New Zealand Food Safety
Haumaru Kai Aotearoa

Annual report concerning Foodborne Diseases in New Zealand 2019

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Cover Image: Computer-generated image of *Yersinia enterocolitica*.
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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 2019

ESR Report FW20013

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 notifications, case enquiries, outbreak investigations and other epidemiological studies of human enteric diseases.

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

The reduction of human cases of foodborne campylobacteriosis is a top priority for NZFS. The current performance target is a reduction of rates of foodborne campylobacteriosis by 10% from 88.4 in 2015 to 79.6 by the end 2020. Progress toward this target is reported in the section entitled Reporting against targets. The surveillance data indicates that during the last ten years the rates of foodborne campylobacteriosis are consistently, albeit slowly, decreasing. NZFS underscores that both total numbers of campylobacteriosis cases and rates per 100,000 population notified in 2019 are the lowest since 1992.

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. In 2019, about 78% of human faecal samples were tested using CIDT. However, different laboratories are using different CIDT and six DHBs continue to use culture-based testing methods for enteric pathogens. The implication of improved sensitivity and changes in number of tests is well described in the introduction to the 2019 report.

Shiga toxigenic *Escherichia coli* (STEC) remains a focus for NZFS. A continuing sharp increase in notification of STEC infections is evident, despite the absence of evidence that foodborne sources are increasing. The cause of this is likely to be related to implementation of CIDT and an increase in the number of faecal samples tested for STEC as all community faecal specimens are now screened for STEC.

The selection of diseases covered in the report is based on the potential of the disease to be caused by foodborne transmission and availability of national sources of information related to the disease. The enhanced analysis of risk factors and presentation of the information has resulted in an improved description of foodborne outbreaks in the 2019 report. Although, some outbreaks reported as foodborne with unidentified food source might be attributed to other routes of transmission, such as water, animal contact or person to person. NZFS and ESR will further continue to improve the analysis and presentation of foodborne human illness surveillance and investigation data in future reports.

Science for Communities

ANNUAL REPORT CONCERNING FOODBORNE DISEASE IN NEW ZEALAND 2019

Prepared for New Zealand Food Safety under
Project MRP/19/01 – Systematic reporting of epidemiology of potentially foodborne disease in New Zealand for year 2019,
as part of an overall contract for scientific services

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Disclaimer

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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 2019 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). There are a number of notifiable illnesses which may be caused by transmission of pathogens through foods*, but it is important to remember that most of the information concerns 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. Foodborne transmission is only one of the routes by which humans are exposed to pathogens; other routes include water, animal contact and person to person. There are a number of 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], 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] and published country-specific estimates, for the USA [3], Canada [4], Australia [5, 6], England and Wales [7] and the Netherlands [8] are given in Table 1. In addition, a WHO project to estimate the global burden of foodborne diseases derived estimates for 14 international regions [9, 10]. 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

* Note that water is not considered a food.

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

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

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

Hazard		Percentage foodborne (%)					
	New Zealand (2013)	WHO (2015)[a]	USA (2011)	Canada (2015)	Australia (2005, 2014)	England and Wales (2002)	Netherlands[b] (2008)
Bacteria							
Bacillus cereus	NE	100	100	99	100	100	90
Campylobacter spp.	64	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	30	40–60[d]	68	61	56[c,d]	63	40
STEC non-O157	34	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
Yersinia enterocolitica[e]	63	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 also collected opinions on the proportion of disease due to travel. A proportion of this will also be 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

[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 2019 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 2019 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 [11].

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 fish 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	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 [12]

For some conditions (intoxications from the bacteria *Bacillus cereus*, *Clostridium perfringens* and *Staphylococcus aureus*, ciguatera fish poisoning, histamine (scombroid) fish poisoning, and norovirus and sapovirus infections) not every case is notifiable; only those that are part of a common source outbreak or when the infected person is in a high risk category (e.g. food handler, early childhood service worker, etc.). Such cases are notified under the heading of acute gastroenteritis.

For some conditions (campylobacteriosis, listeriosis, salmonellosis, shiga toxin-producing *Escherichia coli* (STEC) infection, yersiniosis) the attribution of disease incidence to foodborne transmission was estimated by an expert consultation held on 5 June 2013 [2]. 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 two 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 illnesses and occasionally life threatening.

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, NZ diagnostic laboratories have started to introduce changes in enteric testing methods and screening criteria (Table 4). Traditional culture-based methods for enteric pathogens are gradually being replaced by culture-independent diagnostic tests (CIDT) using molecular techniques such as Polymerase Chain Reaction (PCR). All community faecal specimens in the affected DHBs are screened by multiplex PCR for *Campylobacter spp.*, *Shigella spp.*, *Salmonella spp.*, STEC, *Giardia* spp. and *Cryptosporidium spp.* unless noted otherwise. It is likely that the introduction of these more sensitive assays may have triggered an increase in notifications for some enteric diseases in these regions. With this gradual transition of diagnostic laboratories to CIDT for enteric pathogens, it is difficult to determine if a trend is due to a change in illness rate, change in sensitivity of the method, or a combination of the two. Along the same lines a decrease in disease rate as based on culture derived methods may be masked by the increased sensitivity of CIDT. The move towards CIDT for enteric pathogens is likely to have some impact on notification rates for all the affected enteric pathogens. However, the greatest impact is likely to be for STEC and *Shigella*, where there are marked differences between the sensitivity of CIDT compared with traditional culture-based methodology. The number of samples tested effectively increased for some diseases, as outlined below, and this may also impact on the numbers of positive results and subsequently notification rates.

All community faecal specimens in the DHBs listed below (Table 4) are now screened for STEC, when previously only specimens from patients with certain epidemiological or clinical criteria were tested, e.g. aged less than 5 years of age, presence of haemolytic uraemic syndrome (HUS), or bloody diarrhoea recorded. This has led to an increase in the number of faecal samples tested for STEC. Where STEC is detected by screening PCR, specimens are referred to the reference laboratory at ESR to obtain a STEC culture for serotyping.

Also most community faecal specimens are now screened for *Giardia* spp. and *Cryptosporidium* spp. where previously only those specimens where parasite screening was requested were tested. However, several laboratories have not moved to PCR for *Giardia* and *Cryptosporidium* (as per table), continuing with EIA and selective testing.

Different laboratories are using different CIDT, i.e. panels developed by different companies which may not incorporate all the same target organisms. For example, this will lead to some laboratories routinely testing all faecal samples for *V. parahaemolyticus* whereas other laboratories are still only testing for this organism when specifically requested or where certain clinical criteria are present on the request form.

Several DHBs continue to use separate hospital and community laboratories, with differing testing methods for enteric pathogens. All information is summarised in Table 4 below. The current assumption is that the majority of diagnostic laboratories will have transitioned to CIDT for enteric pathogens by 2020. In 2019, about 78% of faecal samples were tested using CIDT.

Table 4. Changes in laboratory testing methods

District Health Board	Change to CIDT[a]		Comment
	Hospital	Community	
Auckland	July 2017	July 2015	June 2017, community lab included *Y. enterocolitica, Vibrio, Entamoeba histolytica*
Bay of Plenty	November 2018	November 2018	*Giardia* and *Cryptosporidium* still tested by EIA
Canterbury	n/a	n/a	
Capital & Coast	January 2018	January 2018	
Counties Manukau	November 2015	July 2015	
Hawke's Bay	n/a	January 2018	
Hutt Valley	January 2018	January 2018	
Lakes	November 2018	November 2018	*Giardia* and *Cryptosporidium* still tested by EIA
MidCentral	n/a	n/a	
Nelson Marlborough	January 2018	January 2018	
Northland	n/a	July 2015	June 2017, community lab included *Y. enterocolitica, Vibrio, Entamoeba histolytica*
South Canterbury	n/a	n/a	
Southern	January 2017	January 2017	
Tairawhiti	n/a	n/a	
Taranaki	n/a	February 2020	
Waikato	n/a	November 2018	*Giardia* and *Cryptosporidium* still tested by EIA
Wairarapa	January 2018	January 2018	
Waitemata	n/a	July 2015	June 2017, community lab included *Y. enterocolitica, Vibrio, Entamoeba histolytica*
West Coast	n/a	n/a	
Whanganui	n/a	n/a	

Data source: New Zealand Microbiology Network CIDT survey, personal communication, March 2020

CIDT = Culture-independent diagnostic tests, EIA = enzyme immunoassay, n/a = not applicable (In 2019 laboratories serving these DHBs were still using traditional culture-dependent methods)

[a] All community faecal specimens in these DHBs are screened by multiplex PCR for *Campylobacter, Shigella, Salmonella*, STEC, *Giardia* and *Cryptosporidium* unless noted otherwise

REPORTING

SUMMARY OF MAIN FOODBORNE DISEASES

The incidence of the main foodborne diseases is summarised for 2019 in Table 5 below.

