	2.8	-	-	0.9
Hepatitis A	50	7	3	17	2	0	**79**	1.9	1.0	-	3.1	-	-	1.5
Listeriosis	21	3	1	8	6	1	**40**	0.8	-	-	1.5	3.6	-	0.8
Salmonellosis	111	20	14	32	22	13	**212**	4.3	2.8	3.2	5.9	13.4	1.9	4.1
Shigellosis	38	10	5	10	4	3	**70**	1.5	1.4	1.1	1.8	-	-	1.4
STEC infection	28	4	9	9	10	7	**67**	1.1	-	2.0	1.7	6.1	1.0	1.3
Yersiniosis	132	27	16	19	4	3	**201**	5.1	3.8	3.6	3.5	-	-	3.9

Note: Where fewer than five cases have been notified, a rate has not been calculated.

Hospital admission data may include multiple admissions (to the same or different hospitals) for the same case and admissions may relate to cases first diagnosed in previous years. The data includes cases who are admitted with the disease as a primary or other diagnosis. -: No hospital admissions.

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.

Table 89. Number of cases of selected notifiable diseases by the 2013 Deprivation Index of area of residence, 2022

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
Campylobacteriosis	653	1228	1188	1064	921	696	**5750**
Cryptosporidiosis	72	127	123	137	82	61	**602**
Gastroenteritis[b]	55	37	35	40	57	53	**277**
Giardiasis	71	149	138	107	115	92	**672**
Hepatitis A	1	11	8	7	5	7	**39**
Listeriosis	4	4	8	8	7	6	**37**
Salmonellosis	80	125	121	99	113	92	**630**
Shigellosis	2	6	2	6	2	7	**25**
STEC infection	141	220	201	163	145	116	**986**
Yersiniosis	147	256	251	240	211	167	**1272**

Note: Analyses excludes notifications which list overseas travel as a possible risk factor.

[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 [44].

[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) single cases of chemical or toxic food poisoning such as botulism, histamine (scombroid) poisoning and any type of toxic shellfish poisoning [14]. Please note that other publications or reports may report botulism and toxic shellfish poisoning separately, resulting in differing case numbers for acute gastroenteritis.

Table 90. Percentage of total cases of selected notifiable diseases by 2013 Deprivation Index of area of residence, 2022

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	11.4	21.4	20.7	18.5	16.0	12.1
Cryptosporidiosis	12.0	21.1	20.4	22.8	13.6	10.1
Gastroenteritis[b]	19.9	13.4	12.6	14.4	20.6	19.1
Giardiasis	10.6	22.2	20.5	15.9	17.1	13.7
Salmonellosis	12.7	19.8	19.2	15.7	17.9	14.6
STEC infection	14.3	22.3	20.4	16.5	14.7	11.8
Yersiniosis	11.6	20.1	19.7	18.9	16.6	13.1

Note: Analyses excludes notifications which list overseas travel as a possible risk factor.

Hepatitis A, listeriosis and shigellosis 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 a case was equally likely to reside in an area assigned to each of the 10 levels, then the cells 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 [44].

[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) single cases of chemical or toxic food poisoning such as botulism, histamine (scombroid) poisoning and any type of toxic shellfish poisoning [14]. Please note that other publications or reports may report botulism and toxic shellfish poisoning separately, resulting in differing case numbers for acute gastroenteritis.

Table 91. Ministry of Health hospital admissions of selected notifiable diseases by the 2013 Deprivation Index of area of residence, 2022

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
Campylobacteriosis	2	188	198	189	208	214	**999**
Cryptosporidiosis	1	11	18	13	18	9	**70**
Giardiasis	0	7	8	8	9	14	**46**
Hepatitis A	0	8	13	12	21	25	**79**
Listeriosis	0	10	4	9	4	13	**40**
Salmonellosis	5	40	35	30	49	53	**212**
Shigellosis	3	9	14	12	13	19	**70**
STEC infection	1	17	13	18	7	11	**67**
Yersiniosis	1	33	38	34	40	55	**201**

Note: Hospital admission data may include multiple admissions (to the same or different hospitals) for the same case and admissions may relate to cases first diagnosed in previous years. The data includes cases who are admitted with the disease as a primary or other diagnosis.

[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 [44].

Table 92. Percentage of total hospital admissions of selected notifiable diseases by the 2013 Deprivation Index of area of residence, 2022

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	0.2	18.8	19.8	18.9	20.8	21.4
Cryptosporidiosis	1.4	15.7	25.7	18.6	25.7	12.9
Giardiasis	0.0	15.2	17.4	17.4	19.6	30.4
Hepatitis A	0.0	10.1	16.5	15.2	26.6	31.6
Salmonellosis	2.4	18.9	16.5	14.2	23.1	25.0
Shigellosis	4.3	12.9	20.0	17.1	18.6	27.1
STEC infection	1.5	25.4	19.4	26.9	10.4	16.4
Yersiniosis	0.5	16.4	18.9	16.9	19.9	27.4

Note: Listeriosis cases are not included in 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 a case was equally likely to reside in an area assigned to each of the 10 levels, then the cells 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 [44].

