New Zealand Food Safety

Haumaru Kai Aotearoa

Annual report concerning Foodborne Diseases in New Zealand 2021

New Zealand Food Safety Technical Paper No: 2022/24

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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 2021

ESR Report FW22014

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 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.

Consumption of contaminated food is only one of the routes by which humans are exposed to pathogens; other routes of exposure include water ingestion, animal contact, and person to person contact.

The limited data available on food preparation and consumption premises and events where enteric diseases are acquired indicate that commercial food premises and the home are roughly equally responsible for outbreaks and individual cases of foodborne illness. Better data are required to effectively inform regulatory and public health action.

For most foodborne illnesses, both notification rates per 100,000 population and hospital admission rates are highest for very young children (0 to 4 years age group) and for elderly people (70+ years). Different demographic groups that make up the New Zealand population are represented differently in the rates of notifications for foodborne illnesses. However, for most foodborne illness Māori and Pacific people have the lowest rate of notifications per 100,000 people in the relevant demographic group. It is not clear whether this might relate to several possibilities such as difficulty in accessing health services, under-reporting of illnesses to the health system or different dietary choices.

In 2021 the COVID-19 pandemic and the public health measures implemented to control the spread of the disease continued to have a strong impact on notification rates of all communicable disease including foodborne disease in New Zealand. Implementation of certain measures such as lockdowns, affected potential exposure to hazards through for example, not being able to dine outside the home, access to medical care and clinical laboratory testing priorities. The same impact of the COVID-19 pandemic on notifications of enteric infections observed in New Zealand was reported by food safety and public health authorities worldwide. To aid the understanding of the impact on the number of cases reported, a list of public health and social measures that are likely to have affected notifications for potentially foodborne diseases is included in the report. Notification rates were compared with those in the previous year, 2020 and in 2019, the last pre-pandemic year in New Zealand.

The reduction of human cases of foodborne campylobacteriosis is a top strategic priority for NZFS. The current performance target is 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 are consistently, albeit slowly, decreasing. A pronounced decrease in cases reported in 2020 is due to a significant drop in notifications during Alert Levels 3 and 4 restrictions from March to mid-May. In 2021, campylobacteriosis notification rates returned to a more predictable level, which was higher than in 2020, but still lower than the 2017-2019 average. NZFS will continue to monitor this trend closely.

There was a pronounced increase in hospital admissions at the end of Alert Levels 2 and 3 restriction periods in force in Auckland. This observation could have resulted from delays, some of which would be unavoidable, in seeking medical attention during which the health of infected people deteriorated such that they then required hospitalisation.

Hospitalisation rates for other foodborne illness remained mostly static with the exception of Shiga toxin-producing *Escherichia coli* (STEC) which showed a small increase on the 2020 total however, the number of cases hospitalised was comparable with recent years. There are significant costs to the health sector associated with hospitalisation of cases of foodborne illness and actions to reduce the overall burden of illness would be economically beneficial.

In 2021, for the first time in more than fifteen years, there were no outbreaks of campylobacteriosis associated with consumption of raw milk. This indicates that NZFS compliance actions and the associated consumer education campaign have been effective in reducing food safety risks associated with consumption of raw milk.

In early 2021, *Salmonella* Enteritidis was isolated in New Zealand poultry environments and following extensive investigation, a new regulatory framework for the industry was designed and implemented. Forty-six human cases of illness caused by the particular strain of *S*. Enteritidis isolated from poultry environments were identified across multiple Public Health Units. This outbreak however, did not materially affect the total number of salmonellosis cases reported for 2021.

Since 2015, NZ diagnostic laboratories have started to replace traditional culture-based methods for enteric pathogens by culture-independent diagnostic tests (CIDT) using molecular polymerase chain reaction (PCR). In May 2021, Mid-Central, Tairawhiti, and Whanganui District Health Boards moved to PCR-based methods, no other laboratory method changes have been recorded during the 2021 year. Multiple different factors (e.g., change in sensitivity of methods, proportion of faecal specimens being tested) related to testing of clinical samples affect the notification rates of illness, on top of any underlying changes to foodborne illness incidence occurring in New Zealand.

Analyses[1] comparing notification trends for bacterial infections in areas using community CIDT and areas yet to change to CIDT suggest the change in methodology is having a significant impact on reporting rates for Shiga toxin-producing *Escherichia coli* (STEC) infections, but not for *Campylobacter spp.*, *Salmonella spp.*, *Shigella spp.* and *Yersinia enterocolitica*.

Observed trends in changes in STEC notification rates between 2015 and 2021 should be considered in the context of changes to testing approaches and the beginning of wider screening. The national increase in STEC notification rates observed since 2015 is due to

[1] Appendix B in https://www.mpi.govt.nz/dmsdocument/47986-Annual-report-concerning-Foodborne-Diseases-in-New-Zealand-2020-Report

ascertainment, that is **diagnosing** more people with STEC infection from an existing constant burden of disease, rather than an underlying real increase in the rate of incidence of STEC infections in New Zealand. Notably, most of the increase in notifications is for non-O157 STEC serogroups which are difficult to identify using traditional culture-based methods. This is in line with the internationally reported increase in the detection of non-O157 STEC, due to the implementation of PCR methods to detect all STEC serogroups.

In contrast to other enteric diseases, yersiniosis has a wide range of clinical manifestations and sequelae. Consequently, case notifications often rely on laboratory results only. Wider screening of clinical samples by CIDT is now occurring in New Zealand with more samples being screened for *Yersinia* spp. than previously, which may contribute to the observed trend. Notably, yersiniosis is not a nationally notifiable disease in many countries, including Australia.

Although all efforts were made to investigate risk factors for all potentially foodborne outbreaks, some outbreaks reported as foodborne with an unidentified food source could be attributed to other routes of transmission, such as water, animal contact, or person to person. In addition, NZFS will remain mindful of potential emerging issues as a result of e.g. climate change where warming of seawaters could give rise to greater risks of foodborne pathogens such as *Vibrio* spp.. NZFS and ESR alongside the newly established Public Health Agency will continue to further improve the reporting, analysis, and presentation of human foodborne illness surveillance and investigation data.

ESR
Science for Communities
He Pūtaiao, He Tāngata

ANNUAL REPORT CONCERNING FOODBORNE DISEASE IN NEW ZEALAND 2021

Prepared for New Zealand Food Safety under
Project MRP/21/01 – Systematic reporting of epidemiology of potentially foodborne disease in New Zealand for year 2021,
as part of an overall contract for scientific services

by

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

Client Report FW22014

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INTRODUCTION

New Zealand Food Safety, part 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 New Zealand Food Safety's 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 New Zealand Food Safety and its stakeholders.

This report for the calendar year 2021 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 indicators from which we can get information on the proportion of cases caused by foodborne transmission:
    - Outbreak reports: the circumstances of an outbreak (multiple cases from a single event) mean that an investigation is more likely to identify a source of exposure to the pathogen than investigation of sporadic cases.
    - Expert opinion: based on their experience in laboratories and epidemiological investigations, as well as knowledge of factors influencing the risk, experts can provide estimates of the proportion of cases caused by foodborne transmission. Estimates for New Zealand have been developed for some foodborne diseases [2, 3], as presented in relevant report sections. These are not fixed values; future changes to the New Zealand food chain may require the values to be amended.
    - Overseas analyses and estimates: information for 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 USA [4], Canada [5], Australia [6, 7], England and Wales [8] and the Netherlands [9] are given in Table 1. In addition, a WHO project to estimate the global burden of foodborne diseases derived estimates for 14 international regions [10, 11]. The estimates for New Zealand, Australia, Canada, the Netherlands and the international WHO estimates are based on expert opinion, the estimates for England and Wales are based on outbreak analysis, while the US estimates are based on data from surveillance, risk factor studies and a literature review.

* Note that water is not considered a food in this context.

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] [10, 11]	USA (2011) [4]	Canada (2015) [5]	Australia (2005, 2014) [6, 7]	England and Wales (2002) [8]	Netherlands[b] (2008) [9]
Bacteria							
Bacillus cereus	NE	100	100	99	100	100	90
Campylobacter spp.	75	51–76	80	62	77[c]	80	42
Clostridium perfringens	NE	100	100	93	98[c]	94	91
Shiga toxin-producing *Escherichia coli* (STEC) O157:H7	20	40–60[d]	68	61	56[c,d]	63	40
STEC non-O157	40	40–60[d]	82	60	56[c,d]	63	42
Listeria monocytogenes	88	100	99	77	98[c]	99	69
Salmonella non-typhoidal	62	46–76	94	63	72[c]	92	55
Shigella spp.	NE	7–36	31	26	12[c]	8	NE
Staphylococcus aureus	NE	100	100	78	100	96	87
Vibrio parahaemolyticus	91	NE	86	83	71[c]	NE	NE
Yersinia enterocolitica[e]	75	NE	90	83	84	90	NE
Parasites							
Cryptosporidium parvum	NE	8–16	8	11	10	6	12
Giardia lamblia	NE	11–14	7	7	5	10	13
Viruses							
Hepatitis A virus	NE	29–42	7	30	12[c]	11	11
Norovirus	33	12–26	26	18	18[c]	NE	17
Sapovirus	NE	NE	<1	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 2014 Australian publication did not cover the full range of organisms covered in the 2005 publication. Estimates marked with a superscript are from the 2014 publication

[d] Estimate was derived for total STEC

[e] 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 2021 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 2021 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 [12].

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 [13]

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) single cases of chemical or toxic food poisoning such as botulism,

histamine (scombroid) poisoning and any type of toxic shellfish poisoning [12]. 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 the conditions listeriosis and 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 New Zealand Food Safety (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 were subtracted from the total cases before application of the food-associated proportion. Travel-associated cases are those where the individual reported being 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(s)	Comment
Guillain-Barré syndrome (GBS)	H (G61.0 Guillain-Barré syndrome)	Sequela to infection with *Campylobacter* [a]
Haemolytic uraemic syndrome (HUS)	H (D59.3 Haemolytic-uraemic syndrome)	Sequela to infection with STEC

Data Sources: Ministry of Health hospitalisations (H)

[a] 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 72 in Appendix B.

For the 2021 reporting year, nationally reported notification rates are a mixture of notifications based on PCR and non-PCR approaches. In May 2021, MidCentral, Tairawhiti and Whanganui DHBs moved to PCR-based methods, no other laboratory method changes have been recorded during the 2021 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

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

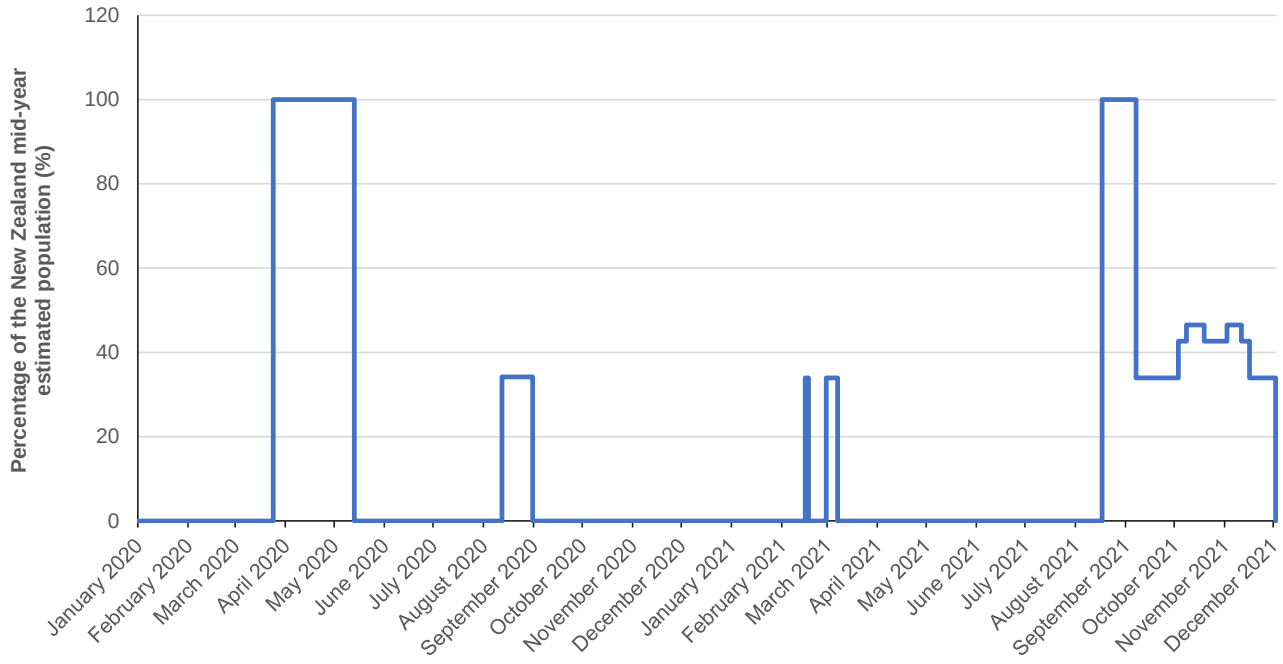
rates of individual diseases is disease specific and is therefore discussed in more detail in the respective sections of this report.

Initial analyses comparing notification trends for bacterial infections in areas using community 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* [14]. Any observed trends in changes in STEC notification rates between 2015 and 2021 must be considered in the context of changes to testing approaches.

Impact of the COVID-19 pandemic and public health measures on notification rates of foodborne disease in New Zealand

The global pandemic of coronavirus disease 19 (COVID-19), caused by SARS-CoV-2, started to unfold in early 2020 with the first confirmed case reported in New Zealand on 26 February 2020. To prevent the spread of COVID-19, New Zealand introduced a range of public health measures, including border restrictions, followed by border closure to all but New Zealand citizens and residents on 20 March 2020. Other measures included national and regional lockdowns, contact tracing and potential case testing. Thereafter, for the rest of 2020 and until December 2021, firm restrictions (Alert Level 3) and lockdown periods (Alert Level 4) alternated with less restrictive periods (Alert Levels 1 and 2) as the whole country, or certain regions, moved up and down COVID-19 Alert Levels (Appendix C, Table 73) [15]. These measures, in particular the more restrictive Alert Levels 3 (restrict) and 4 (lockdown), are likely to have had some impact on the transmission and/or notification rates of some of the potentially foodborne diseases. An approximate timeline of restrictive periods is provided in Figure 1 below.

Figure 1. Percentage of New Zealand Population at Alert Level 3 or 4, 2020 and 2021



Reduced notification rates (either due to under reporting or reduced infection rates) during 2020/2021 may be attributed to several contributing factors, including:

- Changes in testing priorities of laboratories, with resources diverted to the COVID-19 response.
- More emphasis on personal hygiene, e.g. hand sanitiser use.

- Travel restrictions within New Zealand and overseas.
- Physical distancing requirements and limits on hospitality businesses leading to less socialising and private functions.
- Changes in the food supply; supermarkets were the only food retailers open during lockdown periods; restaurants and cafes were closed or had limited functionality, possibly resulting in more home cooking and and more takeway food consumption.
- Behavioural changes such as fewer visits to healthcare providers (e.g., due to anxiety related to COVID-19, financial insecurity, replacement of GP visits by phone consultations); this factor was less pronounced in 2021, when people were encouraged to visit their GP if feeling unwell.

Some of these changes may have continued after lockdown restrictions were lifted.

The impact of public health and social measures on notifications for potentially foodborne diseases is likely to have been complex. In 2020 and 2021, some diseases did show a marked reduction in notifications in comparison to pre-COVID-19 years, while others appeared to be little affected. In 2021, notification rates of some diseases were higher compared to 2020 but still lower compared to pre-COVID-19 years. This may be due to more people seeking healthcare in 2021 than in 2020, resulting in higher rates of disease identification and notification. Also, for most of New Zealand, people were able to visit restaurants and cafes during 2021, and social events increased, where transmission of enteric disease and larger outbreaks are more likely to occur. A similar pattern of changes in disease notifications was reported in other countries [16].

The combined contributions of all the above-mentioned factors make it difficult to quantify the impact of any individual factor. The monthly disease rate graphs for individual diseases show the 2020 and 2021 notification rates compared to the three-year mean of pre-COVID-19 notification rates (2017-2019). This provides an indication of the possible impact of COVID-19 on the 2021 notification rates, although the possibility of true changes in disease incidence cannot be excluded.

REPORTING

SUMMARY OF MAIN FOODBORNE DISEASES

The incidence of the main foodborne diseases is summarised for 2021 in Table 4 below.

Table 4. Estimated proportion and incidence of the main foodborne diseases for 2021

	Total notified[a]		Estimated foodborne transmission[b]		
	Cases	Rate[c]	Cases	Proportion (%)	Rate[c]
Campylobacteriosis	5729	111.8	4292	75	83.8
Cryptosporidiosis	702	13.7	NE	-	-
Giardiasis	1040	20.3	NE	-	-
Hepatitis A	8	0.2	NE	-	-
Listeriosis	32	0.6	28	88[d]	0.5
Salmonellosis	714	13.9	443	62	8.6
Shigellosis	5	0.1	NE	-	
STEC infection	913	17.8	364	40[e]	7.1
Yersiniosis	1410	27.5	1056	75	20.6

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 [12]. 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 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 travel-related cases. Estimated foodborne transmission proportions were derived from two expert consultations in 2013 and 2020, respectively [2, 3]

[c] Rate per 100,000, 2021 mid-year estimated population

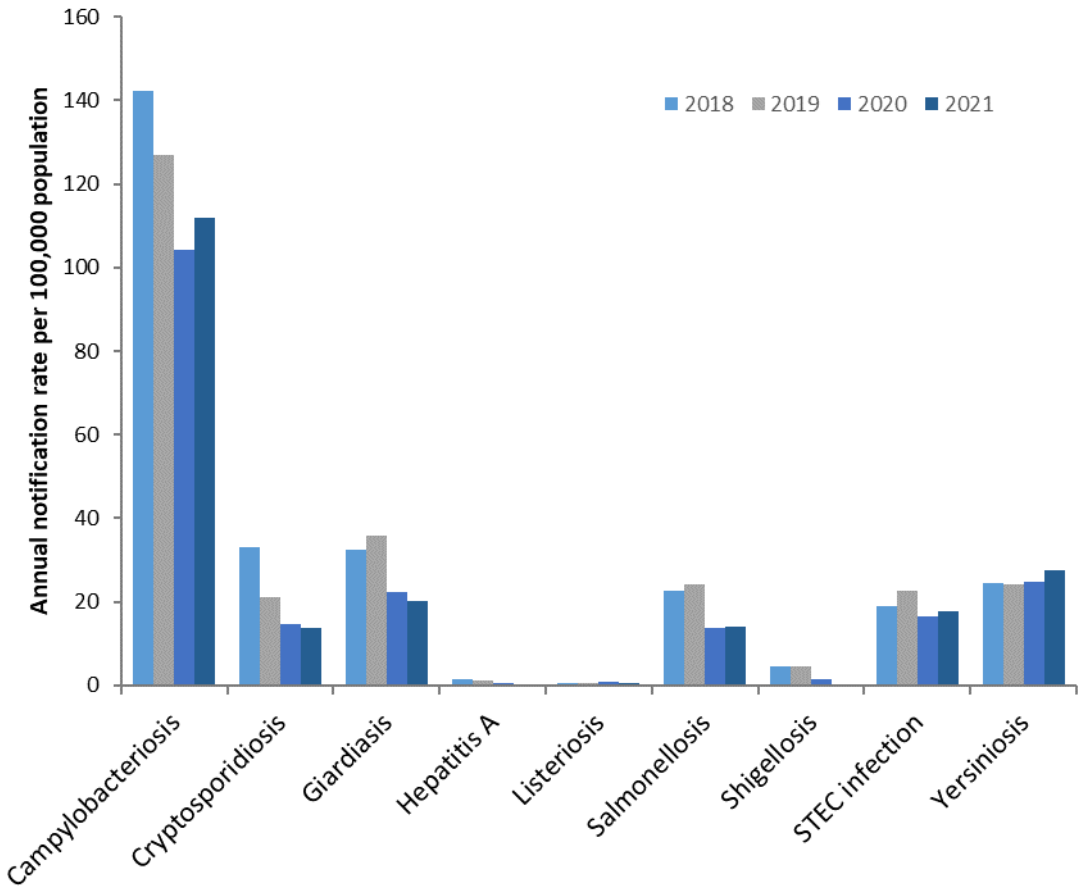
[d] For listeriosis sources other than food are unlikely

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

In 2021, notification rates for all main foodborne diseases apart from yersiniosis and campylobacteriosis were similar to 2020 and lower than 2018 or 2019 (Figure 2). The campylobacteriosis notification rate increased from 104.0 cases per 100,000 population in 2020 to 111.8 in 2021 but remained below 2018 and 2019 rates. The 2021 yersiniosis notification rate is slightly higher than each of the previous three years; ~25 cases per 100,000 population in 2018–2020, rising to 27.5 in 2021.

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. These multiple aspects make it difficult to attribute any changes to notification rates to specific COVID-19 related factors. This is discussed in more detail in the Introduction (see page 5) and the individual sections of this report.

Figure 2. Notification rates of the main foodborne diseases, 2018–2021



Reporting against targets

Performance targets for potentially foodborne diseases are reviewed by New Zealand Food Safety on an annual basis. In 2020, New Zealand Food Safety introduced the goal of reducing the incidence of domestically acquired human cases of 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 New Zealand Food Safety and conducted in 2018–2019 [17], provided updated information on how New Zealanders become infected with the *Campylobacter* bacterium. The study identified that food remained the dominant pathway for exposure and infection in New Zealand, with poultry meat still being the main source of *Campylobacter* infections, especially for the urban population.

Other potentially foodborne illnesses are currently covered by core business activities within New Zealand Food Safety, which includes close monitoring of notifications and outbreaks. Specific targets are introduced if warranted by the current situation or changing trends. New Zealand Food

* https://www.mpi.govt.nz/dmsdocument/42766-Campylobacter-Action-Plan-2020-21 (Accessed 5th April 2022)

Safety continues to closely monitor sources and potential pathways that are most often associated with potentially foodborne illness in New Zealand.

Methodology, tools and reporting

Historical baseline data on the number of notified cases of the targeted potentially foodborne diseases are available from the *Notifiable Diseases in New Zealand Annual Report,* produced by ESR for the Ministry of Health (MoH) [18].

To assess reporting against targets, the annual number of notified cases is adjusted for the proportion of cases reported as 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 proportion of campylobacteriosis due to foodborne transmission was estimated through an expert elicitation process in 2020 to be 75% of cases, taking new studies and increased knowledge into account [3].

The annual incidence of campylobacteriosis is reported in terms of calendar year cases per 100,000 population (*Notifiable Diseases in New Zealand Annual Report,* ESR) [18]. This allows for demographic changes within the New Zealand population to be appropriately captured. The proportion of infections acquired overseas is estimated through data from the EpiSurv programme administered by ESR and MoH.

Campylobacteriosis 2020 to 2024 performance target

The incidence of human cases of 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 (see page 5).

The estimated incidence of domestically acquired foodborne campylobacteriosis in 2021 is given in Table 5.

Table 5. Estimated proportion and incidence of foodborne campylobacteriosis for 2021

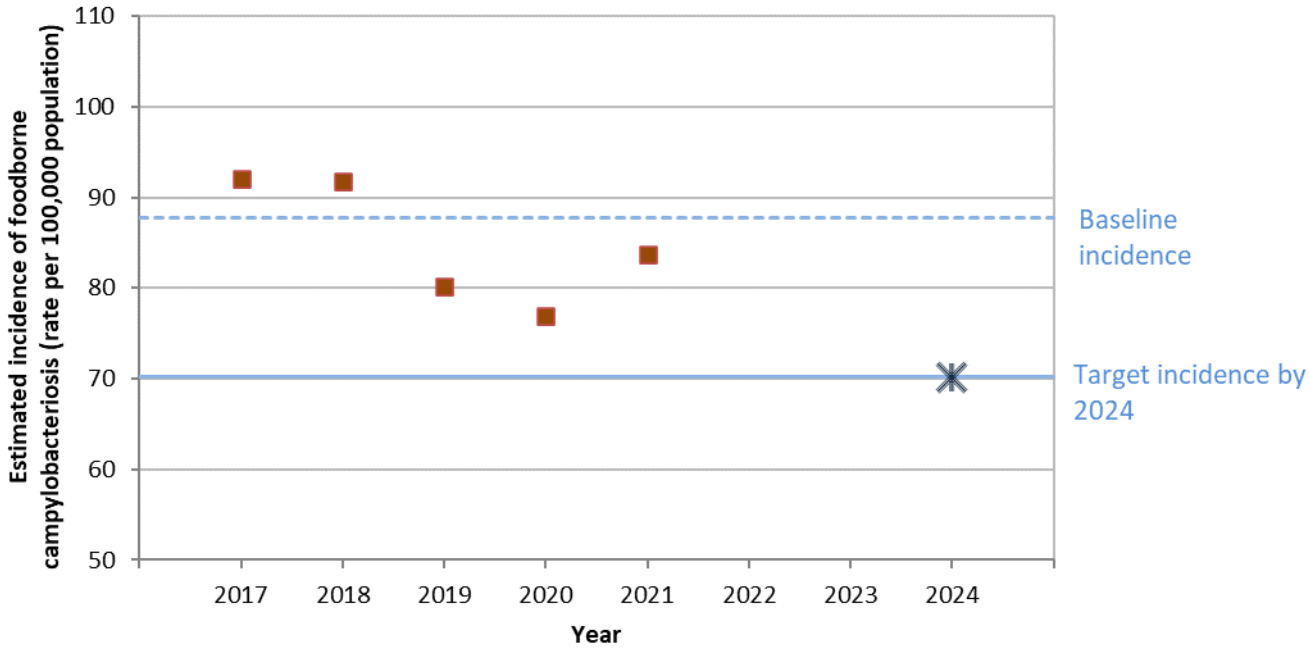
	Cases	Proportion of total notified cases (%)	Rate (per 100,000, mid-year estimated population)
Total notified	5729	-	111.8
Total not related to overseas travel[a]	5722	99.9	111.7
Estimated foodborne transmission[b]	4292	75	83.8

[a] The number of cases listing overseas travel as a risk factor in 2021 is 7.
[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 3. The rates observed in 2020 and 2021 are between the performance target baseline and 2024 target rates.

Figure 3. Estimated incidence of domestically acquired foodborne campylobacteriosis compared to 2020 to 2024 performance target



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

Reporting of incidence and severity of selected foodborne conditions

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

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

- statement of estimated foodborne percentage and range provided by expert elicitation processes conducted in 2013 [2] and 2020 [3]. Note that these estimates are only available for some of the conditions included in this report.
- statement of estimated foodborne percentage and range for any specific foods provided by the same expert elicitation process.
- information on pathogen typing (principally from data generated by ESR's Enteric Reference Laboratory 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 the 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, 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 ≥10^3/g *Bacillus cereus* from a clinical specimen or ≥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 2021 by data source

During 2021, one individual case of *B. cereus* intoxication was reported in EpiSurv in April.

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).

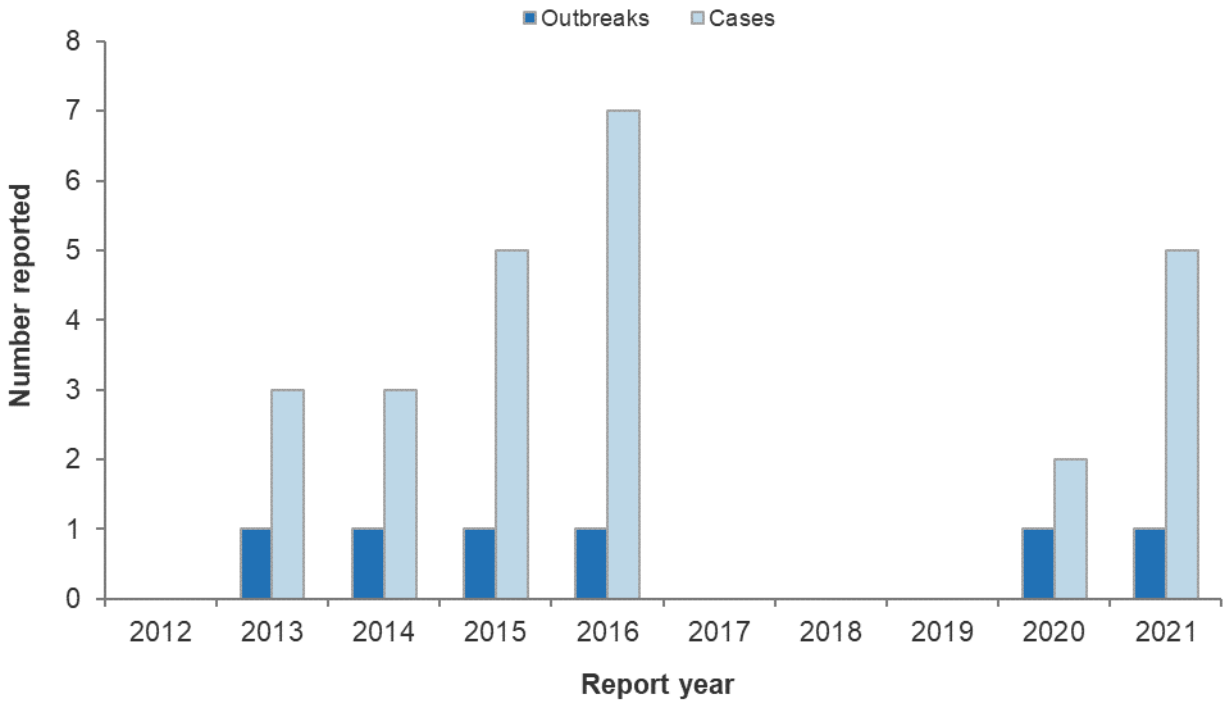
The international statistical classification of diseases and related health problems 10th revision (ICD-10) code A05.4 was used to extract foodborne *B. cereus* intoxication hospitalisation data from the MoH National Minimum Dataset (NMDS). There was one hospital admission (0.02 admissions per 100,000 population) recorded in 2021 with *B. cereus* intoxication as the primary diagnosis. This was not the same case as notified in EpiSurv.

Outbreaks reported as caused by *Bacillus cereus*

During 2021, there were no outbreaks reported in EpiSurv with *B. cereus* confirmed as the causative agent. The New Zealand Food Safety Compliance team recorded an investigation of five possible cases of *B. cereus* intoxication associated with a food service operator in the region covered by Community and Public Health (Canterbury, West Coast and the Chatham Islands). Temperature control failure was identified as a contributing factor.

Outbreaks of *B. cereus* intoxication are rare, with only six outbreaks reported since 2012. The number of cases associated with individual outbreaks ranged between two and seven cases (Figure 4).

Figure 4. *B. cereus* intoxication outbreaks with food reported as a possible mode of transmission and associated cases reported by year, 2012–2021



Note: The 2021 outbreak information is from New Zealand Food Safety Compliance Team records and is not recorded in EpiSurv.

Recent surveys

Nil.

Relevant New Zealand studies and publications

Nil.

Relevant regulatory developments

Nil.

Campylobacteriosis

Summary data for campylobacteriosis in 2021 are given in Table 6.

Table 6. Summary of surveillance data for campylobacteriosis, 2021

Parameter	Value in 2021	Source
Number of notified cases	5729	EpiSurv
Notification rate (per 100,000)	111.8	EpiSurv
Hospitalisations[a]	846	MoH NMDS
Deaths	0	EpiSurv
Travel-related cases (%)[b, c]	7 (0.1%)	EpiSurv
Estimated food-related cases (%)[d]	4292 (75%)	Expert consultation

[a] Cases hospitalised may not be notified on EpiSurv
[b] Percentage of the number of notified cases
[c] New Zealand borders were closed in March 2020 with travel restrictions in place for the rest of 2020 and 2021.
[d] For estimation of food-related cases, the proportions derived from expert consultation [3] exclude travel-related cases

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. In 2021, community faecal specimens in all DHBs except for Canterbury, South Canterbury, and West Coast were screened by PCR methods for *Campylobacter* spp. The MidCentral, Tairawhiti, and Whanganui DHBs changed to PCR testing in May 2021.

There is no evidence that campylobacteriosis notification rates have been affected by the introduction of PCR methods by diagnostic laboratories [3, 14].

Effect of COVID-19 on campylobacteriosis notification rates

Public health and social measures to prevent the spread of COVID-19 in New Zealand were introduced in March 2020 and remained in place through December 2021. These measures will have affected exposure behaviours and pathways, access to medical care and laboratory testing priorities. These multiple aspects make it difficult to attribute any changes in notification rates, either to specific COVID-19 related factors, which are discussed in more detail in the Introduction (see page 5), or true changes in disease incidence.

In 2020, a reduction in campylobacteriosis notifications from March to mid-May, compared with the same period in the previous three years (2017-2019), coincided with the Alert Level 3 and 4 periods.

In 2021, notification rates in March-May increased compared to the same period in 2020 but were not as high as the 2017-2019 average. From August to October 2021, campylobacteriosis notification rates continued to be lower than the 2017–2019 average and were slightly lower than the same period in 2020. These relative rates may reflect the effect of Alert Level 3 and 4 restrictions for all of New Zealand (August – September 2021), Northland, parts of Waikato and Auckland (August – November 2021) (Figure 7).

The frequency of overseas travel has changed due to border restrictions from March 2020 until the end of 2021. This is reflected in the notifications; in 2021, there were seven campylobacteriosis notifications in EpiSurv listing overseas travel as a risk factor, compared to 394 in 2019 and 66 in 2020.

Campylobacteriosis individual cases reported in 2021 by data source

During 2021, 5729 individual cases (111.8 per 100,000 population) of campylobacteriosis and no resulting deaths were reported in EpiSurv. Of the 5729 cases, the symptoms of 5228 cases (91%) were reported as fitting the clinical description for campylobacteriosis, the symptoms were unknown for 493 cases, and for eight 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 NMDS database. Of the 846 hospital admissions (16.5 admissions per 100,000 population) recorded in 2021, 709 cases were reported with campylobacteriosis as the primary diagnosis and 137 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.

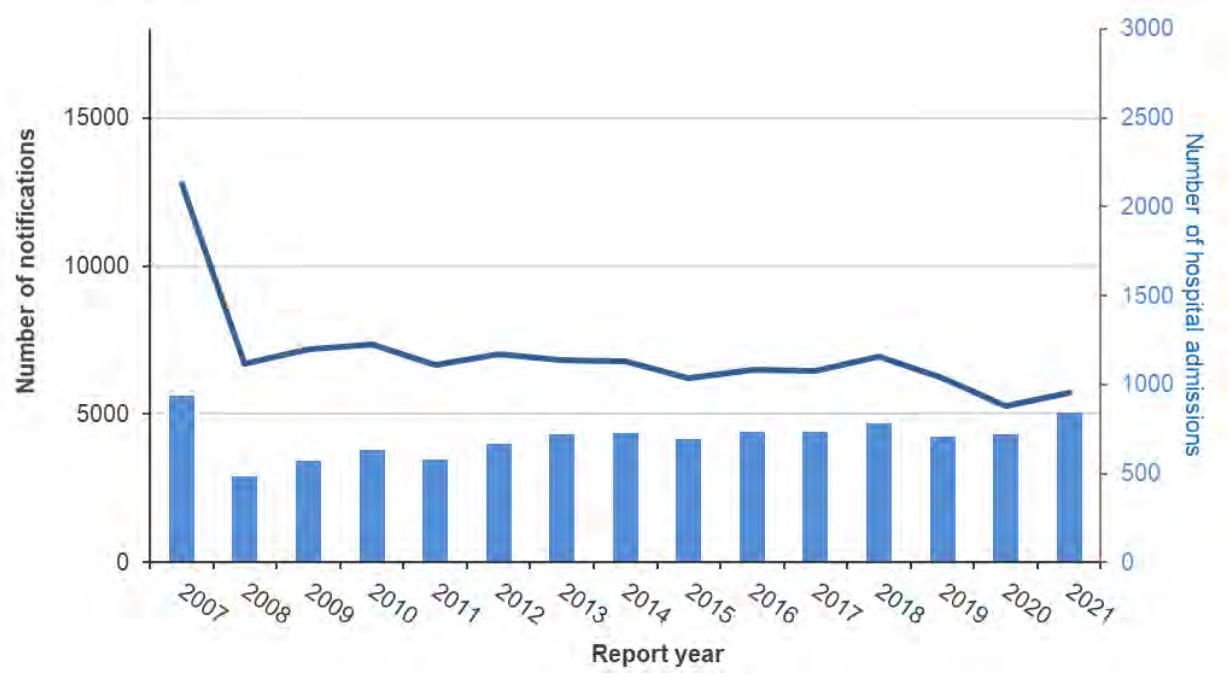
Foodborne transmission

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

The number of campylobacteriosis notifications reported each year generally increased year-on-year up to the highest number recorded in 2006 (15,873 cases). Due to the measures taken by New Zealand Food Safety 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 2019, with a drop in notifications in 2020 and a slight increase in 2021 (Figure 5 and Figure 6). The number of hospital admissions with campylobacteriosis as a primary or secondary diagnosis varied slightly year by year.

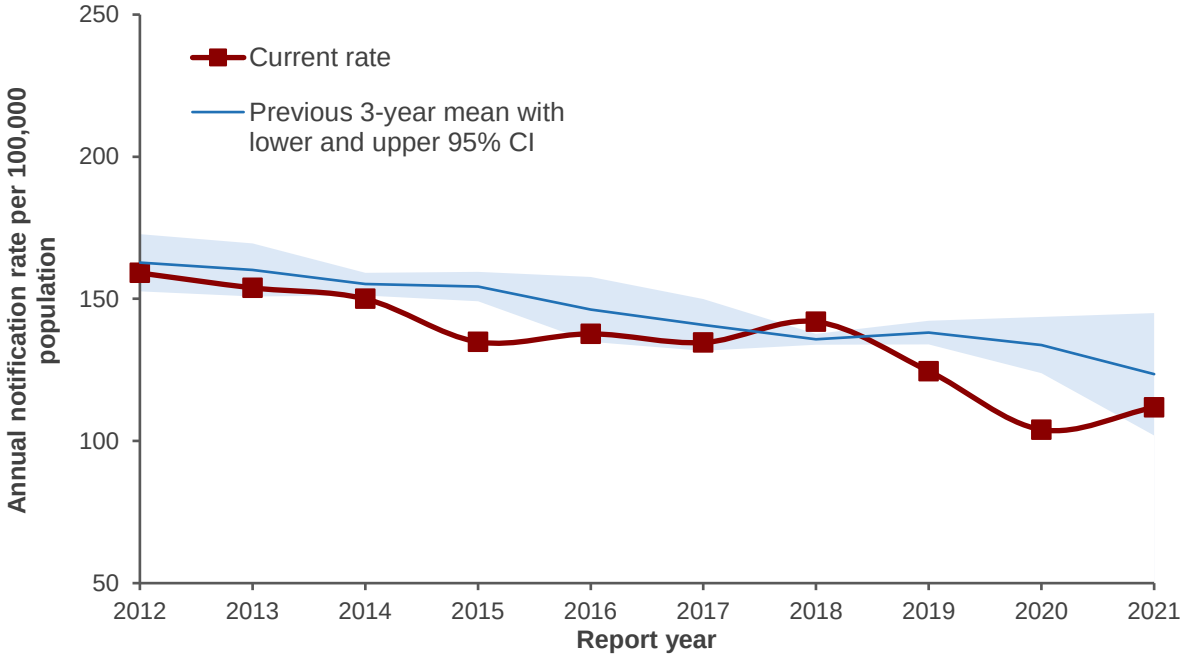
Figure 5. Campylobacteriosis EpiSurv notifications (line) and NMDS hospitalisations (bar) by year, 2007–2021



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

Between 2012 and 2019, the notification rate of campylobacteriosis was in the range of 124.6 to 159.2 notifications per 100,000 population (Figure 6). The trend for the calculated previous three-year mean is generally downward over that period. In 2020, the campylobacteriosis notification rate (104.0 cases per 100,000 population) was much lower compared to 2019 (124.6 cases per 100,000 population), likely due to the impact of COVID-19, but increased to 111.8 cases per 100,000 population in 2021.