Table 5. Estimated proportion and incidence of the main foodborne diseases for 2019

	Total notified		Estimated foodborne transmission[a]		
	Cases	Rate[b]	Cases	Proportion (%)[c]	Rate[d]
Campylobacteriosis	6202	126.1	3394	63.8 (44.1-83.2)	69.0 (47.7-90.0)
Cryptosporidiosis	1035	21.0	NE	-	-
Giardiasis	1749	35.6	NE	-	-
Hepatitis A	58	1.2	NE	-	-
Listeriosis	31	0.6	26	87.8 (57.9-98.5)	0.5 (0.3-0.6)
Salmonellosis	1188	24.2	484	62.1 (35.2-86.4)	9.8 (5.6-13.7)
Shigellosis	222	4.5	NE	-	
STEC infection	1101	22.4	331	34.0 (3.5-63.5)[e]	6.7 (0.7-12.6)
Yersiniosis	1186	24.1	680	63.2 (29.0-91.5)	13.8 (6.3-20.0)

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

[a] For estimation of food-related cases the proportions derived from expert consultation [2] exclude travel-related cases

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

[c] Most likely (95th percentile credible interval) estimates of proportion foodborne, from expert consultation

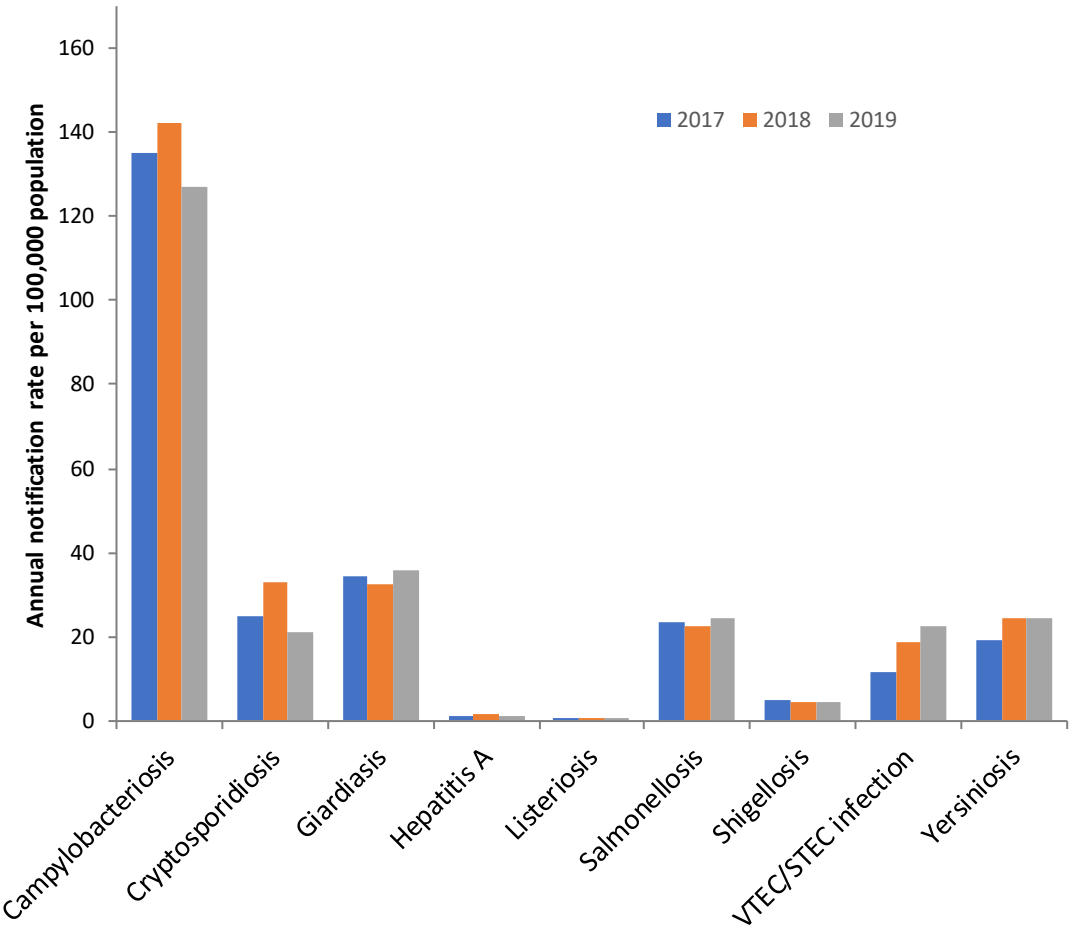
[d] Most likely (95th percentile credible interval) estimates of foodborne rate

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

In 2019, a continued increase in notification rates was apparent for STEC infection compared to 2017 and 2018; yersiniosis, salmonellosis and shigellosis notification rates were similar to previous year (Figure 1). Campylobacteriosis and cryptosporidiosis notifications have decreased compared to the previous two years.

The increase in STEC notifications might be due to additional laboratories changing their methodology to molecular methods and to the increased numbers of specimens routinely being tested (see section on Changes in laboratory testing methodology).

Figure 1. Notification rates of the main foodborne diseases, 2017–2019



Reporting against targets

The performance targets for potentially foodborne diseases come under scrutiny by New Zealand Food Safety on an annual basis. In 2015, the predecessor to New Zealand Food Safety at MPI established a new performance target for campylobacteriosis to reduce the number of human cases of foodborne campylobacteriosis by 10% from 88.4 to 79.6 per 100,000 per head of population by the end of 2020.

Rationale

Campylobacteriosis is the most commonly notified potentially foodborne disease in New Zealand.

Specific targets for salmonellosis and listeriosis were removed from 2015 onwards and the monitoring and review of these two pathogens in relation to any foodborne illness in New Zealand is now covered by core business activities within New Zealand Food Safety. There continues to be very little evidence of any significant ongoing foodborne illness associated with these pathogens that warrants application of a specific target.

A performance target for foodborne illness due to STEC infections is not included as there has been little association of STEC with foodborne outbreaks in New Zealand. Norovirus is also not incorporated at this stage because of the large fluctuations that occur in annual statistics (norovirus infection is not a notifiable disease but may be notified as acute gastroenteritis during investigation of a common source outbreak) and the major transmission route for norovirus is via the person-to-person pathway. The major transmission route for norovirus is outside the influence of New Zealand Food Safety.

New Zealand Food Safety continues to closely monitor sources and potential pathways that are most often (albeit weakly) associated with foodborne illness in New Zealand.

Methodology, tools and reporting

Historical baseline data on the number of reported 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) [13]. New Zealand Food Safety supports additional projects to increase the quality of data and has funded surveillance projects that provide primary information on food attribution such as the advanced attribution study of human campylobacteriosis cases conducted by Massey University and Mid-Central Health within the Manawatu.

The measurement is adjusted for the proportion of cases reported as having travelled overseas during the likely incubation period. It is adjusted also for the proportion of disease estimated to be due to foodborne transmission. In the event of very large outbreaks of campylobacteriosis (>300 notified cases) with a confirmed non-food cause, these cases will also be subtracted from the total number of cases before calculation of the target metric. Estimates for the proportion of disease due to foodborne transmission were revised in 2013, through an expert elicitation process [2]. The new estimates differ slightly from those used previously and have been applied retrospectively to all disease rate estimates presented in this section.

The annual incidence of campylobacteriosis is reported in terms of calendar year totals of cases per 100,000 population (*Notifiable Diseases in New Zealand Annual Report,* ESR) [13]. This allows for demographic changes within the New Zealand population to be appropriately captured. The proportion of infections acquired overseas is estimated through the EpiSurv programme administered by ESR and MoH*.

Campylobacteriosis

Performance target

- Campylobacteriosis: The number of human cases of foodborne campylobacteriosis reduced by 10% from 88.4 to 79.6 per 100,000 population by the end 2020.

Measurement

The measurement used is the annual (calendar year) rate (per 100,000 mid-year population estimate) of notified cases of human foodborne campylobacteriosis, with the baseline being the average foodborne rate for 2012 to 2014 (88.4 cases per 100,000 mid-year population). The estimated incidence of foodborne campylobacteriosis in 2019 is given in Table 6.

Table 6. Estimated proportion and incidence of foodborne campylobacteriosis for 2019

	Cases	Proportion (%)	Rate (per 100,000, mid-year estimated population)
Total notified	6202	-	126.1
Estimated not related to overseas travel[a]	5320	85.8	108.2
Estimated foodborne transmission	3394	63.8 (44.1-83.2)[b]	69.0 (47.7-90.0)[c]

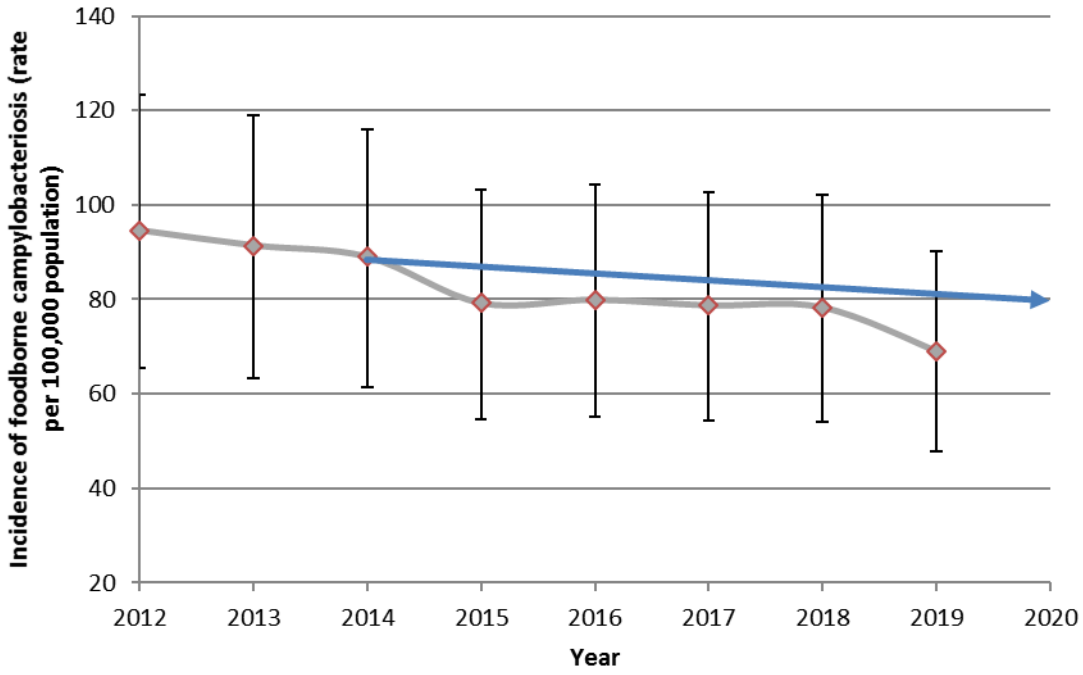
[a] The estimated percentage of cases relating to overseas travel is 14.2%
[b] Most likely (95th percentile credible interval) estimates of proportion foodborne, from expert consultation
[c] Most likely (95th percentile credible interval) estimates of foodborne rate

* Assuming that the cases for which travel information was provided are representative of all cases, a Poisson distribution can be used to estimate the total number of potentially travel related cases.