Table 93. Potential foodborne outbreaks with a common source and associated cases by pathogen/condition as reported in EpiSurv, 2022

Pathogen/Condition	Outbreaks (n = 27)[a]		Cases (n = 193)[a]	
	No.	%[b]	No.	%[c]
Norovirus infection	5	18.5	23	11.9
Salmonellosis	3	11.1	33	17.1
Campylobacteriosis	3	11.1	12	6.2
Hepatitis A	1	3.7	35[d]	18.1
Clostridium perfringens intoxication	1	3.7	5	2.6
Giardiasis	1	3.7	3	1.6
STEC infection	1	3.7	3	1.6
Histamine (scombroid) fish poisoning	1	3.7	2	1.0
Listeriosis	1	3.7	2	1.0
Pathogen not identified [e]	10	37.0	75	38.9

Note:

[a] Data excludes a nationwide *V. parahaemolyticus* gastroenteritis outbreak (60 cases) which did not have a common location or supplier for the source of infection.

[b] Percentage of outbreaks for each pathogen/condition, calculated using the total number of foodborne outbreaks (27). 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 preparation of food was conducted.

[c] Percentage of cases for each pathogen/condition, calculated using the total number of associated cases (193)

[d] Hepatitis A outbreak associated with imported frozen berries continued into 2023. In 2022 there were 35 cases associated with the outbreak.

[e] All enteric outbreaks with no pathogen identified in 2022 were recorded as gastroenteritis

Table 94. Potential foodborne outbreaks with a common source and associated cases by exposure setting as reported in EpiSurv, 2022

Exposure setting	Outbreaks (n = 27)[a]		Cases (n = 193)[a]	
	No.	%[b]	No.	%[c]
Commercial food operators	**16**	**59.3**	**104**	**53.9**
Restaurant/cafe/bakery	12	44.4	63	32.6
Cruise ship, airline, tour bus, train	1	3.7	25	13.0
Caterers	1	3.7	11	5.7
Temporary or mobile service	1	3.7	3	1.6
Takeaway	1	3.7	2	1.0
Institutions	4	**14.8**	**29**	**15.0**
Childcare centre	2	7.4	18	9.3
School	1	3.7	5	2.6
Other institution	1	3.7	6	3.1
Other	**7**	**25.9**	**60**	**31.1**
Home	5	18.5	22	11.4
Farm	1	3.7	3	1.6
Mixed	1[d]	3.7	35[d]	18.1

[a] Data excludes a nationwide *V. parahaemolyticus* gastroenteritis outbreak (60 cases) which did not have a common location or supplier for the source of infection.

[b] Percentage of outbreaks for each exposure setting, calculated using the total number of foodborne outbreaks (27). An outbreak has been 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 preparation of food was conducted.

[c] Percentage of cases for each exposure setting, calculated using the total number of associated cases (193)

[d] Hepatitis A outbreak associated with imported frozen berries continued into 2023. In 2022 there were 35 cases associated with the outbreak.

Table 95. Potential foodborne outbreaks with a common source and associated cases by preparation setting as reported in EpiSurv, 2022

Preparation setting	Outbreaks (n = 27)[a]		Cases (n = 193)[a]	
	No.	%[b]	No.	%[c]
Commercial food operators	**14**	**51.9**	**79**	**40.9**
Restaurant/cafe/bakery	10	37.0	58	30.1
Caterers	2	7.4	16	8.3
Temporary or mobile service	1	3.7	3	1.6
Takeaway	1	3.7	2	1.0
Institutions	**3**	**11.1**	**24**	**12.4**
Childcare centre	2	7.4	18	9.3
Other institution	1	3.7	6	3.1
Other	**7**	**25.9**	**60**	**31.1**
Home	5	18.5	22	11.4
Farm	1	3.7	3	1.6
Mixed	1[d]	3.7	35[d]	18.1
Unknown	**3**	**11.1**	**30**	**15.5**

[a] Data excludes a nationwide *V. parahaemolyticus* gastroenteritis outbreak (60 cases) which did not have a common location or supplier for the source of infection.

[b] Percentage of outbreaks for each exposure setting, calculated using the total number of foodborne outbreaks (27). An outbreak has been 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 preparation of food was conducted

[c] Percentage of cases for each exposure setting, calculated using the total number of associated cases (193)

[d] Hepatitis A outbreak associated with imported frozen berries continued into 2023. In 2022 there were 35 cases associated with the outbreak.