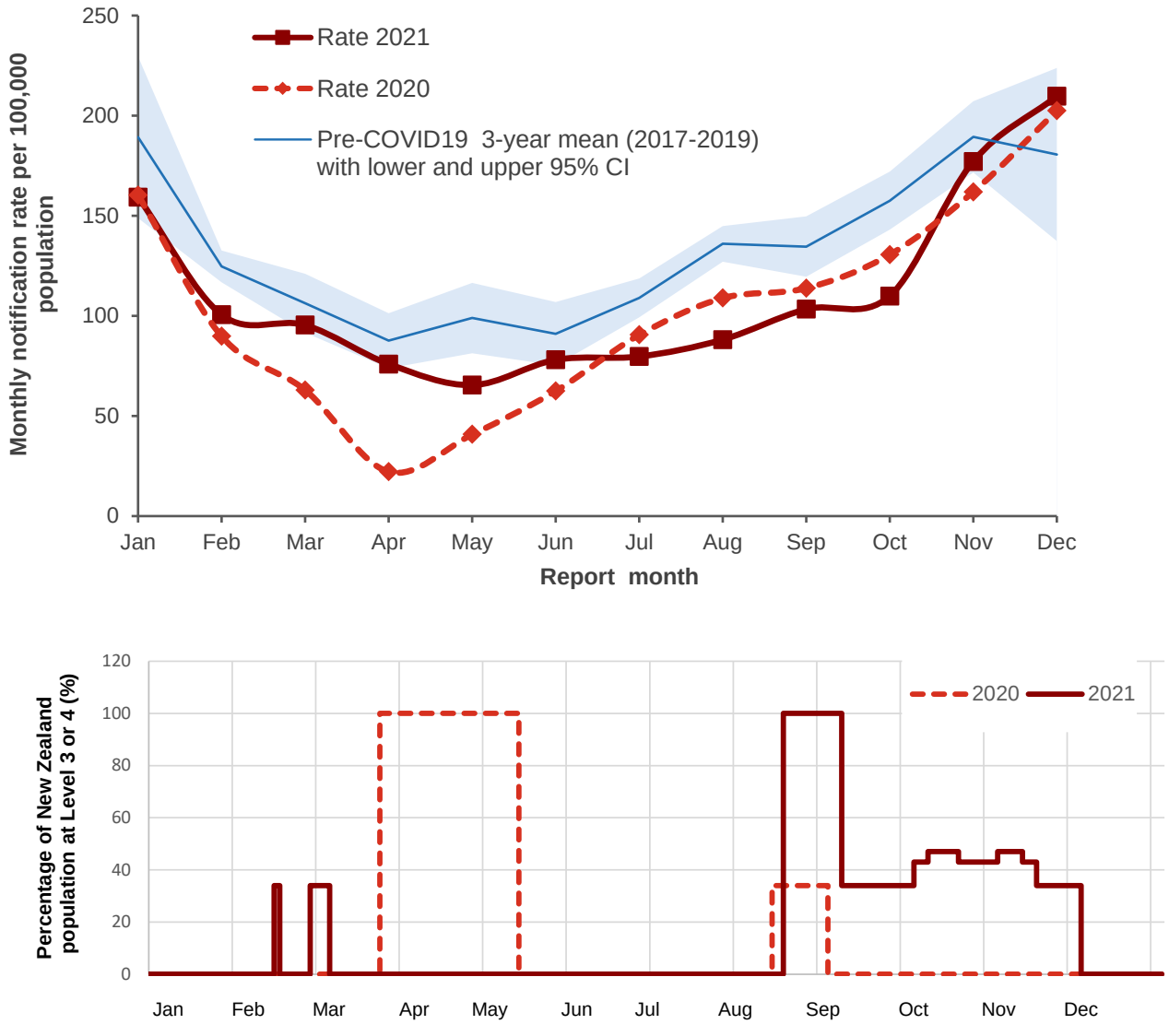
Figure 6. Campylobacteriosis notification rate by year, 2012–2021



Seasonal data

Campylobacteriosis notification rates per 100,000 population by month for 2020 and 2021 are shown in Figure 7 as well as the percentage of the New Zealand population at COVID-19 Alert Levels 3 or 4. In 2021, the monthly notification rates followed a trend similar to the three-year mean of the years 2017-2019 but were generally lower. The monthly number of notifications in 2021 ranged from 279 notifications (May, 65 per 100,000 population) to 895 notifications (December, 210 per 100,000 population). The monthly notification rates in 2020 showed a pronounced drop in April and May, co-inciding with and probably due to the COVID-19 Alert Level 4 public health response.

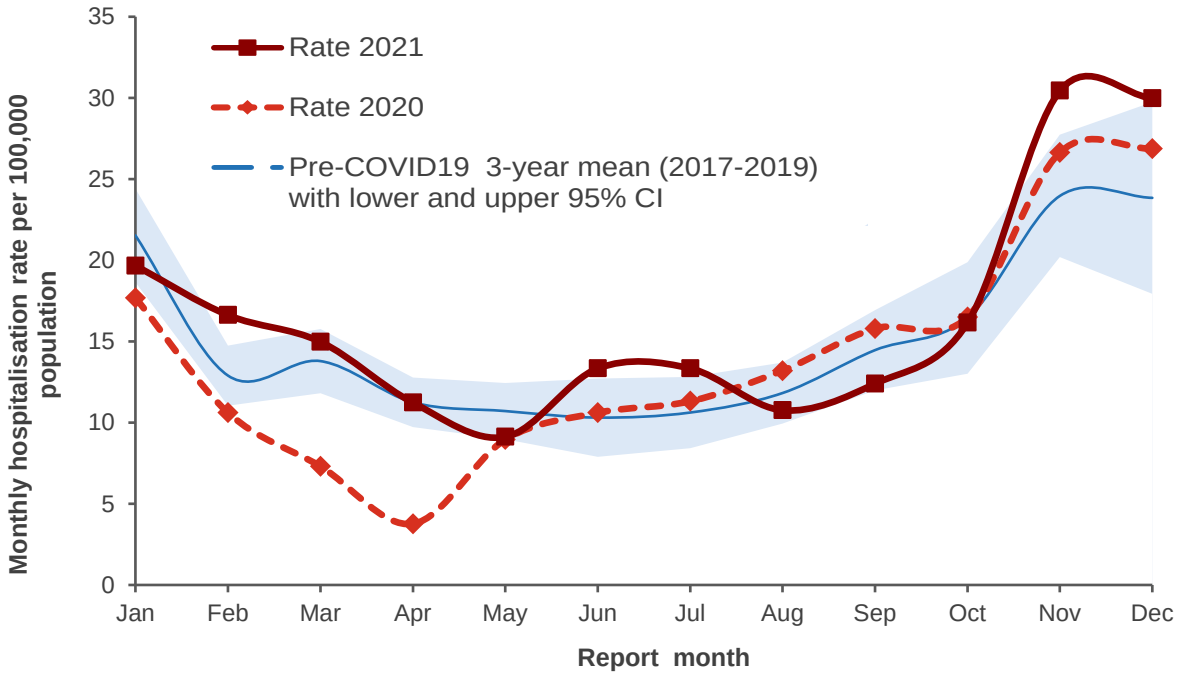
Figure 7. Campylobacteriosis monthly notification rate (annualised) and percentage of New Zealand population at COVID-19 Alert Levels 3 or 4, 2020 and 2021



Note: A detailed timeline of all COVID-19 Alert Level changes for 2020 and 2021 is included in Appendix C (Table 73).

In 2021, the monthly hospitalisation rates were mostly very similar to the three-year average of the years 2017–2019, with slightly higher rates in some months (Figure 8).

Figure 8. Campylobacteriosis monthly hospitalisation rate (annualised), 2020 and 2021



Demographics

In 2021, the rates of notifications and hospitalisations for campylobacteriosis were higher for males (126.7 and 18.4 per 100,000 population) compared with females (96.9 and 14.6 per 100,000 population) (Table 7).

Table 7. Campylobacteriosis cases by sex, 2021

Sex	EpiSurv notifications		Hospitalisations[a]	
	No.	Rate[b]	No.	Rate[b]
Male	3222	126.7	469	18.4
Female	2501	96.9	377	14.6
Total[c]	**5729**	**111.8**	**846**	**16.5**

[a] MoH NMDS data for hospital admissions
[b] per 100,000 population in this sex group
[c] total includes notifications where sex is unknown

The highest age-specific notification rate for campylobacteriosis in 2021 was reported for children aged 0 to 4 years (212.4 per 100,000 population, 649 cases). The highest hospitalisation rate was for the 70 years and over age group (47.0 admissions per 100,000 population, 266 cases) (Table 8).

Table 8. Campylobacteriosis cases by age group, 2021

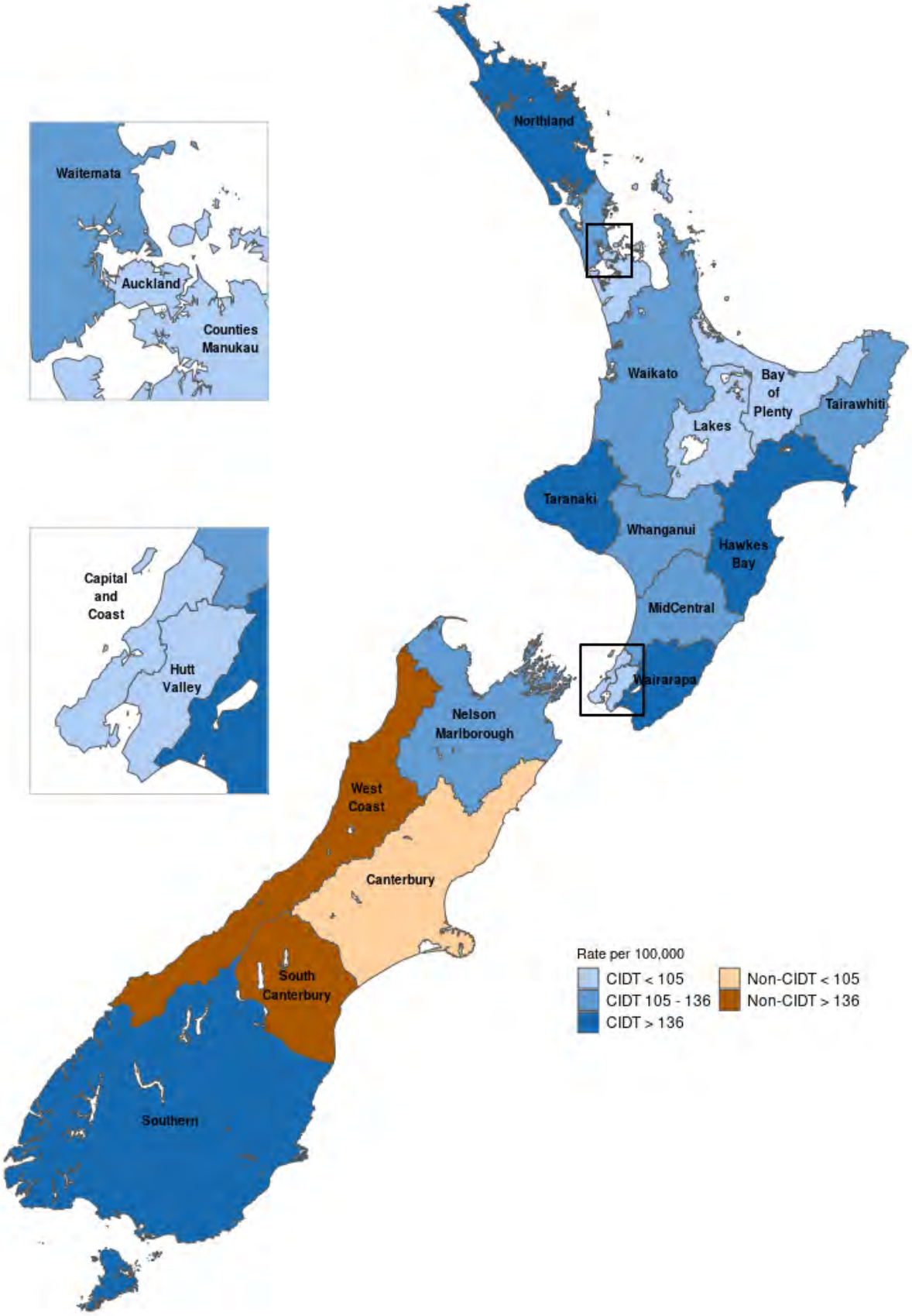
Age group (years)	EpiSurv notifications		Hospitalisations[a]	
	No.	Rate[b]	No.	Rate[b]
0 to 4	649	212.4	52	17.0
5 to 9	231	71.0	19	5.8
10 to 14	192	56.9	17	5.0
15 to 19	305	96.9	38	12.1
20 to 29	783	111.0	95	13.5
30 to 39	621	85.6	70	9.7
40 to 49	571	89.8	64	10.1
50 to 59	740	112.9	103	15.7
60 to 69	735	133.2	122	22.1
70+	900	159.2	266	47.0
Total[c]	**5729**	**111.8**	**846**	**16.5**

[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 9 (see also Table 82). Blue shading is used in DHBs which are using CIDT community testing, the brown shading is used for DHBs using culture-based community testing.

Figure 9. Geographic distribution of campylobacteriosis notifications, 2021



Note: Whanganui, MidCentral and Tairawhiti DHBs testing moved to CIDT methods in May 2021. The rates for these DHBs will be based on a mixture of CIDT and non-CIDT test results.

In 2021, the DHB notification rates of campylobacteriosis ranged from 79 per 100,000 population (475 cases) in Counties Manukau DHB to 246 per 100,000 population (153 cases) in South Canterbury DHB. The South Canterbury, Wairarapa (220 per 100,000 population, 110 cases), West Coast (211 per 100,000 population, 69 cases), and Taranaki (200 per 100,000 population, 253 cases) DHBs had notification rates at or above 200 per 100,000 population.

Historically, notification rates for campylobacteriosis have been variable across New Zealand with the Southern, South Canterbury, Wairarapa, and Taranaki DHBs consistently in the highest quartile of notification rates since 2016.

Outbreaks reported as caused by *Campylobacter* spp.

In 2021, there were 12 campylobacteriosis outbreak notifications in EpiSurv, five (42%) of which recorded food as a possible mode of transmission (Table 9). It is important to note that a single outbreak may have multiple pathogens, settings and possible modes of transmission.

Table 9. Campylobacteriosis outbreaks reported in EpiSurv, 2021

	Possible foodborne transmission with a suspected or confirmed source	Possible foodborne transmission but no suspected source	Total number of campylobacteriosis outbreaks
Outbreaks	3	2	12
Outbreak-associated cases	8	7	32
Hospitalised cases	1	1	2

Table 10 contains details of the five campylobacteriosis outbreaks reported in 2021 with food as a possible mode of transmission. Of the three outbreaks with a suspected food source, the evidence for the source being the cause of the outbreak was weak for the January and March outbreaks, with no leftover food available for testing. For the June outbreak, the same organism subtype was detected in case samples and in associated foods samples, but no further information was available at the time of writing. In addition to the outbreaks recorded in EpiSurv at the cut-off date for this report (12 May 2022) (Table 10), New Zealand Food Safety investigated three further outbreaks. Two outbreaks reported chicken pâté as a suspected source (two cases recorded by the Community and Public Health public health unit (PHU) in February and one case plus two probable cases recorded by the Toi Te Ora PHU in May). One outbreak reported lambs' fry as a suspected source (two cases recorded by Toi Te Ora PHU in March).

Table 10. Details of campylobacteriosis outbreaks notified in EpiSurv with food reported as a possible mode of transmission, 2021

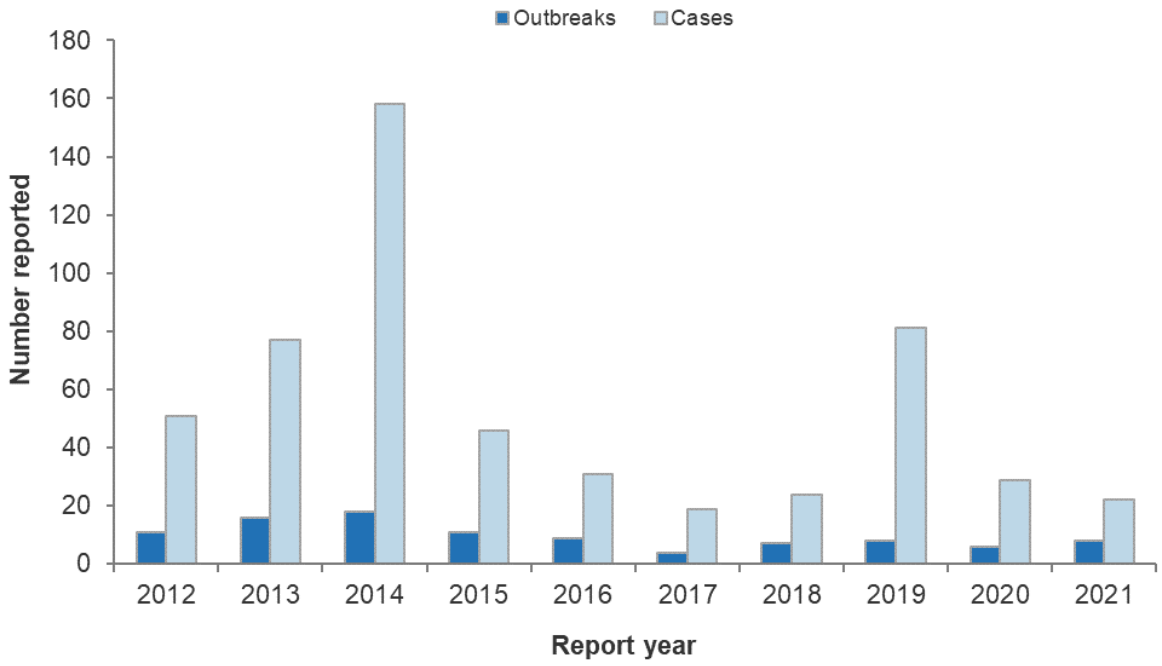
PHU	Report Month	Suspected source	Evidence	Setting	No. ill
C and PH	January	Potluck dinner	Common meal	Home	1C 4P
PH South	January	Potluck dinner	Common meal/social function	Home preparation for sports social function	2C
Regional PH	January	Liver pâté or Cranberry/ Pistachio terrine	Common foods	Home consumption of commercially prepared pate or terrine, or homemade pâté	3C 1P
PH South	March	Smoked fish or chicken	Household cluster	Home	2C
Regional PH	June	Lambs' Fry	Same organism and subtype detected in case and food samples.	Restaurant/cafe/bakery	2C

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

Number ill: C: confirmed, P: probable

Over the 10-year period 2012 to 2021, excluding 2014, the number of outbreaks of campylobacteriosis with food reported as a possible mode of transmission has ranged between four and 16 outbreaks each year with between 15 (2021) and 81 (2019) annual outbreak-associated cases (Figure 10). The greater number of outbreak-associated cases in 2014 was due to three outbreaks with high numbers of cases (51, 32 and 17).

Figure 10. Campylobacteriosis outbreaks with food reported as a possible mode of transmission and associated cases reported by year, 2012–2021



Note: The 2021 outbreak information includes five outbreaks reported in EpiSurv plus three further outbreaks from New Zealand Food Safety Compliance Team records that were not recorded in EpiSurv at the cut-off date for this report (12 May 2022).

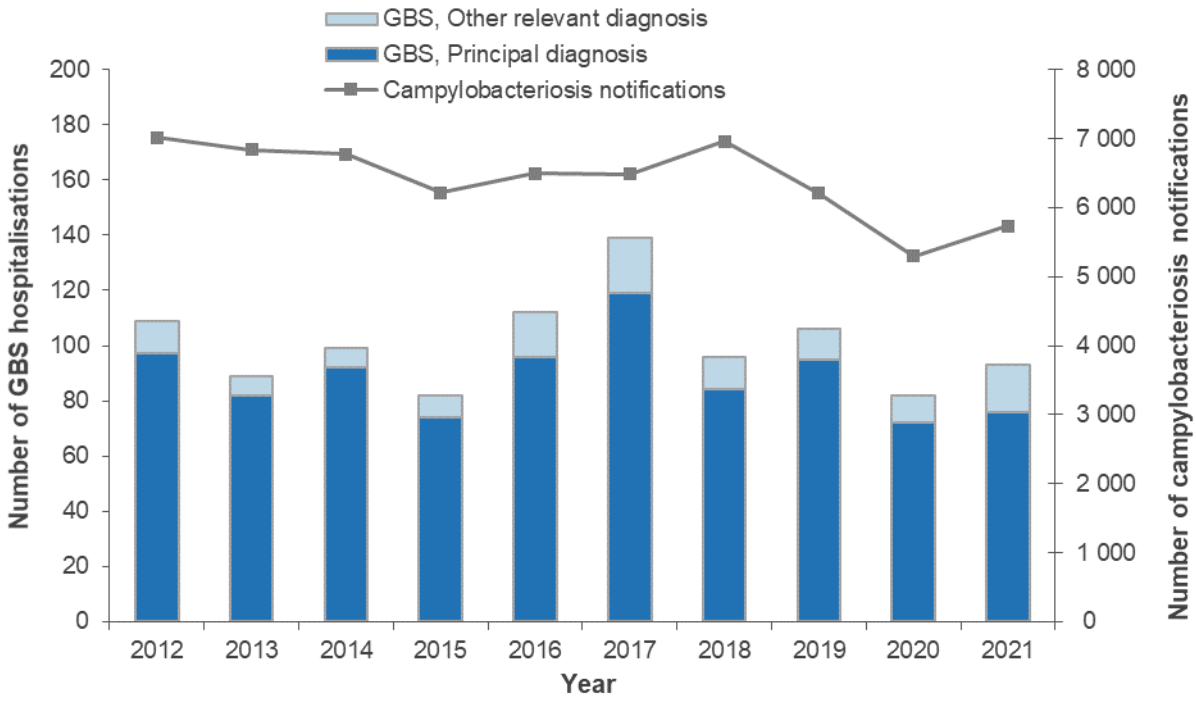
Disease sequelae - Guillain-Barré syndrome

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.

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 2021 were considered, rather than all cases that were hospitalised in 2021. That is, if a GBS case hospitalised in 2021 had been hospitalised with GBS in a previous year, the 2021 admission was considered to be a readmission, rather than an incident case. There were 93 incident hospitalised cases recorded in 2021 (1.8 admissions per 100,000 population), 76 were reported with GBS as the primary diagnosis and 17 with GBS as another relevant diagnosis.

Between 2012 and 2021, the annual number of incident hospitalised cases (any diagnosis code) for GBS ranged from 82 to 139 (Figure 11). The numbers of campylobacteriosis notifications during the same period are also included in Figure 11 for comparison.

Figure 11. Guillain-Barré syndrome hospitalised cases, 2012–2021



In 2021, the number of incident hospitalised cases due to GBS was higher for males than for females (Table 11). 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 2021 (Table 7).

Table 11. Guillain-Barré syndrome hospitalised cases by sex, 2021

Sex	Hospitalised cases[a]	
	No.	Rate[b]
Male	59	2.3
Female	34	1.3
Total	**93**	**1.8**

[a] MoH NMDS data for hospital admissions
[b] per 100,000 population

In 2021, the highest rates of incident hospitalisation for GBS were in the 60-69 years age group, followed by the 50-59 years age group (Table 12).

Table 12. Guillain-Barré syndrome hospitalised cases by age group, 2021

Age group (years)	Hospitalised cases	
	No.	Rate[b]
0 to 4	4	-
5 to 9	1	-
10 to 14	1	-
15 to 19	7	2.2
20 to 29	18	2.6
30 to 39	8	1.1
40 to 49	2	-
50 to 59	18	2.7
60 to 69	22	4.0
70+	12	2.1
Total	**93**	**1.8**

[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

Source attributed case control study of campylobacteriosis in New Zealand study - Lake et al. (2021).

While this paper was published in 2021 [19], the details are taken from a report published in 2020 [17] and the details of the study were included in the previous year's edition of the current report.

Survey of New Zealand poultry consumers' handling of raw poultry and food safety awareness to provide insight into risk factors for campylobacteriosis – Al-Sakkaf et al. (2021)

A cross sectional survey composed of 31 multiple-choice questions was designed, piloted, and used to collect information about the last time consumers purchased and prepared raw poultry at home [20]. Overall, 301 valid responses were obtained. Approximately 30% of the respondents reported symptoms of a foodborne disease experienced once to four times during the past 12 months. The study identified low adherence to current recommended food safety practices, including safe food storage and temperature control.

Transmission dynamics of an antimicrobial resistant Campylobacter jejuni lineage in New Zealand's commercial poultry network – Greening et al. (2021)

Whole-genome sequencing was performed on 167 *C. jejuni* ST- 6964 isolates sampled from across 30 New Zealand commercial poultry enterprises [21]. The genetic relatedness between isolates was determined using whole genome multilocus sequence typing (wgMLST). Overall, a significant association was found between the pairwise genetic relatedness of the *C. jejuni* isolates and the parent company, the road distance and the network distance of transporting feed vehicles. This

result suggests that the transportation of feed within the commercial poultry industry as well as other local contacts between flocks, such as the movements of personnel, may have played a significant role in the spread of *C. jejuni*.

Prevalence and genotyping of Campylobacter jejuni and Campylobacter coli from ovine carcasses in New Zealand– Rivas et al. (2021)

A pilot survey was performed to determine the prevalence of *Campylobacter jejuni* and *Campylobacter coli* on three age classes (lamb, hogget, and mutton) of ovine carcass trim postdressing and prechill [22]. A total of 120 trim samples were collected from 11 processing plants across New Zealand. Enumeration of *Campylobacter* from lamb trim samples showed that *Campylobacter* bacteria were present in very low numbers (<10 CFU/g). The overall prevalence of *Campylobacter* for ovine trim based on PCR detection was 33% (39 of 120 samples), with prevalences for hogget, lamb, and mutton carcass trim of 56% (28 of 50), 11% (4 of 35) and 20% (7 of 35), respectively.

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 [23], 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 2021 by data source

During 2021, one individual case of ciguatera poisoning was reported in EpiSurv. The case had consumed tropical fish.

The ICD-10 code T61.0 was used to extract foodborne ciguatera poisoning hospitalisation data from the NMDS database. Of the two hospital admissions (0.04 admissions per 100,000 population) recorded in 2021, 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.

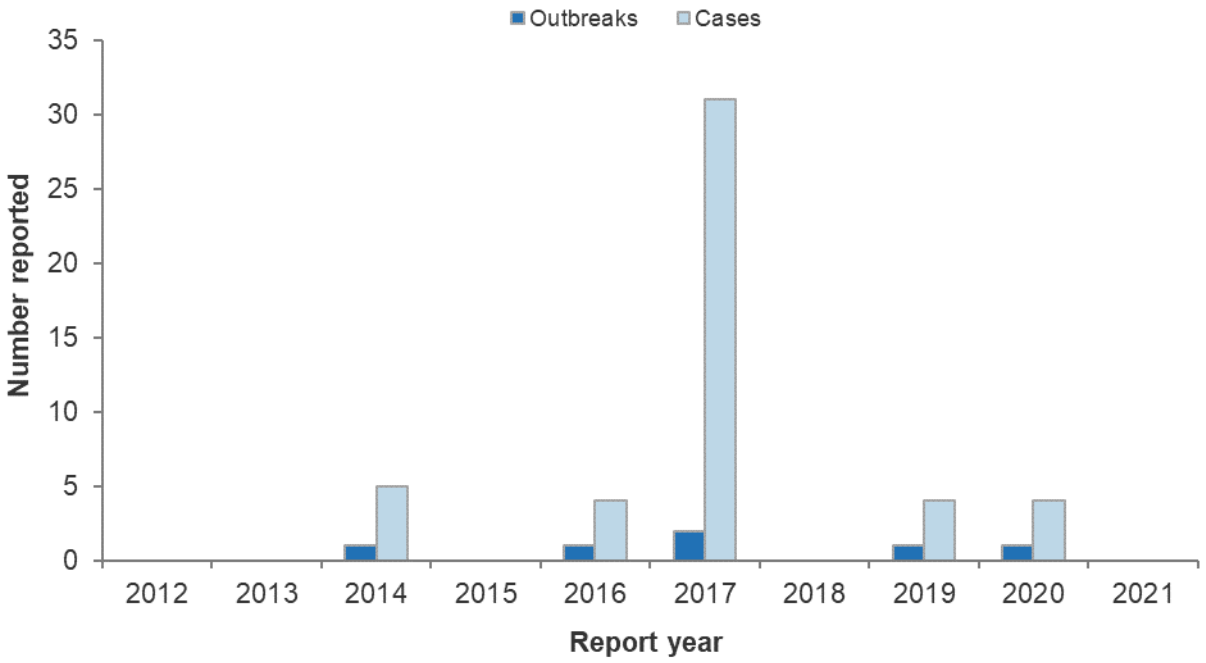
Outbreaks reported as caused by ciguatera poisoning

During 2021, 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 2012 to 2021, six outbreaks of ciguatera poisoning were reported, with no more than two outbreaks reported in a single year (Figure 12). 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 12. Ciguatera poisoning outbreaks and associated cases reported by year, 2012–2021



Recent surveys

Nil.

Relevant New Zealand studies and publications

Journal papers

Ciguatera poisoning and confirmation of ciguatoxins in fish imported into New Zealand– Murray et al. (2021)

In May 2020, five people became ill and one was hospitalised following the consumption of Fiji Kawakawa (camouflage grouper; *Epinephelus polyphekadion*) [24]. The fish was purchased in New Zealand but imported from Fiji. The meal remnants were analysed for ciguatoxins, the causative compounds of ciguatera poisoning, and showed the presence of the three main toxic fish metabolites. Other fish tested from the same shipment did not contain detectable levels of ciguatoxins, indicating they were likely not toxic.

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 ≥10^6/g or isolation of ≥10^5/g *Clostridium perfringens* in leftover food.
Case classification:	
Probable	A clinically compatible illness.
Confirmed	A clinically compatible illness that is laboratory confirmed, OR a clinically compatible illness and a common exposure associated with a laboratory confirmed case.

Clostridium perfringens intoxication cases reported in 2021 by data source

During 2021, 27 outbreak-related cases and no individual cases of confirmed *C. perfringens* intoxication were reported in EpiSurv.

The ICD-10 code A05.2 was used to extract foodborne *C. perfringens* intoxication hospitalisation data from the MoH NMDS database. There were no hospital admissions recorded in 2021 with *C. perfringens* intoxication as the primary diagnosis.

Outbreaks reported as caused by *Clostridium perfringens*

In 2021, there was one *C. perfringens* intoxication outbreak (27 cases) reported in EpiSurv with food as a possible mode of transmission (Table 13).

Table 13. *C. perfringens* intoxication outbreaks reported, 2021

	Possible foodborne transmission but no suspected source	Total number of *C. perfringens* intoxication outbreaks
Outbreaks	1	1
Outbreak-associated cases	27	27
Hospitalised cases	0	0

Table 14 contains details of the outbreak at a prison. Cases came from different independent units at the prison, so the only common exposure factor would have been the food consumed. All of the 12 cases who provided information on their meals had eaten the corned beef meal. No leftover food was available for testing.

A review of kitchen processes for the corned beef meal found the meat stock solution saved from cooking the corned beef and used to make gravy two days later was unlikely to have been cooled sufficiently quickly to meet cooling criteria.

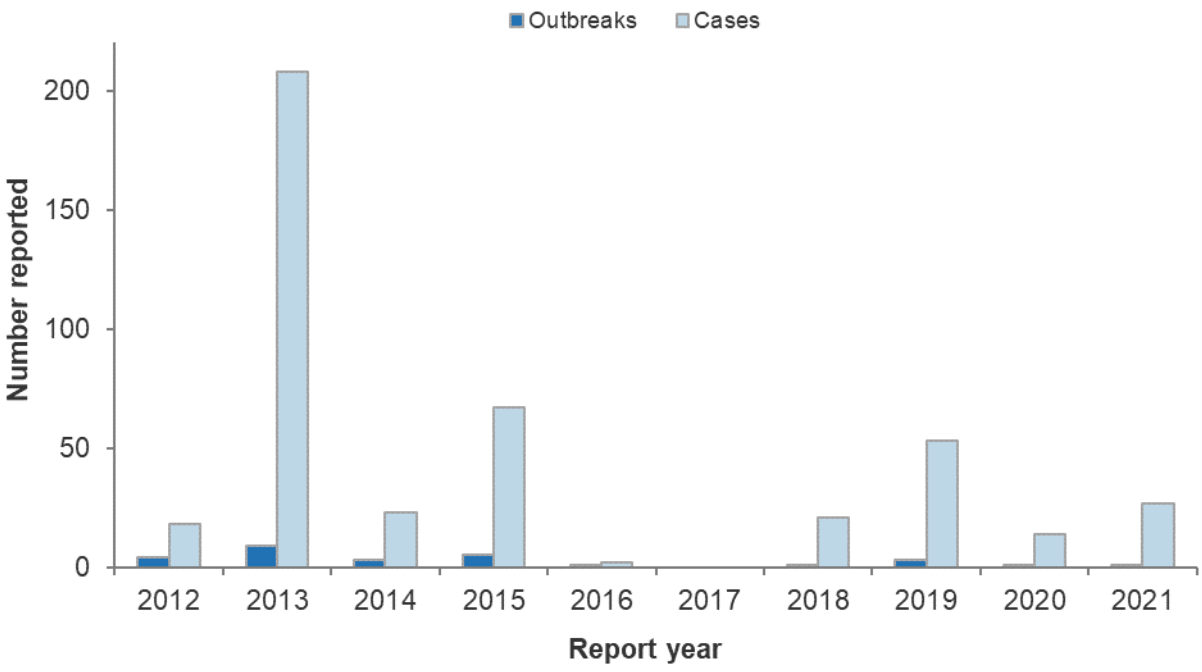
Table 14. Details of *C. perfringens* intoxication outbreaks with food reported as a possible mode of transmission, 2021

PHU	Month	Suspected source	Evidence	Setting	No. ill
PH South	April	Corned beef stock	Food was the only common exposure factor for cases. Review of stock cooling processes used in the kitchen showed the potential for growth of *C. perfringens* during cooling.	Prison	1C 26P

PHU: Public health unit, PH South: Public Health South
Number ill: C: confirmed, P: probable

Over the 10-year period 2012-2021, 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 13). 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 13. *C. perfringens* intoxication outbreaks with food reported as a possible mode of transmission and associated cases reported by year, 2012–2021



Recent surveys

Nil.

Relevant New Zealand studies and publications

Nil.

Relevant regulatory developments

Nil.

Cryptosporidiosis

Summary data for cryptosporidiosis in 2021 are given in Table 15.

Table 15. Summary of surveillance data for cryptosporidiosis, 2021

Parameter	Value in 2021	Source
Number of notified cases	702	EpiSurv
Notification rate (per 100,000)	13.7	EpiSurv
Hospitalisations[a]	47	MoH NMDS
Deaths	0	EpiSurv
Travel-related cases (%)[b, c]	0 (0%)	EpiSurv
Estimated food-related cases (%)	NE	-

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

[a] Cases hospitalised may not be notified on EpiSurv

[b] Percentage of the number of notified cases

[c] New Zealand borders were closed in March 2020 with travel restrictions in place for the rest of 2020 and 2021

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. In 2021, 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. The MidCentral, Tairawhiti, and Whanganui DHBs changed to PCR testing in May 2021.

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 [25].

Effect of COVID-19 on cryptosporidiosis notification rates

Public health and social measures to prevent the spread of COVID-19 in New Zealand were introduced in March 2020 and remained in place through December 2021. These measures will have affected exposure behaviours and pathways, access to medical care and laboratory testing priorities. These multiple aspects make it difficult to attribute any changes to notification rates, either to specific COVID-19 related factors, which is discussed in more detail in the Introduction (see page 5), or true changes in disease incidence.

In 2021, the monthly cryptosporidiosis notification rate followed the same trend but was below the range of the pre-COVID-19 years 2017-2019 (Figure 15). Monthly notification rates in 2021 were very similar to 2020.

The frequency of overseas travel has changed due to border restrictions from March 2020 until the end of 2021. This is reflected in the notifications; in 2021, there were no cryptosporidiosis notifications in EpiSurv listing overseas travel as a risk factor, compared to 50 in 2019 and seven in 2020.

Cryptosporidiosis individual cases reported in 2021 by data source

During 2021, 702 individual cases (13.7 per 100,000 population) of cryptosporidiosis and no resulting deaths were reported in EpiSurv. Of the 702 cases, the symptoms of 652 cases (93%) were reported as fitting the clinical description for cryptosporidiosis, the symptoms were unknown for 49 cases, and for one case the symptoms were reported as not fitting the clinical description

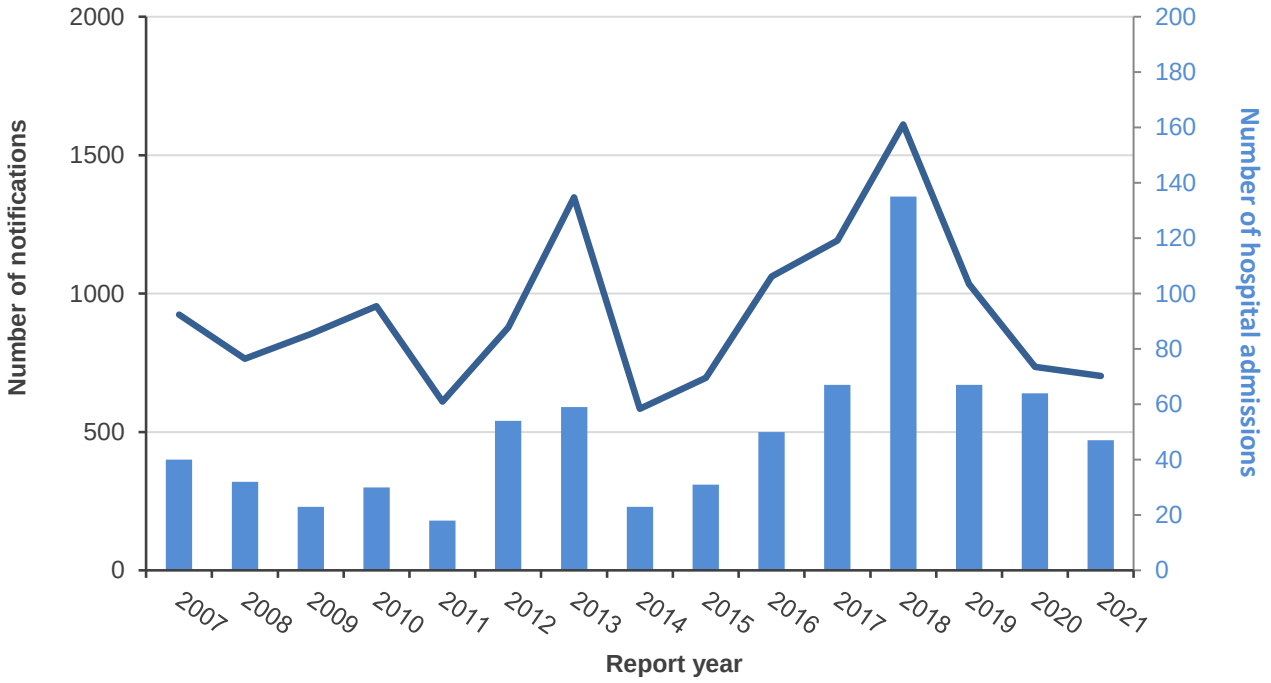
The ICD-10 code A07.2 was used to extract cryptosporidiosis hospitalisation data from the MoH NMDS database. Of the 47 hospital admissions (0.9 admissions per 100,000 population) recorded in 2021, 33 cases were reported with cryptosporidiosis as the primary diagnosis and 14 were reported with cryptosporidiosis 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

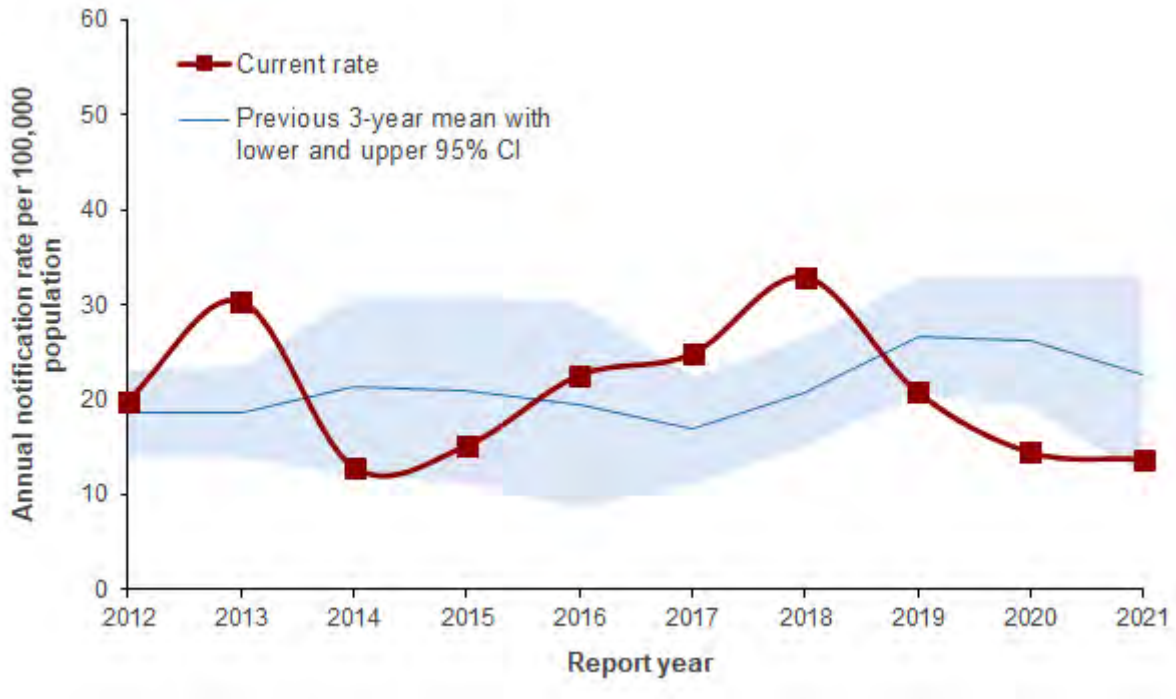
In 2018, the highest number of cryptosporidiosis notifications (1613 notifications) was recorded since cryptosporidiosis became a notifiable disease in 1996. Over the last 15-year time period there were no clear trends regarding the number of cryptosporidiosis notifications (Figure 14). After the peak in 2018, the number of notifications in 2020 and 2021 (735 and 702 cases, respectively) returned to within the range seen in the previous 20 years. 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).