Presentation

The trend in relative rates (most likely estimates) compared with the 2014 to 2020 goal is shown in Figure 2. The estimated foodborne rates for 2012 to 2019 are calculated using the estimates of the proportion foodborne from the expert consultation in 2013.

Figure 2. Incidence of foodborne campylobacteriosis



The blue arrowed line represents the target for 2014 to 2020

Note: In 2020, New Zealand Food Safety introduced the next goal of reducing human foodborne campylobacteriosis in New Zealand by 20% by the end of 2025*.

* https://www.mpi.govt.nz/food-safety/food-safety-and-suitability-research/managing-the-risk-of-campylobacter/ (Accessed 31st July 2020)

Incidence and severity of selected foodborne conditions

This section includes a summary of the overall 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 examination has been performed.

These data are followed by contextual information on the foodborne proportion of the overall incidence of illness. This section will include information on the following topics, where available:

- statement of estimated foodborne percentage and range provided by an expert elicitation process conducted in 2013 [2]. 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), where it is available and informative about foodborne disease;
- comments on specific food related incidents or outbreaks of the condition that were reported to the notification system during the calendar year;
- studies on 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 as a result of surveys conducted during the calendar year; and,
- 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 district health board (DHB) of the place of residence.

Because of the low numbers of cases for some foodborne illnesses such as listeriosis, conditions and age groups, etc. 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 cases reported in 2019 by data source

During 2019, no cases of *B. cereus* intoxication were reported in Episurv. Note that not every case of *B. cereus* intoxication is necessarily notifiable; only those where there is a suspected common source.

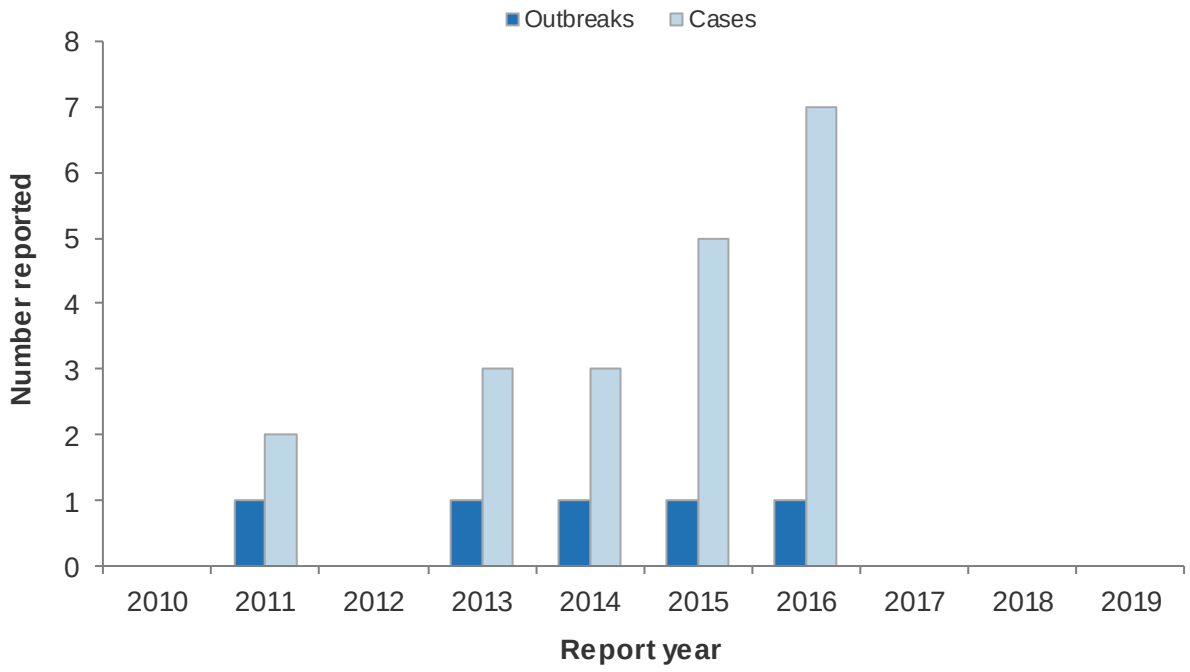
The ICD-10 code A05.4 was used to extract foodborne *B. cereus* intoxication hospitalisation data from the MoH National Minimum Dataset (NMDS). There were no hospital admissions recorded in 2019 with *B. cereus* intoxication as the diagnosis.

Expert consultation estimated that 97% (minimum = 90%, maximum = 100%) of *B. cereus* intoxication will be due to foodborne transmission [14]. The expert consultation also estimated that approximately 60% of the foodborne transmission would be due to consumption of rice.

Outbreaks reported as caused by *Bacillus cereus*

Since 2016, no *B. cereus* intoxication outbreaks have been reported in EpiSurv. Outbreaks of *B. cereus* intoxication are rare, with only five outbreaks reported since 2010. The number of cases associated with the outbreaks ranged between two and seven cases (Figure 3).

Figure 3. *Bacillus cereus* intoxication outbreaks and associated cases reported by year, 2010–2019



Recent surveys

Nil.

Relevant New Zealand studies and publications

Nil.

Relevant regulatory developments

Nil.

Campylobacteriosis

Summary data for campylobacteriosis in 2019 are given in Table 7.

Table 7. Summary of surveillance data for campylobacteriosis, 2019

Parameter	Value in 2019	Source
Number of notified cases	6202	EpiSurv
Notification rate (per 100,000)	126.1	EpiSurv
Hospitalisations[a]	702	MoH NMDS
Deaths	0	EpiSurv
Estimated travel-related cases (%)[b]	882 (14%)	EpiSurv
Estimated food-related cases (%)[c]	3394 (64%)	Expert consultation

[a] Cases hospitalised may not be notified on EpiSurv
[b] Percentage of the number of notified cases
[c] For estimation of food-related cases the proportions derived from expert consultation [2] 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

Since 2015 laboratories across New Zealand have gradually changed the methodology for testing faecal specimens. In 2019, community faecal specimens in all DHBs with the exception of Canterbury, MidCentral, South Canterbury, Tairawhiti, Taranaki, West Coast and Whanganui were screened by multiplex PCR for a range of pathogens, including *Campylobacter* spp.. The introduction of these more sensitive assays may have triggered an increase in notifications for some enteric diseases. It is unclear at this stage how laboratory changes have affected the notification rates for campylobacteriosis as a decrease in disease rate may be masked by the increased sensitivity of the PCR methodology.

Campylobacteriosis cases reported in 2019 by data source

During 2019, 6202 cases (126.1 per 100,000 population) of campylobacteriosis and no resulting deaths were reported in Episurv. Approximately 9% of cases notified in EpiSurv were recorded as hospitalised in 2019.

The ICD-10 code A04.5 was used to extract campylobacteriosis hospitalisation data from the NMDS database. Of the 702 hospital admissions (14.3 admissions per 100,000 population) recorded in 2019, 582 cases were reported with campylobacteriosis as the primary diagnosis and 120 were reported with campylobacteriosis as another relevant diagnosis.

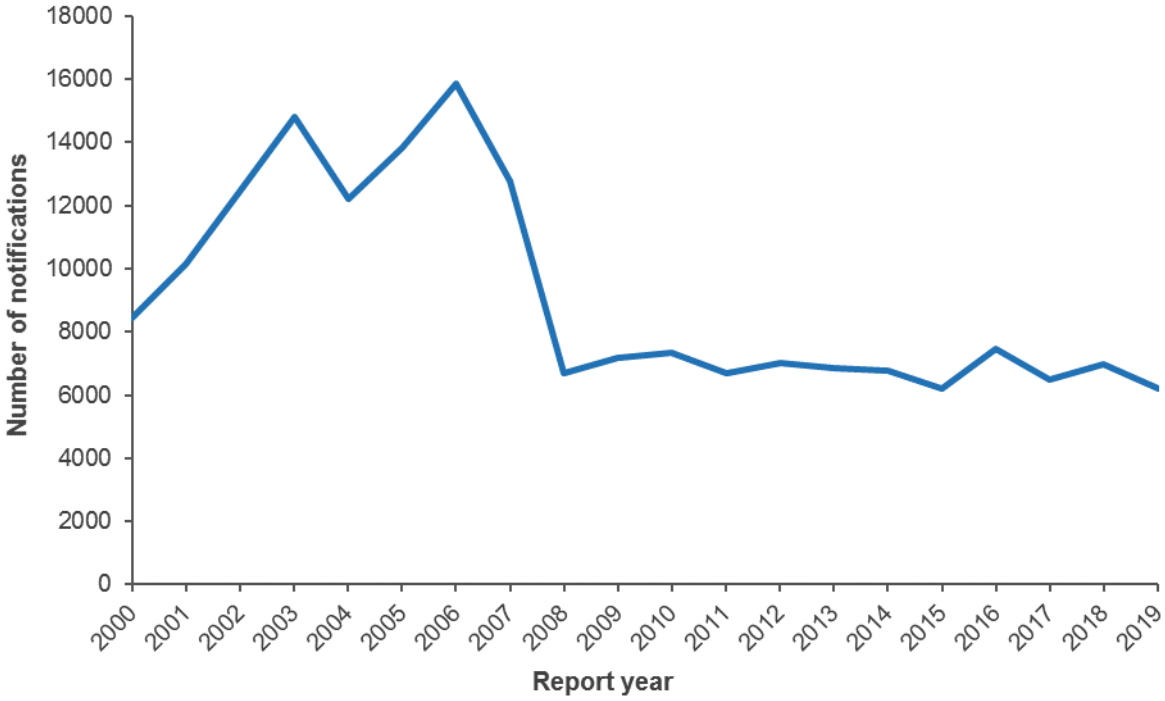
It has been estimated by expert consultation that 63.8% (95th percentile credible interval: 44.1%–83.2%) of campylobacteriosis incidence is due to foodborne transmission [2]. It was further estimated that 75.4% of foodborne transmission would be due to transmission via poultry.