Table 96. All non-O157 STEC serotypes identified from human isolates by the Enteric Reference Laboratory, 2018–2022

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 58), 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	2018	2019	2020	2021	2022
O1:H7	0	0	0	2	0
O2:H6	0	0	1	0	3
O2:H29	0	0	0	1	0
O3:H12	0	0	0	0	1
O3:H21	0	1	0	0	0
O5:H19	0	0	3	1	2
O5:HNM	4	0	0	0	0
O5:HNT	0	8	13	12	9
O6:H10	0	0	1	0	0
O6:H34	0	1	0	0	0
O6:HNM	1	0	0	0	0
O7:H14	0	0	0	1	1
O8:H8	0	0	0	0	1
O8:H9	1	0	1	1	1
O8:H16	0	0	2	1	3
O8/O30:H25	0	0	0	3	2
O8:HNM	1	0	0	0	0
O9:H30	0	0	0	1	1
O11:H25	0	0	1	0	0
O15:H2	1	2	3	2	1
O15:H4	0	0	0	0	2
O15:H16	0	1	0	0	0
O15:H27	0	1	1	0	2
O17:H18	0	2	1	1	1
O17/O106:H45	0	0	1	0	0
O18:H5	0	0	0	1	0
O18:H7	0	0	0	1	0
O21:H2	0	0	0	1	0
O21:H21	0	0	0	0	1
O22:H16	0	1	0	1	0
O23:H8	0	1	0	0	0
O25:H4	0	1	0	0	0
O26:H8	0	1	0	0	0
O26:H11	76	119	121	131	109
O26:HNM	1	0	0	0	0
O26:HNT	1	7	0	0	0
O29:H4	1	0	0	0	0
O38:H26	19	27	33	27	38
O38:HNT	0	2	0	0	0
O41:H21	0	2	0	0	0
O43:H2	0	1	0	1	1
O45:H2	1	0	1	0	0
O45:H19	0	0	0	1	0
O51:H24	0	1	2	0	0
O53:H45	0	0	1	0	0
O55:H12	0	1	2	4	3
O61:H2	0	1	0	0	0
O64:H20	4	7	5	5	5
O65:H2	1	1	0	0	0
O66:H25	0	0	0	1	1
O69:H11	0	1	0	0	0
O71:H2	0	1	0	0	0
O74:H20	0	1	1	0	0
O75:H5	0	0	1	0	0
O75:H7	0	0	2	0	0
O75:H8	1	1	0	3	1
O75:HNT	1	0	0	0	0
O76:H19	0	1	0	2	0
O76:H21	1	0	0	0	0
O77:HNM	1	0	0	0	0
O78:H4	0	0	1	1	0
O80:H2	0	0	0	0	1

Serotype	2018	2019	2020	2021	2022
O80:HNM	1	0	0	0	0
O81:H21	1	0	0	0	0
O82:H8	0	1	0	0	0
O83:H27	0	0	1	0	0
O84:H2	0	4	10	10	10
O84:HNM	2	0	0	0	0
O84:HNT	0	3	0	0	0
O85:H49	0	2	1	1	3
O87:H2	1	0	0	0	0
O87:H16	0	0	0	1	1
O88:H8	0	7	7	11	8
O88:HNM	2	0	0	0	0
O88:HNT	2	2	0	0	0
O91:H14	0	12	12	28	19
O91:H21	2	1	1	0	2
O91:HNM	5	0	0	0	0
O91:HNT	1	1	0	0	1
O93:H28	0	0	0	1	1
O93:H46	0	0	1	0	0
O99:H11, H35	0	1	0	0	0
O100:H20	0	1	0	0	1
O101:H19	1	0	0	0	0
O103:H2	7	11	0	20	11
O103:H8	0	0	0	0	1
O103:H25	4	12	1	5	10
O103:HNT	1	1	0	0	0
O103:HRough	1	0	0	0	0
O104:H7	1	1	1	5	2
O107/O117:H7	0	0	0	1	0
O108:H9	0	1	0	0	0
O108:H21	0	0	0	0	1
O108:H25	1	0	0	0	0
O100/O154:H25	0	0	0	0	3
O111:H2	0	0	1	0	1
O111:H8	0	0	0	0	2
O111:H21	1	0	0	0	0