Figure 14. Cryptosporidiosis EpiSurv notifications (line) and NMDS hospitalisations (bar) by year, 2007–2021



Due to the peak in 2018, the cryptosporidiosis notification rates in 2020 and 2021 (14.4 and 13.7 cases per 100,000 population) were lower than the previous three-year average (22.7 cases per 100,000 population) (Figure 15).

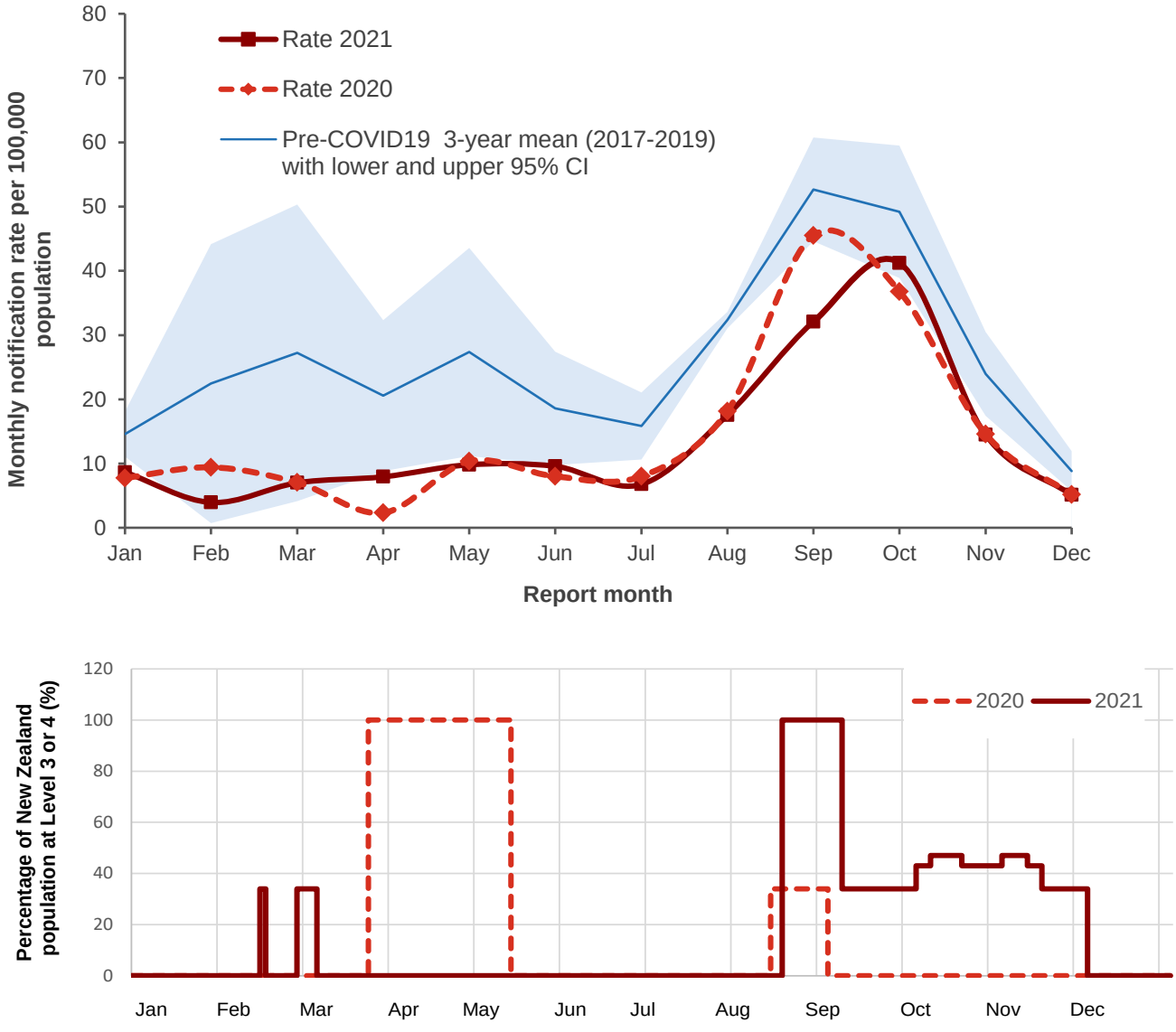
Figure 15. Cryptosporidiosis notification rate by year, 2012–2021



Seasonal data

Cryptosporidiosis notification rates per 100,000 population by month for 2020 and 2021 are shown in Figure 16 as well as the percentage of the New Zealand population at COVID-19 Alert Levels 3 or 4. In 2021, monthly notification rates followed the same trend but were generally lower than the three-year mean of the years 2017-2019. The monthly number of notifications in 2021 ranged from 17 notifications (February, 4 per 100,000 population) to 176 notifications (October, 41 per 100,000 population).

Figure 16. Cryptosporidiosis monthly notification rate (annualised) and percentage of New Zealand population at COVID-19 Alert Levels 3 or 4, 2020 and 2021



Note: A detailed timeline of all COVID-19 Alert Level changes for 2020 and 2021 is included in Appendix C (Table 73).

Demographics

In 2021, the rate of notifications for cryptosporidiosis was higher for females (15.3 per 100,000 population) compared with males (12.1 per 100,000 population) whereas the rate of hospitalisations was the same (Table 16).

Table 16. Cryptosporidiosis cases by sex, 2021

Sex	EpiSurv notifications		Hospitalisations[a]	
	No.	Rate[b]	No.	Rate[b]
Male	307	12.1	23	0.9
Female	395	15.3	24	0.9
Total	**702**	**13.7**	**47**	**0.9**

[a] MoH NMDS data for hospital admissions
[b] per 100,000 population in this sex group

In 2021, the highest cryptosporidiosis age-specific notification rate was reported for the 0 to 4 years age group (45.2 per 100,000 population, 138 cases) (Table 17). The hospitalisation rate was highest for the 5 to 9 years age group (3.7 admissions per 100,000 population, 12 cases).

Table 17. Cryptosporidiosis cases by age group, 2021

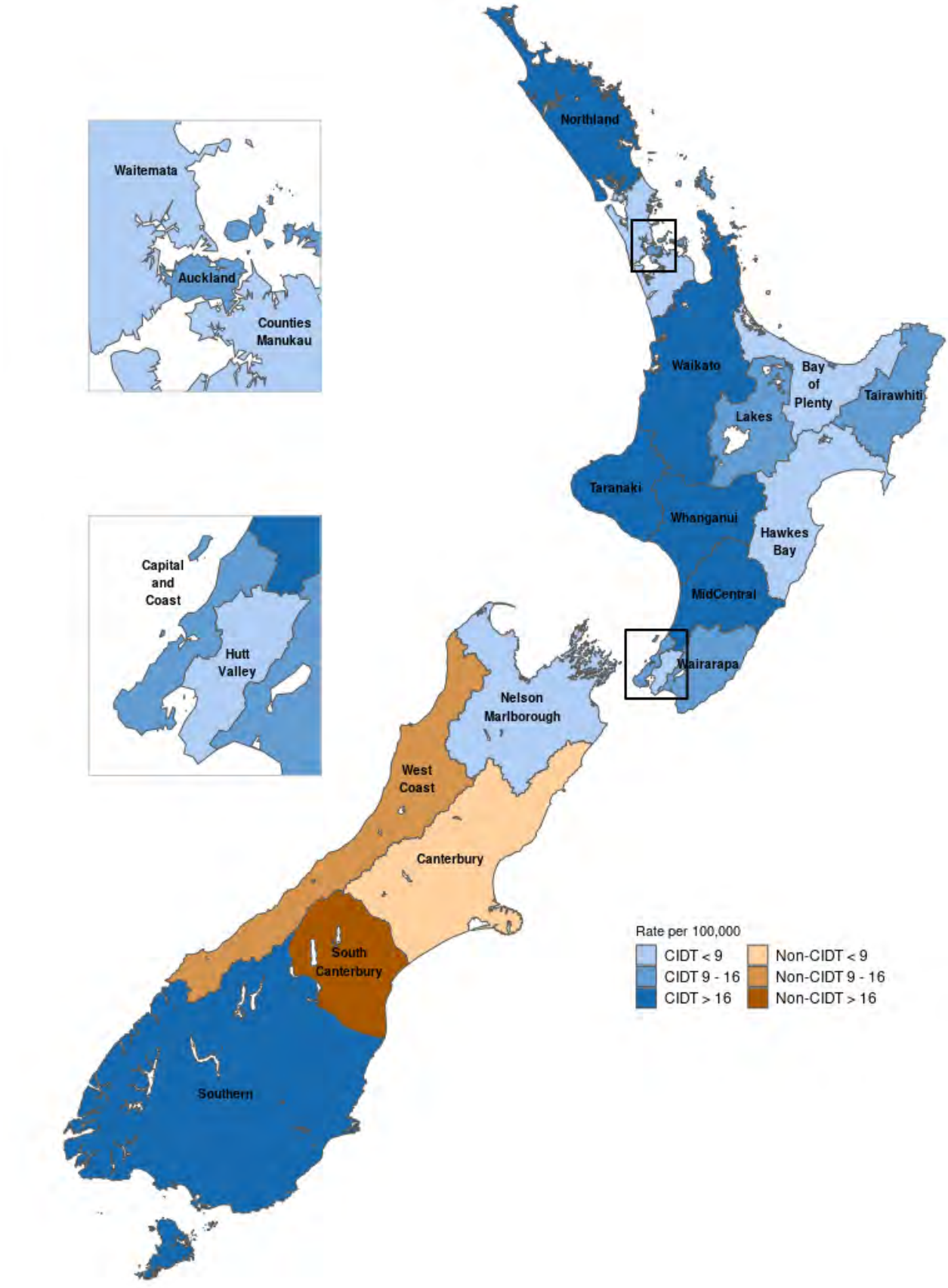
Age group (years)	EpiSurv notifications		Hospitalisations[a]	
	No.	Rate[b]	No.	Rate[b]
0 to 4	138	45.2	6	2.0
5 to 9	79	24.3	12	3.7
10 to 14	52	15.4	3	-
15 to 19	53	16.8	1	-
20 to 29	152	21.6	8	1.1
30 to 39	95	13.1	3	-
40 to 49	57	9.0	2	-
50 to 59	33	5.0	2	-
60 to 69	27	4.9	5	0.9
70+	16	2.8	5	0.9
Total	**702**	**13.7**	**47**	**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 17 (see also Table 82). Blue shading is used in DHBs which are using CIDT community testing, the brown shading is used for DHBs using microscopy or EIA.

Figure 17. Geographic distribution of cryptosporidiosis notifications, 2021



Note: Whanganui, MidCentral and Tairawhiti DHBs testing moved to CIDT methods in May 2021. The rates for these DHBs will be based on a mixture of CIDT and non-CIDT test results.

In 2021, the DHB notification rates of cryptosporidiosis ranged from 6 per 100,000 population (10 cases) in Nelson Marlborough DHB to 50 per 100,000 population (63 cases) in Taranaki DHB. The Taranaki, South Canterbury (39 per 100,000 population, 24 cases), Southern (28 per 100,000 population, 98 cases), Waikato (26 per 100,000 population, 116 cases), and MidCentral (22 per 100,000 population, 42 cases) DHBs had notification rates at or above 20 per 100,000 population.

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

Outbreaks reported as caused by *Cryptosporidium* spp.

In 2021, there were eight cryptosporidiosis outbreak notifications reported in EpiSurv, two of which recorded food as a possible mode of transmission (Table 18). 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 18. Cryptosporidiosis outbreaks reported, 2021

	Possible foodborne transmission with a suspected or confirmed source	Possible foodborne transmission but no suspected source	Total number of cryptosporidiosis outbreaks
Outbreaks	2	0	8
Outbreak-associated cases	17	0	44[a]
Hospitalised cases	1	0	2

[a] One non-foodborne family outbreak did not have case numbers recorded; this number is for the remaining seven outbreak notifications

Both of the outbreaks with food reported as a possible mode of transmission were associated with consumption of raw milk (Table 19). In both outbreaks, multiple-case households consumed milk from the same supplier over the same time period.

The subtype identified in both outbreaks was *Cryptosporidium parvum* subtype IIaA18G3R1, a subtype commonly associated with cattle.

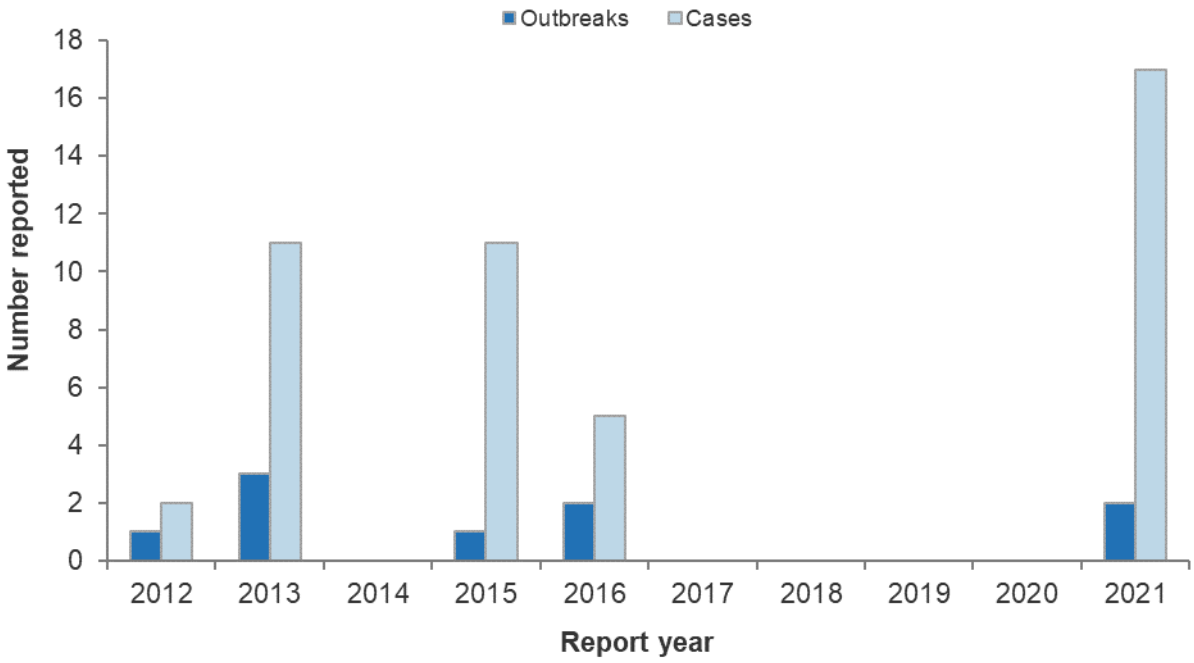
Table 19. Details of cryptosporidiosis outbreaks with food reported as a possible mode of transmission, 2021

PHU	Month	Suspected source	Evidence	Setting	No. ill
Taranaki	April	Raw milk	Common milk supplier	Consumed at home	5C 6P
Taranaki	September	Raw milk	Common milk supplier	Consumed at home	4C 2P

PHU: Public Health Unit, Taranaki: Taranaki Public Health
Number ill: C: confirmed, P: probable

Between 2012 and 2021 there have been a total of nine outbreaks of potentially foodborne cryptosporidiosis (Figure 18), with no outbreaks recorded over the period 2017 to 2020. The number of cases associated with individual outbreaks ranged between two and eleven.

Figure 18. Cryptosporidiosis outbreaks with food reported as a possible mode of transmission and associated cases reported by year, 2012–2021



Recent surveys

Nil.

Relevant New Zealand studies and publications

Journal papers

Absence of Cryptosporidium hominis and dominance of zoonotic Cryptosporidium species in patients after Covid-19 restrictions in Auckland, New Zealand – Knox et al. (2021)

Cryptosporidium infections in humans are almost entirely caused by two species: *C. hominis*, which is primarily transmitted from human to human, and *Cryptosporidium parvum*, which is mainly zoonotic [26]. By monitoring *Cryptosporidium* species and subtype families in human cases of cryptosporidiosis before and after the introduction of COVID-19 control measures in New Zealand, *C. hominis* was found to be completely absent after the first months of 2020 and has remained so until the beginning of 2021. Nevertheless, *C. parvum* has followed its typical transmission pattern and continues to be widely reported. It was concluded that approximately seven weeks of isolation during Level 3 and 4 lockdown period interrupted the human-to-human transmission of *C. hominis* leaving only the primarily zoonotic transmission pathway used by *C. parvum*.

Relevant regulatory developments

Nil.

Giardiasis

Summary data for giardiasis in 2021 are given in Table 20.

Table 20. Summary of surveillance data for giardiasis, 2021

Parameter	Value in 2021	Source
Number of notified cases	1040	EpiSurv
Notification rate (per 100,000)	20.3	EpiSurv
Hospitalisations[a]	57	MoH NMDS
Deaths	0	EpiSurv
Travel-related cases (%)[b, c]	6 (0.6%)	EpiSurv
Estimated food-related cases	NE	-

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

[a] Cases hospitalised may not be notified on EpiSurv

[b] Percentage of the number of notified cases

[c] New Zealand borders were closed in March 2020 with travel restrictions in place for the rest of 2020 and 2021.

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. In 2021, 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. The MidCentral, Tairawhiti, and Whanganui DHBs changed to PCR testing in May 2021.

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 20). This suggests that symptoms of gardiasis were generally well recognised leading to appropriate requests for testing.

Effect of COVID-19 on giardiasis notification rates

Public health and social measures to prevent the spread of COVID-19 in New Zealand were introduced in March 2020 and remained in place through December 2021. These measures will have affected exposure behaviours and pathways, access to medical care and laboratory testing priorities. These multiple aspects make it difficult to attribute any changes to notification rates, either to specific COVID-19 related factors, which is discussed in more detail in the Introduction (see page 5), or true changes in disease incidence.

In 2021, the monthly giardiasis notification rate followed the same trend but was consistently below the range of the pre-COVID-19 years 2017-2019 (Figure 21). Compared to 2020, monthly notification rates were higher from April to June 2021 but lower for the spring and summer months. It is unclear how COVID-19 restrictions have affected giardiasis notification rates in 2021. In 2020, a reduction in giardiasis notifications from March to mid-May – compared to the same period in the previous three years 2017–2019 – coincided with Alert Level 3 and 4 periods and can probably be attributed to the COVID-19 public health response.

The frequency of overseas travel has changed due to border restrictions from March 2020 until the end of 2021. This is reflected in the notifications; in 2021, there were six giardiasis notifications in EpiSurv listing overseas travel as a risk factor, compared to 179 in 2019 and 59 in 2020.

Giardiasis individual cases reported in 2021 by data source

During 2021, 1040 individual cases (20.3 per 100,000 population) of giardiasis and no resulting deaths were reported in EpiSurv. Of the 1040 cases, the symptoms of 945 cases (91%) were reported as fitting the clinical description for giardiasis, the symptoms were unknown for 92 cases, and for three cases the symptoms were reported as not fitting the clinical description.

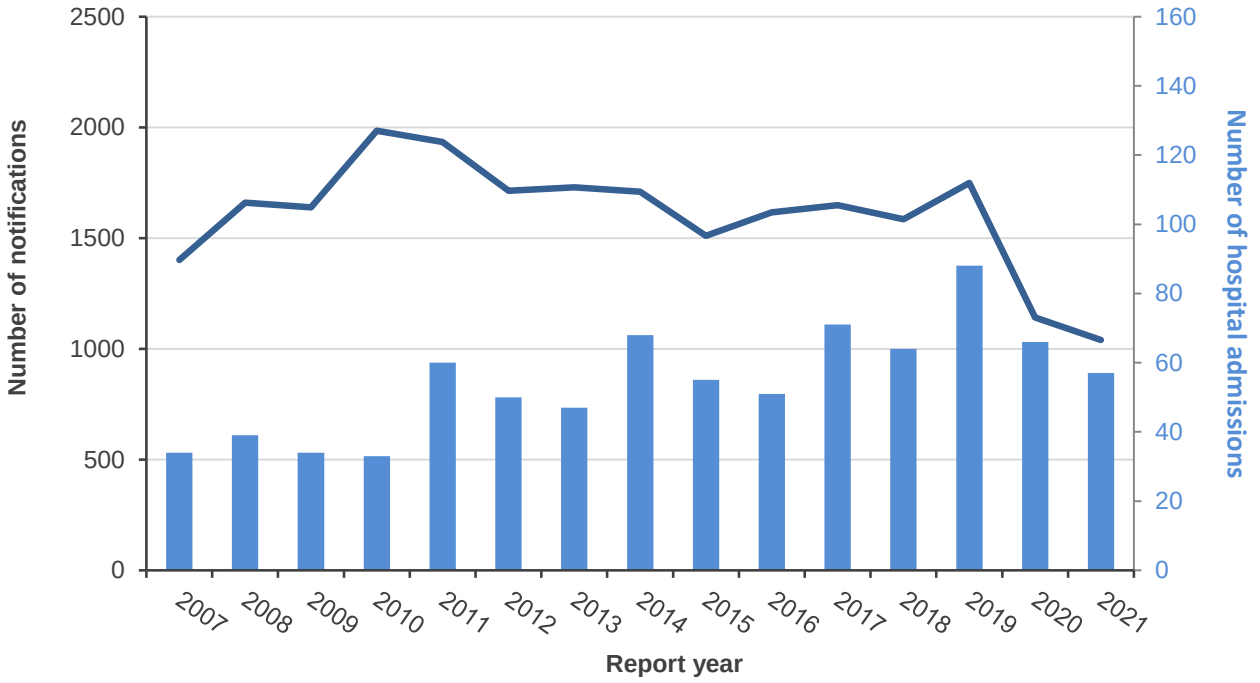
The ICD-10 code A07.1 was used to extract giardiasis hospitalisation data from the MoH NMDS database. Of the 57 hospital admissions (1.1 admissions per 100,000 population) recorded in 2021, 31 cases were reported with giardiasis as the primary diagnosis and 26 were reported with giardiasis as another 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

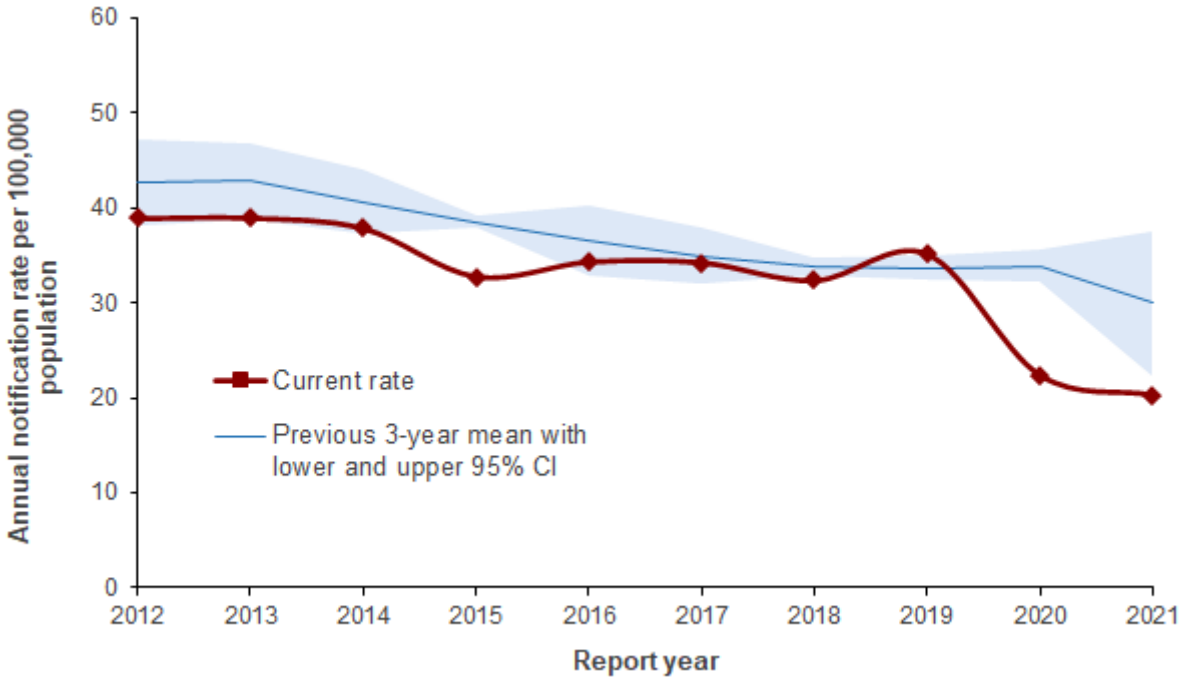
The number of giardiasis cases reported each year decreased until 2006. An increasing trend in the number of notifications was observed from 2006 until 2010 with notification numbers remaining within a similar range since 2012 (range of 1510 to 1749 cases) (Figure 19). There was a pronounced drop in notifications in 2020 and 2021. 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).

Figure 19. Giardiasis EpiSurv notifications (line) and NMDS hospitalisations (bar) by year, 2007–2021



The notification rate in 2021 (20.3 cases per 100,000 population) was much lower than the previous three-year average (29.9 cases per 100,000 population) (Figure 20). This drop in notification rates can be attributed to the COVID-19 pandemic.*

Figure 20. Giardiasis notification rate by year, 2012–2021

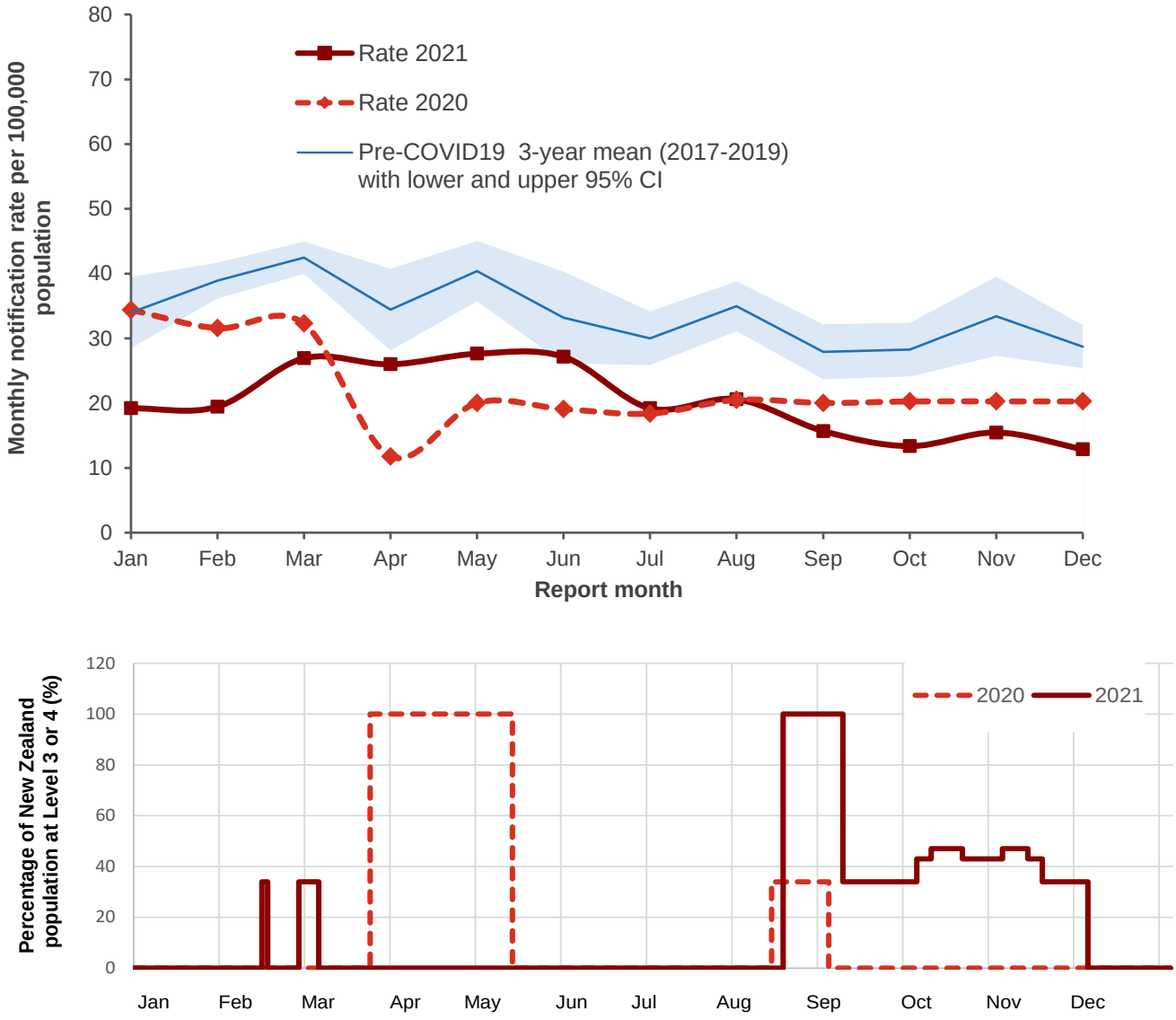


* An overview of the impact of the COVID-19 pandemic on notifications of potentially foodborne diseases is provided in the Introduction, page 5.

Seasonal data

Giardiasis notification rates per 100,000 population by month for 2020 and 2021 are shown in Figure 21 as well as the percentage of the New Zealand population at COVID-19 Alert Levels 3 or 4 at different times in 2020 and 2021. For the months March to June 2021 notification rates were higher compared to the rest of the 2021 year. The monthly number of notifications in 2021 ranged from 55 notifications (December, 13 per 100,000 population) to 118 notifications (May, 28 per 100,000 population). In 2020, a reduction in giardiasis notification rates from March to mid-May – compared to the same period in the previous three years 2017–2019 – coincided with Alert Level 3 and 4 periods and is likely to be attributed to the COVID-19 public health response.

Figure 21. Giardiasis monthly notification rate (annualised) and percentage of New Zealand population at COVID-19 Alert Levels 3 or 4, 2020 and 2021



Note: A detailed timeline of all COVID-19 Alert Level changes for 2020 and 2021 is included in Appendix C (Table 73).

Demographics

In 2021, the rate of notifications for giardiasis was similar for males (20.4 cases per 100,000 population) and females (20.1 cases per 100,000 population). Hospitalisation rates were also similar for females (1.2 admissions per 100,000 population) and males (1.1 admissions per 100,000 population) (Table 21).

Table 21. Giardiasis cases by sex, 2021

Sex	EpiSurv notifications		Hospitalisations[a]	
	No.	Rate[b]	No.	Rate[b]
Male	519	20.4	27	1.1
Female	519	20.1	30	1.2
Total[c]	**1040**	**20.3**	**57**	**1.1**

[a] MoH NMDS data for hospital admissions
[b] per 100,000 population in this sex group
[c] total includes notifications where gender is unknown

In 2021, the highest age-specific notification rate was for the 0 to 4 years age group (76.3 per 100,000 population, 233 cases), (Table 22). The highest hospitalisation rate was also reported for the 0 to 4 years age group (5.2 admissions per 100,000 population, 16 cases).

Table 22. Giardiasis cases by age group, 2021

Age group (years)	EpiSurv notifications		Hospitalisations[a]	
	No.	Rate[b]	No.	Rate[b]
0 to 4	233	76.3	16	5.2
5 to 9	70	21.5	3	-
10 to 14	14	4.1	1	-
15 to 19	13	4.1	1	-
20 to 29	102	14.5	5	0.7
30 to 39	217	29.9	3	-
40 to 49	131	20.6	10	1.6
50 to 59	97	14.8	6	0.9
60 to 69	120	21.8	5	0.9
70+	42	7.4	7	1.2
Total[c]	**1040**	**20.3**	**57**	**1.1**

[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)
[c] total includes notifications where age is unknown

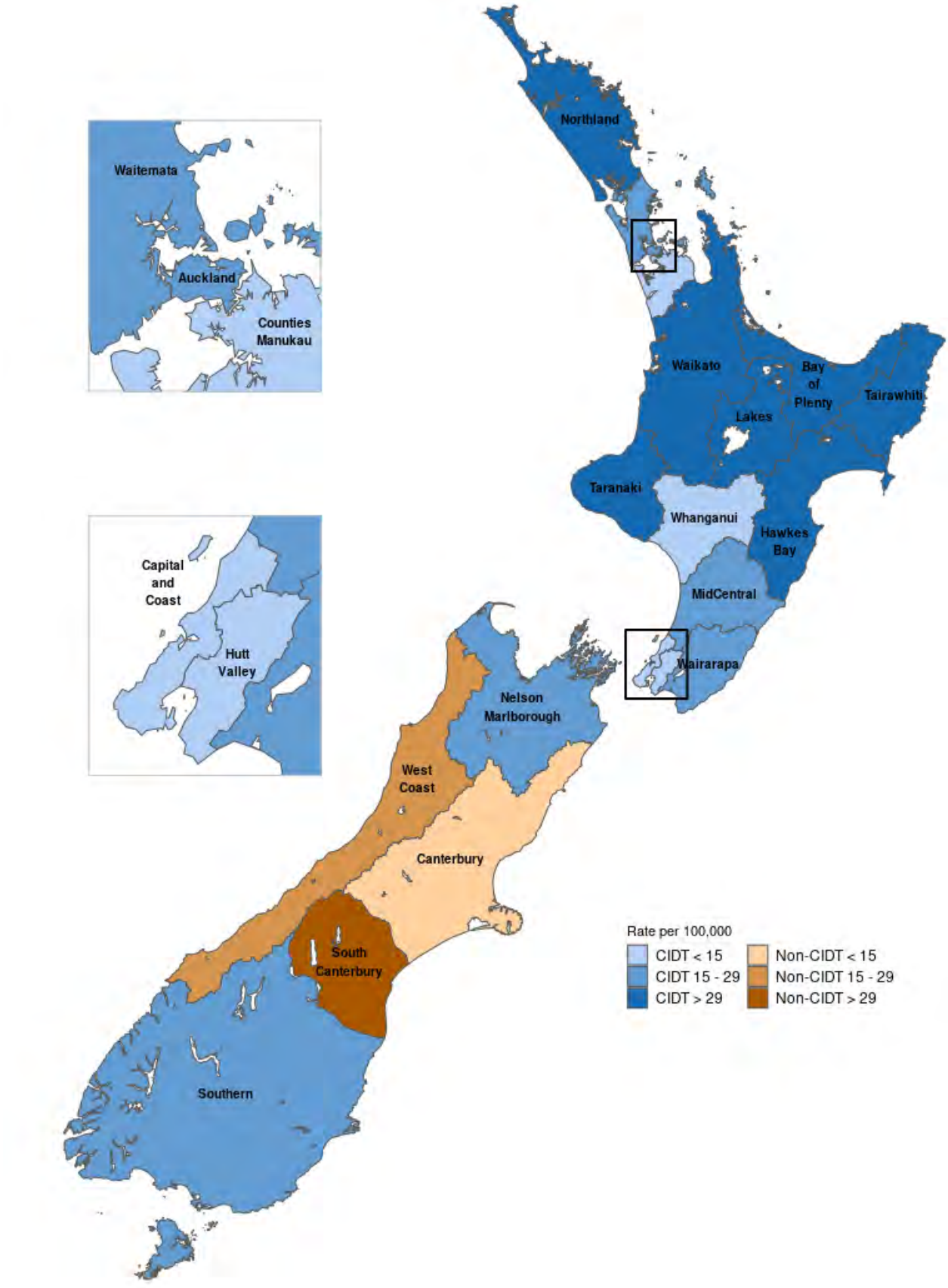
Geographic distribution

The notification rates by DHB calculated per 100,000 resident population are presented in Figure 22 (see also Table 82). Blue shading is used in DHBs which are using CIDT community testing, the brown shading is used for DHBs using microscopy or EIA.

In 2021, the DHB notification rates for giardiasis ranged from 9 per 100,000 population (six cases) in Whanganui DHB to 52 per 100,000 population (27 cases) in Tairawhiti DHB. The Tairawhiti, Bay of Plenty (36 per 100,000 population, 96 cases) and Hawke's Bay (35 per 100,000 population, 63 cases) DHBs had notification rates at or above 35 per 100,000 population.

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

Figure 22. Geographic distribution of giardiasis notifications, 2021



Note: Whanganui, MidCentral and Tairawhiti DHBs testing moved to CIDT methods in May 2021. The rates for these DHBs will be based on a mixture of CIDT and non-CIDT test results.

Outbreaks reported as caused by *Giardia spp.*

In 2021, there were 21 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, 2021

	Possible foodborne transmission with a suspected or confirmed source	Possible foodborne transmission but no suspected source	Total number of giardiasis outbreaks
Outbreaks	0	1	21
Outbreak-associated cases	0	2	119[a]
Hospitalised cases	0	0	0

[a] One non-foodborne family outbreak did not have case numbers recorded; this number is for the 20 completed outbreak notifications.

The evidence linking the possibly foodborne outbreak (Table 24) to a foodborne source was weak with no suspected foods identified. The cases also visited Department of Conservation (DOC) reserves and camped during the incubation period.

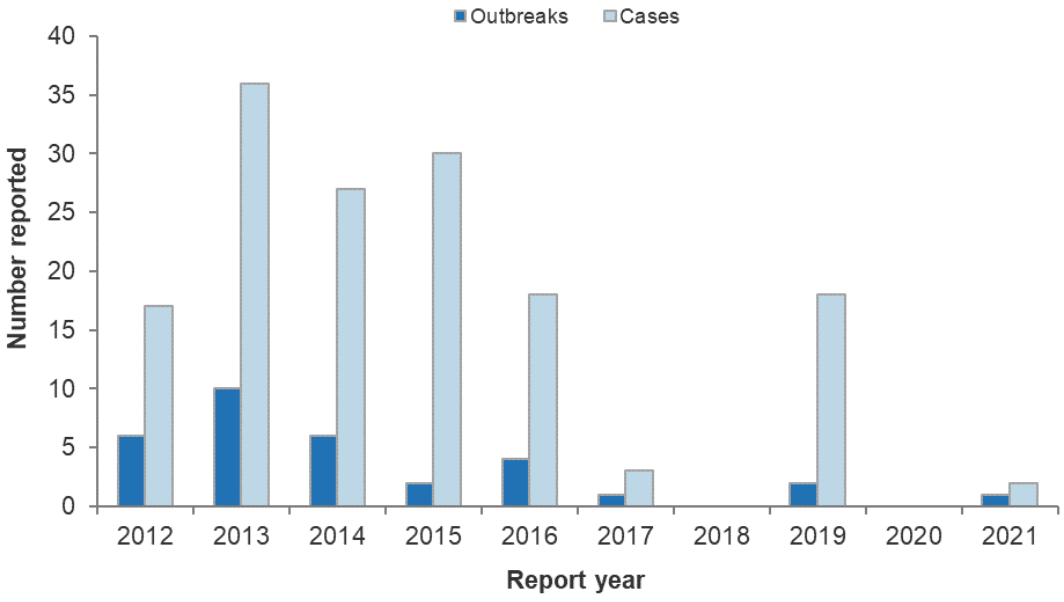
Table 24. Details of giardiasis outbreak with food reported as a possible mode of transmission, 2021

PHU	Month	Suspected source	Evidence	Setting	No. ill
PH Northland	February	Unknown	None	Unknown	2C

PHU: Public health unit, PH Northalnd: Public Health Northland
Number ill: C: confirmed

Over the 10-year period 2012 and 2021, 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 23).

Figure 23. Giardiasis outbreaks with food reported as a possible mode of transmission and associated cases reported by year, 2012–2021



Recent surveys

Nil.

Relevant New Zealand studies and publications

Journal papers

First report of novel assemblages and mixed infections of Giardia duodenalis in human isolates from New Zealand – Garcia-R et al. (2021)

The pathogen is classified into eight assemblages, further divided into sub-assemblages, based on genetic divergence and host specificities [27]. There are two zoonotic subtypes known as assemblages A and B, whilst assemblages C to H are mainly found in domesticated animals, rodents and marine mammals. Assemblage E and sub-assemblage AIII were identified in human isolates from the South Island in New Zealand for the first time. Assemblage E has so far only been found in ruminants in New Zealand, suggesting that the route of transmission to humans is zoonotic, with potential sources of infection from domesticated farm animals.

Relevant regulatory developments

Nil.

Hepatitis A

Summary data for hepatitis A in 2021 are given in Table 25.

Table 25. Summary of surveillance data for hepatitis A, 2021

Parameter	Value in 2021	Source
Number of notified cases	8	EpiSurv
Notification rate (per 100,000)	0.2	EpiSurv
Hospitalisations[a]	9	MoH NMDS
Deaths	0	EpiSurv
Travel-related cases (%)[b,c]	2 (25%)	EpiSurv
Estimated food-related cases	NE	-

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

[a] Hospitalisations with acute hepatitis A as the principal diagnosis. Cases hospitalised may not be notified on EpiSurv

[b] Percentage of the number of notified cases

[c] New Zealand borders were closed in March 2020 with travel restrictions in place for the rest of 2020 and 2021.

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 2021 by data source

There were 40 hospital admissions (0.8 admissions per 100,000 population) recorded in 2021; nine cases were reported with acute hepatitis A as the primary diagnosis and 31 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.