Notifiable disease data

The number of campylobacteriosis notifications reported each year generally increased from 1997, up to the highest number recorded in 2006 (15,873 cases). During 2007 and 2008, there was a significant decrease in the number of cases reported (Figure 4). The number and rate of notifications each year has remained stable from 2008 to 2019, with the exception of 2016, due to an outbreak in Hawke's Bay attributed to contaminated drinking water [15] (Figure 4 and Figure 5).

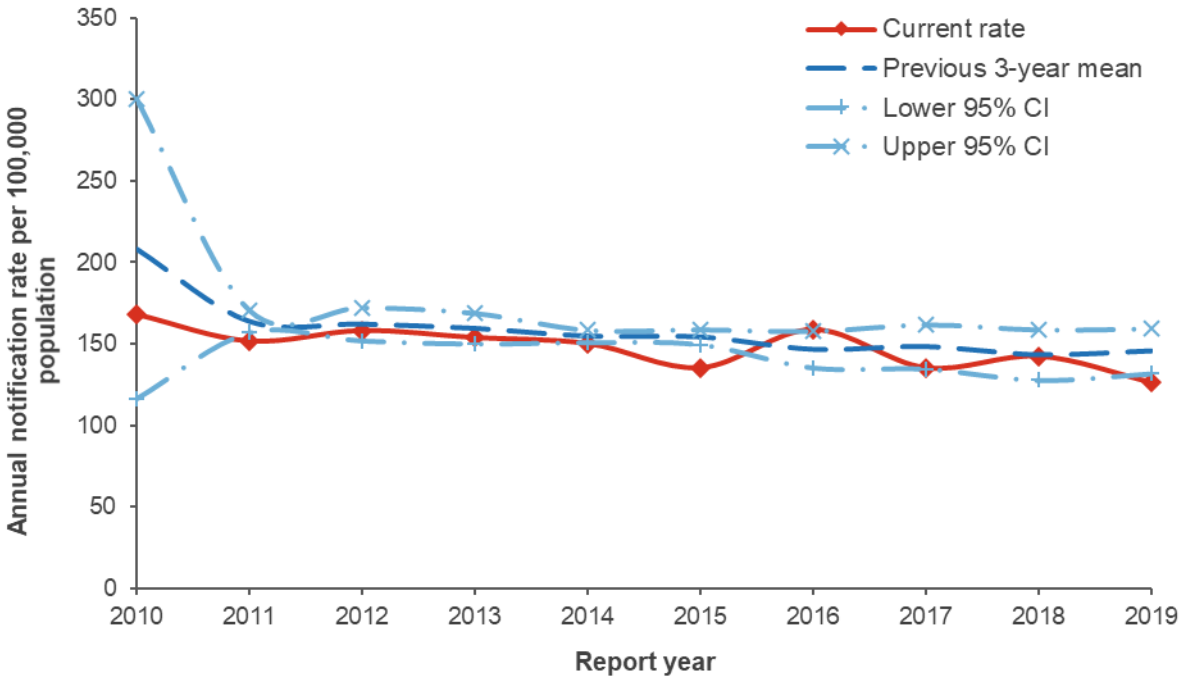
The annual campylobacteriosis rate in 2019 is the lowest rate observed in the period 2000 to 2019.

Figure 4. Campylobacteriosis notifications by year, 2000–2019



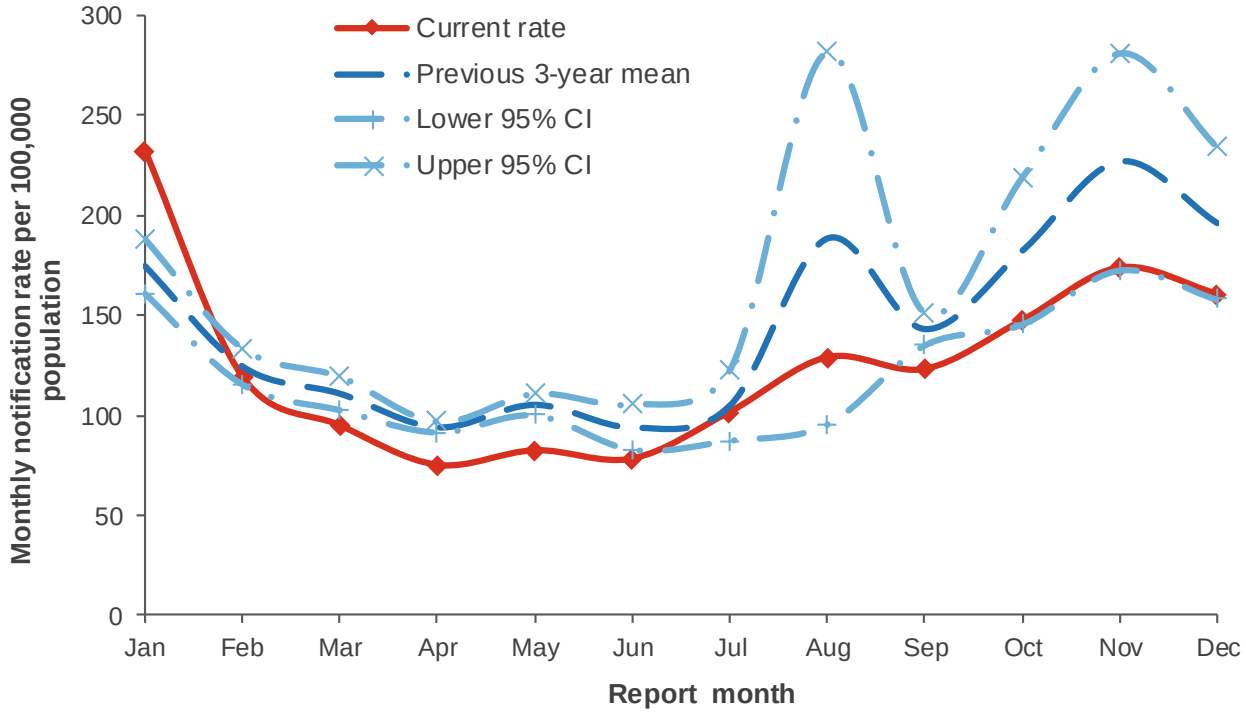
The campylobacteriosis annual rate trend (Figure 5) was very similar to the corresponding annual notification trend (Figure 4); with the notification rate remaining stable between 2010 and 2019. The notification rate was significantly higher in 2016 (158.9 cases per 100,000 population) than the previous three-year average (146.5 cases per 100,000), due to one outbreak in Hawke's Bay attributed to contaminated drinking water [15].

Figure 5. Campylobacteriosis notification rate by year, 2010–2019



The number of notified cases of campylobacteriosis per 100,000 population by month for 2019 is shown in Figure 6. The monthly number of notifications in 2019 ranged from 306 notifications (April) to 951 notifications (January). In 2019, the lowest notification rates occurred between March and July. Rates by month followed a similar pattern as seen in 2017 and 2018. The current previous three-year mean is influenced by an outbreak in Hawke's Bay in 2016 attributed to contaminated drinking water [15]. The actual outbreak occurred in August 2016, however a number of notifications were not reported in EpiSurv until November, resulting in a second peak in reported notifications seen in November 2016.

Figure 6. Campylobacteriosis monthly rate (annualised), 2019



In 2019, the rate of notifications and hospitalisations for campylobacteriosis was higher for males (146.7 and 16.2 per 100,000 population) compared with females (106.1 and 12.5 per 100,000 population) (Table 8).

Table 8. Campylobacteriosis cases by sex, 2019

Sex	EpiSurv notifications		Hospitalisations[a]	
	No.	Rate[b]	No.	Rate[b]
Male	3550	146.7	391	16.2
Female	2650	106.1	311	12.5
Total[c]	**6202**	**126.1**	**702**	**14.3**

[a] MoH NMDS data for hospital admissions

[b] per 100,000 population

[c] total includes notifications where gender is unknown

The highest age-specific notification rates for campylobacteriosis in 2019 were reported for children aged 1 to 4 years (242.7 per 100,000 population, 597 cases) and infants aged less than 1 year (214.6 per 100,000 population, 128 cases). The highest hospitalisation rates were for the 70 years and over age group (41.5 admissions per 100,000 population) and infants aged less than 1 year (26.8 admissions per 100,000 population) (Table 9).