Serotype	2018	2019	2020	2021	2022
O111:HNM	3	0	0	0	0
O112:H8	0	1	0	0	0
O112:H9	0	4	5	7	7
O112:H19	0	1	0	0	1
O112:HNM	2	0	0	0	0
O113:H4	0	1	1	0	0
O113:H21	0	1	1	0	4
O114:HNT	0	1	0	0	0
O117:H4	2	3	1	1	0
O117:H7	2	7	4	1	0
O117:H21	0	0	0	0	1
O117:HNM	1	0	0	0	0
O118:H2	0	1	0	0	0
O119:H4	1	0	0	0	0
O121:H19	0	1	0	1	0
O123:H2	0	3	1	1	2
O123:H10	0	2	11	4	9
O123:H11	0	0	0	0	1
O123/O186:H2	2	0	0	0	0
O123/O186:H10	2	0	0	0	0
O123/O186:HNM	13	0	0	0	0
O124,O8:H19	0	0	0	1	0
O128:H2	22	55	79	82	82
O128:H8	0	1	0	0	0
O128:H45	1	0	0	0	0
O128:HNM	6	0	0	0	0
O128:HNT	1	3	0	0	0
O129:H21	0	0	0	1	0
O130:H11	1	4	11	8	6
O136:H16	1	0	0	0	0
O136:H20	0	0	1	0	0
O141:H2	0	1	0	0	0
O141:HNT	0	1	0	0	0
O144:H2	0	1	0	0	0
O145:H2	1	0	0	3	1
O145:HNT	0	0	0	1	3

Serotype	2018	2019	2020	2021	2022
O146:H21	17	15	28	27	44
O146:H28	0	1	4	3	2
O146:HNM	2	0	0	0	0
O148:H7	0	1	0	0	0
O149:H2	2	2	0	0	0
O150:H8	0	0	0	0	1
O152:H7	0	0	0	0	1
O152:H10	1	0	0	0	0
O152:H38	1	0	0	0	0
O153:H2	3	10	8	8	6
O153:H7	0	0	1	0	0
O153:H21	0	0	1	1	0
O153:HNT	0	1	0	0	0
O153/O178:H7	0	0	0	1	2
O153/O178:H23	0	0	1	0	0
O156:H25	0	2	0	1	0
O158:HNM	1	0	0	0	0
O159:H4	0	0	0	2	0
O159:HNT	0	1	0	0	0
O162:H10	1	0	0	0	0
O163:H19	1	7	1	11	2
O165:H7	0	0	2	2	0
O165:H25	0	0	1	2	3
O165:HNT	0	2	0	0	0
O166:H15	0	1	0	0	1
O171:H2	1	1	1	0	0
O172:H25	0	0	1	0	0
O174:H8	4	10	10	14	16
O174:H21	1	5	7	1	3
O174:HNM	3	0	0	0	0
O174:HNT	2	1	0	0	0
O176:H4	0	12	16	14	24
O176:HNM	9	0	0	0	0
O176:HNT	0	4	0	0	0
O177:H2	0	0	1	0	0
O177:H25	0	2	3	4	4

Serotype	2018	2019	2020	2021	2022
O177:HNM	1	0	0	0	0
O177:HNT	0	1	0	0	0
O178:H7	1	0	0	0	0
O179:H8	0	0	0	2	0
O179:H26	0	1	0	0	0
O181:H16	1	1	0	0	0
O182:H25	0	3	7	5	5
O182:HNM	2	0	0	0	0
O183:H18	0	3	1	1	6
O186:H10	0	2	0	0	0
O186:HNT	0	4	0	0	0
O187:H7	1	0	0	0	0
O187:H52	0	0	0	2	0
O188:H7	1	0	0	0	0
O188:H14	5	0	0	0	0
ONT:H1	0	1	0	0	0
ONT:H2	17	11	0	0	0
ONT:H4	2	0	0	0	0
ONT:H6	0	1	0	0	0
ONT:H7	6	6	0	0	0
ONT:H8	2	4	0	0	0
ONT:H9	2	1	0	0	0
ONT:H10	1	2	0	0	0
ONT:H11	2	0	0	0	0
ONT:H12	1	0	0	0	0
ONT:H14	1	1	0	0	0
ONT:H15	1	0	0	0	0
ONT:H18	0	2	0	0	0
ONT:H19	1	1	0	0	0
ONT:H20	2	0	0	0	0
ONT:H21	4	5	0	0	0
ONT:H25	0	4	1	0	0
ONT:H27	1	0	0	0	0
ONT:H30	1	0	0	0	0
ONT:H31	1	0	0	0	0
ONT:H45	0	0	0	1	0

Serotype	2018	2019	2020	2021	2022
ONT:H49	0	1	0	1	1
ORough:H2	7	0	0	0	0
ORough:H5	1	0	0	0	0
ORough:H10	1	0	0	0	0
ORough:H19	2	0	0	0	0
ORough:H21	1	0	0	0	0
ORough:H26	1	0	0	0	0
ORough:H45	1	0	0	0	0
Onovel1:H16	0	0	1	0	0
Onovel2:H49	0	0	0	1	2
Onovel5:H21	0	0	1	1	0
Onovel21:H14	0	2	0	4	4
Onovel27:H16	0	0	1	0	0
Onovel27:H21	0	1	0	0	0
Onovel32:H10	0	1	0	0	0

NM: Non-Motile. NT: Non-typable

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