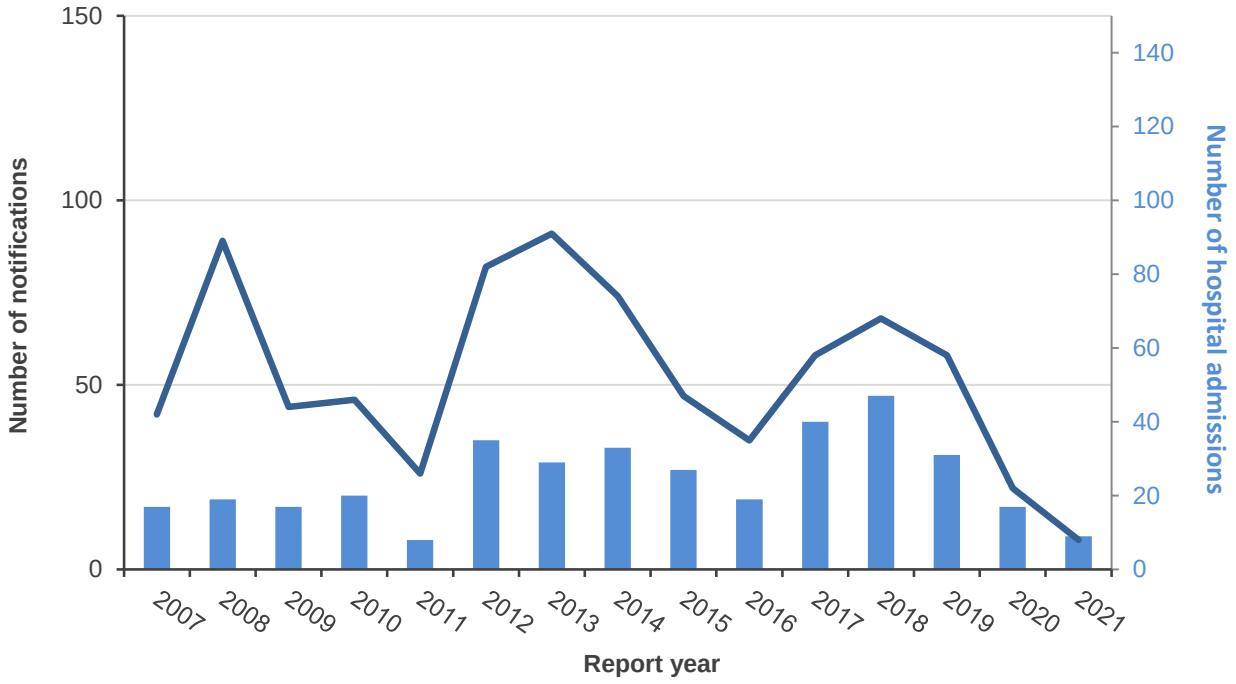
During 2021, eight individual cases (0.2 per 100,000 population) of hepatitis A and no resulting deaths were reported in EpiSurv. Hospitalisation rates are usually high for hepatitis A with 50% of notified cases recorded in EpiSurv as hospitalised in 2021.

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 [13]. 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 2007 and 2019, the annual number of notifications remained in the range of 26 (2011) to 91 (2013) (Figure 24), followed by lower numbers in 2020 and 2021 (22 and eight notifications, respectively). The frequency of overseas travel has changed due to border restrictions from March 2020 until the end of 2021. This is reflected in the notifications; in 2021, there were two hepatitis A notifications in EpiSurv listing overseas travel as a risk factor, compared to 33 in 2019 and 16 in 2020.

Figure 24. Hepatitis A EpiSurv notifications (line) and NMDS hospitalisations (bar) by year, 2007–2021



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 2021, the number of hepatitis A notifications was similar for females (five notified cases) and males (three notified cases). Hospitalisation admissions were higher for females (eight admissions) than for males (one admission) (Table 26).

Table 26. Hepatitis A cases by sex, 2021

Sex	EpiSurv notifications		Hospitalisations[a]	
	No.	Rate[b]	No.	Rate[b]
Male	3	-	1	-
Female	5	0.2	8	0.3
Total	**8**	**0.2**	**9**	**0.2**

[a] MoH NMDS data for hospital admissions with hepatitis A as a primary diagnosis
[b] per 100,000 population in this sex group (rate not calculated when fewer than five cases reported)

In 2021, the hepatitis A notified cases ranged in age from 4 to 65 years old. The age range for hospital admissions was 6 to 83 years old (Table 27).

Table 27. Hepatitis A cases by age group, 2021

Age group (years)	EpiSurv notifications		Hospitalisations[a]	
	No.	Rate[b]	No.	Rate[b]
0 to 4	1	-	0	-
5 to 9	1	-	2	-
10 to 14	0	-	0	-
15 to 19	1	-	1	-
20 to 29	0	-	0	-
30 to 39	1	-	2	-
40 to 49	1	-	1	-
50 to 59	2	-	0	-
60 to 69	1	-	1	-
70+	0	-	2	-
Total	**8**	**0.2**	**9**	**0.2**

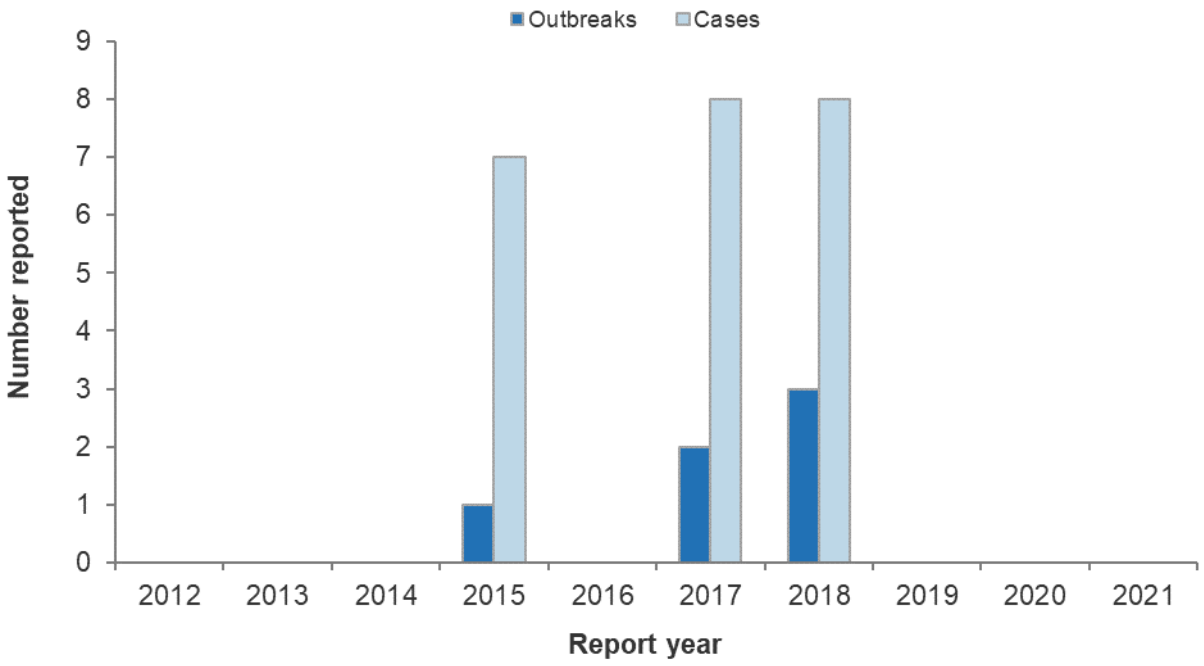
[a] MoH NMDS data for hospital admissions with hepatitis A as a primary diagnosis

[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

From 2019 to 2021 there were no outbreaks of hepatitis A reported in EpiSurv (Figure 25). In the preceding four years (2015 to 2018) there were six outbreaks with a total of 23 associated cases.

Figure 25. Hepatitis A outbreaks with food reported as a possible mode of transmission and associated cases reported by year, 2012–2021



Hepatitis A virus genotypes commonly reported

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

Hepatitis A virus genotypes IA and IIIA were identified in cases in 2021. Hepatitis A virus IA was the most commonly identified sub-genotype between 2017 and 2020.

Table 28. Hepatitis A virus genotypes identified by the Enteric, Environmental and Food Virology Laboratory, 2017–2021

Hepatitis A virus genotypes	2017	2018	2019	2020	2021
IA	20	20	24	10	2
IIIA	4	14	8	4	2
IB	1	0	1	2	0
Unable to genotype	2	3	1	0	0
Total	**27**	**37**	**34**	**16**	**4**

Recent surveys

Nil.

Relevant New Zealand studies and publications

Nil

Relevant regulatory developments

A new version of the Food Notice, *Importing Food*, was published in 2021 [28]. The Notice lists frozen berries as of increased regulatory interest with respect to hepatitis A virus.

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/100 g fish muscle.
Case classification:	Not applicable.

Histamine (scombroid) fish poisoning cases reported in 2021 by data source

During 2021, six individual cases (0.1 admissions per 100,000 population) 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 10 hospital admissions (0.2 admissions per 100,000 population) recorded in 2021, all cases were reported with histamine (scombroid) fish poisoning as the primary diagnosis. No cases were reported with histamine (scombroid) fish 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 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 2021 involving two cases. No 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, 2021

	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 2021. No leftover food was available for testing to confirm the source of the illness.

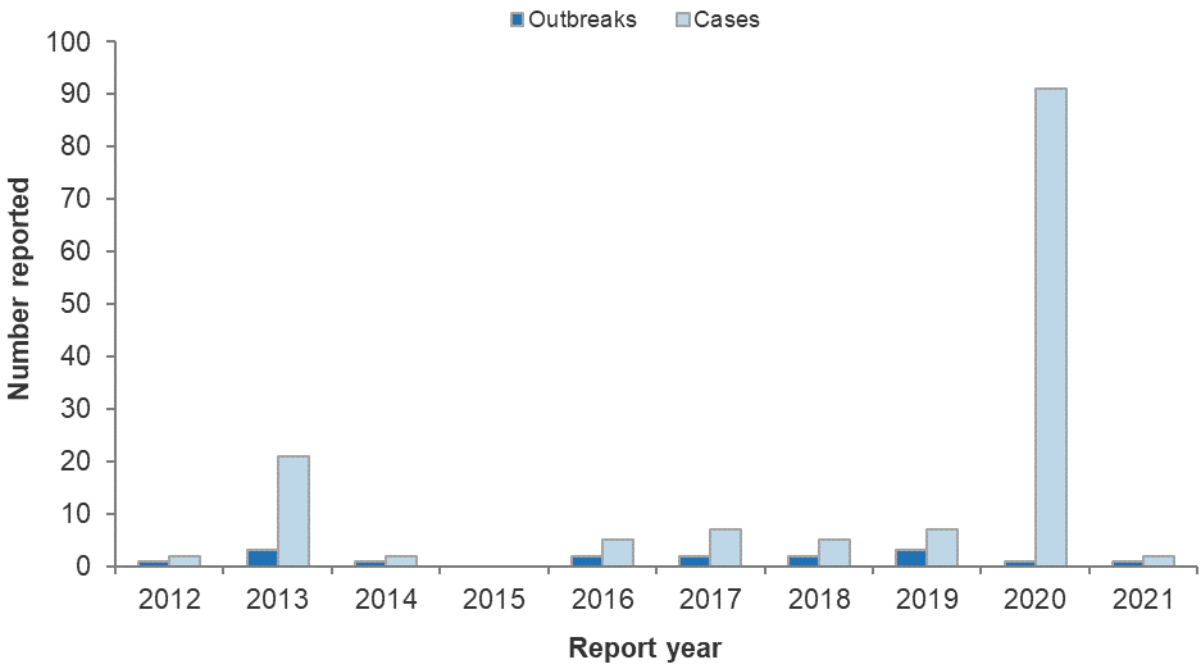
Table 30. Details of histamine (scombroid) fish poisoning outbreaks, 2021

PHU	Report Month	Suspected source	Evidence	Setting	No. Ill
Auckland	June	Soup containing fermented tuna and mackerel	Common source	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 2012 and 2021, 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 26). 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 26. Histamine (scombroid) fish poisoning outbreaks and associated cases reported by year, 2012–2021



Recent surveys

Nil.

Relevant New Zealand studies and publications

Nil.

Relevant regulatory developments

A new version of the Food Notice, *Importing Food*, was published in 2021 [28]. The notice lists histamine susceptible fish and fish products as of high regulatory interest.

Listeriosis

Summary data for listeriosis in 2021 are given in Table 31.

Table 31. Summary of surveillance data for listeriosis, 2021

Parameter	Value in 2021	Source
Number of notified cases[a]	32	EpiSurv
Notification rate (per 100,000)	0.6	EpiSurv
Hospitalisations[b]	38	MoH NMDS
Deaths	4[c]	EpiSurv
Travel-related cases (%)[d]	0 (0%)	EpiSurv
Estimated food-related cases	Sources other than food are unlikely	

[a] Includes non-perinatal (28) and perinatal cases (4)
[b] Cases hospitalised may not be notified on EpiSurv
[c] One perinatal case and three non-perinatal cases died with listeriosis recorded as the primary cause of death
[d] Percentage of the number of notified cases. New Zealand borders were closed in March 2020 with travel restrictions in place for the rest of 2020 and 2021

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 2021 by data source

During 2021, 32 individual cases (0.6 per 100,000 population) of listeriosis (28 non-perinatal cases and four perinatal cases) were reported in EpiSurv, with four resulting deaths. Hospitalisation rates are usually very high for listeriosis with 31 notified cases known to be hospitalised in 2021 (97%). For one case hospitalisation data were not recorded.

The ICD-10 code A32 was used to extract listeriosis hospitalisation data from the MoH NMDS database. Of the 38 hospital admissions (0.7 admissions per 100,000 population) recorded in 2021, 19 were reported with listeriosis as the principal diagnosis and 19 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 [13]. 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.

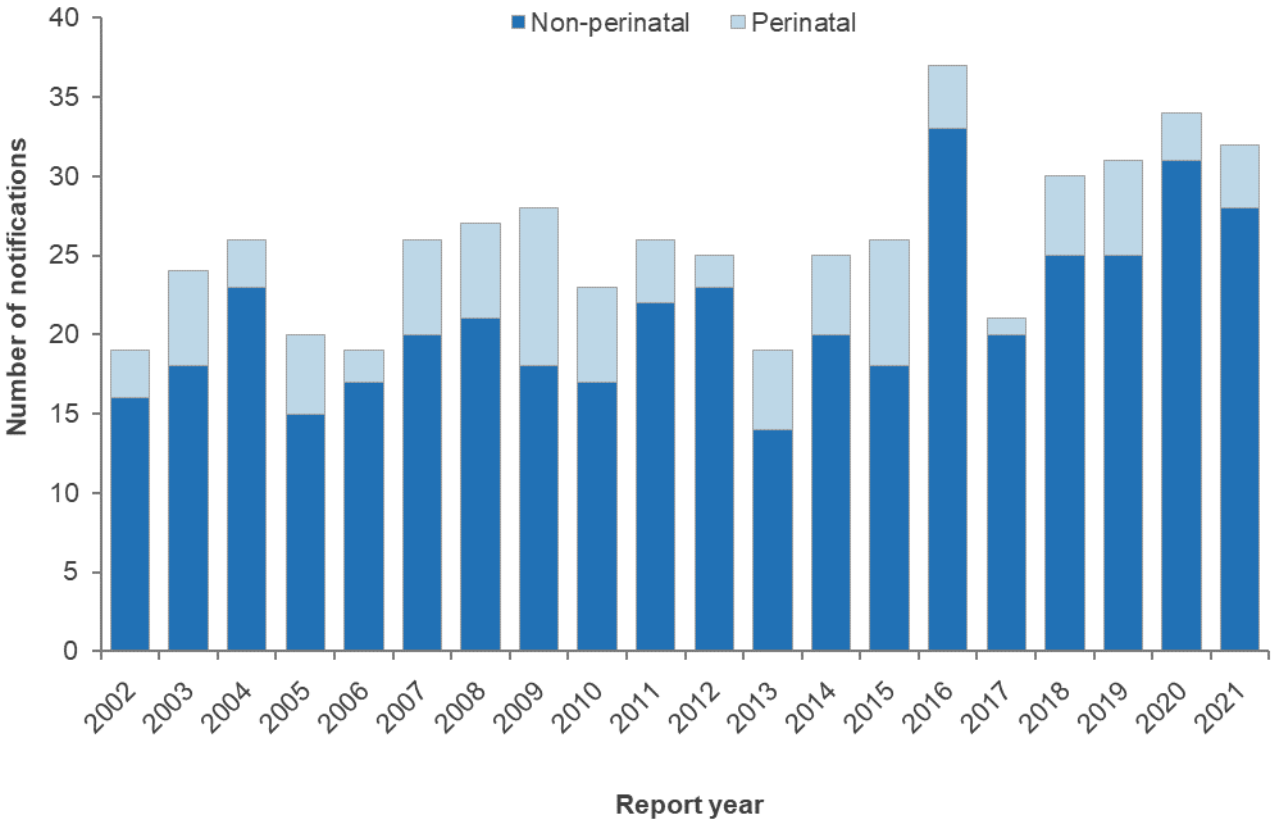
Foodborne transmission

It has been estimated by expert consultation that 87.8% (95th percentile credible interval: 57.9% to 98.5%) 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 2001 and 2021, the annual number of listeriosis notifications has fluctuated between 18 (2001) and 36 (2016) (Figure 27). Overall, the notification rate has been relatively stable for the past 20 years at around 0.6 per 100,000 population.

Figure 27. Listeriosis EpiSurv non-perinatal and perinatal notifications by year, 2002–2021



Demographics

In 2021, the rate and number of notifications for listeriosis was slightly higher for males (0.7 per 100,000 population, 20 cases, 0.8 admissions per 100,000 population, 20 hospitalisations) than females (0.5 per 100,000 population, 12 cases, 0.7 admissions per 100,000 population, 18 hospitalisations) (Table 32). It should be noted that notification case details for perinatal cases are those for the mother, so the female cases will include the four perinatal cases.

Table 32. Listeriosis cases by sex, 2021

Sex	EpiSurv notifications		Hospitalisations[a]	
	No.	Rate[b]	No.	Rate[b]
Male	20	0.8	20	0.8
Female	12	0.5	18	0.7
Total	**32**	**0.6**	**38**	**0.7**

[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 2021, notification and hospitalisation rates for listeriosis were highest in the 70+ years age group (2.7 notified cases and 3.5 admissions per 100,000 population) (Table 33).

Table 33. Listeriosis cases by age group, 2021

Age group (years)	EpiSurv notifications		Hospitalisations[a]	
	No.[b]	Rate[c]	No.	Rate[c]
0 to 4	0	-	0	-
5 to 9	0	-	0	-
10 to 14	0	-	0	-
15 to 19	0	-	0	-
20 to 29	2	-	4	-
30 to 39	2	-	5	0.7
40 to 49	3	-	3	-
50 to 59	6	0.9	4	-
60 to 69	4	-	2	-
70+	15	2.7	20	3.5
Total	**32**	**0.6**	**38**	**0.7**

[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 was believed to have started in December 2020 but was reported in 2021. This outbreak had four confirmed cases and one death reported in EpiSurv.

Table 34 contains details of the listeriosis outbreak reported in 2021. Investigation of the outbreak identified cooked ready-to-eat meats bought from a supermarket as a possible source of the outbreak. Whole genome sequencing of unopened product samples and the processing environment from one producer showed close association with case isolates (https://www.mpi.govt.nz/news/media-releases/pestells-confirmed-as-source-of-listeria-in-ham-products-in-december-2020-food-recall/).

Table 34. Details of listeriosis outbreak, 2021

PHU	Report Month	Suspected source	Evidence	Setting	No. Ill
Nelson Marlborough PHS	January [a]	Ready-to-eat ham product	WGS showed close association between case isolates with product samples and producer's environmental samples	Home consumption of supermarket bought product	4C

PHU: Public health unit, **PHS**: Public Health Service, **WGS**: Whole genome sequencing
Number ill: C: confirmed.
[a] First case was identified in December 2020, but the outbreak was reported in January 2021.

Since 2006 there have been two other listeriosis outbreaks reported. There was an outbreak with two associated cases in 2009 and an outbreak with food reported as the mode of transmission with six associated cases in 2012. 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 33 human isolates of *L. monocytogenes* during 2021. Table 35 shows the number of isolates and percentage of *L. monocytogenes* serotypes reported by the Special Bacteriology Laboratory at ESR between 2017 and 2021. The annual number of isolates identified to be serotype O4 or serotype O1/2 has been in the range of nine to 21 isolates and 11 to 15 isolates, respectively, over the 5-year period. The most common sequence types since 2018 were ST1 and ST4.

Table 35. *L. monocytogenes* serotypes and sequence types identified by the Special Bacteriology Laboratory, 2017–2021

Serotype / Sequence type (ST)	2017	2018	2019	2020	2021
Serotype O1/2	**13**	**11**	**15**	**13**	**12**
ST321	0	1	1	4	1
ST155	1	1	2	1	2
ST120	1	2	2	1	1
ST14	2	3	1	0	0
ST9	0	1	2	1	2
ST59	1	0	2	0	1
ST7	2	0	0	0	0
Other ST	6	3	5	6	5
Serotype O4	**9**	**20**	**15**	**18**	**21**
ST1	1	7	6	10	11
ST4	3	6	3	5	4
ST2	1	2	3	1	3
ST455	0	2	1	2	2
ST220	1	2	1	0	0
Other ST	3	1	1	0	1
Non-serotypable	**0**	**1**	**0**	**0**	**-**
Total	**22**	**32**	**30**	**31**	**33**

Recent surveys

Nil.

Relevant New Zealand studies and publications

Journal papers

Genomic diversity of Listeria monocytogenes isolates from seafood, horticulture and factory environments in New Zealand– Mohan et al. (2021)

New Zealand isolates (*n* = 359) from seafood, fruit and vegetables and the associated processing environments formed unique genetic clusters when compared to the international isolates for which data were available [29]. Characterisation of strains by pulsed-field gel electrophoresis identified that, apart from the Asc0002:Apa0002 pulsotype which was distributed across different sources, other pulsotypes were site or factory associated. Whole-genome analysis of 200 randomly selected *L. monocytogenes* isolates revealed that lineage II dominated the New Zealand *L. monocytogenes* populations.

Relevant regulatory developments

A new version of the Food Notice, *Importing Food*, was published in 2021 [28]. The Notice lists the following foods as of high regulatory interest with respect to *L. monocytogenes*:

- Raw milk products
- Fresh cheese, curd cheese and soft cheese (pasteurised)
- Ready to eat smoked fish and smoke flavoured fish (chilled)
- Fermented meat products, meat paste and pâté
- Ready to eat crustaceans (lobsters, crabs, bugs, shrimps and prawns and their products)
- Ready to eat bivalve molluscan shellfish (BMS) or products containing BMS, other than whole adductor muscle with viscera and roe completely removed.

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 2021 by data source

During 2021, three individual cases of norovirus infection were reported in EpiSurv. It should be noted that not every individual case of norovirus infection is notifiable; only those when the infected person is in a high-risk category (e.g. food handler, early childhood service worker). In contrast to individual case reports of norovirus, 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 235 hospital admissions (4.6 admissions per 100,000 population) recorded in 2021, 137 cases were reported with norovirus infection as the primary diagnosis and 98 were reported with norovirus infection as another relevant diagnosis. Of the 235 hospital admissions, 64 were in the 0 to 4 years age group and 46 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 2021, there were 93 notified outbreaks of norovirus infection, six (6.5%) of which reported food or a food handler as one of the possible modes of transmission (Table 36). There were two 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, 2021

	Possible foodborne transmission with a suspected or confirmed source	Possible foodborne transmission but no suspected source	Total number of norovirus infection outbreaks
Outbreaks	3	3	93
Outbreak-associated cases	127	44	2440[a]
Hospitalised cases	2	0	10

[a] One outbreak did not record number of cases

Table 37 contains details of the six norovirus infection outbreaks with food reported as a possible mode of transmission in 2021. For the May outbreak cooked and shredded chicken breasts were tested at ESR, and no causative pathogens were identified. Food handler sickness was identified as a possible source of food contamination. For the August outbreak, norovirus was detected in raw oysters. Contamination from one or more oyster harvesting workers was considered to be the source of the contamination.

Table 37: Details of norovirus infection outbreaks with food or food handling reported as a possible mode of transmission, 2021

PHU	Month	Suspected source	Evidence	Setting	No. Ill
C and PH	Jan	Food handler	Food prepared by close contact of ill person	Family function	1C 24P
Toi Te Ora	Mar	BBQ food	Common meal / event	School	2C 98P
C and PH	Apr	Unknown	Common location	Long term care facility	13C 3P
Auckland	May	Chicken breast, food handler	Common meal, food handled by ill person	Sports gathering	2C 16P
Regional PH	Jun	Unknown	Common meal	Restaurant/café/bakery	2C 1P
PH Northland	Aug	Raw oysters, food handler	Oyster factory shop, possible contamination from oyster harvesting worker(s)	Other food outlet	1C 8P

PHU: Public health unit, Auckland: Auckland Regional Public Health Service, C and PH: Community and Public Health, Regional PH: Regional Public Health, PH Northland: Public Health Northland, Toi Te Ora: Toi Te Ora - Public Health,
Number ill: C: confirmed, P: probable

During investigation of suspected foodborne illness outbreaks by ESR's Public Health Laboratory and the Enteric, Food and Environmental Virology/Norovirus Reference Laboratory (NRL), faecal specimens relating to six outbreaks (Table 37) were received for norovirus testing. Norovirus was detected in faecal samples from all of those outbreaks. In the April outbreak, *Yersinia* was also detected in faecal samples.

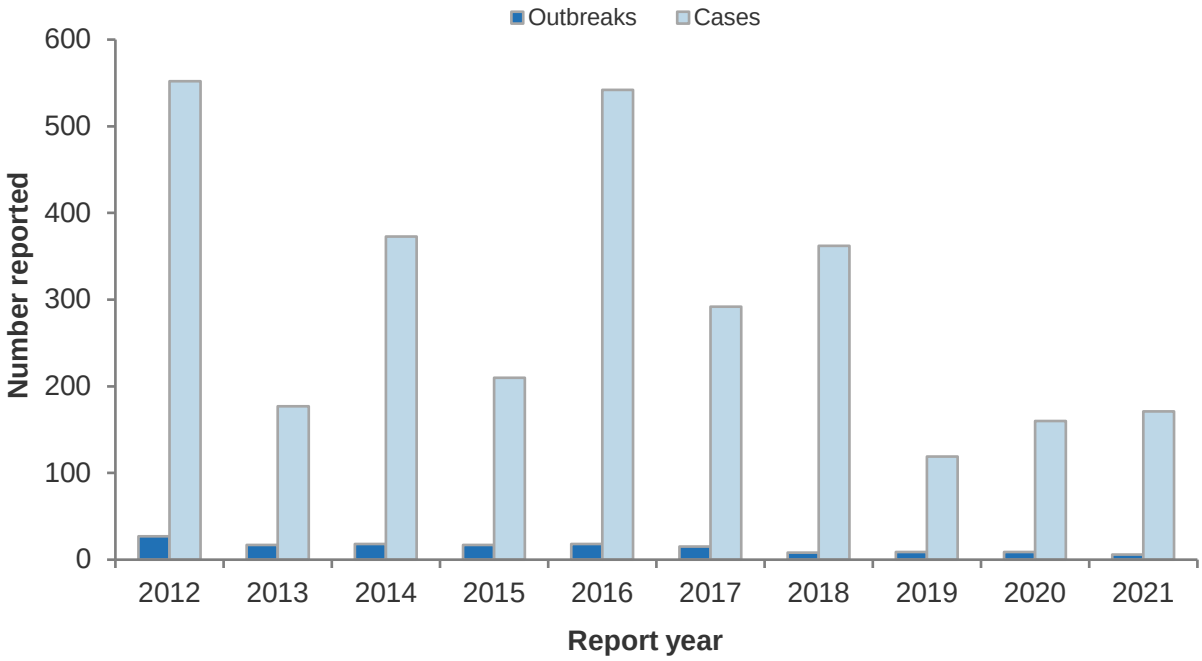
Table 38 shows the total cases by genotype for the six tested outbreaks. The outbreaks were due to two genotypes, with four outbreaks being attributed to one genotype (GII.2[P16]).

Table 38. Norovirus genotypes reported in foodborne outbreaks, 2021

Norovirus genotype	Outbreaks	Total cases
GI.3[P3]	2	25
GII.2[P16]	4	146
Total	**6**	**171**

Over the 10-year period 2011 and 2020, the annual number of norovirus infection outbreaks with food reported as a possible mode of transmission reported each year ranged from six (2021) to 27 (2012) (Figure 28). The total number of cases associated with these outbreaks ranged from 159 (2019) to 552 cases (2012) each year.

Figure 28. Norovirus infection outbreaks with food reported as a possible mode of transmission and associated cases reported by year, 2012–2021



Norovirus types commonly reported

Norovirus genotyping data from the NRL are shown in Table 39. The data relate to outbreaks rather than individual cases and include 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 2021, 97 norovirus outbreaks were ESR laboratory-confirmed. Norovirus genogroup II (GII) was identified in 75/97 (77.3%) outbreaks. In the previous four years, GII was the predominant norovirus genogroup during the period 2017-2021 and was identified in between 77.6% (2020) and 90.8% (2018) of outbreaks.

The norovirus genotype was determined for 93/97 (95.9%) of ESR laboratory-confirmed norovirus outbreaks. Two genotypes were identified at similar rates: GII.2[P16] (35/97, 36.1% of outbreaks), and GII.4 Sydney[P31] (34/97, 35.1% of outbreaks). For foodborne norovirus outbreaks, predominance of GII.2[P16] (66.7%, 4/6 identified) was also observed (see Table 38 above).

Table 39. Norovirus genotypes identified in outbreaks by the Norovirus Reference Laboratory, 2017–2021

Norovirus genotypes[a]	2017	2018	2019	2020	2021
Genogroup I	**51**	**15**	**32**	**33**	**22**
GI untyped	-	-	1	2	2
GI.1[P1]	2	1	-	-	-
GI.2[P2]	-	1	1	-	-
GI.3[P3]	19	4	9	5	-
GI.3[P13]	10	2	4	8	14
GI.4[P4]	1	3	5	-	-
GI.5[P4]	-	2	5	14	1
GI.5[P5]	1	-	1	-	-
GI.5[P12]	-	-	-	1	-
GI.6[P6]	2	1	4	-	-
GI.6[P11]	13	-	1	3	5
GI.7[P7]	1	-	-	-	-
GI.8[P8]	2	-	-	-	-
GI.9[P9]	-	1	1	-	-
Genogroup II	**186**	**158**	**147**	**125**	**75**
GII.2[P16]	18	38	17	93	35
GII.3[P12]	2	8	20	5	-
GII.4 Sydney [P16][b]	103	70	49	6	-
GII.4 Sydney[P31][b]	13	3	21	-	34
GII.4 Sydney[P4 New Orleans][b]	13	2	13	1	-
GII.6[P7]	1	10	13	3	2
GII.9[P7]	-	-	2	-	-
GII.10[P16]	-	-	3	-	-
GII.14[P7]	4	7	2	1	-
GII.17[P17]	5	4	1	6	2
Other[c]	26	16	6	10	2
Mixed GI and GII	**2**	**1**	**3**	**2**	-
Genogroup GIX[d]	**1**	**-**	**-**	**1**	-
Total outbreaks[e]	**239**	**174**	**182**	**161**	**97**

[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], GII.15[P15]

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

[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 40. 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* serotype Paratyphi B var. Java, which is typically associated with gastroenteritis.

Table 40. Summary of surveillance data for salmonellosis, 2021

Parameter	Value in 2021	Source
Number of notified cases	714	EpiSurv
Notification rate (per 100,000)	13.9	EpiSurv
Hospitalisations[a]	217	MoH NMDS
Deaths	0	EpiSurv
Travel-related cases (%)[b, c]	0 (0%)	EpiSurv
Estimated food-related cases (%)[d]	443 (62%)	Expert consultation

[a] Cases hospitalised may not be notified on EpiSurv
[b] Percentage of the number of notified cases
[c] Note: New Zealand borders were closed in March 2020 with travel restrictions in place for the rest of 2020 and 2021
[d] For estimation of food-related cases the proportions derived from expert consultation [2] exclude travel-related cases

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. In 2021, 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. The MidCentral, Tairawhiti, and Whanganui DHBs changed to PCR testing in May 2021. Following the introduction of PCR methods there was no sustained increase in notification rates for salmonellosis [14].

Effect of COVID-19 on salmonellosis notification rates

Public health and social measures to prevent the spread of COVID-19 in New Zealand were introduced in March 2020 and remained in place through December 2021. These measures will have affected exposure behaviours and pathways, access to medical care and laboratory testing priorities. These multiple aspects make it difficult to attribute any changes to notification rates to specific COVID-19 related factors or to true changes in disease incidence. This is discussed in more detail in the Introduction (see page 5).

In 2021, the monthly salmonellosis notification rates were generally lower than the three-year mean of years 2017-2019. Compared to 2020, the notification rates in 2021 were lower from August to October (Figure 31), probably due to the COVID-19 public health response and associated Alert Level restrictions.

The frequency of overseas travel has changed due to border restrictions from March 2020 until the end of 2021. This is reflected in the notifications; in 2021, there were no salmonellosis notifications in EpiSurv listing overseas travel as a risk factor, compared to 349 in 2019 and 49 in 2020.

Salmonellosis individual cases reported in 2021 by data source

During 2021, 714 individual cases (13.9 per 100,000 population) of salmonellosis and no resulting deaths were reported in EpiSurv. Of the 714 cases, the symptoms of 690 cases (97%) were reported as fitting the clinical description for salmonellosis, the symptoms were unknown for 20 cases, and for four 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 217 hospital admissions (4.2 admissions per 100,000 population) recorded in 2021, 182 cases were reported with salmonellosis as the primary diagnosis and 35 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].

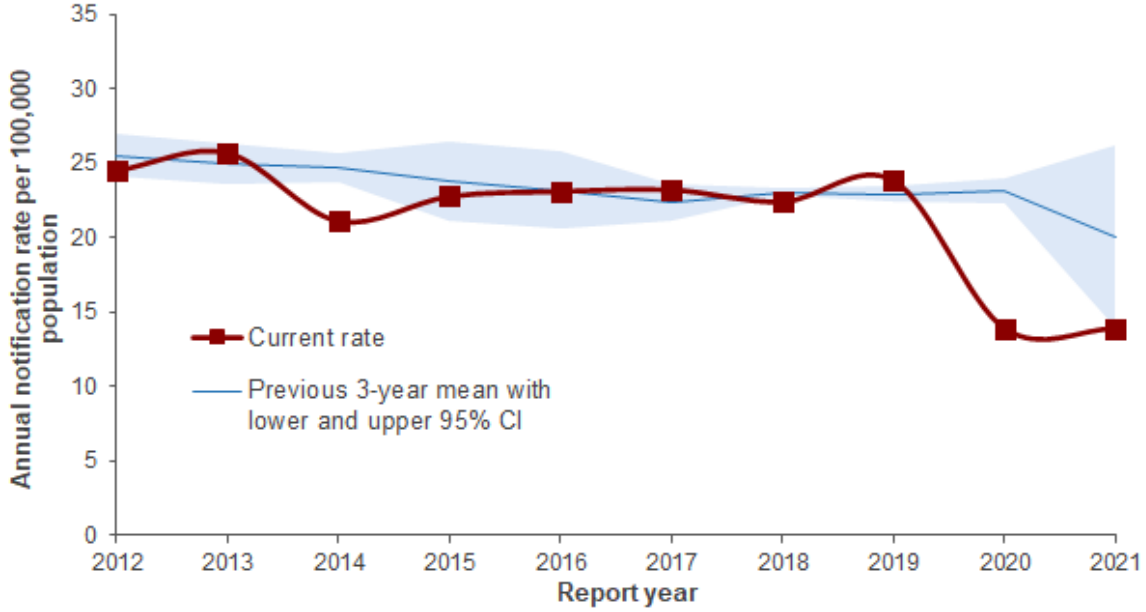
Annual data

Between 2007 and 2019 the number of salmonellosis notifications per year ranged between 955 (2014) and 1337 (2008) (Figure 29), with associated notification rates between 21.1 and 31.3 cases of salmonellosis per 100,000 population per year (Figure 30). The low numbers of notifications in 2020 and 2021 can be attributed to the impact of the COVID-19 public health response. The number of hospital admissions with salmonellosis as a primary or secondary diagnosis varied slightly year by year but did not show the same reduction in 2020 and 2021 as the number of annual notifications.

Figure 29. Salmonellosis EpiSurv notifications (line) and NMDS hospitalisations (bar) by year, 2007–2021

The notification rate in 2021 (13.9 cases per 100,000 population) was much lower than the previous three-year average (20.1 cases per 100,000 population) (Figure 30). This drop in notification rates can be attributed to the COVID-19 pandemic.*

Figure 30. Salmonellosis notification rate by year, 2012–2021

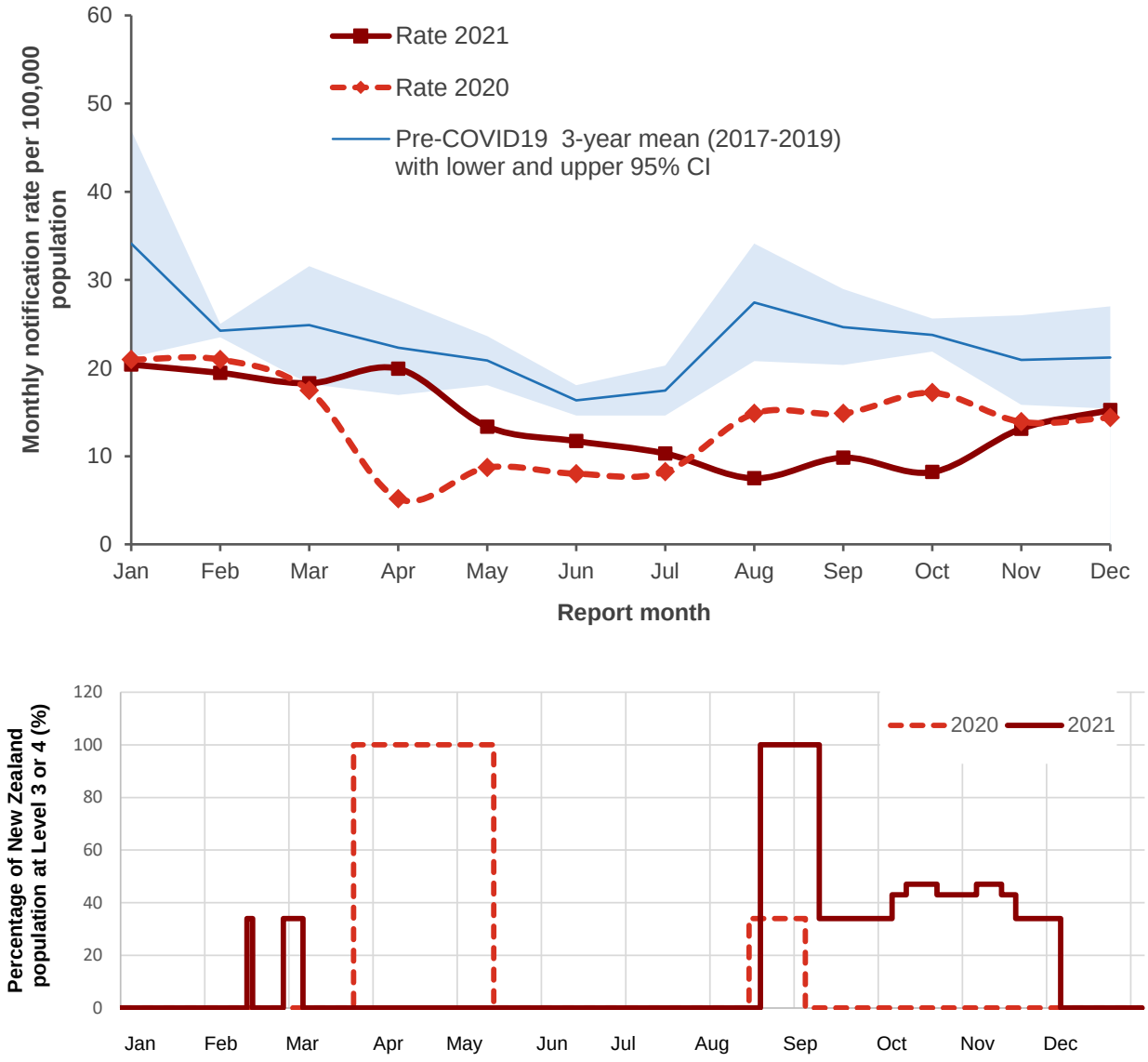


* An overview of the impact of the COVID-19 pandemic on notifications of potentially foodborne diseases is provided in the Introduction, page 5.

Seasonal data

Salmonellosis notification rates per 100,000 population by month for 2020 and 2021 are shown in Figure 31 as well as the percentage of the New Zealand population at COVID-19 Alert Levels 3 or 4. The monthly number of notifications in 2021 ranged from 32 notifications (August, 8 per 100,000 population) to 87 notifications (January, 20 per 100,000 population). The monthly notification rate in 2021 was generally lower than the three-year mean of years 2017-2019. In 2021, the notification rate was lower than 2020 from August to October probably due to the COVID-19 public health response and Alert Level 3 and 4 restrictions.