Table 9. Campylobacteriosis cases by age group, 2019

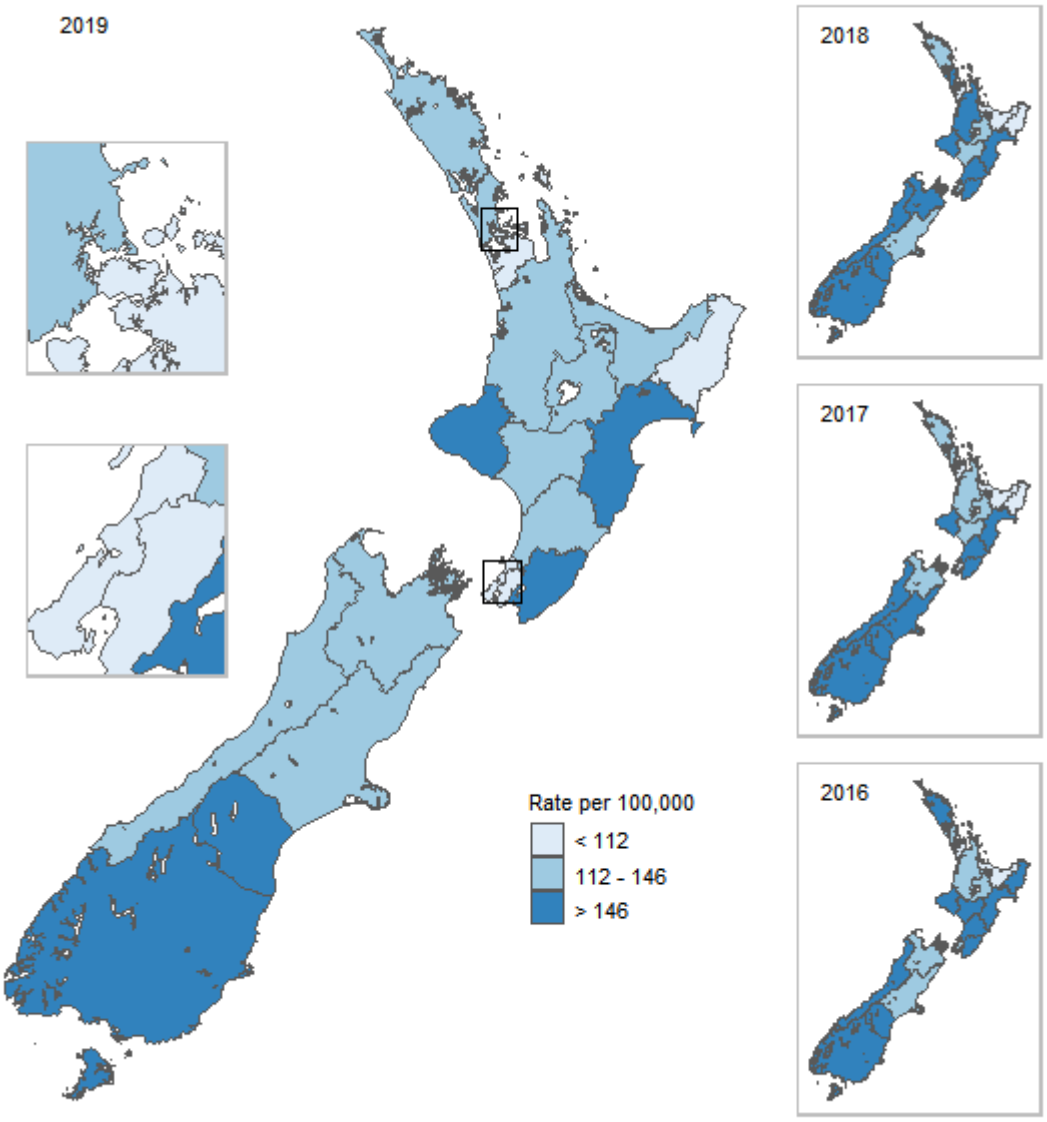
Age group (years)	EpiSurv notifications		Hospitalisations[a]	
	No.	Rate[b]	No.	Rate[b]
<1	128	214.6	16	26.8
1 to 4	597	242.7	29	11.8
5 to 9	269	81.6	16	4.9
10 to 14	219	67.8	14	4.3
15 to 19	324	102.6	26	8.2
20 to 29	865	124.1	91	13.1
30 to 39	667	102.8	60	9.2
40 to 49	660	106.3	51	8.2
50 to 59	809	128.6	77	12.2
60 to 69	804	154.7	103	19.8
70+	860	162.9	219	41.5
Total	**6202**	**126.1**	**702**	**14.3**

[a] MoH NMDS data for hospital admissions

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

Campylobacteriosis rates varied throughout the country in 2019 as shown in Figure 7. In the South Island, the highest rates of campylobacteriosis were reported for South Canterbury DHB (232.4 per 100,000 population, 142 cases) and Southern DHB (158.0 per 100,000 population, 536 cases). In the North Island, Wairarapa DHB (226.9 per 100,000, 108 cases) had the highest rate, followed by Taranaki DHB (181.6 per 100,000, 223 cases). The lowest rate in New Zealand was reported for Counties Manukau DHB (86.3 per 100,000, 487 cases). Southern, South Canterbury, Wairarapa, Taranaki and Hawke's Bay DHBs have consistently been in the highest quantile of notification rates in the last four years.

Figure 7. Geographic distribution of campylobacteriosis notifications, 2016–2019



Note: Since 2015 laboratories across New Zealand have gradually changed the methodology for testing faecal specimens. It is unclear at this stage how laboratory changes have affected the notification rates for campylobacteriosis. Refer to text for details.

For cases where information on travel was provided in 2019, 14% had travelled overseas during the incubation period. Assuming that the cases for which travel information was provided were representative of all campylobacteriosis cases, a Poisson distribution can be used to estimate the total number of potentially travel-related cases of campylobacteriosis in 2019. The resultant distribution has a mean of 882 cases (95% CI 825-942).

If data from the last four years are considered the estimated proportion of cases travelling overseas within the incubation period of the organism was 12% (95% CI 11.0-13%).

Outbreaks reported as caused by *Campylobacter* spp.

In 2019, there were 20 campylobacteriosis outbreak notifications in EpiSurv, eight (40%) of which recorded food as a possible mode of transmission (Table 10). It is important to note that a single outbreak may have multiple pathogens, settings and possible modes of transmission,

Table 10. Campylobacteriosis outbreaks reported, 2019

Measure	Campylobacteriosis outbreaks		
	Possible foodborne transmission with a suspected or confirmed source	Possible foodborne transmission but no suspected source	All
Outbreaks	7	1	20
Cases	79	2	156
Hospitalised Cases	3	0	5

Table 11 contains details of the eight campylobacteriosis outbreaks reported in 2019 with food as a possible mode of transmission.

Table 11. Details of campylobacteriosis outbreaks with food reported as a possible mode of transmission, 2019

PHU	Month	Suspected source	Evidence	Setting	No. ill
MidCentral	Mar	Raw milk	Consumption of milk from same source	Camp	1C 3P
South	Apr	Raw milk	Consumption of milk from same source	Home	2C
Toi Te Ora	Jul	Re-heated rice	Consumption of same food type	Long term care facility	2C
Toi Te Ora	Aug	Raw Milk	Consumption of milk from same source	Home	3C
Regional	Aug	Lamb's fry/liver and bacon	Consumption of same food type	Restaurant/cafe/bakery	3C
Auckland	Sep	Unknown	Household cluster	-	1C 1P
Waikato	Dec	Hot and cold chicken meals, food also being hoarded in rooms	Increase in disease incidence, common meals	Prison	4C 58P
Auckland	Dec	Chicken liver pâté	Common meal	Restaurant/cafe/bakery	3C

PHU MidCentral: MidCentral Public Health Service, South: Public Health South, Toi Te Ora: Toi Te Ora - Public Health, Regional: Regional Public Health, Auckland: Auckland Regional Public Health Service, Waikato: Population Health Service Waikato

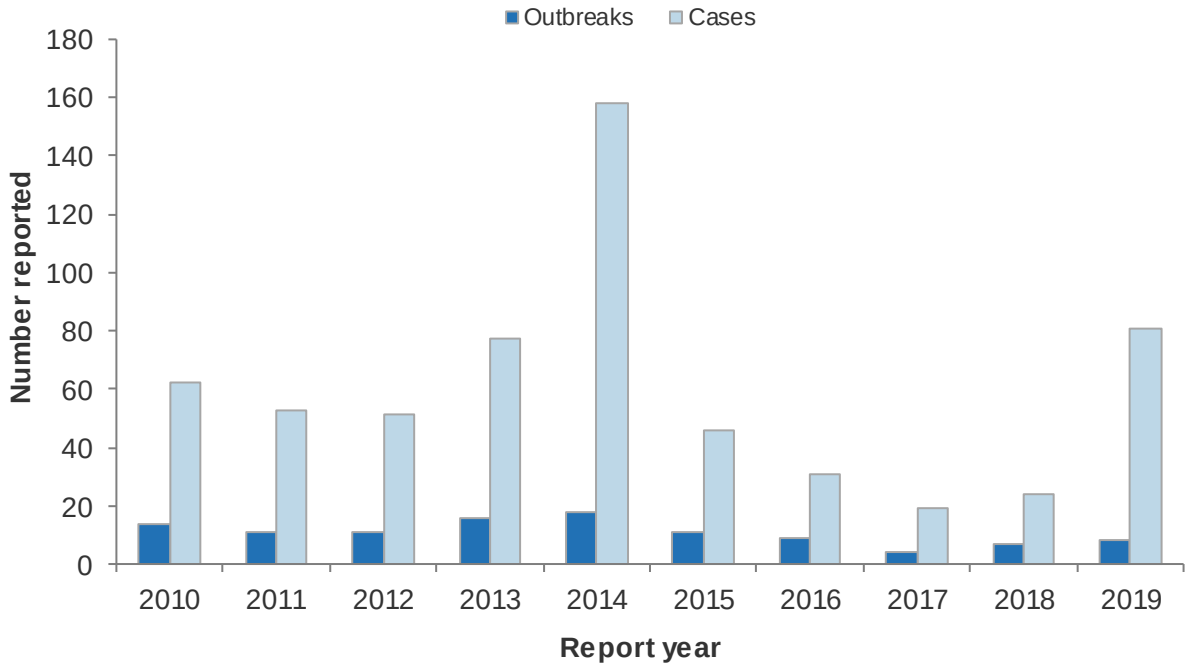
Number ill: C: confirmed, P: probable

Of the eight outbreaks and 81 associated cases where food was identified as a possible mode of transmission (Table 11), three cases were hospitalised from one outbreak at a Waikato Prison. For two outbreaks additional pathogens were implicated; STEC in the Toi Te Ora outbreak in August and *Yersinia* spp. in the Waikato outbreak in December.

Campylobacteriosis outbreaks accounted for 4.0% (20/499) of all enteric outbreaks and 2.0% (156/7824) of all associated cases reported in 2019.

Over the 10 year period 2010 to 2019, excluding 2014, the number of outbreaks of campylobacteriosis with food reported as a possible mode of transmission has ranged between four and 16 outbreaks reported each year with between 19 and 81 annual outbreak-associated cases (Figure 8). The greater number of outbreak-associated cases in 2014 was due to three outbreaks with high numbers of cases (51, 32 and 17).

Figure 8. Campylobacteriosis outbreaks with food reported as a possible mode of transmission and associated cases reported by year, 2010–2019



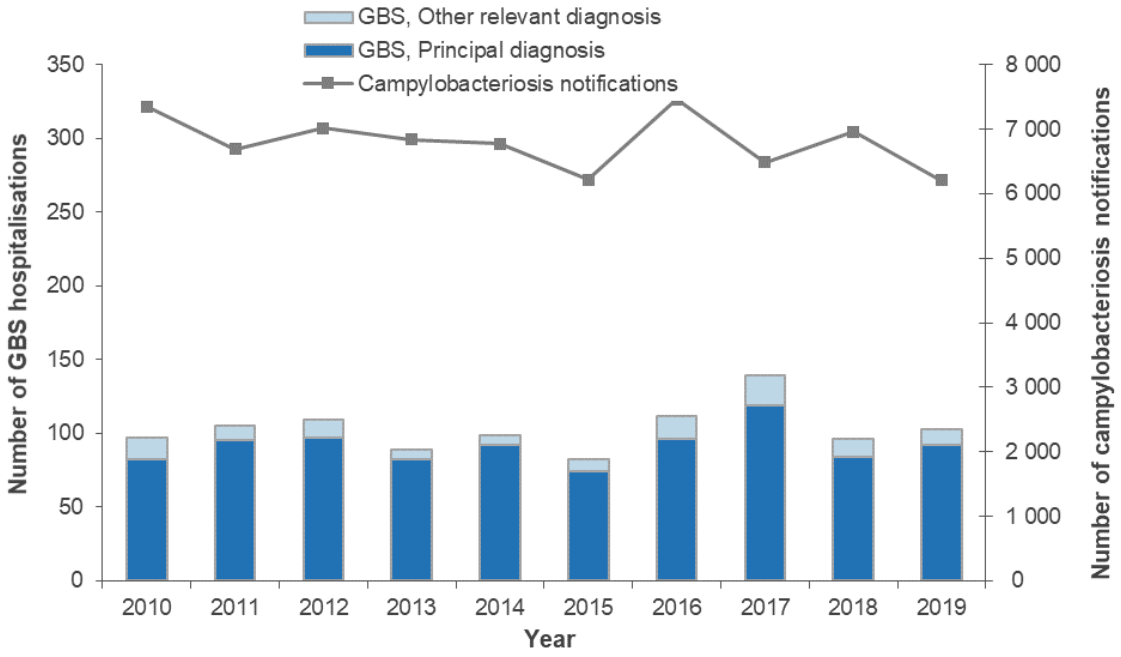
Disease sequelae - Guillain-Barré syndrome

Guillain-Barré syndrome (GBS) may be preceded by an infection with *Campylobacter jejuni*. Other respiratory or intestinal illnesses and other triggers may also precede an episode of GBS.

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 2019 were considered, rather than all cases that were hospitalised in 2019. That is, if a GBS case hospitalised in 2019 had been hospitalised with GBS in a previous year, the 2019 admission was considered to be a readmission, rather than an incident case. There were 103 incident hospitalised cases recorded in 2019 (2.1 admissions per 100,000 population), 92 were reported with GBS as the primary diagnosis and 11 with GBS as another relevant diagnosis.

Between 2010 and 2019, the annual number of incident hospitalised cases (any diagnosis code) for GBS ranged from 82 to 139 (Figure 9). The numbers of campylobacteriosis notifications during the same period are also included in Figure 9 for comparison.

Figure 9. Guillain-Barré syndrome hospitalised cases, 2010–2019



In 2019, the number of incident hospitalised cases due to GBS was slightly higher for males than for females (Table 12). This is consistent with the pattern seen for GBS in most previous years, except 2016 when case numbers for males and females were almost identical. It is also consistent with the gender differences seen in notification rates for campylobacteriosis in males and females in 2019 (Table 8).

Table 12. Guillain-Barré syndrome hospitalised cases by sex, 2019

Sex	Hospitalised cases[a]	
	No.	Rate[b]
Male	54	2.2
Female	49	2.0
Total	**103**	**2.1**

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

In 2019, 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 13).

Table 13. Guillain-Barré syndrome hospitalised cases by age group, 2019

Age group (years)	Hospitalised cases	
	No.	Rate[b]
<5	2	-
5 to 9	2	-
10 to 14	1	-
15 to 19	3	-
20 to 29	8	1.1
30 to 39	8	1.2
40 to 49	12	1.9
50 to 59	24	3.8
60 to 69	25	4.8
70+	18	3.4
Total	**103**	**2.1**

[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

In 2014, antimicrobial drug–resistant *Campylobacter jejuni* sequence type 6964 emerged contemporaneously in poultry from 3 supply companies in the North Island of New Zealand and as a major cause of campylobacteriosis in humans in New Zealand [16]. This lineage, not previously identified in New Zealand, was resistant to tetracycline and fluoroquinolones. Genomic analysis revealed divergence into 2 major clades; both clades were associated with human infection, one with poultry companies A and B and the other with company C. Accessory genome evolution was associated with a plasmid, phage insertions, and natural transformation.

Excretion of the human bacterial pathogen *Campylobacter jejuni* by naturally infected dairy cows was investigated by monitoring 18 and 17 cows on two different commercial farms fortnightly for up to 12 months [17]. *C. jejuni* was enumerated in the collected faeces by a most probable number technique and genotyped by enterobacterial repetitive intergenic consensus (ERIC) sequences. On both farms, *C. jejuni* excretion was highly variable among the studied cows, with excretion patterns ranging from chronic to sporadic. Chronic excretion of *C. jejuni* was associated with long-term predominance of a given genotype, co-excretion of a few genotypes, or succession over time of dominant genotypes. Sporadic excretions separated by less than 1.5 months between *C. jejuni*-positive samples resulted in re-excretion of the same *C. jejuni* genotype. Overall, the results showed the complexity of *C. jejuni* excretion pattern by dairy cows with an animal and farm specificity.

Relevant regulatory developments

Nil.

Ciguatera fish 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 [18], 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. As the FAO/WHO report has only recently been released, the older terminology has been used for the current report.

Ciguatera fish poisoning cases reported in 2019 by data source

During 2019, ten cases of ciguatera fish poisoning (0.2 per 100,000 population) were reported in EpiSurv. Note that not every case of Ciguatera fish poisoning is necessarily notifiable; only those where there is a suspected common source.

The ICD-10 code T61.0 was used to extract foodborne Ciguatera fish poisoning hospitalisation data from the NMDS database. Of the 14 hospital admissions (0.3 admissions per 100,000 population) recorded in 2019, 13 cases were reported with ciguatera fish poisoning as the primary diagnosis and one case was reported with ciguatera fish poisoning as another relevant diagnosis.

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 fish poisoning in hospital are reported in EpiSurv.

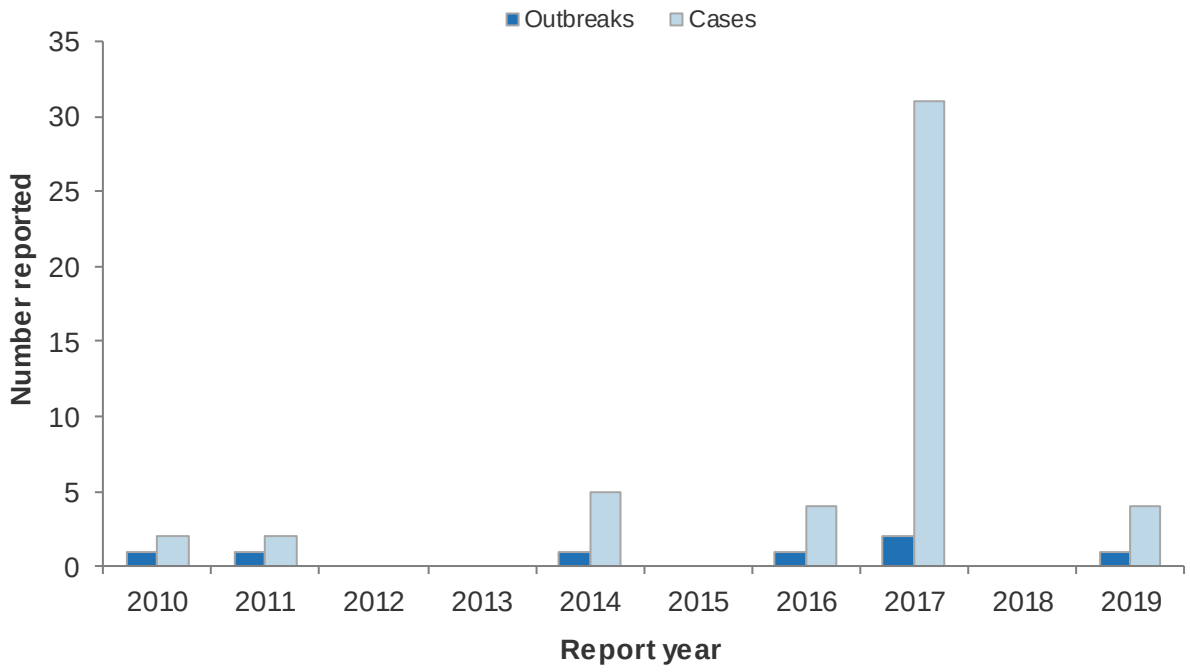
Outbreaks reported as caused by ciguatera fish poisoning

During 2019, one outbreak of possible ciguatera fish poisoning was reported in EpiSurv, with four associated probable cases in a home exposure setting. Consumption of imported fish was the suspected cause of the outbreak.