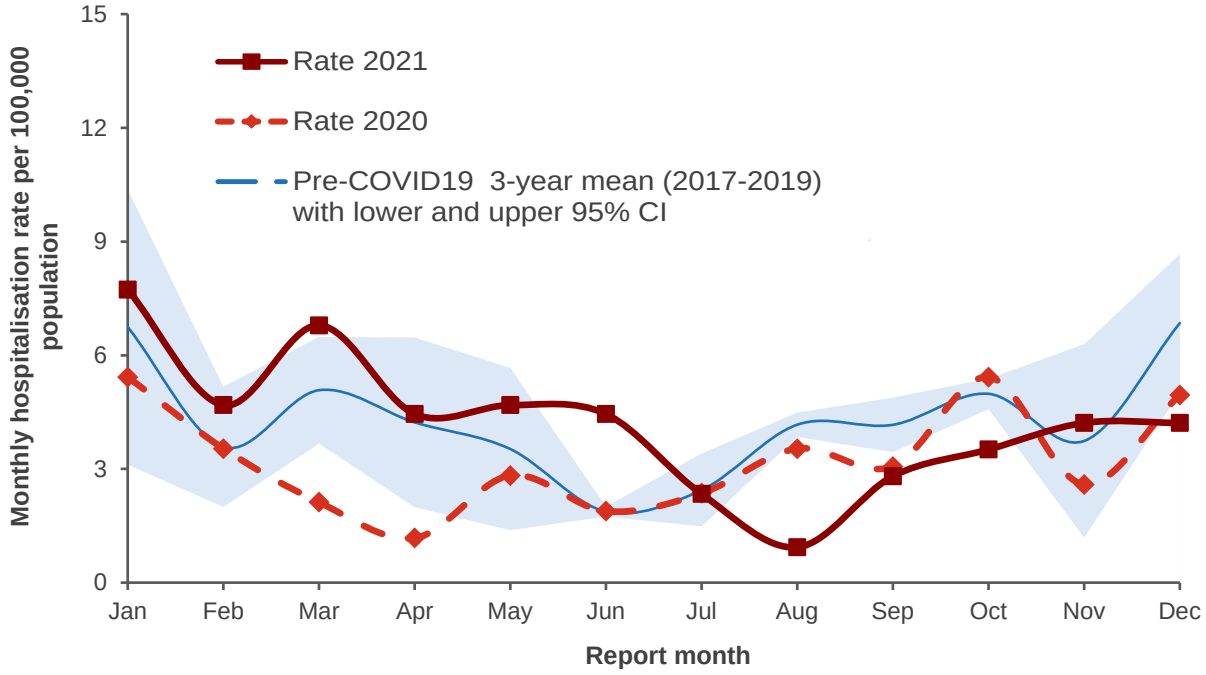
Figure 31. Salmonellosis monthly notification rate (annualised) and percentage of New Zealand population at COVID-19 Alert Levels 3 or 4, 2020 and 2021



Note: A detailed timeline of all COVID-19 Alert Level changes for 2020 and 2021 is included in Appendix C (Table 73).

In 2021, the monthly hospitalisation rates varied over the year and broadly followed the same pattern as the notification rates for 2020 and 2021 (Figure 32). The lowest hospitalisation rate was for August 2021, which coincided with a national lockdown for COVID-19.

Figure 32. Salmonellosis monthly hospitalisation rate (annualised), 2020 and 2021



Demographics

In 2021, the rate of notifications for females was higher (14.5 cases per 100,000 population, 374 cases) than males (13.3 cases per 100,000 population, 339 cases). The rate of hospital admissions was also higher for females (4.8 admissions per 100,000 population, 123 hospitalisations) compared to males (3.7 admissions per 100,000 population, 94 hospitalisations) (Table 41).

Table 41. Salmonellosis cases by sex, 2021

Sex	EpiSurv notifications		Hospitalisations[a]	
	No.	Rate[b]	No.	Rate[b]
Male	339	13.3	94	3.7
Female	374	14.5	123	4.8
Total	**714**	**13.9**	**217**	**4.2**

[a] MoH NMDS data for hospital admissions
[b] per 100,000 population in this sex group

In 2021, notification and hospital admission rates of salmonellosis were highest for children in the 0 to 4 years age group (52.7 cases per 100,000 population, and 10.8 admissions per 100,000 population) (Table 42).

Table 42. Salmonellosis cases by age group, 2021

Age group (years)	EpiSurv notifications		Hospitalisations[a]	
	No.	Rate[b]	No.	Rate[b]
0 to 4	161	52.7	33	10.8
5 to 9	58	17.8	13	4.0
10 to 14	14	4.1	3	-
15 to 19	24	7.6	4	-
20 to 29	73	10.4	22	3.1
30 to 39	43	5.9	10	1.4
40 to 49	69	10.8	15	2.4
50 to 59	93	14.2	35	5.3
60 to 69	88	16.0	26	4.7
70+	90	15.9	56	9.9
Total[c]	**714**	**13.9**	**217**	**4.2**

[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

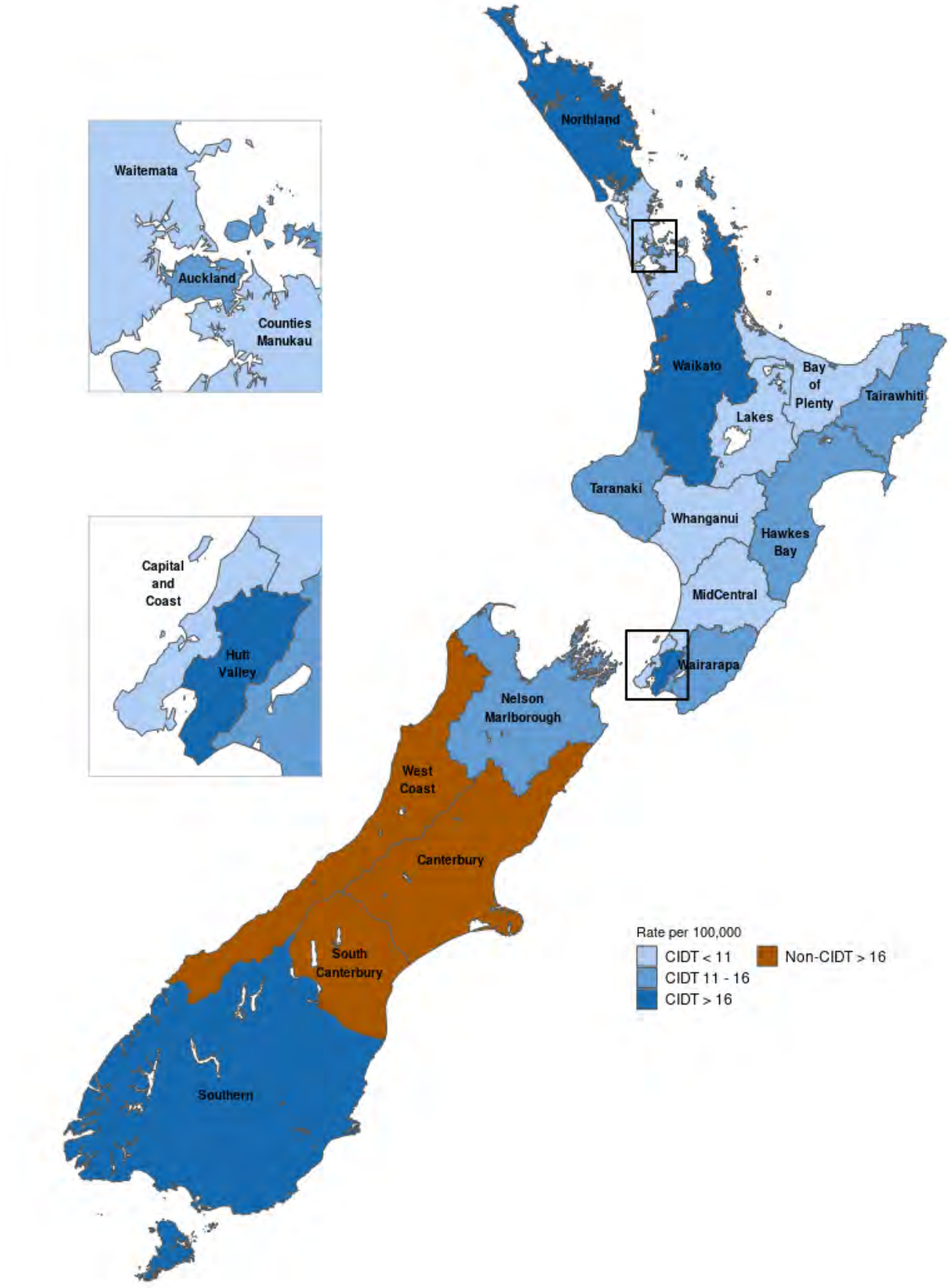
Geographic distribution

The notification rates by DHB calculated per 100,000 resident population are presented in Figure 33 (see also Table 82). Blue shading is used for DHBs which are using CIDT community testing, the brown shading is used for DHBs using culture-based community testing.

In 2021, the DHB notification rates of salmonellosis ranged from 9 per 100,000 population (six cases) in Whanganui DHB to 29 per 100,000 population (103 cases) in Southern DHB. The Southern, South Canterbury (24 per 100,000 population, 15 cases) and West Coast (21 per 100,000 population, seven cases) DHBs had notification rates above 20 per 100,000 population.

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

Figure 33. Geographic distribution of salmonellosis notifications, 2021



Note: Whanganui, MidCentral and Tairawhiti DHBs testing moved to CIDT methods in May 2021. The rates for these DHBs will be based on a mixture of CIDT and non-CIDT test results.

Outbreaks reported as caused by *Salmonella*

In 2021, there were eight salmonellosis notified outbreaks in EpiSurv, five of which reported food as a possible mode of transmission (Table 43). These five outbreaks included 90 cases, of which 18 cases were reported to have been hospitalised. 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 43. Salmonellosis outbreaks reported, 2021

	Possible foodborne transmission with a suspected or confirmed source	Possible foodborne transmission but no suspected source	Total number of salmonellosis outbreaks
Outbreaks	5	0	8
Outbreak-associated cases	90	0	99
Hospitalised cases	18	0	19

Table 44 contains details of the five salmonellosis outbreaks with food reported as a possible mode of transmission reported in 2021.

Table 44. Details of salmonellosis outbreaks with food reported as a possible mode of transmission, 2021

PHU	Report Month	Suspected source	Evidence	Setting	No. Ill	Serotype[a]
South Island PHUs	January	Packaged alfalfa and radish sprouts	WGS of case isolates matching those from opened sprout samples from a cases home/ elevated odds ratio for eating sprouts	Home or restaurant/ café/bakery	28C	*S.* Enteritidis ST183
Toi Te Ora	May	Undercooked chicken	Common meal	Restaurant/ café/bakery	1C 4P	*S.* Weltevreden
PH South	June	Chicken or cross contamination of raw salad	Common meal	Home	1C 2P	*S.* Typhimurium ST568
Auckland	November	Chicken wings or raw fish salad	Household cluster	Home	1C 7P	*S.* Typhimurium ST2297
Multi PHU (mainly North Island)	February to June	Poultry	WGS of case isolates matching those found in poultry flocks in 2021	Work, home or restaurant/ café/bakery	46C	*S.* Enteritidis ST11

PHU: Public health unit, Auckland: Auckland Regional Public Health Service, PH South: Public Health South, Toi Te Ora: Toi Te Ora - Public Health

Number ill: C: confirmed, P: probable

WGS: Whole genome sequencing

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

[b] Cases are still being linked to the outbreak via whole genome sequencing in 2022, but not necessarily to a common source. The number of confirmed cases in the table are those that were part of a distinct temporal cluster of cases in 2021, with illness onset dates from 3rd February 2021 to 29th June 2021.

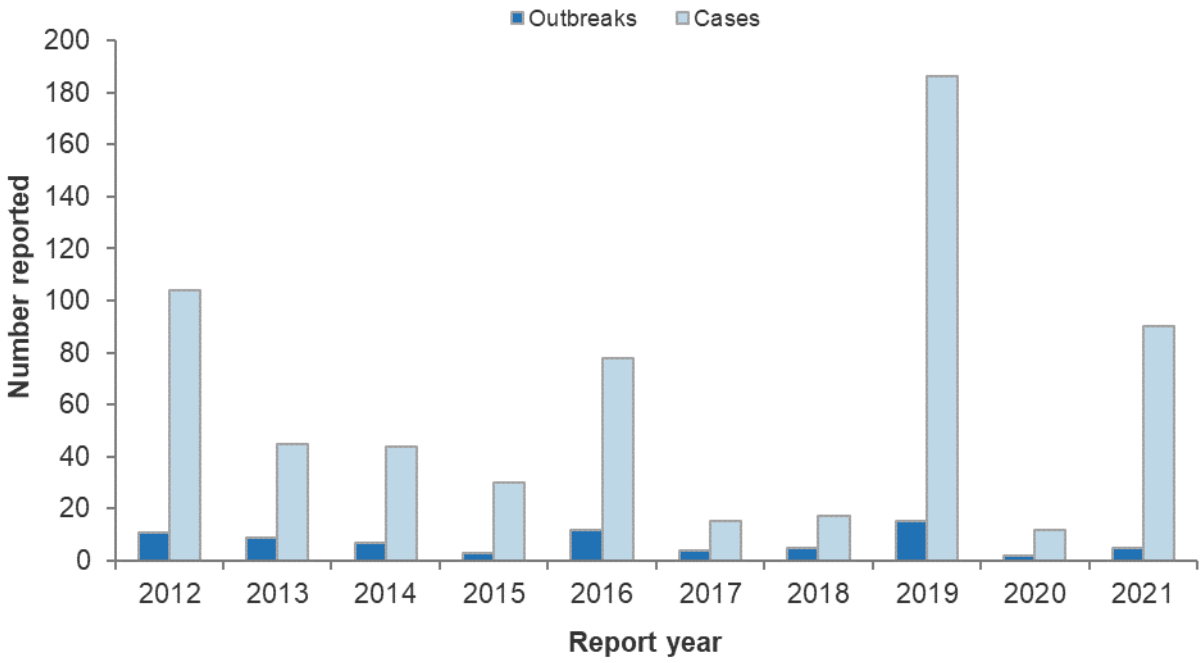
For three outbreaks (May, June and November) the evidence linking the outbreak to a common suspected food source was weak.

For the South Island outbreak in January, whole genome sequencing (WGS) of case isolates matched the WGS of an isolate from an opened packet of sprouts obtained from the home of a case, and there was a significantly elevated odds ratio for eating sprouts from a case/case analysis. Water, seed and final product samples taken from the sprout supplier did not test positive for *Salmonella* spp.

In 2021, there was a multi-PHU outbreak which was detected through a clustering of the same *Salmonella* strain over time. WGS confirmed the case *Salmonella* isolates were genetically clustered. In the 2021 cluster, the outbreak strain was also detected in samples from hatchery, layer and broiler poultry flocks. Person-to-person transmission was reported as a possible risk factor for six of the cases and some of the cases were reported as working on poultry farms.

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 34). The total number of cases associated with the outbreaks over the same period ranged between 15 (2017) and 186 (2019).

Figure 34. Salmonellosis outbreaks with food reported as a possible mode of transmission and associated cases reported by year, 2012–2021



Salmonella types commonly reported

Human isolates

In 2021, isolates from 660 notified cases with non-typhoidal *Salmonella* infections were typed by the ESR Enteric Reference Laboratory (Table 45). *S.* Typhimurium (312 cases) and *S.* Enteritidis (131 cases) were the most common serotypes identified. Other serotypes commonly reported were *S.* Bovismorbificans (50 cases), *S.* Brandenburg (39 cases) and *S.* Saintpaul (30 cases).

EpiSurv records for 2021 indicate that 36% to 39% of cases infected with *S.* Typhimurium, *S.* Enteritidis, *S.* Bovismorbificans or *S.* Brandenburg were hospitalised. In contrast, hospitalisation rates for cases infected with *S.* Saintpaul were lower (20%). Note that the hospitalisation status for between 2% and 14% of cases infected with each serotype was not recorded.

There were no non-typhoidal *Salmonella* overseas travel-related cases recorded in EpiSurv for 2021 due to the COVID-19 travel restrictions and, consequently, Table 45 does not provide the proportion of cases with different serotypes who travelled overseas. Of the 714 cases, 21% (153) notifications did not include travel information.

Table 45. Annual number of notifications with different *Salmonella* serotypes identified by the Enteric Reference Laboratory, 2018–2021

Serotype[a]	2018	2019	2020	2021
S. Typhimurium[b]	360	482	330	312
S. Enteritidis[b]	130	153	70	131
S. Bovismorbificans	81	47	60	50
S. Brandenburg	42	37	36	39
S. Saintpaul	37	22	26	30
S. Thompson	9	11	11	10
S. Stanley	34	41	11	9
S. Infantis	15	27	7	9
S. Pensacola	9	6	1	8
S. Mississippi	16	15	17	7
S. Hvittingfoss	5	5	1	6
S. Agona	26	13	4	4
S. Weltevreden	22	19	11	3
S. Paratyphi B var. Java	30	26	9	3
S. Newport	9	10	3	1
Other[c]	186	161	49	39
Unknown[d]	89	113	63	54
Total	1100	1188	709	714

Please note that one case in 2021 had a mixed infection, i.e. an individual case is represented by two *Salmonella* serotypes

[a] Excludes *S.* Typhi and *S.* Paratyphi (except *S.* Paratyphi B var Java which which is typically associated with gastroenteritis). Table lists the serotypes which had four or more associated cases in 2020 or had more than 10 annual cases in the previous three years

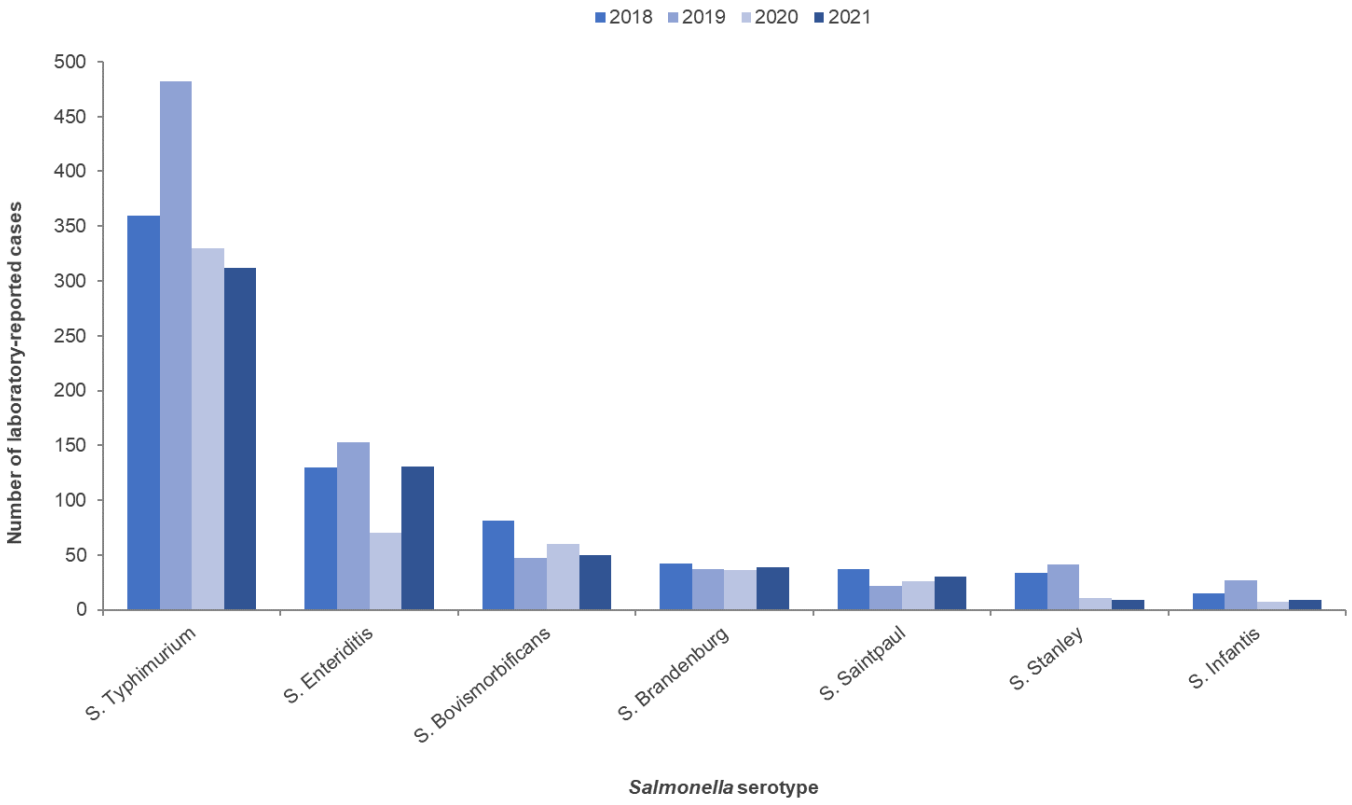
[b] From 1st November 2019, all phage typing of *Salmonella* isolates ceased. From this time, serotypes that were historically phage typed (Typhimurium and Enteritidis) have all been typed using whole genome sequencing. *Salmonella* Subsp. (I) ser. 4,5,12 : i : - is being reported as monophasic *Salmonella*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

[c] Serotypes where able to be determined, but there were three or less associated notified cases in 2021

[d] No isolates received by the Enteric Reference Laboratory for typing

Figure 35 shows the annual trend for selected *Salmonella* serotypes from 2018 to 2021. 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. There was a drop in *S*. Enteritidis cases in 2020 compared to 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.

Figure 35. Number of laboratory-reported case related isolates for selected *Salmonella* serotypes by year, 2018–2021



Non-human isolates

A total of 1015 non-human *Salmonella* isolates were serotyped by the Enteric Reference Laboratory during 2021. *S.* Typhimurium (330 isolates) and *S.* Enteritidis (188 isolates) were the most common serotypes in non-human samples in 2021. The next most common serotypes were *S.* Bovismorbificans (127 isolates), *S.* Brandenburg (89 isolates) and *S.* Give (88 isolates) (Table 46). In 2021, there was a shift in the proportion of different 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 46. *Salmonella* serotypes from non-human sources identified by the Enteric Reference Laboratory, 2017–2021

Serotype	2017	2018	2019	2020	2021	Major sources, 2021
S. Typhimurium	**372**	**282**	**320**	**336**	**330**	Bovine (198), poultry environmental (37), canine (26), equine (18), feline (17), avian (9)
S. Enteritidis	**11**	**5**	**8**	**5**	**188**[a]	Poultry environmental (172), poultry miscellaneous[b] (5), feline (4)
Other serotypes	**589**	**561**	**598**	**492**	**497**	
S. Agona	17	18	9	9	7	Bovine (3), poultry miscellaneous[b] (3)
S. Bovismorbificans	292	297	309	247	127	Bovine (106), canine (5), ovine (4), feline(4)
S. Brandenburg	137	106	133	91	89	Bovine (41), ovine (23), canine (15) food[c](7)
S. Give	0	0	12	78	88	Bovine (58), canine (12), poultry environmental (7), poultry miscellaneous[b] (7)
S. Hindmarsh	27	26	28	8	23	Ovine (20)
S. Infantis	26	8	3	3	17	Poultry environmental (14)
S. Mbandaka	9	4	16	7	39	Poultry environmental (27), poultry feed (6)
S. Saintpaul	12	12	14	8	9	Reptile (6)
S. Thompson	1	1	6	1	46	Poultry environmental (43)
Other or unknown serotypes	68	89	68	40	52	-
Total	**972**	**848**	**926**	**833**	**1015**	

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

[b] Including product

[c] Includes animal carcasses from meat works

Recent surveys

Nil.

Relevant New Zealand studies and publications

Nil.

Relevant regulatory developments

Food Notices

A new version of the Food Notice, *Importing Food*, was published in 2021 [28]. The Notice lists the following foods as of high regulatory interest with respect to *Salmonella*:

- Raw milk products
- Fermented meat products, meat paste and pâté
- Tahini and crushed sesame seeds and any products containing these
- Ready to Eat (RTE) crustaceans – lobsters, crabs, bugs, shrimps and prawns and their products
- Pepper, chilli and paprika

Animal products order

In response to the detections of *Salmonella* Enteritidis in commerical chick flocks, new rules for commercial chicken operators were introduced in October 2021 by the Ministry for Primary Industries. The rules apply to the commercial chicken meat or egg supply chain and are detailed in Animal Products Order. Emergency Control Scheme –Managing *Salmonella* Enteritidis in Commercial Chicken Flocks [30] and its supporting guidance document [31].

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 2021 by data source

During 2021, one individual case of sapovirus infection was reported in EpiSurv. Note that not every individual case of sapovirus infection is necessarily notifiable; only those when the infected person is in a high-risk category (e.g. food handler, early childhood service worker).

Laboratory testing for sapovirus began in New Zealand in 2009. Since 2009, specimens from gastroenteritis outbreaks found to be negative for norovirus have been tested for the presence of sapovirus.

Outbreaks reported as caused by sapovirus

In 2021, nine sapovirus infection outbreaks were notified in EpiSurv. One of the outbreaks (11%), with 11 associated cases, reported food as a possible mode of transmission (Table 47). The suspected source of infection was an infected food handler at the childcare centre (Table 48), there was no suspected food source recorded in EpiSurv.

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 47. Sapovirus infection outbreaks reported, 2021

	Possible foodborne transmission with a suspected or confirmed source	Total number of sapovirus outbreaks
Outbreaks	1	9
Outbreak-associated cases	11	124
Hospitalised cases	0	1

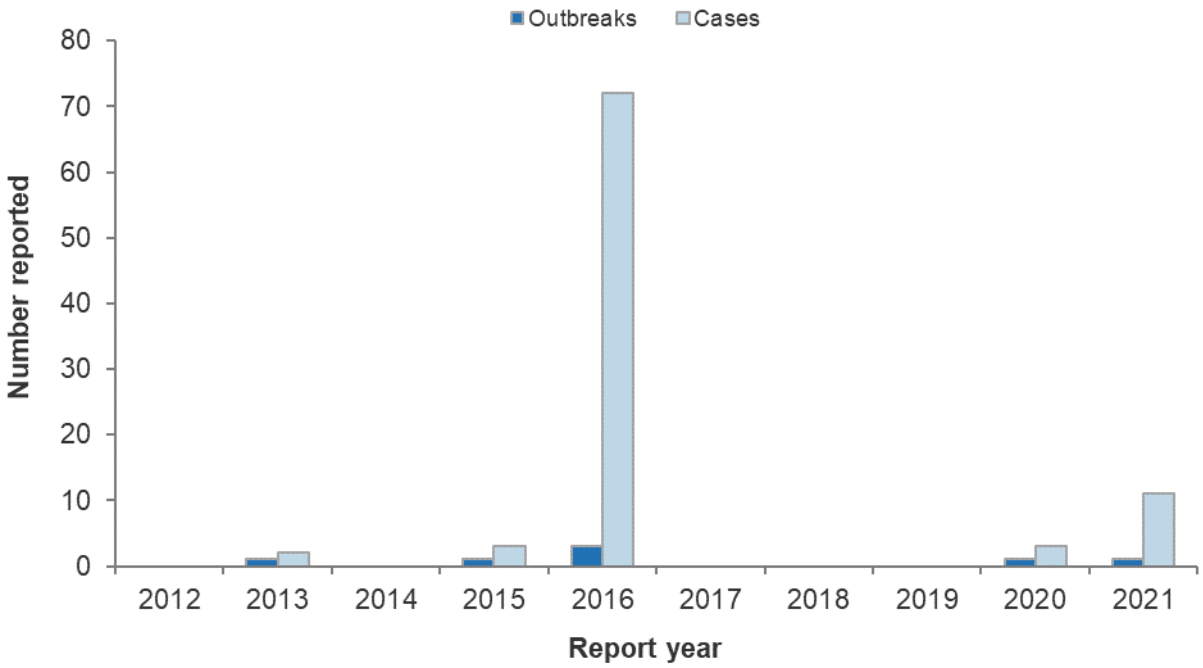
Table 48. Details of sapovirus infection outbreak with food reported as a possible mode of transmission, 2021

PHU	Month	Suspected source	Evidence	Setting	No. ill
Auckland	January	Infected food handler	Common location	Childcare centre	1C 10P

PHU: Public health unit, Auckland: Auckland Regional Public Health Service
Number ill: C: confirmed, P: probable

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 36).

Figure 36. Sapovirus infection outbreaks with food reported as a possible mode of transmission and associated cases reported by year, 2012–2021



Recent surveys

Nil.

Relevant New Zealand studies and publications

Nil.

Relevant regulatory developments

Nil.

Shigellosis

Summary data for shigellosis in 2021 are given in Table 49.

Table 49. Summary of surveillance data for shigellosis, 2021

Parameter	Value in 2021	Source
Number of notified cases	5	EpiSurv
Notification rate (per 100,000)	0.1	EpiSurv
Hospitalisations[a]	26	MoH NMDS
Deaths	0	EpiSurv
Travel-related cases (%)[b, c]	0 (0%)	EpiSurv
Estimated food-related cases (%)	NE	-

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

[a] Cases hospitalised may not be notified on EpiSurv

[b] Percentage of the number of notified cases

[c] Note: New Zealand borders were closed in March 2020 with travel restrictions in place for the rest of 2020 and 2021.

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. In 2021, 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. The MidCentral, Tairawhiti, and Whanganui DHBs changed to CIDT in May 2021. Following the introduction of CIDT there was no sustained increase in notification rates for shigellosis [14].

Effect of COVID-19 on shigellosis notification rates

Public health and social measures to prevent the spread of COVID-19 in New Zealand were introduced in March 2020 and remained in place through December 2021. These measures will have affected exposure behaviours and pathways, access to medical care and laboratory testing priorities. These multiple aspects make it difficult to attribute any changes to notification rates, either to specific COVID-19 related factors, which is discussed in more detail in the Introduction (see page 5), or true changes in disease incidence.

From April 2020 and all of 2021 the monthly shigellosis notification rates were very low and often no cases were notified in a month, which can be attributed to overseas travel limitations due to the COVID-19 border restrictions (Figure 39). In 2021, there were no shigellosis notifications in EpiSurv

listing overseas travel as a risk factor, compared to 82 in 2019 and 26 in 2020 (two during April to December 2020).

Shigellosis individual cases reported in 2021 by data source

In 2021, five individual cases (0.1 per 100,000 population) of shigellosis and no resulting deaths were reported in EpiSurv. All cases were reported as fitting the clinical description for shigellosis.

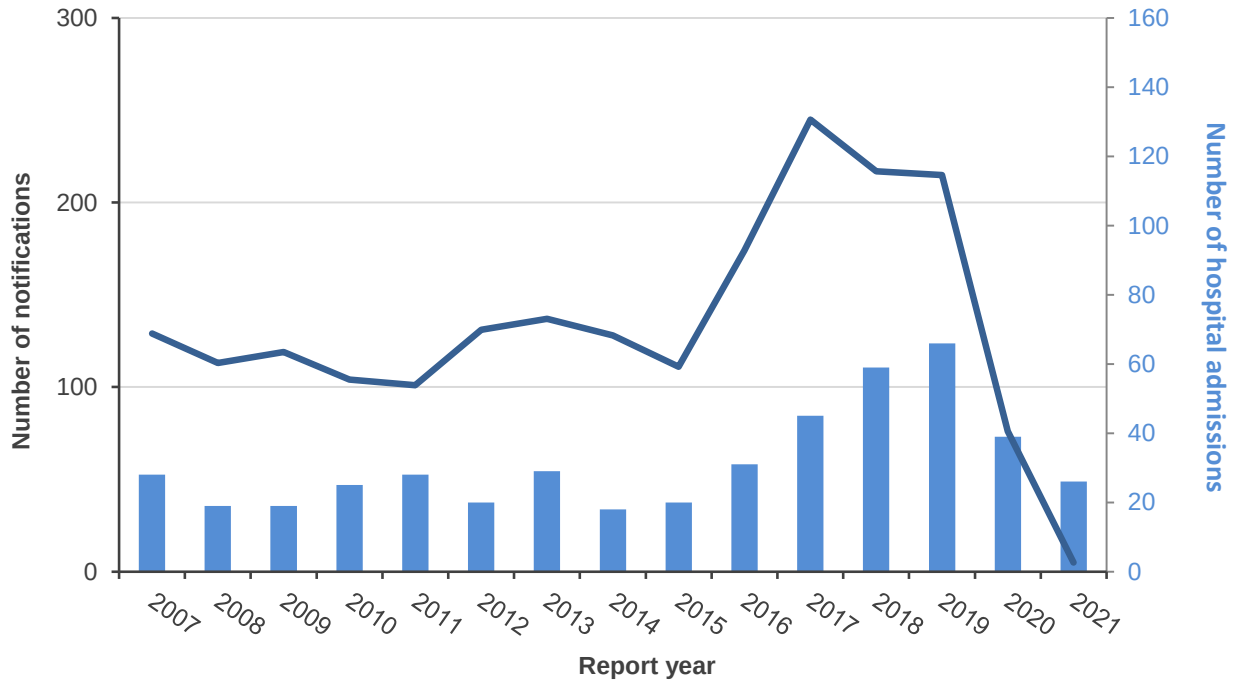
The ICD-10 code A03 was used to extract shigellosis hospitalisation data from the MoH NMDS database. Of the 26 hospital admissions (0.5 admissions per 100,000 population) recorded in 2021, seven were reported with shigellosis as the principal diagnosis and 19 with shigellosis as another relevant diagnosis.

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 2007 and 2015 the number of shigellosis notifications has been in the range of 101 to 137 cases. In 2016 to 2017 there was an increase in notifications and the notification rate per 100,000 population, which was sustained in 2018 (217 cases) and 2019 (215 cases) (Figure 37 and Figure 38). The drop in notifications in 2020 and 2021 can be attributed to travel restrictions due to the COVID-19 pandemic. 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.

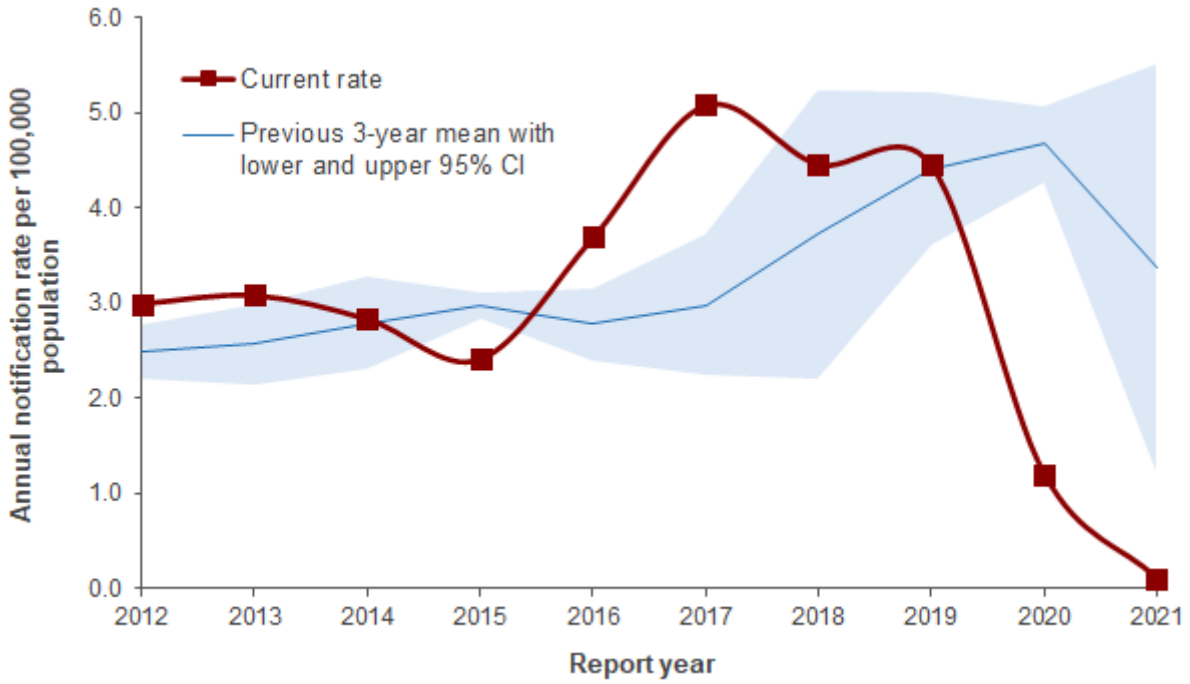
Figure 37. Shigellosis EpiSurv notifications (line) and NMDS hospitalisations (bar) by year, 2007–2021



The notification rate in 2021 (0.1 cases per 100,000 population) was much lower than the previous three-year average (3.4 cases per 100,000 population) (Figure 38). This drop in notification rates can be attributed to the COVID-19 pandemic and ongoing travel restrictions in 2021.*

* An overview of the impact of the COVID-19 pandemic on notifications of potentially foodborne diseases is provided in the Introduction, page 5.

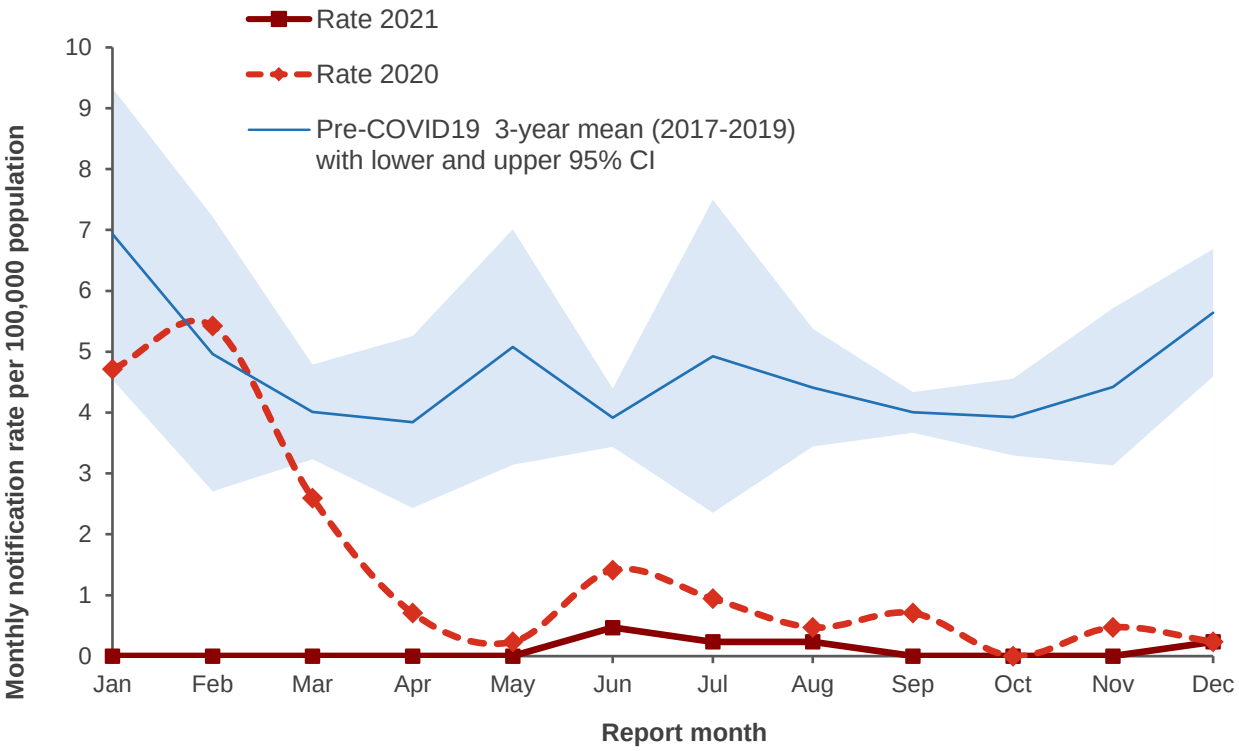
Figure 38. Shigellosis notification rate by year, 2012–2021



Seasonal data

Shigellosis notification rates per 100,000 population by month for 2020 and 2021 are shown in Figure 39. The number of notifications per month for the first three months of the year 2020 was in the range of the three-year average of the years 2017–2019. From April 2020 and all of 2021 the monthly notification rates were very low and often zero, which can likely be attributed to overseas travel limitations due to the COVID-19 border restrictions.

Figure 39. Shigellosis monthly notification rate (annualised), 2020 and 2021



Demographics

In 2021, there were four male cases and a single female case recorded in EpiSurv. Hospitalisation rates were the same for both genders (Table 50).

Table 50. Shigellosis cases by sex, 2021

Sex	EpiSurv notifications		Hospitalisations[a]	
	No.	Rate[b]	No.	Rate[b]
Male	4	-	12	0.5
Female	1	-	14	0.5
Total	**5**	**0.1**	**26**	**0.5**

[a] MoH NMDS data for hospital admissions
[b] per 100,000 population in this sex group (rate not calculated when fewer than five cases reported)

In 2021, the shigellosis notification rates, and hospitalisations rates were spread across age groups (Table 51), with the largest proportion of hospitalisations in age groups over 50 years of age.

Table 51. Shigellosis cases by age group, 2021

Age group (years)	EpiSurv notifications		Hospitalisations[a]	
	No.	Rate[b]	No.	Rate[b]
0 to 4	0	-	3	-
5 to 9	1	-	2	-
10 to 14	0	-	1	-
15 to 19	1	-	1	-
20 to 29	1	-	1	-
30 to 39	0	-	2	-
40 to 49	0	-	0	-
50 to 59	0	-	5	0.8
60 to 69	1	-	5	0.9
70+	1	-	6	1.1
Total	**5**	**0.1**	**26**	**0.5**

[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)

Outbreaks reported as caused by *Shigella spp.*

In 2021, there was a single shigellosis outbreak reported in EpiSurv. The outbreak was reported with food as one possible mode of transmission (Table 52). 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 52. Shigellosis outbreaks reported, 2021

	Possible foodborne transmission but no suspected source	Total number of shigellosis outbreaks
Outbreaks	1	1
Outbreak-associated cases	2	2
Hospitalised cases	0	0

Table 53 contains details of the household shigellosis outbreak with food reported as a possible mode of transmission. No suspected food source was recorded and the evidence that food was the source of the outbreak was weak.

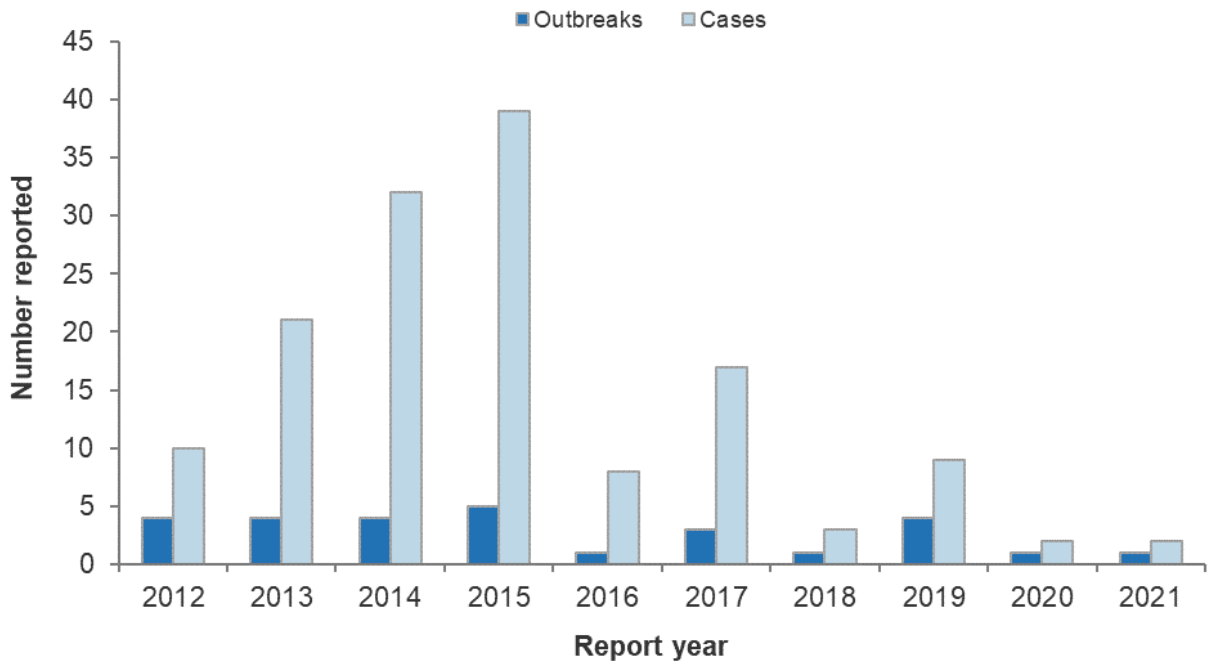
Table 53. Details of shigellosis outbreak with food reported as a possible mode of transmission, 2021

PHU	Report Month	Suspected source	Evidence	Setting	No. Ill
Auckland	March	Unknown	Household cluster	Home	2C

PHU: Public health unit, Auckland: Auckland Regional Public Health Service
Number ill: C: confirmed

Over the 10-year period 2012–2021, 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 40).

Figure 40. Shigellosis outbreaks with food reported as a possible mode of transmission and associated cases reported by year, 2012–2021



Shigella species commonly reported

In 2021, isolates from three notified cases infected with *Shigella* spp. were typed by the Enteric Reference Laboratory at ESR. *S. flexneri* was the species identified for two of the cases and *S. boydii* for the other case (Table 54).

Table 54. *Shigella* species and subtypes identified by the Enteric Reference Laboratory, 2017–2021

Species	2017	2018	2019	2020	2021
S. sonnei	**99**	**99**	**107**	**28**	**0**
biotype a	30	37	33	9	0
biotype f	1	1	1	2	0
biotype g	68	61	73	17	0
S. flexneri	**126**	**84**	**84**	**34**	**2**
1b	31	36	14	2	0
1c	0	0	0	0	1
2a	18	15	19	12	0
6 biotype Boyd 88	43	13	12	1	0
Other	34	20	39	19	1
Other	**14**	**14**	**8**	**2**	**1**
S. boydii	13	10	3	2	1
S. dysenteriae	1	4	4	0	0
Shigella species not identified	0	0	1	0	0
Total	**239**	**197**	**199**	**64**	**3**

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 $\geq 10^3$ */*gram coagulase-positive *S. aureus* from faecal or vomit specimen or $\geq 10^5$ 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 2021 by data source

In 2021, 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. Three hospital admissions were recorded in 2021 with *S. aureus* intoxication as the primary diagnosis and no cases were reported with *S. aureus* intoxication as another relevant diagnosis.

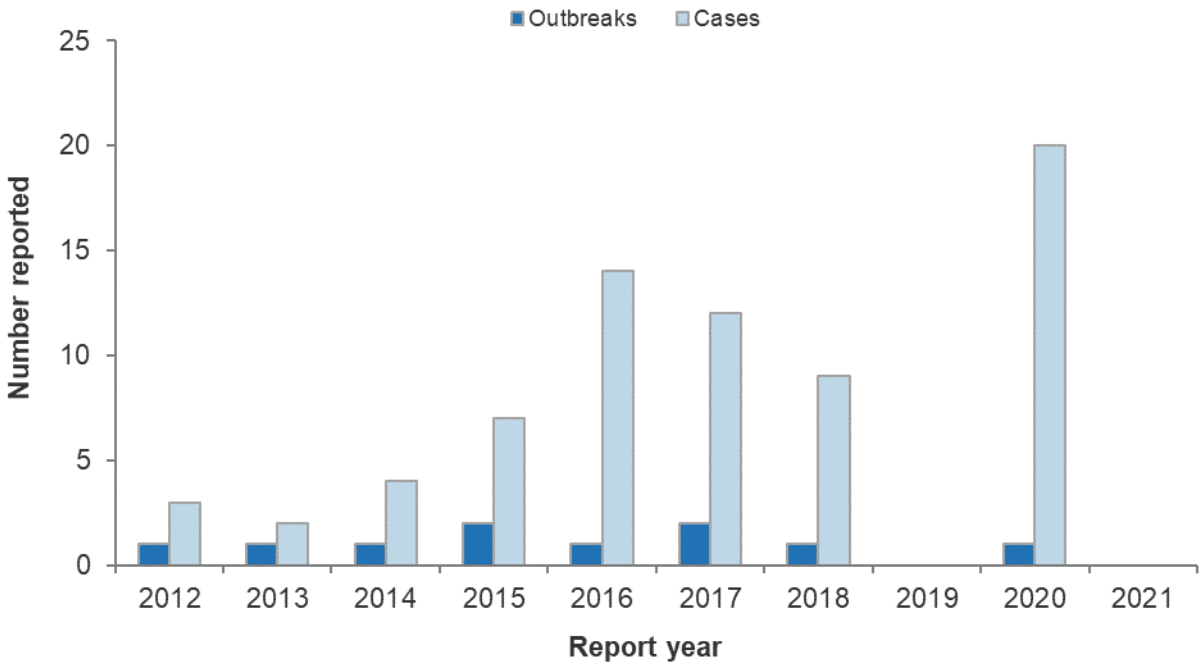
It should be noted that EpiSurv and the MoH NMDS database are separate systems and hospital admission can occur without cases being notified in EpiSurv. This means that not all cases diagnosed with staphylococcal intoxication in hospital are reported in EpiSurv.

Outbreaks reported as caused by *Staphylococcus aureus*

During 2021, no outbreaks of *S. aureus* intoxication were reported in EpiSurv. It is important to note that an outbreak may have multiple pathogens, modes of transmission, settings where exposure occurred, or settings where preparation of food was conducted.

Over the 10-year period 2012 to 2021, 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 with food reported as a possible mode of transmission and associated cases reported by year, 2012–2021



Recent surveys

Nil.

Relevant New Zealand studies and publications

Journal papers

Defects and bacterial pathogens in udders of non-dairybreed ewes from New Zealand – Ridler et al. (2021)

Milk samples were aseptically collected from 110 ewes (195 udder halves) on 11 sheep farms in the lower North Island of New Zealand for bacterial culture [32]. A range of bacterial species was isolated from milk samples, but *Staphylococcus aureus* was the most common species.

Relevant regulatory developments

A new version of the Food Notice, *Importing Food*, was published in 2021 [28]. The Notice lists fermented meat products, meat paste and pâté as of high regulatory interest with respect to coagulase-positive *Staphylococci*.

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 2021 are given in Table 55.

Table 55. Summary of surveillance data for STEC infection, 2021

Parameter	Value in 2021	Source
Number of notified cases	913	EpiSurv
Notification rate (per 100,000)	17.8	EpiSurv
Hospitalisations[a]	43	MoH NMDS
Deaths	0	EpiSurv
Travel-related cases (%)[b,c]	2 (0.2%)	EpiSurv
Estimated food-related cases (%)[b,d]	364 (40%)	Expert consultation

[a] Cases hospitalised may not be notified on EpiSurv
[b] Percentage of the number of notified cases
[c] New Zealand borders were closed in March 2020 with travel restrictions in place for the rest of 2020 and 2021
[d] For estimation of food-related cases the proportions derived from expert consultation [3] exclude travel-related cases. 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. In 2021, 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. The MidCentral, Tairawhiti, and Whanganui DHBs changed to CIDT in May 2021.

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 some STEC infection, particularly O157. With multiplex PCR testing, all faecal samples are screened for all STEC, approximately doubling the number of samples tested for O157 (Michael Addidle, ESR, personal communication). This has led to an increase in the number of faecal samples tested for STEC, resulting 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 2021, 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. Some community West Coast DHB samples are tested at Grey Hospital. 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 has 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.

Effect of COVID-19 on STEC notification rates

Public health and social measures to prevent the spread of COVID-19 in New Zealand were introduced in March 2020 and remained in place through December 2021. These measures have affected exposure behaviours and pathways, access to medical care and laboratory testing priorities. These multiple aspects make it difficult to attribute changes in notification rates to specific COVID-19 related factors, which is discussed in more detail in the Introduction (see page 5).

In 2021, monthly STEC infection notification rates were similar to the three-year mean of the years 2017-2019. There was no apparent direct effect of COVID-19 Alert Level restrictions on the monthly pattern of notifications. In 2020, a reduction in STEC infection notification rates from March to mid-May – compared to the same period in the previous three years 2017-2019 – coincided with Alert Level 3 and 4 restrictions and was probably due to the COVID-19 public health response.

The frequency of overseas travel has changed due to border restrictions from March 2020 until the end of 2021. Consequently in 2021, there were only two STEC infection notifications in EpiSurv listing overseas travel as a risk factor, compared to 113 in 2019 and 18 in 2020.

STEC infection individual cases reported in 2021 by data source

During 2021, 913 individual cases (17.8 cases per 100,000 population) of STEC infection and no resulting deaths were reported in EpiSurv. All cases were reported as fitting the clinical description for STEC infection.

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 [33], but ICD-10 uses EHEC rather than STEC. Of the 43 hospital admissions (0.8 admissions per 100,000 population) recorded in 2021, 24 cases were reported with enterohaemorrhagic *E. coli* infection as

the primary diagnosis and 19 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

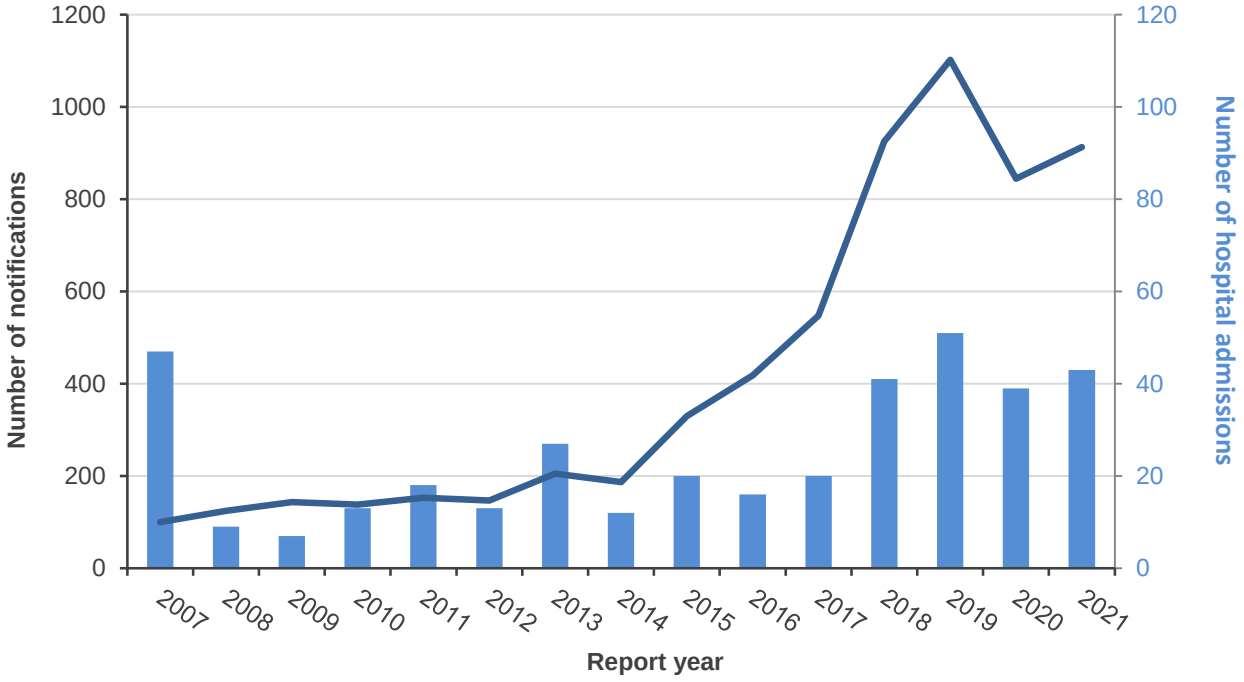
It has been estimated by expert consultation that 20% of O157 STEC (20%) and 40% of non-O157 STEC (40%) incidence is due to foodborne transmission [3]. It was further estimated that approximately 34% of foodborne O157 STEC infections and 27% of foodborne non-O157 STEC infections were due to transmission 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 a modest increase in 2021 (Figure 42). The decrease in 2020 compared to 2019 data is related to the reduction in monthly cases reported during the COVID-19 Alert Level period months (Figure 45).

The number of hospital admissions with STEC infection as a primary or secondary diagnosis varies year to year. The last four years (2018-2021) have seen hospital admission numbers consistently higher than the previous 10 years. Of the hospitalisations in 2021, ~30% were identified with the O157:H7 serotype, ~40% 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.

Figure 42. STEC infection EpiSurv notifications (line) and NMDS hospitalisations (bar) by year, 2007–2021

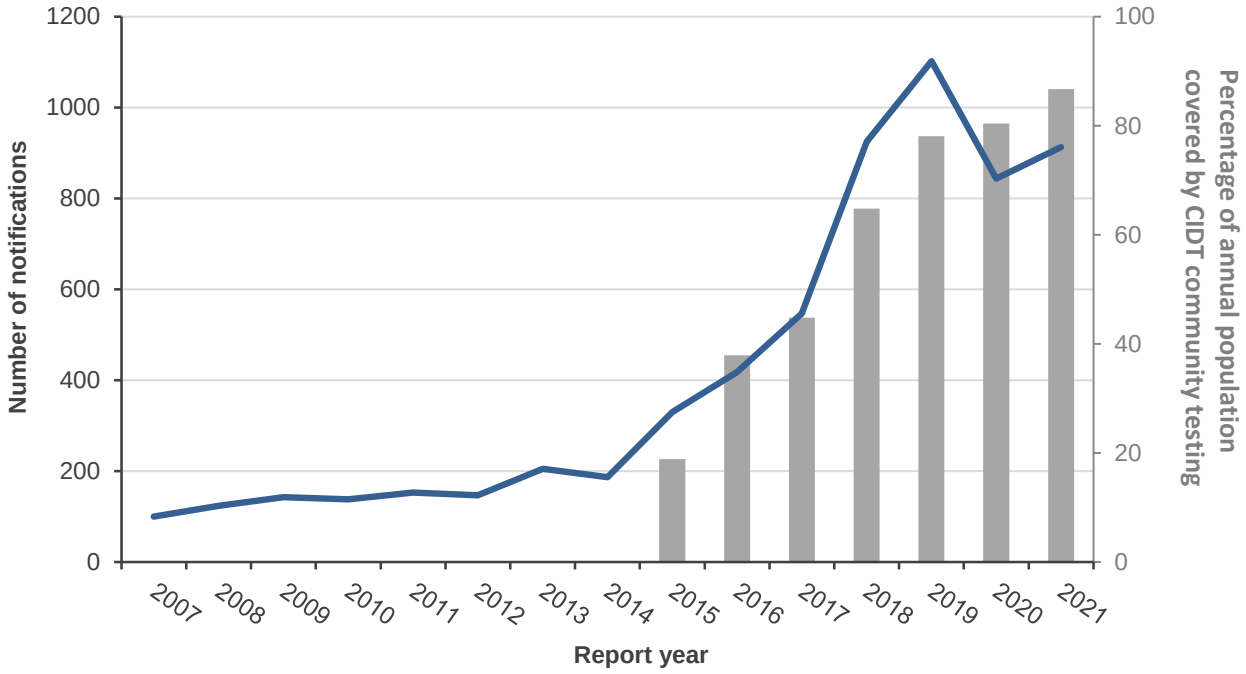


Between 2015 and 2019, the annual increases in STEC infection notifications correspond to the increase in the population being tested by community laboratory CIDT (Appendix B page 120) (Figure 43). The increased sensitivity of CIDT to detect non-O157 STEC serotypes (Table 60) and the increased number of samples routinely tested for STEC appears to have caused the majority of

the increase in STEC notifications [34]. Areas and time periods that have not used CIDT or increased screening for STEC, show no increase in notification rates for STEC [14].

In 2021, approximately 87% of the New Zealand population was covered by community laboratories using CIDT for STEC testing.

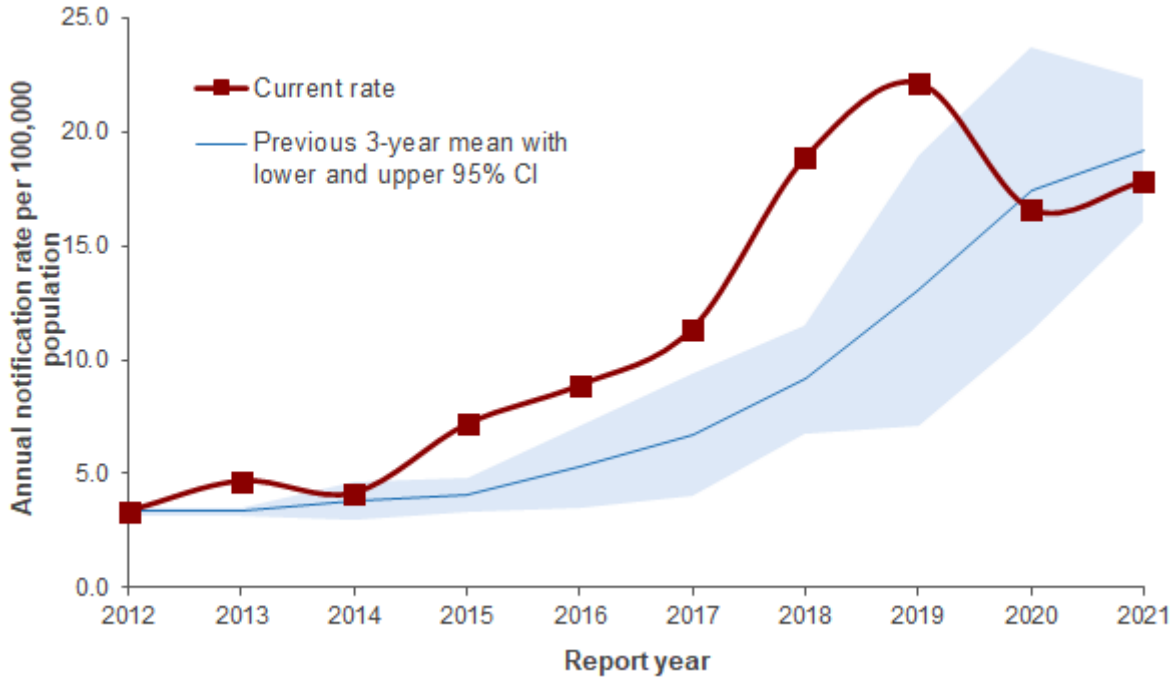
Figure 43. STEC infection EpiSurv notifications (line) and proportion of the NZ population covered by community CIDT (bar) by year, 2007–2021



From 2012 to 2014, the notification rate of STEC infection was in the range of 3.3 to 4.7 notifications per 100,000 population (Figure 44). Increasing rates have been noted every year from 2015 to 2019 (22.1 cases per 100,000 population), followed by a drop in 2020, attributed to the COVID-19 pandemic* and a small increase in 2021 (17.8 cases per 100,000 population). The previous three-year average was 19.2 cases per 100,000 population.

* An overview of the impact of the COVID-19 pandemic on notifications of potentially foodborne diseases is provided in the Introduction, page 5.

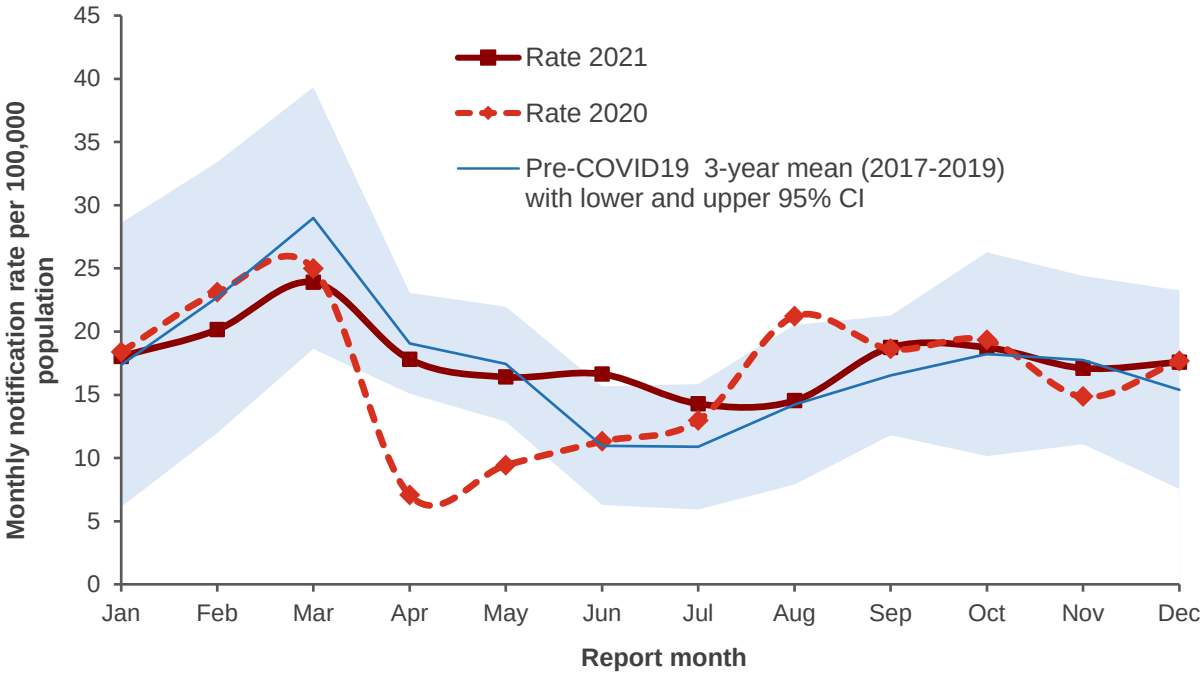
Figure 44. STEC infection notification rate by year, 2012–2021

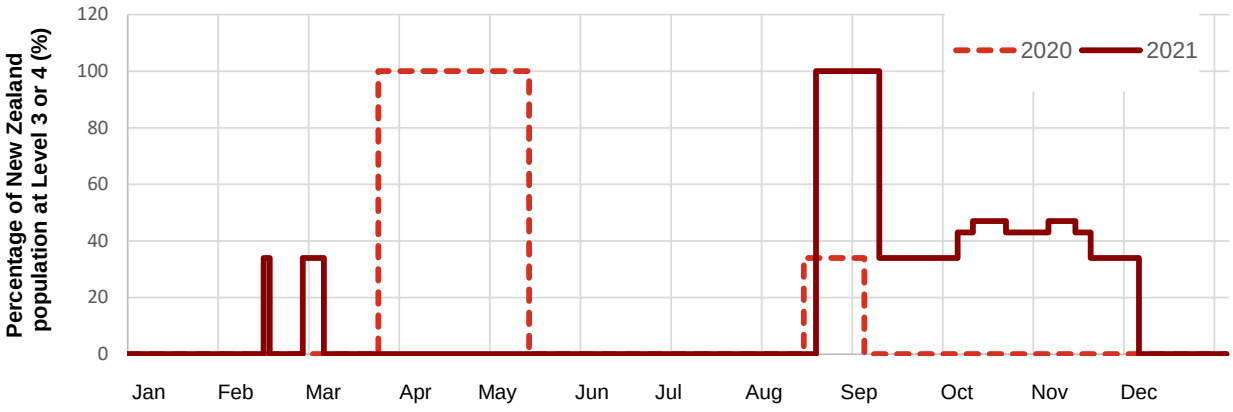


Seasonal data

STEC infection notification rates per 100,000 population by month for 2020 and 2021 are shown in Figure 45 as well as the percentage of the New Zealand population at COVID-19 Alert Levels 3 or 4. In 2021, monthly notification rates were similar to the three-year mean of years 2017-2019. The monthly number of notifications in 2021 ranged from 61 notifications in July (14 per 100,000 population) to a peak of 102 notifications in March (24 per 100,000 population).

Figure 45. STEC infection monthly notification rate (annualised) and percentage of New Zealand population at COVID-19 Alert Levels 3 or 4, 2020 and 2021





Note: A detailed timeline of all COVID-19 Alert Level changes for 2020 and 2021 is included in Appendix C (Table 73).

In 2021, 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 56).

Table 56. STEC infection monthly NMDS hospitalisation admissions 2017-2021

Month	Hospital admissions with a primary or secondary diagnosis of STEC infection				
	2017	2018	2019	2020	2021
January	2	4	9	3	3
February	0	7	4	8	4
March	3	5	9	3	4
April	1	3	9	0	9
May	1	4	1	3	4
June	2	0	1	2	5
July	2	3	3	2	1
August	0	1	6	1	2
September	3	5	5	3	2
October	2	2	0	4	4
November	4	1	3	3	1
December	0	6	1	7	4
Total	**20**	**41**	**51**	**39**	**43**

Demographics

In 2021, notification rates and hospitalisation rates were higher for females (18.4 cases and 1.0 admissions per 100,000 population) than for males (17.2 cases and 0.7 admissions per 100,000 population) (Table 57).

Table 57. STEC cases by sex, 2021

Sex	EpiSurv notifications		Hospitalisations[a]	
	No.	Rate[b]	No.	Rate[b]
Male	437	17.2	17	0.7
Female	476	18.4	26	1.0
Total	**913**	**17.8**	**43**	**0.8**

[a] MoH NMDS data for hospital admissions
[b] per 100,000 population in this sex group

In 2021, the STEC infection notification rate was highest for the 0 to 4 years age group followed by the 70+ years age group (68.4 cases and 27.1 cases per 100,000 population, respectively). The hospital admission rate was also highest for the 0 to 4 years age group, followed by the 70+ age group (3.9 and 1.4 hospital admissions per 100,000 population) (Table 58).

Table 58. STEC cases by age group, 2021

Age group (years)	EpiSurv notifications		Hospitalisations[a]	
	No.	Rate[b]	No.	Rate[b]
0 to 4	209	68.4	12	3.9
5 to 9	58	17.8	2	-
10 to 14	43	12.7	2	-
15 to 19	47	14.9	3	-
20 to 29	92	13.0	3	-
30 to 39	75	10.3	2	-
40 to 49	58	9.1	3	-
50 to 59	90	13.7	5	0.8
60 to 69	88	16.0	3	-
70+	153	27.1	8	1.4
Total	**913**	**17.8**	**43**	**0.8**

[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).

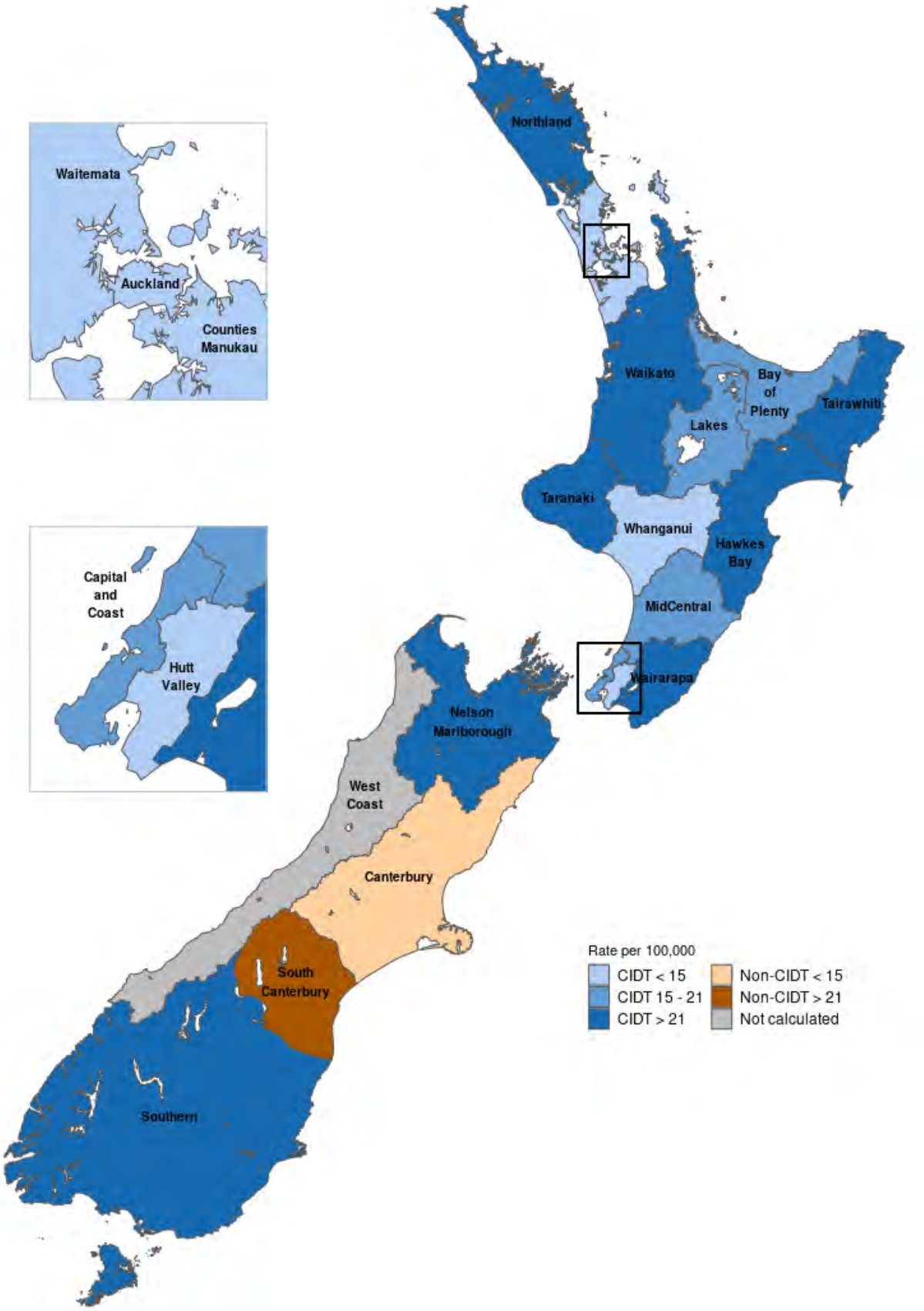
Geographic distribution

The notification rates by DHB calculated per 100,000 resident population are presented in Figure 46 (see also Table 82). 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 (one case). The West Coast DHB used culture-based testing for STEC during the reporting period.

In 2021, the DHB notification rates of STEC infection ranged from 8 per 100,000 population (40 cases) in Auckland DHB to 46 per 100,000 (58 cases) in Taranaki DHB. The Taranaki, South Canterbury (44 per 100,000 population, 27 cases) and Southern (42 per 100,000 population, 146 cases) DHBs had notification rates above 40 per 100,000 population.

Historically, notification rates for STEC infection have been variable across New Zealand with the Southern and Northland DHBs consistently in the highest quartile of notification rates since 2017.

Figure 46. Geographic distribution of STEC infection notifications, 2021



Note: Whanganui, MidCentral and Tairawhiti DHBs testing moved to CIDT methods in May 2021. The rates for these DHBs will be based on a mixture of CIDT and non-CIDT test results.

Outbreaks reported as caused by STEC

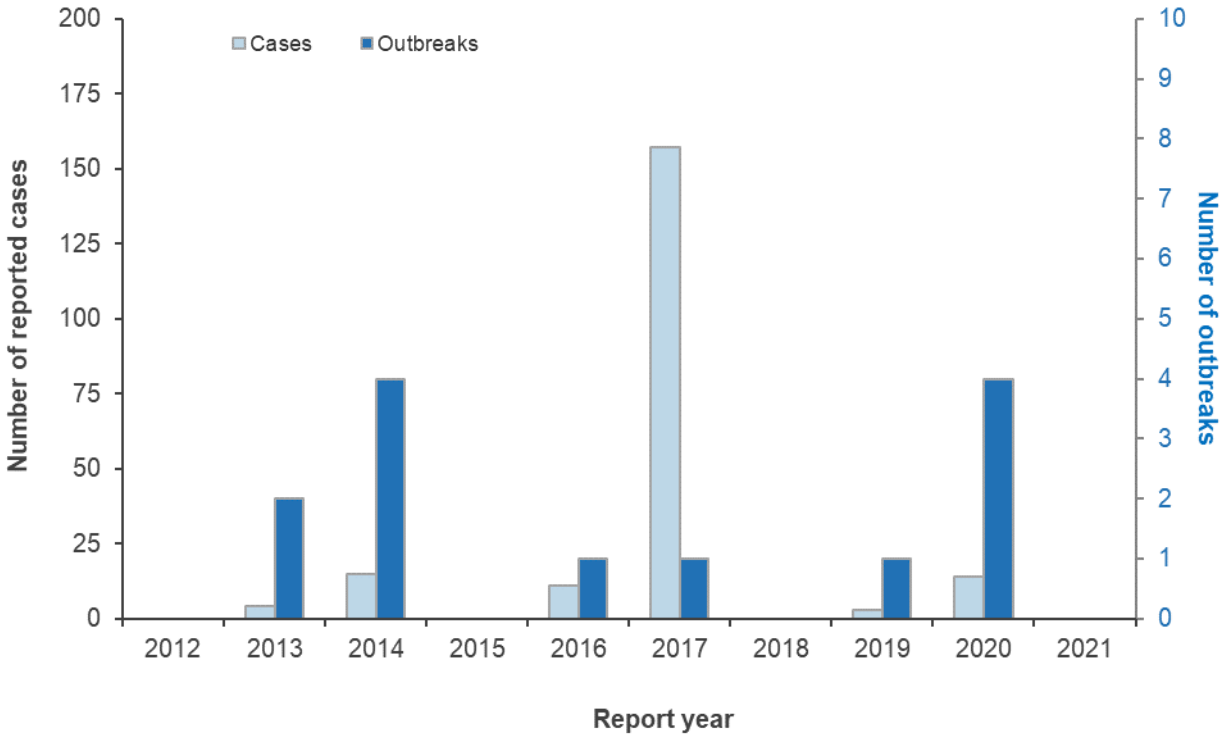
In 2021, there was one outbreak (two cases) of STEC infection notified in EpiSurv. This outbreak did not report food as a possible mode of transmission (Table 59). It is important to note that an outbreak may have multiple pathogens, modes of transmission, settings where exposure occurred, or settings where preparation of food was conducted.

Table 59. STEC infection outbreaks reported, 2021

	Possible foodborne transmission	Total number of STEC infection outbreaks
Outbreaks	0	1
Outbreak-associated cases	0	2
Hospitalised Cases	0	0

Over the 10-year period 2012 to 2021, the annual number of STEC outbreaks with food reported as a possible mode of transmission ranged from zero to four per year, with no outbreaks with food reported as a possible mode of transmission reported for four of the ten years (Figure 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 with food reported as a possible mode of transmission and associated cases reported by year, 2012–2021



STEC types reported for notified cases

Isolates from 619 notified cases infected with STEC were typed by the ESR Enteric Reference Laboratory (ERL) in 2021. A single STEC serotype was confirmed from 612 cases but two different STEC serotypes were isolated and serotyped from each of the remaining seven cases giving a total of 626 isolates. Of the 626 typed isolates, 182 (29.1%) were identified as *E. coli* O157:H7 and 443 (70.8%) as non-O157 (Table 60). As in the previous three years, the most frequently typed non-O157:H7 serotypes were *E. coli* O26:H11 and *E. coli* O128:H2.

Table 60. Annual number of notifications with different STEC serotypes identified by the Enteric Reference Laboratory, 2018–2021

Serotype	2018	2019	2020	2021
O157	**188**	**196**	**166**	**183**
O157:H7[a]	184	191	165	182
Non-O157	**292**	**417**	**391**	**443**
O26:H11	70	113	112	127
O128:H2	17	45	61	62
O146:H21	11	12	18	24
O91:H14	-	11	10	24
O38:H26	18	22	27	22
O103:H2	6	6	9	17
O176:H4	-	10	14	14
O5:HNT[b]	-	6	12	12
O174:H8	1	7	9	11
O88:H8	-	5	8	9
O153:H2	4	10	6	8
O130:H11	1	6	7	7
O84:H2	-	2	10	7
Other Types[c]	167	172	79	99
Cases without typing information	**445**	**491**	**292**	**294**

[a] Whole genome sequencing of human O157:H7 isolates from 2020 to 2021 revealed a wide diversity of genotypes present, with most of the isolates quite distinct to each other

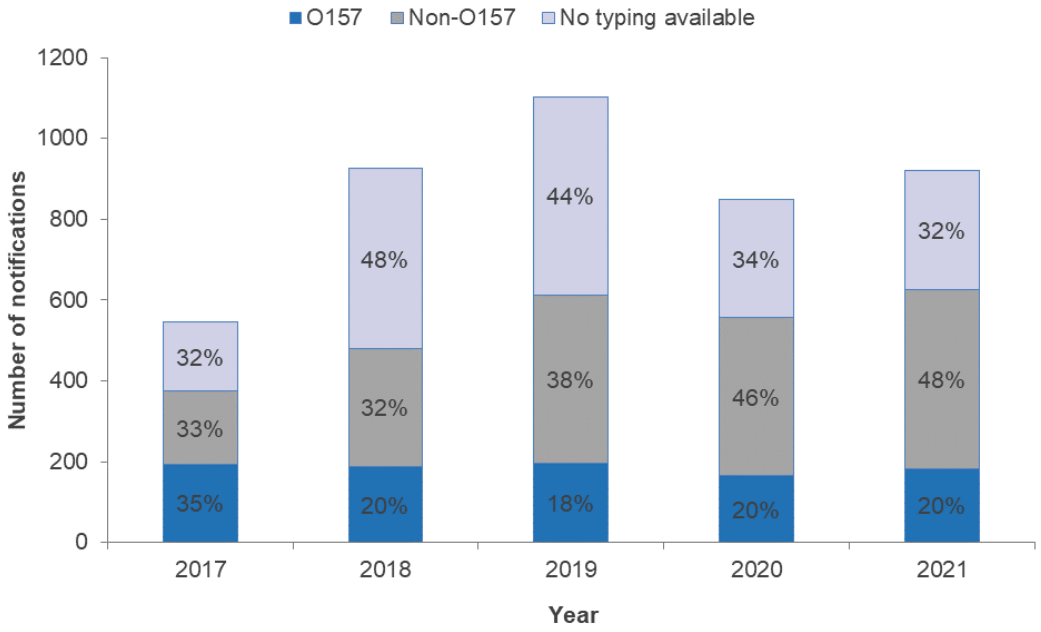
[b] HNT: Non-typable

[c] Isolates with identifiable non-O157 serotypes, not listed in table. Full list available in the Appendix D, Table 88

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

For 294 (32%) of the 913 STEC notifications in 2021, 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, 2017–2021



Investigation of the 2021 EpiSurv-recorded hospitalisation status for the three most commonly identified serotypes found that *E. coli* O157:H7-infected cases were most frequently reported to have been hospitalised (30% of cases hospitalised, 8% no hospitalisation information recorded). The proportion of cases hospitalised was less for *E. coli* O26:H11 (26% cases hospitalised, 9% no hospital data recorded) and *E. coli* O128:H2 (10% cases hospitalised, 19% no hospital data recorded).