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

Over the 10 year period 2010 to 2019, seven outbreaks of ciguatera fish poisoning were reported, with no more than two outbreaks reported in a year (Figure 10). 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 10. Ciguatera fish poisoning outbreaks and associated cases reported by year, 2010–2019



Recent surveys

Nil.

Relevant New Zealand studies and publications

New Zealand benthic and epiphytic dinoflagellate records increased in recent years as harmful algal bloom research increased [19]. This was largely due to risk assessments of micro-algal biotoxins for the seafood industry and concerns regarding ciguatera fish poisoning in humans from toxic finfish. High-throughput sequencing enabled the detection of dinoflagellate species that were previously overlooked by microscopy, particularly where diatoms or sediments obscured visual identification. This checklist includes new species records for New Zealand and species usually considered planktonic, but which have benthic life stages. Thirty-one dinoflagellate genera were recorded from isolations and descriptions of living cells, including the ciguatera-associated genera *Fukuyoa* and *Gambierdiscus*.

Relevant regulatory developments

Nil.

Clostridium perfringens intoxication

Case definition

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

Clostridium perfringens intoxication cases reported in 2019 by data source

During 2019, no individual cases of confirmed *C. perfringens* intoxication were reported in EpiSurv. One probable case was reported as gastroenteritis with elevated levels of *C. perfringens* in lab sample. Note that not every case of *C. perfringens* intoxication is necessarily notifiable; only those where there is a suspected common source.

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 2019 with *C. perfringens* intoxication as the diagnosis.

Outbreaks reported as caused by *Clostridium perfringens*

In 2019, all three *C. perfringens* intoxication outbreaks (53 associated cases and zero hospitalisations) reported food as a possible mode of transmission (Table 14). While details of these outbreaks were reported in EpiSurv, details for the individual cases involved in the outbreaks were not reported in EpiSurv. It is important to note that a single outbreak may have multiple pathogens, settings and modes of transmission.

Table 14. *C. perfringens* intoxication outbreaks reported, 2019

Measure	*C. perfringens* intoxication outbreaks	
	Possible foodborne transmission with a suspected or confirmed source	All
Outbreaks	3	3
Cases	53	53
Hospitalised Cases	0	0

Table 15 contains details of the three *C. perfringens* intoxication outbreaks reported in 2019.

Table 15. Details of foodborne *C. perfringens* intoxication outbreaks with food reported as a possible mode of transmission, 2019

PHU	Month	Suspected source	Evidence	Setting	No. ill
Auckland	July	Roast lamb	Common meal	Catered event	2C 18P
C and PH	July	Chicken burrito (chicken, vegetables and rice)	Consumption of same food type at common meal	Restaurant/cafe/bakery	3P
C and PH	Dec	Beef sirloin with condiments / pork belly / leafy vegetables	Common meal and epidemiological investigation	Catered event	30C

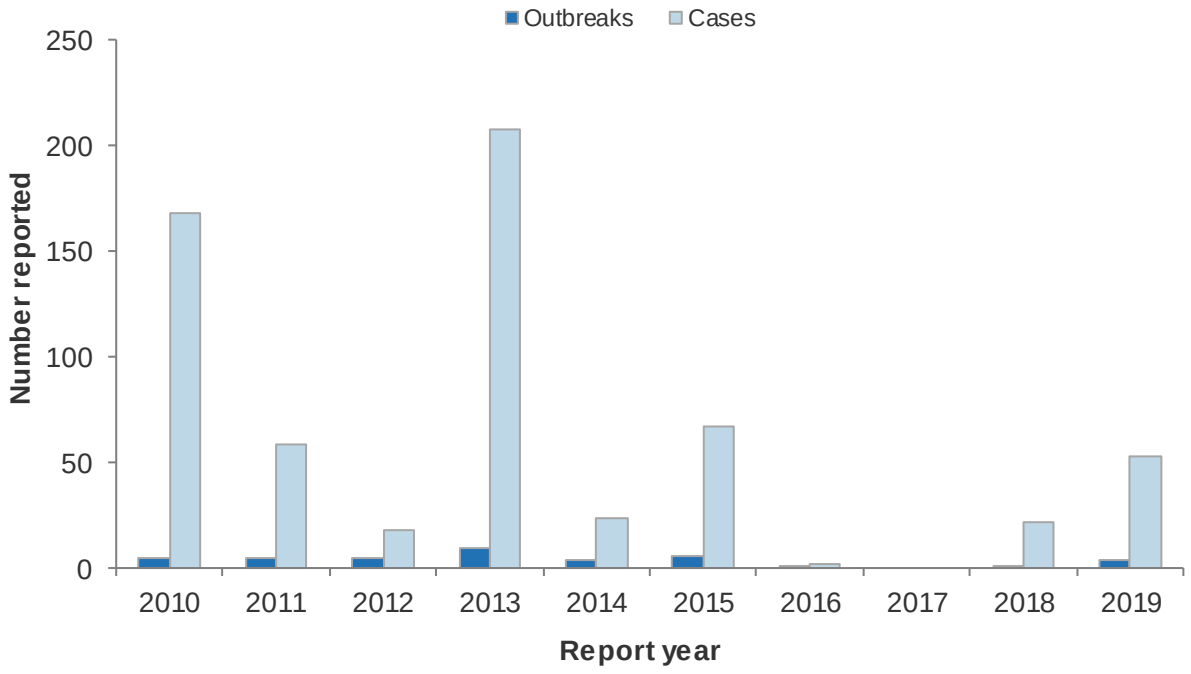
PHU Auckland: Auckland Regional Public Health Service, C and PH: Community and Public Health

Number ill: C: confirmed, P: probable

For all three outbreaks a suspected source of infection was recorded. The suspected sources of infection for the December outbreak included beef sirloin meal with condiments, pork belly and leafy vegetables. The level of evidence was strong. The source for one outbreak in July was suspected to be roast lamb, for the second outbreak in July it was chicken burrito. The level of evidence was weak for both July outbreaks.

Over the 10 year period 2010 and 2019, the number of outbreaks of *C. perfringens* intoxication with food reported as a possible mode of transmission ranged from one (2016 and 2018) to nine outbreaks (in 2013) (Figure 11). The number of cases associated with outbreaks of *C. perfringens* intoxication has also varied markedly over time. The highest number of cases associated with an outbreak of *C. perfringens* intoxication with possible transmission by food occurred in 2013 (208 cases).

Figure 11. *C. perfringens* intoxication outbreaks with food reported as a possible mode of transmission and associated cases reported by year, 2010–2019



Recent surveys

Nil.

Relevant New Zealand studies and publications

Nil.

Relevant regulatory developments

Nil.

Cryptosporidiosis

Summary data for cryptosporidiosis in 2019 are given in Table 16.

Table 16. Summary of surveillance data for cryptosporidiosis, 2019

Parameter	Value in 2019	Source
Number of notified cases	1035	EpiSurv
Notification rate (per 100,000)	21.0	EpiSurv
Hospitalisations[a]	67	MoH NMDS
Deaths	0	EpiSurv
Estimated travel-related cases (%)[b]	92 (9%)	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

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

Since 2015 laboratories across New Zealand have gradually changed the methodology for testing faecal specimens. In 2019, community faecal specimens in all DHBs with the exception of Canterbury, MidCentral, South Canterbury, Tairawhiti, Taranaki, West Coast and Whanganui were screened by multiplex PCR for a range of pathogens, including *Cryptosporidium*. Most community faecal specimens are now screened for *Cryptosporidium* spp. when previously only those specimens where parasite screening was requested were tested. It is unclear at this stage how laboratory changes have affected the notification rates. The increased number of samples screened for *Cryptosporidium* spp. may impact on the numbers of positive results and subsequently increased notification rates. There does not seem to be a large difference in sensitivity between enzyme immunoassay tests (EIA, used by most laboratories prior to enteric PCR introduction) and PCR for the detection of *Cryptosporidium* spp.