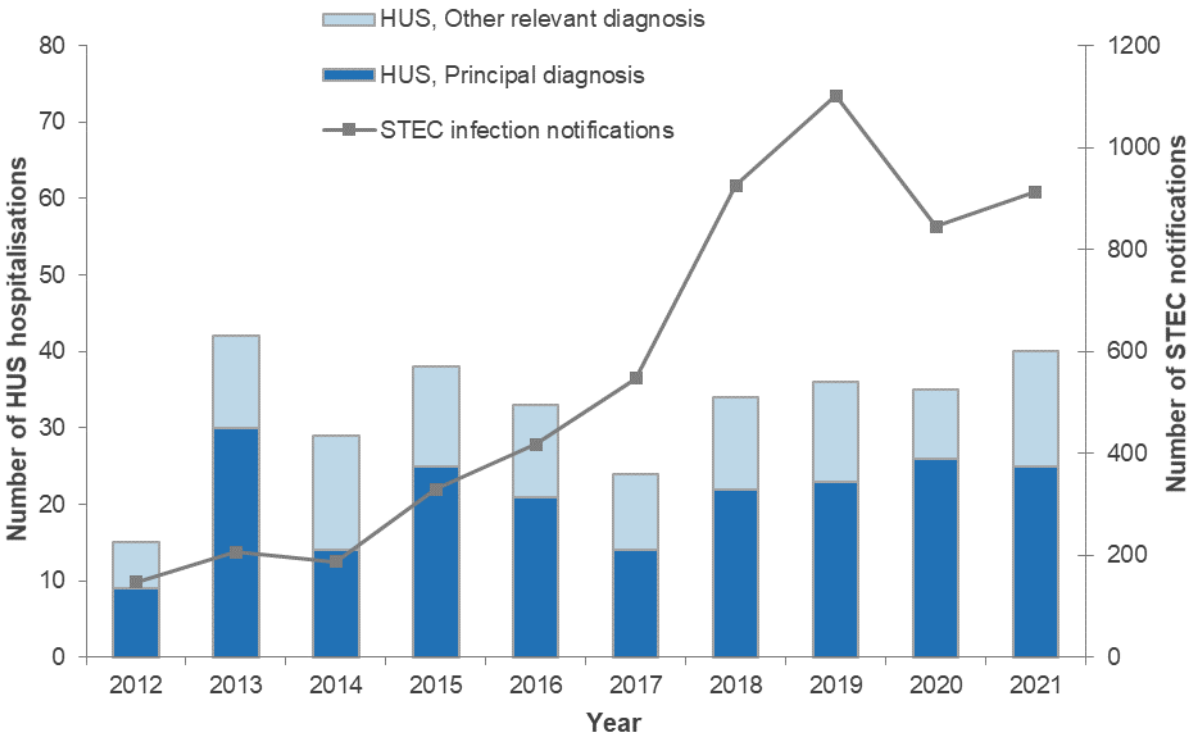
Disease sequelae – haemolytic uraemic syndrome (HUS)

HUS is a serious sequela that may result from an STEC infection. HUS is usually preceded by an STEC infection [35]. 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 [36], the most recent European data report that *E. coli* O26 was most frequently associated with HUS cases [37]. In 2021, 16 STEC cases notified in EpiSurv were reported to have developed HUS. The associated serotypes were O157:H7 (7), O26:H11 (7), while for two cases the serotype was not reported.

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 2021 year were considered, rather than all cases that were hospitalised in that year. That is, if an HUS case hospitalised in 2021 had been hospitalised with HUS in a previous year, the 2021 admission was considered as a re-admission, rather than an incident case. Of the 40 incident hospital admissions recorded in 2021 (0.8 per 100,000 population), 25 were reported with HUS as the primary diagnosis and 15 with HUS as another relevant diagnosis.

Between 2012 and 2021, the number of incident hospitalised cases (any diagnosis code) of HUS each year ranged from 15 to 42 (Figure 49). In 2021, the number of incident hospitalised cases (40) was slightly higher than 2020 (35). STEC notifications have increased steadily over this period (Figure 42). However annual numbers of HUS cases have remained similar over the last decade.

Figure 49. Haemolytic uraemic syndrome (HUS) hospitalised cases, 2012–2021



In 2021, the number of female cases hospitalised due to HUS was slightly less than the number of male cases (Table 61). This is the opposite of the pattern seen in most years other than 2017, with more females usually hospitalised with HUS than males.

Table 61. Haemolytic uraemic syndrome hospitalised cases by sex, 2021

Sex	Hospitalised cases[a]	
	No.	Rate[b]
Male	21	0.8
Female	19	0.7
Total	**40**	**0.8**

[a] MoH NMDS data for hospital admissions

[b] per 100,000 population.

In 2021, the highest age-specific rates of incident hospitalised cases due to HUS were for children in the 0 to 4 years age group (Table 62).

Table 62. Haemolytic uraemic syndrome hospitalised cases by age group, 2021

Age group (years)	Hospitalised cases [a]	
	No.	Rate[b]
0 to 4	23	7.5
5 to 9	4	-
10 to 14	1	-
15 to 19	1	-
20 to 29	1	-
30 to 39	2	-
40 to 49	3	-
50 to 59	-	-
60 to 69	1	-
70+	4	-
Total	**40**	**0.8**

[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

Nil.

Journal papers

Transmission dynamics of Shiga toxin-producing Escherichia coli in New Zealand cattle from farm to slaughter – Browne et al. (2021)

Animal and environmental samples (*n* = 2580) were collected from six farms and three meat processing plants in New Zealand during multiple sampling sessions in spring of 2015 and 2016 [38]. PCR/MALDI-TOF analysis revealed that 6.2% were positive for "Top 7" STEC (O157, O26, O45, O103, O111, O121, and O145). A marked increase in the Top 7 STEC prevalence was observed between calf hides on farm (6.3% prevalence) and calf hides at processing plants (25.1% prevalence). Whole-genome sequencing was performed on the Top 7 STEC bacterial isolates (*n* = 40). Analysis of STEC O26 (*n* = 25 isolates) revealed relatively low genetic diversity on individual farms, consistent with the presence of a resident strain disseminated within the farm environment.

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 status

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 ppm 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 TSP 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)

Toxic shellfish poisoning cases reported in 2021 by data source

During 2021, three individual cases of toxic shellfish poisoning were reported in EpiSurv.

The ICD-10 code T61.2 was used to extract hospitalisation data for 'other fish and shellfish poisoning' from the MoH NMDS database. All of the four hospital admissions (0.1 admissions per 100,000 population) recorded in 2021 were reported with 'other fish and shellfish poisoning' as the primary 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 2021, no toxic shellfish poisoning outbreaks were notified. 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 six years. The last outbreaks were in 2014 (13 cases) and 2012 (29 cases).

Recent surveys

Nil.

Relevant New Zealand studies and publications

Journal papers

Overview of Australian and New Zealand harmful algal species occurrences and their societal impacts in the period 1985 to 2018, including a compilation of historic records – Hallegraeff et al. (2021)

Similarities and differences between Australia and New Zealand in harmful algal species occurrences and harmful algal events impacting on human society (HAEDAT) are reported and factors that explain their differences explored [39]. Paralytic shellfish toxin (PST)-producing blooms of *Alexandrium catenella* in 2000 in New Zealand caused significant economic damage from restrictions on the movement of greenshell mussel spat. The biggest biotoxin event in New Zealand was an unexpected outbreak of neurotoxic shellfish poisoning (NSP) in 1993 in the Hauraki Gulf (putatively due to *Karenia* cf. *mikimotoi*) with 180 reported cases of human poisonings as well as reports of respiratory irritation north of Auckland. Notably, NSP has not recurred in New Zealand since.

Limited diarrhoeic shellfish poisoning (DSP) illnesses have been reported in New Zealand. No human illnesses from amnesic shellfish poisoning (ASP) have been reported in either Australia or New Zealand.

Relevant regulatory developments

A new version of the Food Notice, *Importing Food*, was published in 2021 [28]. The Notice lists bivalve molluscan shellfish (BMS) and products containing BMS as of high regulatory interest with respect to marine biotoxins:

Vibrio parahaemolyticus infection

Case definition

Clinical description:	Gastroenteritis with watery diarrhoea and abdominal cramps.
Laboratory test for diagnosis:	Isolation of Kanagawa-positive or pathogenic serotype of *Vibrio parahaemolyticus* from a faecal specimen or isolation of ≥10^5/gram *V. parahaemolyticus* from leftover food.
Case classification:	
Probable	A clinically compatible illness.
Confirmed	A clinically compatible illness that is laboratory confirmed, OR a clinically compatible illness and a common exposure associated with a laboratory confirmed case.

Changes to laboratory methods

Since 2015, laboratories across New Zealand have changed the methodology for testing faecal specimens. Three of the four PCR panels used across New Zealand include *Vibrio* species, in addition to other faecal pathogens. In 2021, 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 2021 by data source

During 2021, 51 individual cases (1.0 per 100,000 population) of *Vibrio parahaemolyticus* infection were reported in EpiSurv.

The ICD-10 code A05.3 was used to extract foodborne *V. parahaemolyticus* infection hospitalisation data from the MoH NMDS database. Of the four hospital admissions (0.1 admissions per 100,000 population) recorded in 2021, all four cases were reported with *V. parahaemolyticus* infection as the primary 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.

Foodborne transmission

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

Outbreaks reported as caused by *Vibrio parahaemolyticus*

Two outbreaks of *V. parahaemolyticus* infection with food as a possible mode of transmission were reported in EpiSurv for 2021, before the cut-off date for this report (12 May 2022), involving 28 associated cases, eight of whom were listed as hospitalised (Table 63).

Table 63. *V. parahaemolyticus* infection outbreaks reported in EpiSurv, 2021

	Possible foodborne transmission with suspected source	Total number of *V. parahaemolyticus* infection outbreaks
Outbreaks	2	2
Outbreak-associated cases	28	28
Hospitalised cases	8	8

Table 64 provides details of the two *V. parahaemolyticus* infection outbreaks with food reported as a possible mode of transmission in EpiSurv. Between February and May 2021, 24 cases from six different DHBs were reported to be part of a *V. parahaemolyticus* outbreak. Of the case isolates, 16 were the same sequence type, ST50, with three ST199 and one ST36 types. *V. parahaemolyticus* ST2549 was isolated from three of the cases in the November outbreak.

Table 64. Details of *V. parahaemolyticus* infection outbreaks reported in EpiSurv with food reported as a possible mode of transmission, 2021

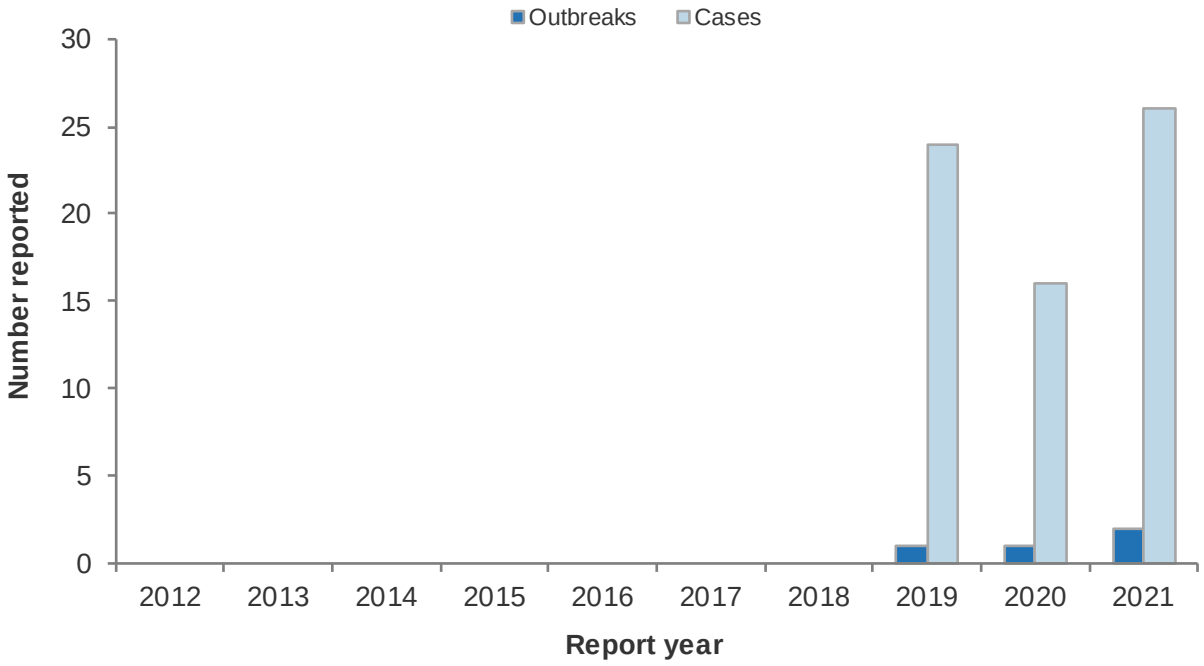
PHU	Report Month	Suspected source	Evidence	Setting	No. Ill
Multi PHU	March	Raw mussels	Common food type eaten by cases	Home or Restaurant/café/bakery consumption of commercially harvested or self-caught mussels	19C 5P
PH Northland	November	Raw oysters	Common food outlet	Home consumption of commercially harvested oysters	4C

PHU: Public Health Unit, PH Northland: Public Health Northland
Number ill: C: confirmed, P: probable

In addition to the two outbreaks listed in EpiSurv at the cut-off date for this report, three further suspected outbreaks were investigated by the New Zealand Food Safety Compliance team during 2021.

In the last 10 years there were three years with potentially foodborne *V. parahaemolyticus* outbreaks recorded (2019, 2020 and 2021), with between two and 24 outbreak-associated cases per year (Figure 50).

Figure 50. *V. parahaemolyticus* infection outbreaks with food reported as a possible mode of transmission and associated cases reported by year, 2012–2021



V. 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 *Vibrio parahaemolyticus* isolates, predominantly those that were positive for the virulence markers *tdh* and *trh* (Table 65).

Table 65. *V. parahaemolyticus* 7-gene multi locus sequence types identified by the Enteric Reference Laboratory, 2019–2021

Sequence type	2019	2020	2021
ST36	14	2	1
ST50	2*	24	24
ST199	-	-	3
ST675	1*	-	-
ST2549	-	-	3
Total	**17**	**26**	**31**

*Infection acquired overseas and genetically distinct from New Zealand acquired infections

Recent surveys

Nil.

Relevant New Zealand studies and publications

Nil.

Relevant regulatory developments

Nil.

Yersiniosis

Summary data for yersiniosis in 2021 are given in Table 66.

Table 66. Summary of surveillance data for yersiniosis, 2021

Parameter	Value in 2021	Source
Number of notified cases (Total)	1410	EpiSurv
Notification rate (per 100,000)	27.5	EpiSurv
Hospitalisations[a]	193	MoH NMDS
Deaths	0	EpiSurv
Travel-related cases (%)[b,c]	2 (0.1%)	EpiSurv
Estimated food-related cases (%)[d]	1056 (75%)	Expert consultation

[a] Cases hospitalised may not be notified on EpiSurv
[b] Percentage of the number of notified cases
[c] New Zealand borders were closed in March 2020 with travel restrictions in place for the rest of 2020 and 2021.
[d] For estimation of food-related cases the proportions derived from expert consultation [3] exclude travel-related cases.

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.

* 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. In 2021, 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.* The MidCentral, Tairawhiti, and Whanganui DHBs changed to CIDT in May 2021.

Within the DHBs that have moved to CIDT, all community faecal specimens are routinely tested for *Y. enterocolitica and Y. pseudotuberculosis* in the Capital & Coast, Hawke's Bay, Hutt Valley, MidCentral, Nelson Marlborough, Southern, Tairawhiti, Taranaki, Wairarapa, and Whanganui DHBs. Faecal specimens in Auckland, Bay of Plenty, Counties Manukau, Lakes, Northland, Waikato, and Waitemata DHBs are only being screened for *Y. enterocolitica* [40]. This corresponds to 54% of the New Zealand population now only being screened for *Yersinia 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. The cultural methods previously in use identified isolates as belonging to the *Yersinia* genus, with additional testing identifying the isolates to the species level.

The introduction of CIDT methods has had no significant impact on notifications for yersiniosis [14].

Effect of COVID-19 on yersiniosis notification rates

Public health and social measures to prevent the spread of COVID-19 in New Zealand were introduced in March 2020 and remained in place through December 2021. These measures will have affected exposure behaviours and pathways, access to medical care and laboratory testing priorities. These multiple aspects make it difficult to attribute any changes to notification rates, either to specific COVID-19 related factors, which is discussed in more detail in the Introduction (see page 5), or true changes in disease incidence.

In 2021, monthly yersiniosis notification rates were generally higher or similar to the three-year average of 2017-2019. The seasonal trend differed from recent years (2017–2019) with higher rates in autumn and winter (Figure 53). In 2020, the impact of the national Alert Level 3 and 4 restrictions in April and May was apparent with a pronounced drop in notifications. In 2021, the impact of COVID-19 restrictions from August to December for varying parts of the country is unclear.

The frequency of overseas travel has changed due to border restrictions from March 2020 until the end of 2021. This is reflected in the notifications; in 2021, there were two yersiniosis notifications in EpiSurv listing overseas travel as a risk factor, compared to 58 in 2019 and 11 in 2020.

Yersiniosis cases reported in 2021 by data source

During 2021, 1410 individual cases (27.5 per 100,000 population) of yersiniosis and no resulting deaths were reported in EpiSurv. Of the 1410 cases, the symptoms of 1144 cases (81%) were reported as fitting the clinical description for yersiniosis infection, the symptoms were unknown for 156 cases, and for 10 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 193 hospital admissions (3.8 admissions per 100,000 population) recorded in 2021, 120 cases were reported with yersiniosis as the primary diagnosis and 73 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.

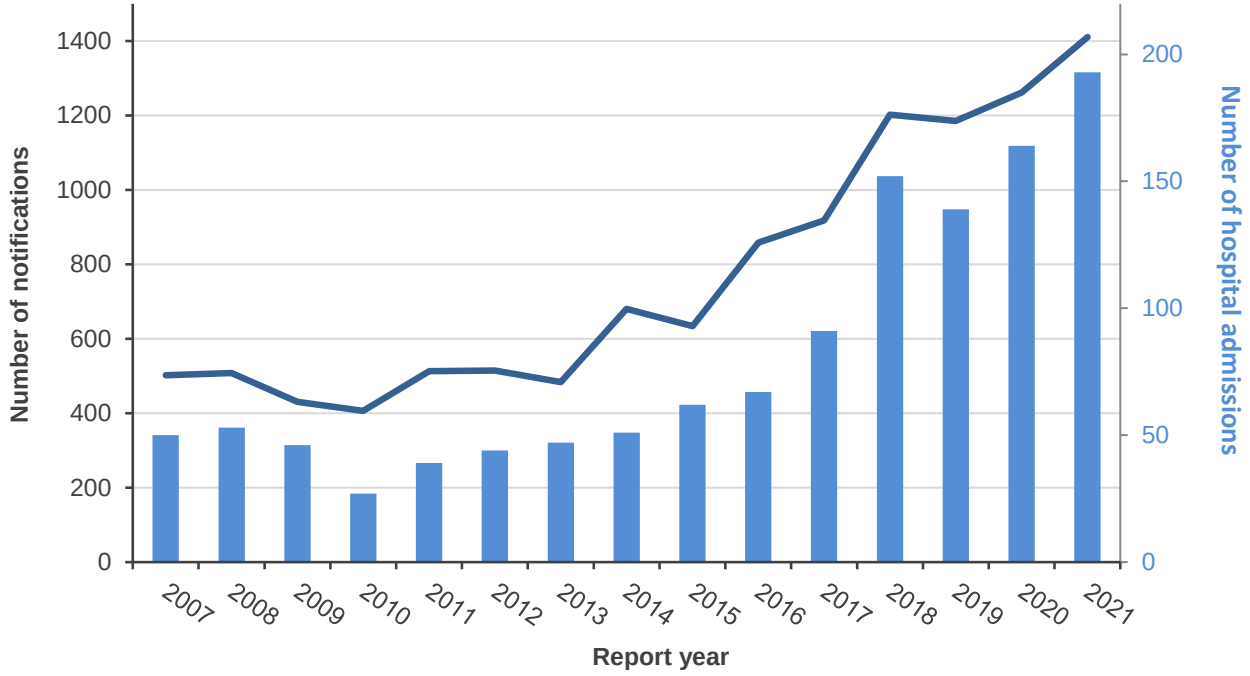
Foodborne transmission

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

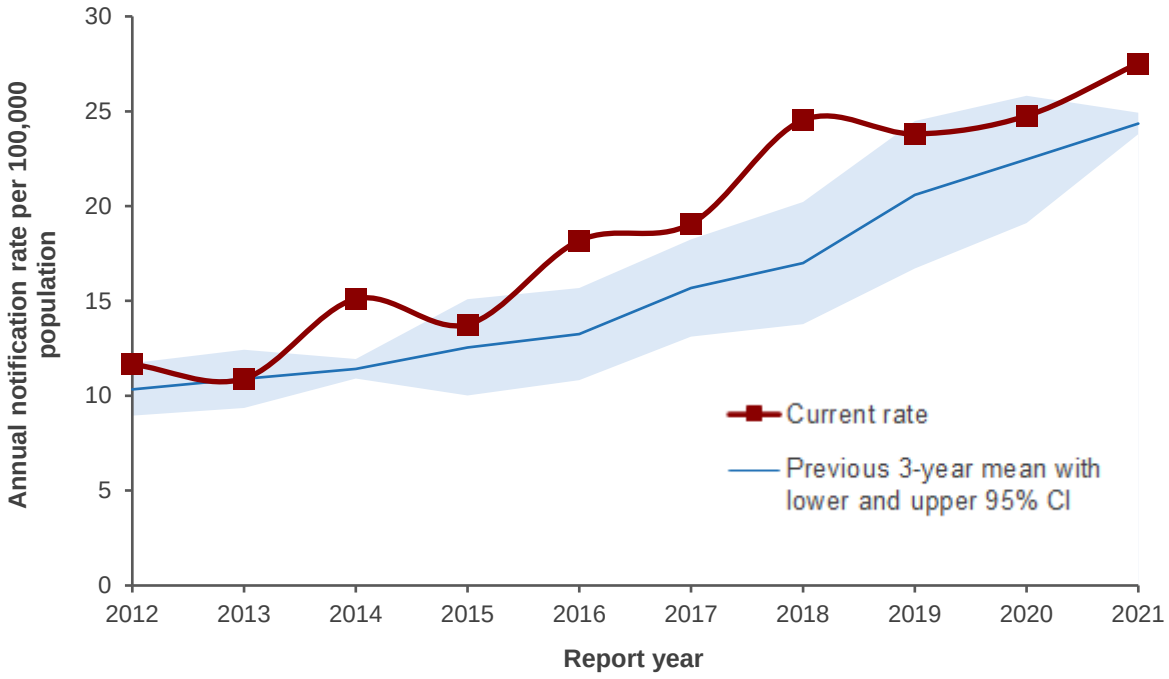
Between 2007 and 2013 the annual number of notifications reported ranged between 406 and 514. Since 2013, the number of notifications for yersiniosis and the rate of yersiniosis notifications per 100,000 population has been increasing, with 1260 cases reported in 2020 and 1410 cases in 2021 (Figure 51 and Figure 52). The number of hospital admissions with yersiniosis as a primary or secondary diagnosis has also increased in line with the number of notifications.

Figure 51. Yersiniosis EpiSurv notifications (line) and NMDS hospitalisations (bar) by year, 2007–2021



The yersiniosis annual notification rate has been generally increasing since 2013 (Figure 52). The 2021 notification rate was 27.5 per 100,000 population, higher than the previous three-year average (24.4 cases per 100,000).

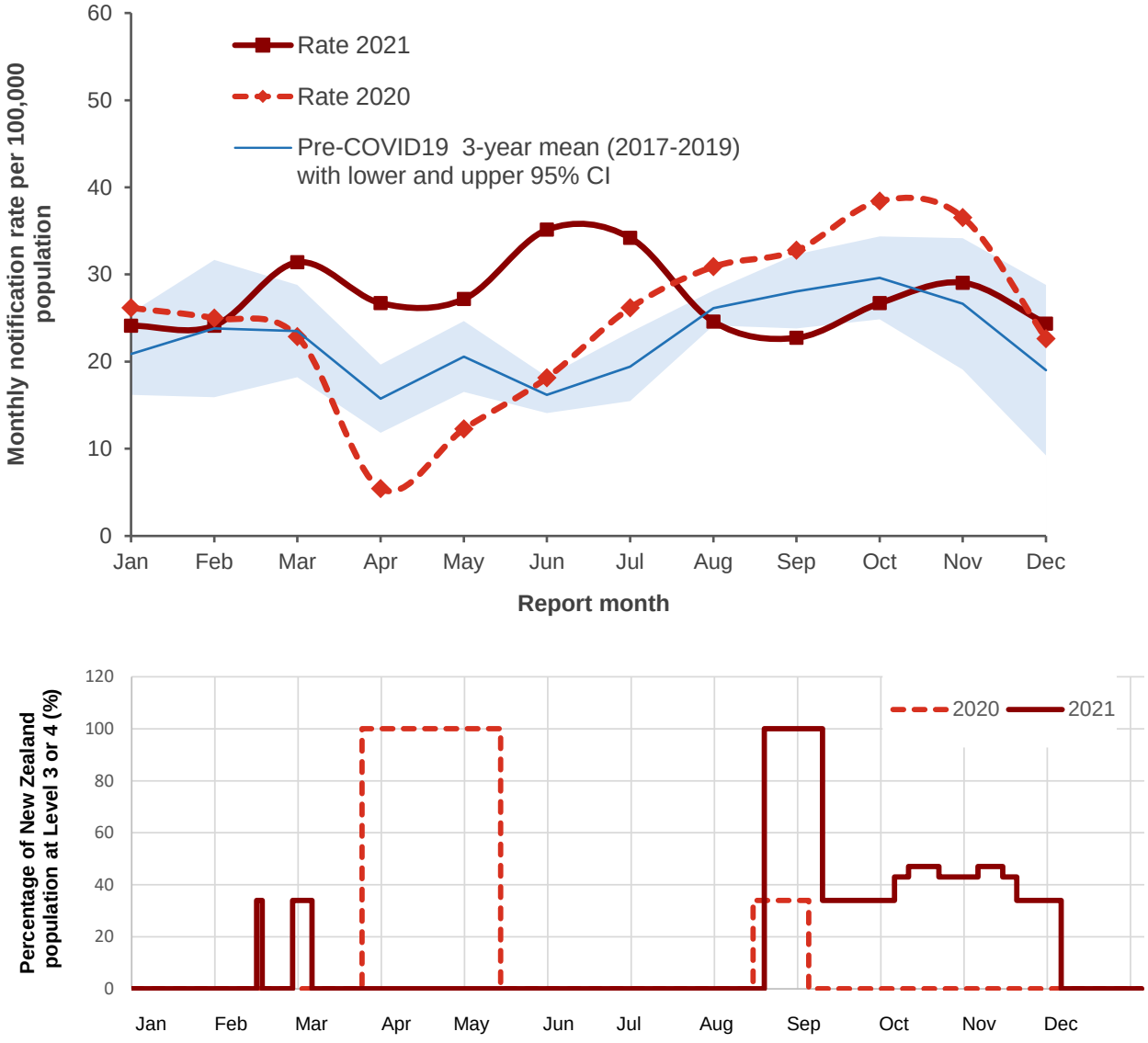
Figure 52. Yersiniosis notification rate by year, 2012–2021



Seasonal data

Yersiniosis notification rates per 100,000 population by month for 2020 and 2021 are shown in Figure 53 as well as the percentage of the New Zealand population at COVID-19 Alert Levels 3 or 4. The monthly number of notifications in 2021 ranged from 97 notifications (September, 23 per 100,000 population) to a peak of 150 notifications (June, 35 per 100,000 population). In 2021, monthly notification rates were generally higher or similar to the three-year average of 2017-2019. The seasonal trend in monthly notification rates in 2021 differed from recent years (2017–2019) with higher rates in autumn and winter and a pronounced increase in June and July. It is unclear how COVID-19 restrictions have affected yersiniosis notification rates in 2021.

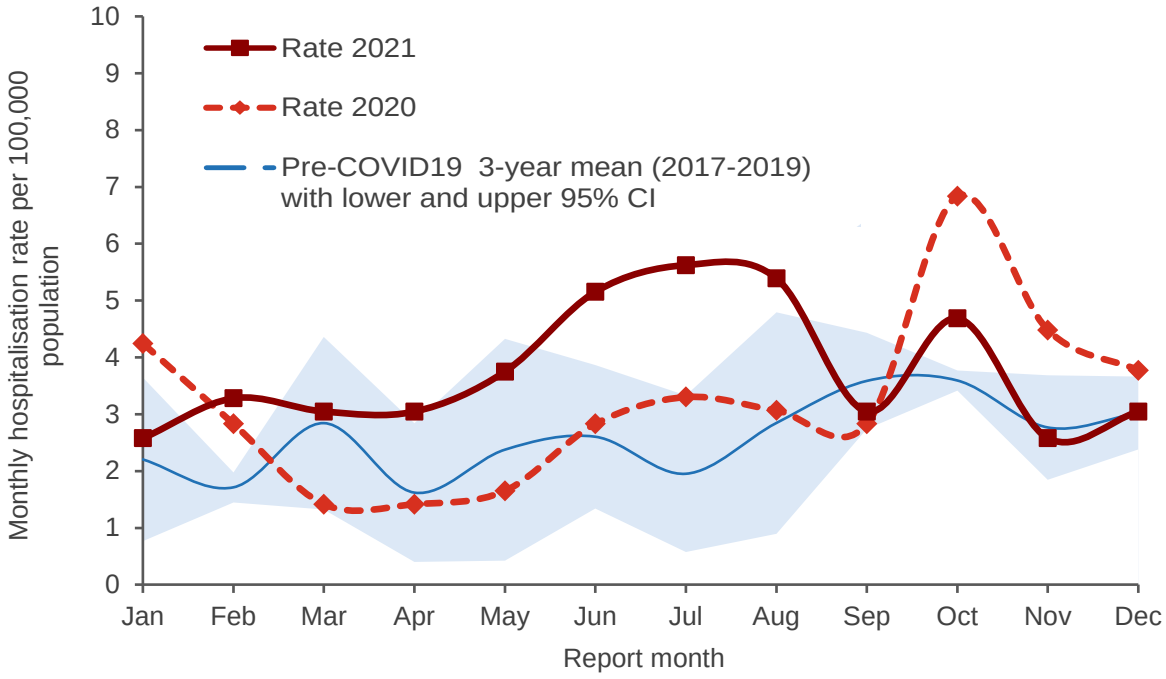
Figure 53. Yersiniosis monthly notification rate (annualised) and percentage of New Zealand population at COVID-19 Alert Levels 3 or 4, 2020 and 2021



Note: A detailed timeline of all COVID-19 Alert Level changes for 2020 and 2021 is included in Appendix C (Table 73).

In 2021, the monthly hospitalisation rates were generally higher than the three-year average range of the years 2017-2019, except for the months September, November and December where hospitalisation rates were similar to the years 2017-2019 (Figure 54). The seasonal trend in monthly hospitalisation rates followed the seasonal trend in monthly notification rates in 2021 (Figure 53).

Figure 54. Yersiniosis monthly hospitalisation rate (annualised), 2020 and 2021



Demographics

In 2021, the yersiniosis notification and hospitalisation rates were higher for males (28.4 cases and 3.9 admissions per 100,000 population) than females (26.6 cases and 3.6 admissions per 100,000 population) (Table 67).

Table 67. Yersiniosis cases by sex, 2021

Sex	EpiSurv notifications		Hospitalisations[a]	
	No.	Rate[b]	No.	Rate[b]
Male	723	28.4	99	3.9
Female	687	26.6	94	3.6
Total	**1410**	**27.5**	**193**	**3.8**

[a] MoH NMDS data for hospital admissions
[b] per 100,000 population in this sex group

In 2021, the highest yersiniosis notification rates and hospitalisation rates were for the 0 to 4 years age group (88.0 cases and 10.8 admissions per 100,000 population) (Table 68).

Table 68. Yersiniosis cases by age group, 2021

Age group (years)	EpiSurv notifications		Hospitalisations[a]	
	No.	Rate[b]	No.	Rate[b]
0 to 4	269	88.0	33	10.8
5 to 9	62	19.0	3	-
10 to 14	44	13.0	3	-
15 to 19	44	14.0	6	1.9
20 to 29	167	23.7	21	3.0
30 to 39	210	29.0	29	4.0
40 to 49	147	23.1	17	2.7
50 to 59	157	24.0	23	3.5
60 to 69	152	27.6	25	4.5
70+	158	27.9	33	5.8
Total	**1410**	**27.5**	**193**	**3.8**

[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)

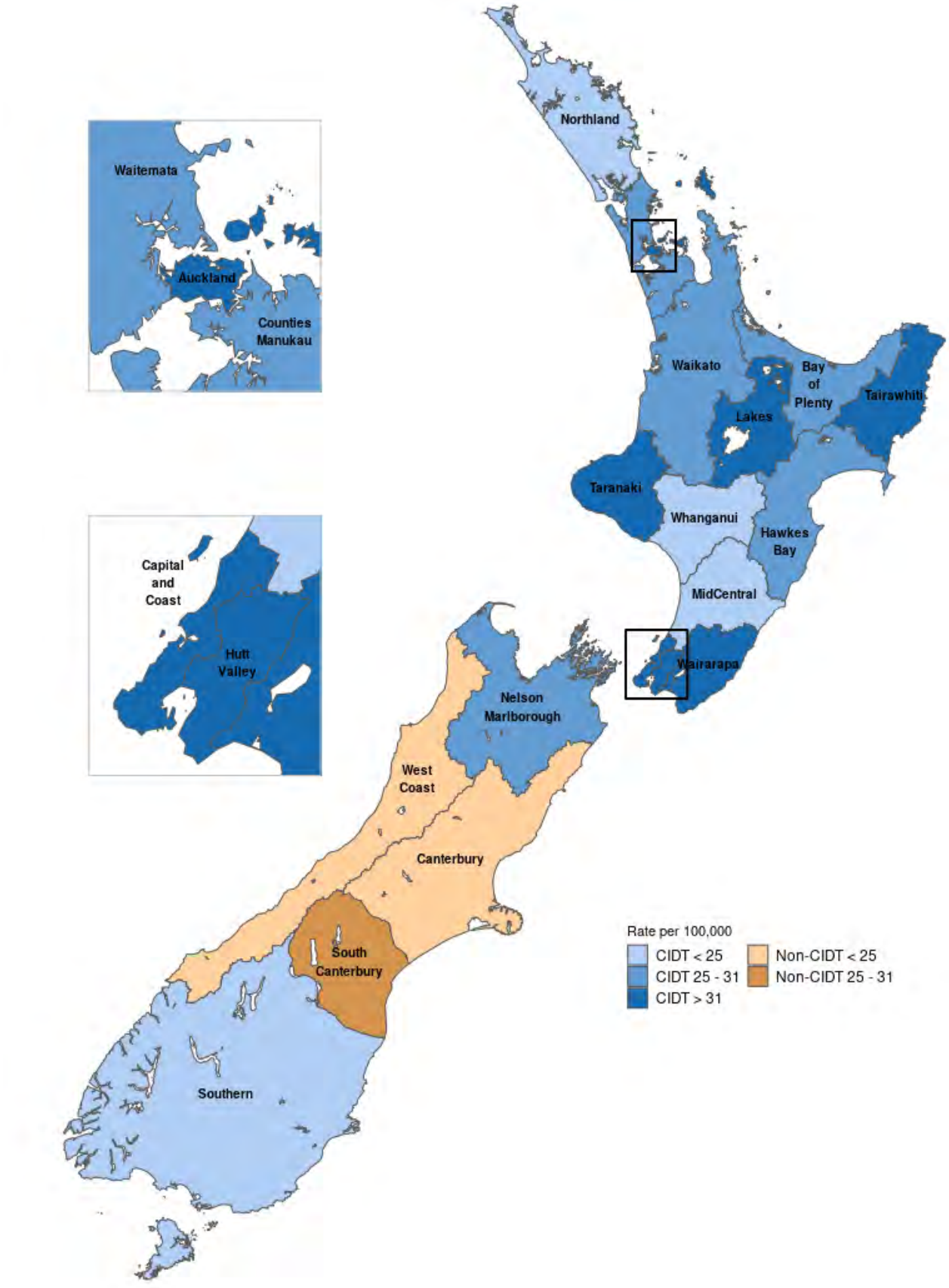
Geographic distribution

The notification rates by DHB calculated per 100,000 resident population are presented in Figure 55 (see also Table 82). Blue shading is used for DHBs which are using CIDT community testing, the brown shading is used for DHBs using culture-based community testing.

In 2021, the DHB notification rates of yersiniosis ranged from 7 per 100,000 population (five cases) in Whanganui DHB to 48 per 100,000 for Taranaki DHB (61 cases). The Taranaki, Wairarapa (46 per 100,000 population, 23 cases), and Tairawhiti (45 per 100,000 population, 23 cases) DHBs had rates above 40 cases per 100,000 population.

Historically, notification rates for yersiniosis have been variable across New Zealand with Wairarapa and Hutt Valley DHBs consistently in the highest quartile of notification rates since 2017.

Figure 55. Geographic distribution of yersiniosis notifications, 2021



Note: Whanganui, MidCentral and Tairawhiti DHBs testing moved to CIDT methods in May 2021. The rates for these DHBs will be based on a mixture of CIDT and non-CIDT test results.

Outbreaks reported as caused by *Yersinia* spp.

In 2021, there were four yersiniosis outbreaks reported in EpiSurv, with food reported as a possible mode of transmission for three outbreaks (Table 69). 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 69. Yersiniosis outbreaks reported, 2021

	Possible foodborne transmission with suspected source	Possible foodborne transmission but no suspected source	Total number of yersiniosis outbreaks
Outbreaks	2	1	4
Outbreak-associated cases	8	16	29
Hospitalised cases	0	0	0

Table 70 contains details of the yersiniosis outbreaks with food reported as a possible mode of transmission reported in 2021. The evidence for foodborne transmission was weak in all three outbreaks. In the April outbreak norovirus was also detected in associated clinical samples.

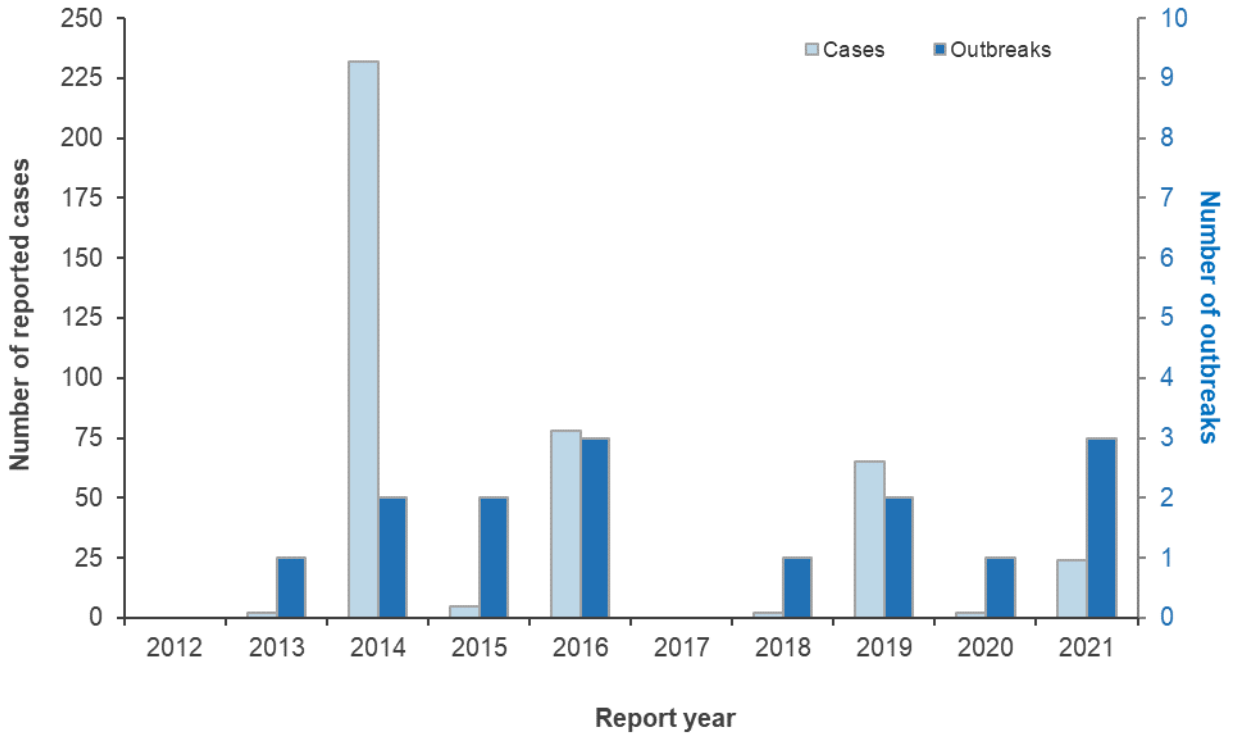
Table 70. Details of yersiniosis outbreaks with food reported as a possible mode of transmission, 2021

PHU	Report Month	Suspected Vehicle	Evidence	Setting	No. Ill
PH South	March	Raw milk, untreated drinking water	Household cluster	Home	1C 4P
C and PH	April	Unknown	Common location	Long term care facility	13C 3P
Toi Te Ora	October	Bacon (consumed long after the 'use by date')	Household cluster	Home	3C

PHU: Public health unit, PH South: Public Health South, C and PH: Community and Public Health, Toi Te Ora: Toi Te Ora - Public Health
Number ill: C: confirmed, P: probable

Over the 10-year period 2012 to 2021, 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 two to 232 (Figure 56). The number of outbreaks in 2014 (two outbreaks) and 2016 (three outbreaks) was not unusual, but the number of cases involved (232 and 78, respectively) was higher than has been seen in New Zealand previously or since. The increased number of outbreak cases in 2019 was due to an outbreak in a prison setting.

Figure 56. Yersiniosis outbreaks with food reported as a possible mode of transmission and associated cases reported by year, 2012–2021



Yersinia species commonly reported

In 2021, isolates from 1076 out of 1410 cases (76%) of notified yersiniosis were typed by the Enteric Reference Laboratory (ERL).

Table 71 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 57. 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 76% in 2021, and

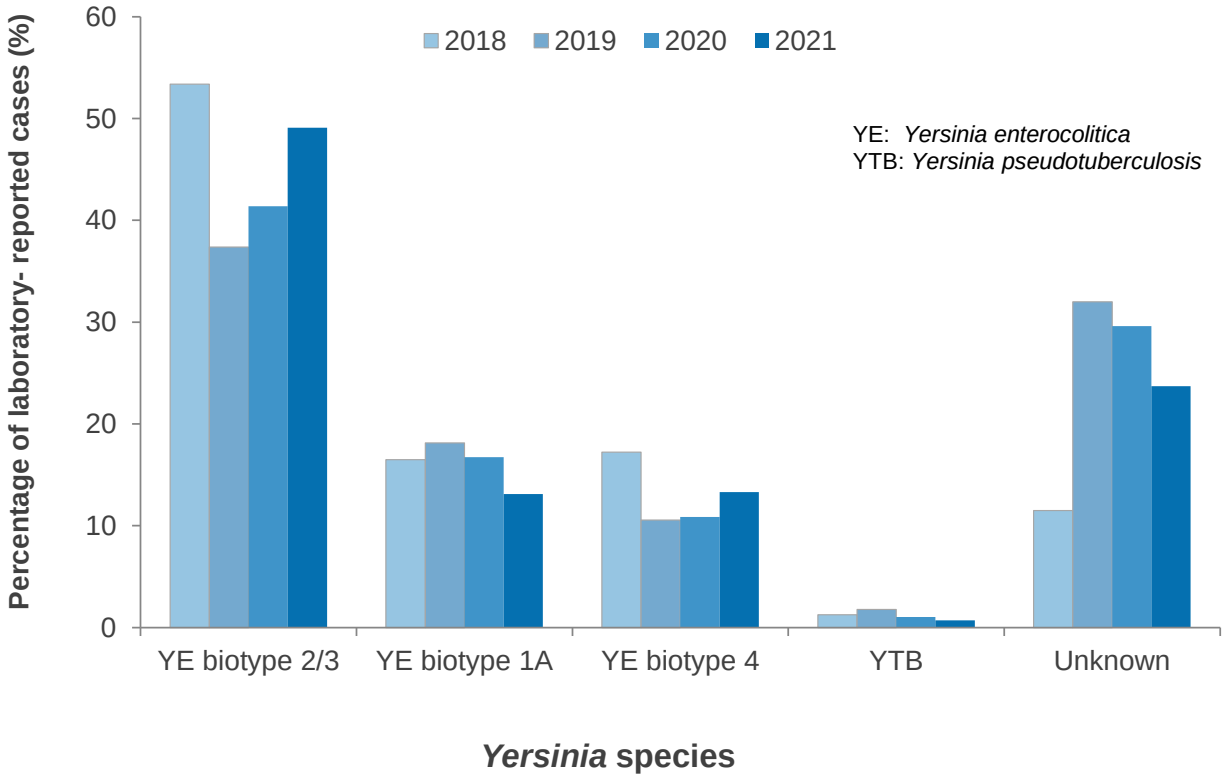
c) successful detection and identification of *Yersinia* spp. is influenced by the methods used by the laboratories. Newer nucleic acid-based (PCR) methods have not been shown to be more sensitive than the historical culture-based methods, but >50% of New Zealand samples are no longer being tested for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

Between 2018 and 2021, each year the largest proportion of cases was due to *Y. enterocolitica* (Table 71 and Figure 57). The most prevalent type of *Y. enterocolitica* has been biotype 2/3, serotype O:9 in each year since 2018. This type is associated with over 50% of the notified cases with typing information, and at least 38% of all cases. In the same time period (2018 to 2021), *Y. enterocolitica* biotype 1A accounted for between 13% and 18% of yersiniosis notifications and biotype 4 accounted for between 10% and 17% of annual yersiniosis notified cases.

Table 71. Annual number of notifications of different *Yersinia* spp. biotypes and serotypes identified by the Enteric Reference Laboratory, 2018–2021

Species	2018	2019	2020	2021
Yersinia enterocolitica	**1048**	**785**	**874**	**1066**
biotype 1A	**198**	**215**	**211**	**185**
serotype O:5	-	18	38	19
serotype O:8	-	18	38	35
biotype 2/3	**641**	**443**	**522**	**693**
serotype O:5, 27	43	16	40	26
serotype O:9	598	425	482	667
biotype 4	**207**	**125**	**137**	**187**
serotype O:3	207	125	137	187
biotype not identified	**2**	**2**	**4**	**1**
Yersinia pseudotuberculosis	**15**	**21**	**13**	**10**
Cases without typing information	**138**	**379**	**373**	**334**

Figure 57. Percentage of notified yersiniosis cases by species and biotype by year, 2018–2021



Recent surveys

Nil.

Relevant New Zealand studies and publications

Journal papers

Yersiniosis in New Zealand – Rivas et al. (2021)

Most human cases of yersiniosis are considered sporadic without an identifiable source [41]. Key restrictions in previous investigations included insufficient sensitivity for the isolation of *Yersinia* spp. from foods, although foodborne transmission is the most likely route of infection. In New Zealand, *Yersinia enterocolitica* has been isolated from a variety of sick and healthy domestic and farm animals but the pathways from zoonotic reservoir to human remain unproven.

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 2021, 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 overseas travel risk factor is reported.

Further information about notifiable diseases can be found in the *Notifiable Diseases in New Zealand: Annual Report* [18].

Laboratory-based surveillance

For a number of organisms (e.g. *Salmonella*, *Escherichia coli*), clinical laboratory isolates are forwarded to reference laboratories at ESR for confirmation and typing. The number of isolates forwarded differs by 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 general decrease in the number of isolate forward 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 [13]. 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

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 preparation of food was conducted. 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.

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 organism, 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. See analytical methods section for further details.

New Zealand Food Safety project reports and other publications

New Zealand Food Safety 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 New Zealand Food Safety 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 New Zealand Food Safety is the authority and expert in this area and the regulatory developments summarised in this report were confirmed with New Zealand Food Safety.

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 17 March 2022. Outbreak data contained in this report are based on information recorded as an outbreak in EpiSurv as at 12 May 2022. Changes made to EpiSurv data by PHU staff after these dates will not be reflected in this report. Consequently, future analyses of these data may produce revised results. Disease numbers are reported according to the date of notification.

Case status for notifications

All notifications recorded in EpiSurv that meet the case definitions [12] 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 2021 mid-year population estimates and are crude rates unless otherwise stated. At 30 June 2021, the New Zealand population was estimated to be 5,122,600. The population estimates for 2014 to 2020 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 2020 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

This report provides rates for current district health boards (DHBs). 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.

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 being 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 graphs, the historical mean is calculated from the previous three years' data (2018−2020). For seasonal graphs, the historical mean is calculated from the data based on the three years prior to the COVID-19 pandemic (2017-2019).

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APPENDIX B - LABORATORIES CHANGING TO PCR-BASED DETECTION OF ENTERIC PATHOGENS

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

An overview of when laboratories servicing different DHBs moved to PCR-based detection methods and which pathogens are included in the respective PCR panels is summarised in Table 72 below. In 2021 there were four different commercial panels used across New Zealand.

In 2021, Hawke's Bay, Northland, Waikato and Waitemata DHBs used separate hospital and community laboratories with differing testing methods for enteric pathogens.

Table 72. 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	X	X	X	X	X	X	X	X	X
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	X	X	X	Dec 2016	X	X	X	X	X
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 2022

[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 –NEW ZEALAND PUBLIC HEALTH MEASURES IN RESPONSE TO THE COVID-19 PANDEMIC

Table 73. New Zealand public health measures in response to the COVID-19 pandemic

Dates	Alert Level[a]	Public Health Measures
28 Feb 2020	-	First COVID-19 case reported in New Zealand
19 Mar 2020	-	Borders closed to all but New Zealand citizens and residents
22 Mar 2020	L2	4-tiered Alert Level system introduced
24 Mar 2020	L3	
26 Mar 2020	L4	Lockdown/self-isolation, State of National Emergency is declared
29 Mar 2020	L4	First COVID-19-related death reported in New Zealand
28 Apr 2020	L3	
14 May 2020	L2	State of National Emergency ends
9 Jun 2020	L1	No more acrive cases of COVID-19 in New Zealand
12 Aug 2020	L2, AKL L3	Four new COVID-19 cases are recorded in the community
31 Aug 2020	L2	
22 Sep 2020	L1, AKL L2	
8 Oct 2020	L1	
15 Feb 2021	L2, AKL L3	Three new cases are recorded in the community
17 Feb 2021	L1, AKL L2	
22 Feb 2021	L1	
28 Feb 2021	L2, AKL L3	
7 Mar 2021	L1, AKL L2	
12 Mar 2021	L1	
23 Jun 2021	L1, WEL L2	
29 Jun 2021	L1	
17 Aug 2021	L4	Nationwide lockdown
31 Aug 2021	L3, AKL & NOR L4	
2 Sep 2021	L3, AKL L4	
7 Sep 2021	L2, AKL L4	
21 Sep 2021	L2, AKL & HAU L3	
25 Sep 2021	L2, AKL L3	
3 Oct 2021	L2, AKL & parts of WAI L3	Some Alert Level 3 restricitons are gradually eased for AKL on Oct 5th and Oct 7th, WAI Alert Level 3 boundary extended on Oct 7th
8 Oct 2021	L2, AKL & NOR & parts of WAI L3	
19 Oct 2021	L2, AKL & parts of WAI L3	Some further easing of Alert Level 3 restriction is introduced on Oct 27th
2 Nov 2021	L2, AKL & NOR & parts of WAI L3	
11 Nov 2021	L2, AKL & parts of WAI L3	
16 Nov 2021	L2, AKL L3	
2 Dec 2021	-	All of New Zealand moves to the COVID-19 Protection Framework: The South Island and lower half of the North Island are at the 'Orange' setting, the upper North Island[b] are at the 'Red' setting.

[a] Alert levels applied to all of New Zealand unless stated otherwise

[b] Northland, Auckland, Taupō and Rotorua Lakes Districts, Kawerau, Whakatane, Ōpōtiki Districts, Gisborne District, Wairoa District, Rangitikei, Whanganui and Ruapehu Districts

L1, Alert Level 1 – prepare (COVID-19 is contained in New Zealand)

L2, Alert Level 2 – reduce (low risk of community transmission of COVID-19 within applied area)

L3, Alert Level 3 – restrict (medium risk of community transmission COVID-19 – active but managed clusters)

L4, Alert Level 4 – lockdown (likely COVID-19 is not contained)

AKL, Auckland; WEL, Wellington; NOR, Northland; HAU, Upper Hauraki; WAI, Waikato

Source: For details on the individual alert levels please refer to https://covid19.govt.nz/about-our-covid-19-response/history-of-the-covid-19-alert-system/#alert-levels

For details on the COVID-19 Traffic Light Protection Framework refer to https://covid19.govt.nz/traffic-lights/

APPENDIX D - SUMMARY TABLES

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

Table 74. Number of cases and rate per 100,000 population of selected notifiable diseases in New Zealand, 2020–2021

Disease	2020		2021	
	Cases	Rate	Cases	Rate
Campylobacteriosis	5292	104.0	5729	111.8
Cryptosporidiosis	735	14.4	702	13.7
Gastroenteritis[a]	358	7.0	244	4.8
Giardiasis	1139	22.4	1040	20.3
Hepatitis A	22	0.4	8	0.2
Listeriosis	35	0.7	32	0.6
Salmonellosis	709	13.9	714	13.9
Shigellosis	61	1.2	5	0.1
STEC infection	845	16.6	913	17.8
Yersiniosis	1260	24.8	1410	27.5

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

Note: Annual decreases of many enteric diseases may be due to COVID-19 related Alert Level periods and travel restrictions (fo more information see Introduction, page 5, and Appendix C, Table 73). Please also refer to individual sections for details relating to specific diseases.

Table 75. Deaths due to selected notifiable diseases recorded in EpiSurv, 2002–2021

Disease	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021
Campylobacteriosis	1	0	0	1	1	1	0	0	0	0	0	1	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]	1	0	0	0	0	0	0	0	0	0	0	0	2	0	1	0	0	0	1	0
Giardiasis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Listeriosis- nonperinatal	0	2	3	1	0	2	3	2	3	1	4	2	3	1	0	0	2	0	1	3
Listeriosis- perinatal	2	2	2	4	1	2	2	2	4	0	2	3	2	3	2	0	0	4	0	1
Salmonellosis	1	0	0	1	1	1	1	1	0	0	0	0	0	0	0	1	0	0	0	0
Shigellosis	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0
STEC infection	0	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0	2	0	0	0
Yersiniosis	0	0	1	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 [12]. 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 the primary cause of death. Information on deaths is most likely to be reported by Public Health Services when it occurs close to the time of notification and investigation.

Table 76. Ministry of Health hospitalisations data for selected notifiable diseases, 2019–2021

Disease	ICD 10 Codes	2019		2020		2021	
		Principal diagnosis	Other relevant diagnosis	Principal diagnosis	Other relevant diagnosis	Principal diagnosis	Other relevant diagnosis
Campylobacteriosis	A04.5	588	123	609	110	709	137
Cryptosporidiosis	A07.2	43	24	49	15	33	14
Giardiasis	A07.1	42	46	40	27	31	26
Hepatitis A	B15	31	44	17	40	9	31
Listeriosis	A32	22	24	19	19	19	19
Salmonellosis[a]	A02.0	206	27	138	27	182	35
Shigellosis	A03	45	21	15	24	7	19
STEC infection[b]	A04.3	28	23	17	22	24	19
Yersiniosis	A04.6	69	70	98	66	120	73

[a] *Salmonella* enterocolitis.

[b] Enterohaemorrhagic *Escherichia coli* infection.

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.

Table 77. Number of cases and rate per 100,000 population of selected notifiable diseases by ethnic group, 2021

Disease	Ethnic group[a]											
	Māori		Pacific peoples		Asian		MELAA		European or Other		Total[b]	
	Cases	Rate	Cases	Rate	Cases	Rate	Cases	Rate	Cases	Rate	Cases	Rate
Campylobacteriosis	631	73.9	140	40.5	359	46.1	63	84.5	4476	145.8	5729	111.8
Cryptosporidiosis	79	9.3	19	5.5	39	5.0	6	8.0	555	18.1	702	13.7
Gastroenteritis[c]	45	5.3	18	5.2	19	2.4	5	6.7	152	4.9	244	4.8
Giardiasis	120	14.1	8	2.3	60	7.7	11	14.7	832	27.1	1040	20.3
Hepatitis A	4	-	0	-	2	-	0	-	2	-	8	0.2
Listeriosis	5	0.6	2	-	7	0.9	0	-	18	0.6	32	0.6
Salmonellosis	108	12.7	30	8.7	73	9.4	6	8.0	493	16.1	714	13.9
Shigellosis	1	-	1	-	1	-	0	-	2	-	5	0.1
STEC infection	97	11.4	22	6.4	60	7.7	17	22.8	709	23.1	913	17.8
Yersiniosis	160	18.7	65	18.8	394	50.6	17	22.8	754	24.6	1410	27.5

[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] Total includes cases where ethnicity was unknown

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

Not all individual cases of acute gastroenteritis are notifiable, only those when: (i) the infected person is in a high-risk category (e.g. food handler, early childhood service worker, or another person with increased risk of spreading the disease), (ii) it is an infectious gastroenteritis of public health importance such as *C. perfringens, 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 [12]. 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.

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

Table 78. Number of cases and rate per 100,000 population of selected notifiable diseases by sex, 2021

Disease	Sex					
	Male		Female		Total[a]	
	Cases	Rate[b]	Cases	Rate	Cases	Rate
Campylobacteriosis	3222	126.7	2501	96.9	5729	111.8
Cryptosporidiosis	307	12.1	395	15.3	702	13.7
Gastroenteritis[b]	118	4.6	124	4.8	244	4.8
Giardiasis	519	20.4	519	20.1	1040	20.3
Hepatitis A	3	-	5	0.2	8	0.2
Listeriosis[c]	20	0.8	12	0.5	32	0.6
Salmonellosis	339	13.3	374	14.5	714	13.9
Shigellosis	4	-	1	-	5	0.1
STEC infection	437	17.2	476	18.4	913	17.8
Yersiniosis	723	28.4	687	26.6	1410	27. 5

[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 [12]. 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 perinatal cases are those for the mother, so the female cases will include all four perinatal cases

Note: Rate is not calculated for fewer than five cases

Table 79. Number of cases of selected notifiable diseases by age group, 2021

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	111	538	231	192	305	783	621	571	740	735	900	5729
Cryptosporidiosis	6	132	79	52	53	152	95	57	33	27	16	702
Gastroenteritis[b]	3	17	7	6	9	35	29	29	39	27	31	244
Giardiasis	19	214	70	14	13	102	217	131	97	120	42	1040
Hepatitis A	0	1	1	0	1	0	1	1	2	1	0	8
Listeriosis	0	0	0	0	0	2	2	3	6	4	15	32
Salmonellosis[c]	61	100	58	14	24	73	43	69	93	88	90	714
Shigellosis	0	0	1	0	1	1	0	0	0	1	1	5
STEC infection	46	163	58	43	47	92	75	58	90	88	153	913
Yersiniosis	85	184	62	44	44	167	210	147	157	152	158	1410

[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 [12]. 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 four perinatal cases are those for the mother.

Table 80. Rate per 100,000 population of selected notifiable diseases by age group, 2021

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	181.6	220.2	71.0	56.9	96.9	111.0	85.6	89.8	112.9	133.2	159.2	111.8
Cryptosporidiosis	9.8	54.0	24.3	15.4	16.8	21.6	13.1	9.0	5.0	4.9	2.8	13.7
Gastroenteritis[a]	-	7.0	2.2	1.8	2.9	5.0	4.0	4.6	6.0	4.9	5.5	4.8
Giardiasis	31.1	87.6	21.5	4.1	4.1	14.5	29.9	20.6	14.8	21.8	7.4	20.3
Hepatitis A	-	-	-	-	-	-	-	-	-	-	-	0.2
Listeriosis	-	-	-	-	-	-	-	-	0.9	-	2.7	0.6
Salmonellosis[c]	99.8	40.9	17.8	4.1	7.6	10.4	5.9	10.8	14.2	16.0	15.9	13.9
Shigellosis	-	-	-	-	-	-	-	-	-	-	-	0.1
STEC infection	75.2	66.7	17.8	12.7	14.9	13.0	10.3	9.1	13.7	16.0	27.1	17.8
Yersiniosis	139.0	75.3	19.0	13.0	14.0	23.7	29.0	23.1	24.0	27.6	27.9	27.5

[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 [12]. 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 four 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 81. Number of cases of selected notifiable diseases by District Health Board, 2021

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	281	683	422	475	572	123	253	69	253	251	77	250	146	261	110	188	69	594	153	499	5729
Cryptosporidiosis	32	54	51	38	116	15	19	7	63	15	14	42	13	32	7	10	5	47	24	98	702
Gastroenteritis[a]	22	9	12	9	19	5	27	0	0	2	0	2	19	32	4	14	1	40	3	24	244
Giardiasis	63	100	98	68	131	35	96	27	40	63	6	49	21	46	11	35	5	74	19	53	1040
Hepatitis A	0	0	2	0	1	0	1	0	0	1	0	3	0	0	0	0	0	0	0	0	8
Listeriosis	1	2	5	3	3	1	2	1	2	2	1	1	0	1	0	3	0	3	0	1	32
Salmonellosis	33	56	59	65	72	13	28	6	20	23	6	20	27	32	7	22	7	100	15	103	714
Shigellosis	0	1	2	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0	5
STEC infection	57	77	40	51	95	23	52	11	58	39	6	37	22	51	17	43	1	60	27	146	913
Yersiniosis	26	176	188	152	115	38	73	23	61	46	5	33	59	111	23	50	7	123	17	84	1410

[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 [12]. 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 82. Rate per 100,000 population of selected notifiable diseases by District Health Board, 2021

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	142.0	106.8	84.6	79.0	128.5	103.9	93.8	134.0	199.8	138.4	111.4	132.2	91.1	79.9	220.4	114.6	211.0	101.3	246.0	142.0	111.8
Cryptosporidiosis	16.2	8.4	10.2	6.3	26.1	12.7	7.0	13.6	49.8	8.3	20.3	22.2	8.1	9.8	14.0	6.1	15.3	8.0	38.6	27.9	13.7
Gastroenteritis[a]	11.1	1.4	2.4	1.5	4.3	4.2	10.0	-	-	-	-	-	11.9	9.8	-	8.5	-	6.8	-	6.8	4.8
Giardiasis	31.8	15.6	19.6	11.3	29.4	29.6	35.6	52.4	31.6	34.7	8.7	25.9	13.1	14.1	22.0	21.3	15.3	12.6	30.5	15.1	20.3
Hepatitis A	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0.2
Listeriosis	-	-	1.0	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0.6
Salmonellosis	16.7	8.8	11.8	10.8	16.2	11.0	10.4	11.7	15.8	12.7	8.7	10.6	16.8	9.8	14.0	13.4	21.4	17.1	24.1	29.3	13.9
Shigellosis	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0.1
STEC infection	28.8	12.0	8.0	8.5	21.3	19.4	19.3	21.4	45.8	21.5	8.7	19.6	13.7	15.6	34.1	26.2	-	10.2	43.4	41.5	17.8
Yersiniosis	13.1	27.5	37.7	25.3	25.8	32.1	27.1	44.7	48.2	25.4	7.2	17.5	36.8	34.0	46.1	30.5	21.4	21.0	27.3	23.9	27.5

[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 [12]. 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 gastroenterit

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 83. Number of cases of selected notifiable diseases by year, 1992–2021

Disease	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006
Campylobacteriosis	5144	8101	7714	7442	7635	8924	11,572	8161	8418	10,146	12,493	14,788	12,215	13,836	15,873
Cryptosporidiosis[a]	-	-	-	-	119	357	866	977	775	1208	975	817	611	888	737
Gastroenteritis[a b]	-	-	-	-	555	316	493	608	730	942	1088	1030	1362	559	926
Giardiasis[a]	-	-	-	-	1235	2127	2183	1792	1688	1604	1547	1570	1514	1231	1214
Hepatitis A	288	257	179	338	311	347	144	119	107	61	106	70	49	51	123
Listeriosis	16	11	8	13	10	35	17	19	22	18	19	24	26	20	19
Salmonellosis	1239	1340	1522	1334	1141	1177	2069	2077	1795	2417	1880	1401	1081	1382	1335
Shigellosis	124	128	185	191	167	117	122	147	115	157	112	87	140	183	102
STEC infection[b]	-	3	3	6	7	13	48	64	67	76	73	104	89	92	87
Yersiniosis[a]	-	-	-	-	330	488	546	503	396	429	472	436	407	383	453

Disease	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021
Campylobacteriosis	12,778	6692	7177	7346	6686	7016	6837	6782	6218	7457	6482	6957	6203	5289	5729
Cryptosporidiosis	924	765	854	954	610	877	1348	584	696	1062	1192	1613	1035	735	702
Gastroenteritis[b]	617	676	713	502	570	765	558	775	506	513	324	231	486	358	244
Giardiasis	1402	1660	1639	1985	1934	1714	1729	1709	1510	1616	1648	1585	1749	1141	1040
Hepatitis A	42	89	44	46	26	82	91	74	47	35	58	68	58	22	8
Listeriosis	26	27	28	23	26	25	19	25	26	36	21	30	31	34	32
Salmonellosis	1275	1337	1128	1146	1055	1081	1143	955	1051	1091	1127	1100	1188	708	714
Shigellosis	129	113	119	104	101	131	137	128	111	174	244	217	215	76	5
STEC infection	100	122	143	138	153	147	205	187	330	417	547	925	1103	844	913
Yersiniosis	502	508	430	406	513	514	483	680	634	858	917	1201	1185	1261	1410

[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 84. 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 (2021)	Australia[a] (2020)	USA[b] (2020)	Canada[d] (2019)	UK[e] (2019)	EU Total[e] (2020)	Other high
Campylobacteriosis	111.8	124.6	14.4	27.2	88.1	40.3	163.8 (Czech Republic)[f] 116.4 (Luxembourg)[f]
Cryptosporidiosis	13.7	9.6	4.3[c]	4.0	8.8[g]	4.4[g]	20.0 (Netherlands)[g] 12.8 (Ireland)[g]
Giardiasis	20.3	NN	5.8[c]	10.3	7.9[g]	5.5[g]	17.6 (Belgium)[g] 12.2 (Estonia)[g]
Hepatitis A	0.2	0.3	5.7[c]	1.0	0.8[g]	2.4[g]	25.0 (Slovakia)[g] 22.7 (Bulgaria)[g]
Listeriosis	0.6	0.2	0.2	0.46	0.23	0.42	1.7 (Finland)[f] 1.2 (Slovenia)[f]
Salmonellosis	13.9	47.5	13.3	15.6	14.6	13.7	98.4 (Czech Republic)[f] 62.1 (Slovakia)[f]
Shigellosis	0.1	6.3	3.1	2.4	3.1[g]	1.7[g]	4.7 (Slovakia)[g] 4.3 (Bulgaria)[g]
STEC infection	17.8	2.3	3.6	3.0	2.4	1.5	14.8 (Ireland)[f] 8.4 (Switzerland)[f]
Yersiniosis	27.5	NN	0.9	NN	0.2	1.8	7.1 (Denmark)[f] 7.0 (Finland)[f]

NN: Not notifiable

[a] The Australian National Notifiable Diseases Surveillance System (NNDSS) is currently being decommissioned and replaced by a new system. At the time of preparation of the current report notification rates for the 2021 year were not available

[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) http://dsol-smed.phac-aspc.gc.ca/dsol-smed/ndis/index-eng.php.

[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 2020 Zoonoses Report https://www.efsa.europa.eu/en/efsajournal/pub/6971

[g] European Centre for Disease Prevention and Control (ECDC). Annual epidemiological report on communicable diseases in Europe http://ecdc.europa.eu/en/publications/surveillance_reports/annual_epidemiological_report/Pages/epi_index.aspx (ECDC data presented here relate to the 2019 year for yersiniosis, the 2018 year for cryptosporidiosis, the 2017 year for giardiasis and shigellosis and the 2016 year for hepatitis A)

Table 85. Potential foodborne outbreaks and associated cases by pathogen/condition as reported in EpiSurv, 2021

Pathogen/Condition	Outbreaks (n = 40)		Cases (n = 465)	
	No.	%[c]	No.	%[d]
Norovirus infection [a]	6	15.0	171	36.8
Salmonellosis	5	12.5	90	19.4
Campylobacteriosis	5	12.5	15	3.2
Yersiniosis	3	7.5	24	5.2
V. parahaemolyticus gastroenteritis	2	5.0	28	6.0
Cryptosporidiosis	2	5.0	17	3.7
Clostridium perfringens intoxication	1	2.5	27	5.8
Sapovirus infection	1	2.5	11	2.4
Listeriosis	1	2.5	4	0.9
Histamine (scombroid) fish poisoning	1	2.5	2	0.4
Shigellosis	1	2.5	2	0.4
Giardia	1	2.5	2	0.4
Pathogen not identified [b, e]	12	30.0	88	18.9

Note: Two agents were reported in one outbreak, therefore percentage totals add to more than 100%

[a] For one norovirus outbreak, Yersinia was also reported (16 cases)

[b] One gastroenteritis outbreak with no identified pathogen and associated with a restaurant/café/bakery setting, had no cases numbers recorded in EpiSurv

[c] Percentage of outbreaks for each pathogen/condition, calculated using the total number of foodborne outbreaks (40). 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

[d] Percentage of cases for each pathogen/condition, calculated using the total number of associated cases (465)

[e] All enteric outbreaks with no pathogen identified in 2021 were recorded as gastroenteritis

Table 86. Potential foodborne outbreaks and associated cases by exposure setting as reported in EpiSurv, 2021

Exposure setting	Outbreaks (n = 40)		Cases (n = 465)	
	No.	%[a]	No.	%[b]
Commerical food operators	**18**	**45.0**	**199**	**42.8**
Restaurant/cafe/bakery	14	35.0	131	28.2
Other food outlet	3	7.5	66	14.2
Supermarket/delicatessan	1	2.5	2	0.4
Institutions	**5**	**12.5**	**160**	**34.4**
School	2	5.0	106	22.8
Prison	1	2.5	27	5.8
Long term care facility	1	2.5	16	3.4
Childcare centre	1	2.5	11	2.4
Other	**20**	**50.0**	**206**	**43.9**
Home	18	45.0	184	39.6
Community, church, sports gathering	2	5.0	20	4.3
Unknown	**1**	**2.5**	**2**	**0.4**

Note: Three outbreaks had both home and Restaurant/cafe/bakery exposure settings (24, 28 and 46 cases) and one outbreak had home and supermarket/delicatessen exposure settings (two cases)

One gastroenteritis outbreak with no identified pathogen and associated with a restaurant/café/bakery setting, had no cases numbers recorded in EpiSurv

[a] Percentage of outbreaks for each exposure setting, calculated using the total number of foodborne outbreaks (40). 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

[b] Percentage of cases for each exposure setting, calculated using the total number of associated cases (465)

Table 87. Potential foodborne outbreaks and associated cases by preparation setting as reported in EpiSurv, 2021

Preparation setting	Outbreaks (n = 40)		Cases (n =465)	
	No.	%[a]	No.	%[b]
Commerical food operators	**21**	**52.5**	**222**	**47.3**
Restaurant/cafe/bakery	14	35.0	131	28.2
Other food outlet	6	15.0	89	18.7
Supermarket/delicatessan	1	2.5	2	0.4
Institutions	**5**	**12.5**	**160**	**34.4**
School	2	5.0	106	22.8
Prison	1	2.5	27	5.8
Long term care facility	1	2.5	16	3.4
Childcare centre	1	2.5	11	2.4
Other	**16**	**40.0**	**181**	**38.9**
Home	15	37.5	163	35.1
Community, church, sports gathering	1	2.5	18	3.9
Unknown	**1**	**2.5**	**2**	**0.4**

Note: Three outbreaks had both home and Restaurant/cafe/bakery preparation settings (24, 28 and 46 cases)

One gastroenteritis outbreak with no identified pathogen and associated with a restaurant/café/bakery setting, had no cases numbers recorded in EpiSurv

[a] Percentage of outbreaks for each preparation setting, calculated using the total number of foodborne outbreaks (40). 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

[b] Percentage of cases for each implicated vehicle/source, calculated using the total number of associated cases (465)

Table 88. All non-O157 STEC serotypes identified from human isolates by the Enteric Reference Laboratory, 2017–2021

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 60), which are reported in the calendar year of their report date. This table also includes data relating to human isolates where the persons symptoms did not meet the case definition and the person would not become a notified case.

Serotype	2017	2018	2019	2020	2021
O1:H7	0	0	0	0	2
O2:H6	0	0	0	1	0
O2:H29	0	0	0	0	1
O3:H21	0	0	1	0	0
O5:H19	0	0	0	3	1
O5:HNT	0	0	8	13	12
O5:HNM	1	4	0	0	0
O6:H10	0	0	0	1	0
O6:H34	0	0	1	0	0
O6:HNM	0	1	0	0	0
O7:H14	0	0	0	0	1
O8:H7	1	0	0	0	0
O8:H9	0	1	0	1	1
O8:H16	0	0	0	2	1
O8/O30:H25	0	0	0	0	3
O8:HNM	1	1	0	0	0
O9:H2	1	0	0	0	0
O9:H30	0	0	0	0	1
O11:H25	0	0	0	1	0
O15:H2	0	1	2	3	2
O15:H14	1	0	0	0	0
O15:H16	0	0	1	0	0
O15:H21	1	0	0	0	0
O15:H27	0	0	1	1	0
O17:H18	0	0	2	1	1
O17/O106:H45	0	0	0	1	0
O18:H5	0	0	0	0	1
O18:H7	1	0	0	0	1
O20:HNM	1	0	0	0	0
O21:H2	0	0	0	0	1
O22:H16	1	0	1	0	1

Serotype	2017	2018	2019	2020	2021
O23:H8	0	0	1	0	0
O23:H39	1	0	0	0	0
O25:H4	0	0	1	0	0
O26:H8	0	0	1	0	0
O26:H11	44	76	119	121	131
O26:HNT	2	1	7	0	0
O26:HNM	4	1	0	0	0
O29:H4	0	1	0	0	0
O38:H26	7	19	27	33	27
O38:HNT	1	0	2	0	0
O41:H21	0	0	2	0	0
O43:H2	0	0	1	0	1
O45:H2	0	1	0	1	0
O45:H19	0	0	0	0	1
O51:H24	0	0	1	2	0
O53:H45	0	0	0	1	0
O55:H12	0	0	1	2	4
O55:HNT	0	0	0	0	0
O60:HNM	1	0	0	0	0
O61:H2	0	0	1	0	0
O63:H6	0	0	0	0	0
O64:H20	2	4	7	5	5
O65:H2	0	1	1	0	0
O66:H25	0	0	0	0	1
O69:H11	0	0	1	0	0
O71:H2	0	0	1	0	0
O74:H20	0	0	1	1	0
O75:H5	0	0	0	1	0
O75:H7	0	0	0	2	0
O75:H8	2	1	1	0	3
O75:HNT	0	1	0	0	0

Serotype	2017	2018	2019	2020	2021
O76:H19	1	0	1	0	2
O76:H21	0	1	0	0	0
O77:HNM	0	1	0	0	0
O78:H4	0	0	0	1	1
O78:HNT	1	0	0	0	0
O80:H2	1	0	0	0	0
O80:HNM	0	1	0	0	0
O81:H21	0	1	0	0	0
O82:H8	0	0	1	0	0
O83:H27	0	0	0	1	0
O84:H2	0	0	4	10	10
O84:HNM	6	2	0	0	0
O84:HNT	0	0	3	0	0
O85:H49	0	0	2	1	1
O87:H2	0	1	0	0	0
O87:H16	0	0	0	0	1
O88:H8	0	0	7	7	11
O88:HNT	1	2	2	0	0
O88:HNM	1	2	0	0	0
O91:H14	0	0	12	12	28
O91:H21	0	2	1	1	0
O91:HNM	2	5	0	0	0
O91:HNT	0	1	1	0	0
O93:H28	0	0	0	0	1
O93:H46	0	0	0	1	0
O99:H11, H35	0	0	1	0	0
O100:H20	0	0	1	0	0
O101:H19	0	1	0	0	0
O103:H2	3	7	11	0	20
O103:H25	1	4	12	1	5
O103:HNT	0	1	1	0	0
O103:HRough	0	1	0	0	0
O104:H7	0	1	1	1	5
O107:H7	1	0	0	0	0
O107/O117:H7	0	0	0	0	1
O108:H9	0	0	1	0	0
O108:H25	0	1	0	0	0
O111:H2	0	0	0	1	0

Serotype	2017	2018	2019	2020	2021
O111:H21	0	1	0	0	0
O111:HNM	2	3	0	0	0
O112:H8	0	0	1	0	0
O112:H9	0	0	4	5	7
O112:H19	0	0	1	0	0
O112:HNM	0	2	0	0	0
O113:H4	0	0	1	1	0
O113:H21	2	0	1	1	0
O114:HNT	0	0	1	0	0
O117:H4	0	2	3	1	1
O117:H7	1	2	7	4	1
O117:HNM	0	1	0	0	0
O118:H2	0	0	1	0	0
O119:H4	0	1	0	0	0
O121:H19	0	0	1	0	1
O123:H2	1	0	3	1	1
O123/O186:H2	0	2	0	0	0
O123:H10	0	0	2	11	4
O123/O186:H10	0	2	0	0	0
O123/O186:HNM	0	13	0	0	0
O124,O8:H19	0	0	0	0	1
O128:H2	7	22	55	79	82
O128:H8	0	0	1	0	0
O128:H45	0	1	0	0	0
O128:HNM	1	6	0	0	0
O128:HNT	1	1	3	0	0
O129:H21	0	0	0	0	1
O130:H11	1	1	4	11	8
O130:H23	1	0	0	0	0
O136:H16	0	1	0	0	0
O136:H20	0	0	0	1	0
O141:H2	0	0	1	0	0
O141:HNT	0	0	1	0	0
O144:H2	0	0	1	0	0
O145:H2	0	1	0	0	3
O145:HNT	0	0	0	0	1
O145:HNM	1	0	0	0	0
O146:H11	1	0	0	0	0

Serotype	2017	2018	2019	2020	2021
O146:H21	13	17	15	28	27
O146:H28	0	0	1	4	3
O146:HNM	3	2	0	0	0
O146:HNT	1	0	0	0	0
O148:H7	0	0	1	0	0
O148:H21	1	0	0	0	0
O149:H2	0	2	2	0	0
O152:H10	0	1	0	0	0
O152:H38	0	1	0	0	0
O153:H2	0	3	10	8	8
O153:H7	0	0	0	1	0
O153/O178:H7	0	0	0	0	1
O153:H21	0	0	0	1	1
O153/O178:H23	0	0	0	1	0
O153:HNT	2	0	1	0	0
O156:H19	1	0	0	0	0
O156:H25	0	0	2	0	1
O158:HNM	0	1	0	0	0
O159:H4	0	0	0	0	2
O159:HNT	0	0	1	0	0
O162:H10	0	1	0	0	0
O163:H19	0	1	7	1	11
O165:H7	0	0	0	2	2
O165:H25	0	0	0	1	2
O165:HNM	3	0	0	0	0
O165:HNT	0	0	2	0	0
O166:H15	0	0	1	0	0
O171:H2	0	1	1	1	0
O172:H25	0	0	0	1	0
O174:H8	1	4	10	10	14
O174:H21	0	1	5	7	1
O174:HNT	0	2	1	0	0
O174:HNM	0	3	0	0	0
O176:H4	0	0	12	16	14
O176:HNM	4	9	0	0	0
O176:HNT	0	0	4	0	0
O176:HRough	1	0	0	0	0
O177:H2	0	0	0	1	0

Serotype	2017	2018	2019	2020	2021
O177:H25	0	0	2	3	4
O177:HNM	1	1	0	0	0
O177:HNT	0	0	1	0	0
O178:H7	0	1	0	0	0
O179:H8	2	0	0	0	2
O179:H26	0	0	1	0	0
O181:H16	0	1	1	0	0
O182:H25	0	0	3	7	5
O182:HNM	2	2	0	0	0
O183:H18	0	0	3	1	1
O183:HNM	0	0	0	0	0
O186:H10	2	0	2	0	0
O186:HNM	4	0	0	0	0
O186:HNT	0	0	4	0	0
O187:H7	0	1	0	0	0
O187:H52	0	0	0	0	2
O188:H7	0	1	0	0	0
O188:H14	0	5	0	0	0
ONT:H1	0	0	1	0	0
ONT:H2	22	17	11	0	0
ONT:H4	0	2	0	0	0
ONT:H6	0	0	1	0	0
ONT:H7	7	6	6	0	0
ONT:H8	1	2	4	0	0
ONT:H9	1	2	1	0	0
ONT:H10	0	1	2	0	0
ONT:H11	1	2	0	0	0
ONT:H12	0	1	0	0	0
ONT:H14	2	1	1	0	0
ONT:H15	0	1	0	0	0
ONT:H18	0	0	2	0	0
ONT:H19	2	1	1	0	0
ONT:H20	0	2	0	0	0
ONT:H21	4	4	5	0	0
ONT:H25	0	0	4	1	0
ONT:H26	4	0	0	0	0
ONT:H27	1	1	0	0	0
ONT:H30	0	1	0	0	0

Serotype	2017	2018	2019	2020	2021
ONT:H31	1	1	0	0	0
ONT:H45	1	0	0	0	1
ONT:H49	0	0	1	0	1
ORough:H2	4	7	0	0	0
ORough:H5	0	1	0	0	0
ORough:H10	0	1	0	0	0
ORough:H19	0	2	0	0	0
ORough:H21	0	1	0	0	0
ORough:H25	1	0	0	0	0
ORough:H26	0	1	0	0	0
ORough:H45	0	1	0	0	0
Onovel1:H16	0	0	0	1	0
Onovel2:H49	0	0	0	0	1
Onovel5:H21	0	0	0	1	1
Onovel21:H14	0	0	2	0	4
Onovel27:H16	0	0	0	1	0
Onovel27:H21	0	0	1	0	0
Onovel32:H10	0	0	1	0	0

NM: Non-Motile. NT: Non-typable

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