Cryptosporidiosis cases reported in 2019 by data source

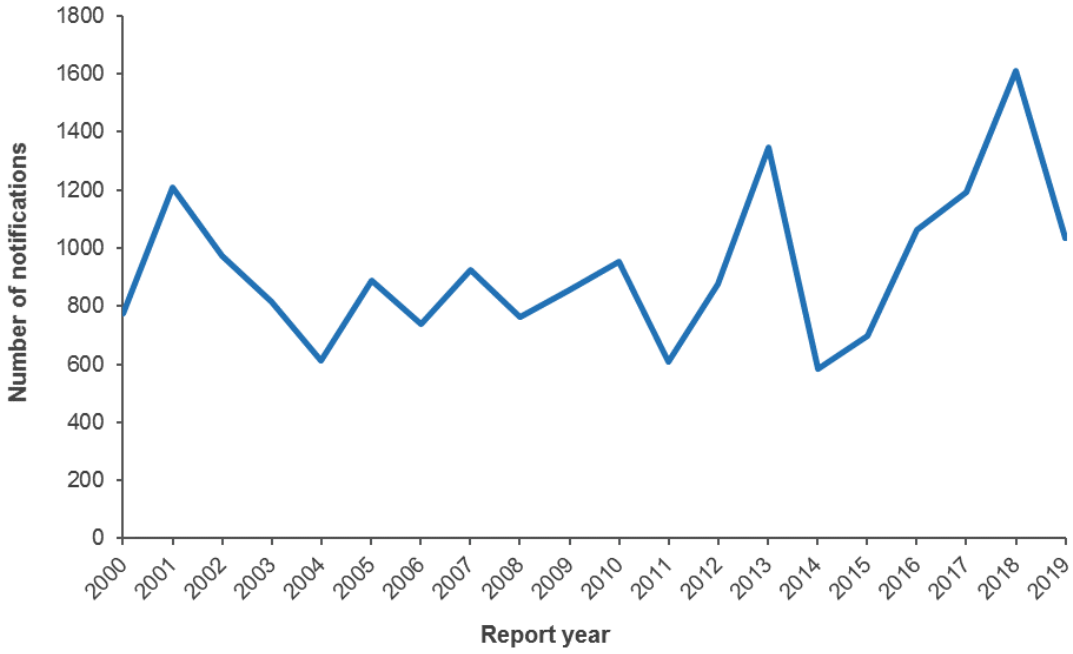
During 2019, 1035 cases (21.0 per 100,000 population) of cryptosporidiosis and no resulting deaths were reported in EpiSurv. Approximately 6% of cases notified in EpiSurv are recorded as hospitalised in 2019.

The ICD-10 code A07.2 was used to extract cryptosporidiosis hospitalisation data from the MoH NMDS database. Of the 67 hospital admissions (1.4 admissions per 100,000 population) recorded in 2019, 43 cases were reported with cryptosporidiosis as the primary diagnosis and 24 were reported with cryptosporidiosis as another relevant diagnosis.

Notifiable disease data

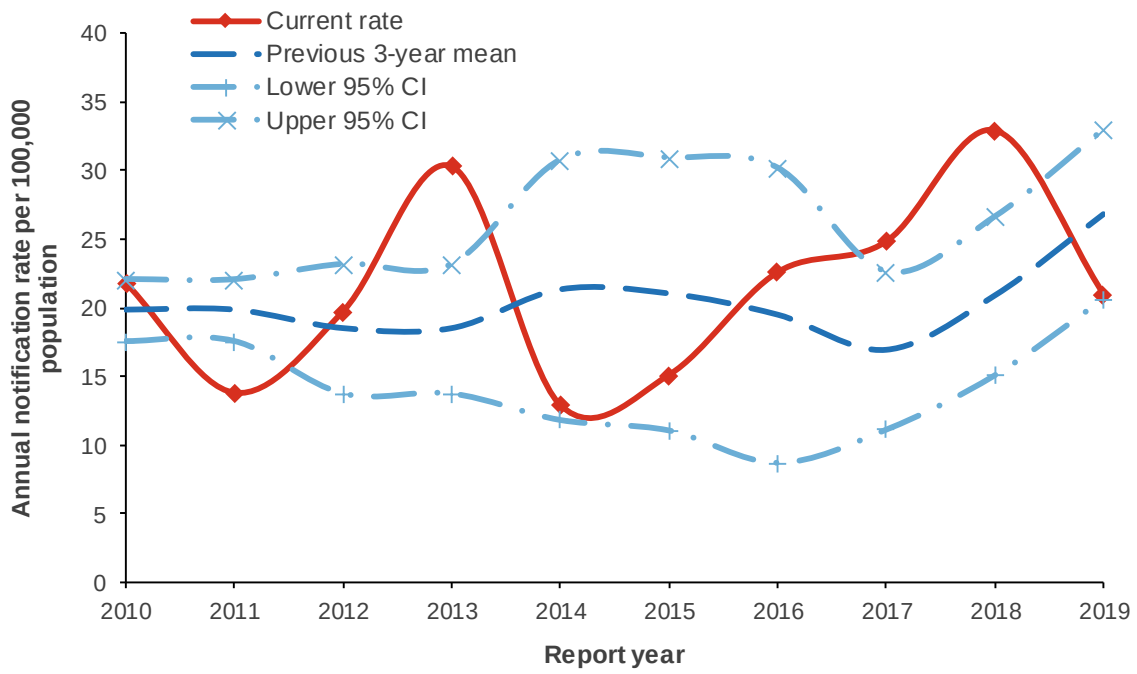
In 2018, the highest number of cryptosporidiosis notifications (1611 notifications) was recorded since cryptosporidiosis became a notifiable disease in 1996. Over the last 20 year time period there were no clear trends regarding the number of cryptosporidiosis notifications (Figure 12). After the peak in 2018, the number of notifications in 2019 (1035 cases) has returned to within the range seen in the previous 20 years.

Figure 12. Cryptosporidiosis notifications by year, 2000–2019



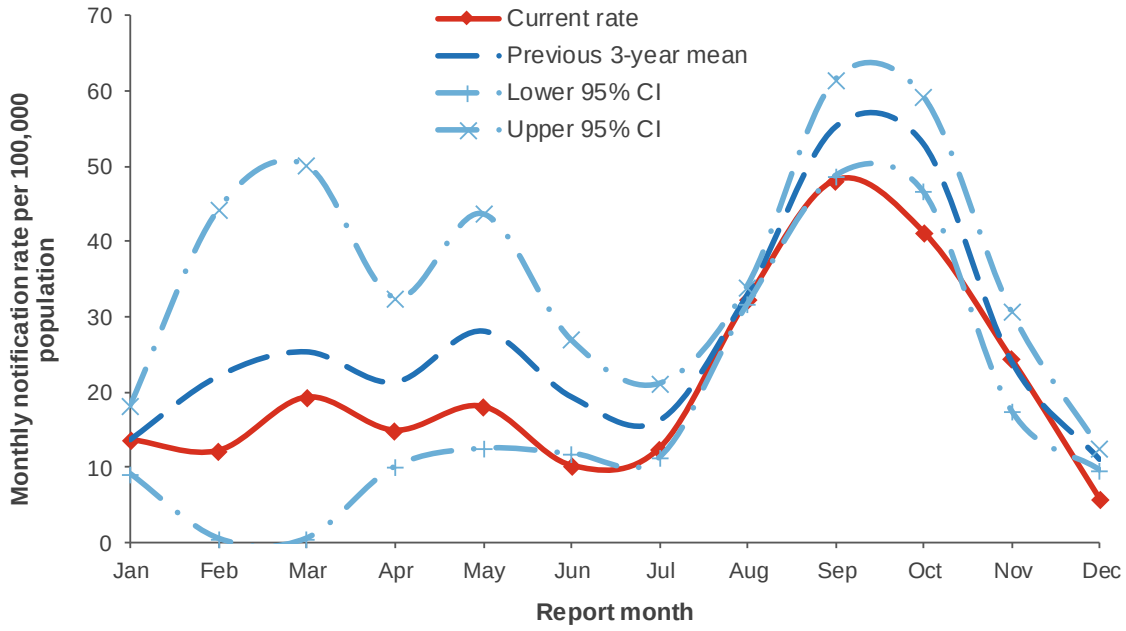
Due to the peak in 2018, the cryptosporidiosis notification rate in 2019 (21.1 cases per 100,000 population) was lower than the previous three year average (26.9 cases per 100,000 population) (Figure 13).

Figure 13. Cryptosporidiosis notification rate by year, 2010–2019



The number of notified cases of cryptosporidiosis reported per 100,000 population by month for 2019 is shown in Figure 14. The monthly number of notifications in 2019 ranged from 24 notifications (December) to 197 notifications (September). In 2019 there was a distinct seasonal pattern of cryptosporidiosis cases, with the highest number of notifications reported during spring, which is similar to the pattern observed before 2018. In 2018, higher than usual monthly rates were reported in the first half of the year, most likely due to two large outbreaks (not foodborne) between January and April 2018 in the Wellington region and a significant increase in notifications in the Auckland region compared to previous years.

Figure 14. Cryptosporidiosis monthly rate (annualised), 2019



In 2019, the rate of notifications for cryptosporidiosis was higher for females (22.4 per 100,000 population) compared with males (19.6 per 100,000 population) whereas the rate of hospitalisations was similar (Table 17).

Table 17. Cryptosporidiosis cases by sex, 2019

Sex	EpiSurv notifications		Hospitalisations[a]	
	No.	Rate[b]	No.	Rate[b]
Male	474	19.6	34	1.4
Female	560	22.4	33	1.3
Total[c]	**1035**	**21.0**	**67**	**1.4**

[a] MoH NMDS data for hospital admissions

[b] per 100,000 population

[c] total includes notifications where gender is unknown

During 2019, the highest cryptosporidiosis age-specific notification rates were for the 1 to 4 years age group (101.6 per 100,000 population, 250 cases), followed by the less than 1 year (33.5 per 100,000, 20 cases) and the 5 to 9 (30.3 per 100,000, 100 cases) age groups (Table 18). The hospitalisation rate was also highest in the 1 to 4 years age group.

Table 18. Cryptyosporidiosis cases by age group, 2019

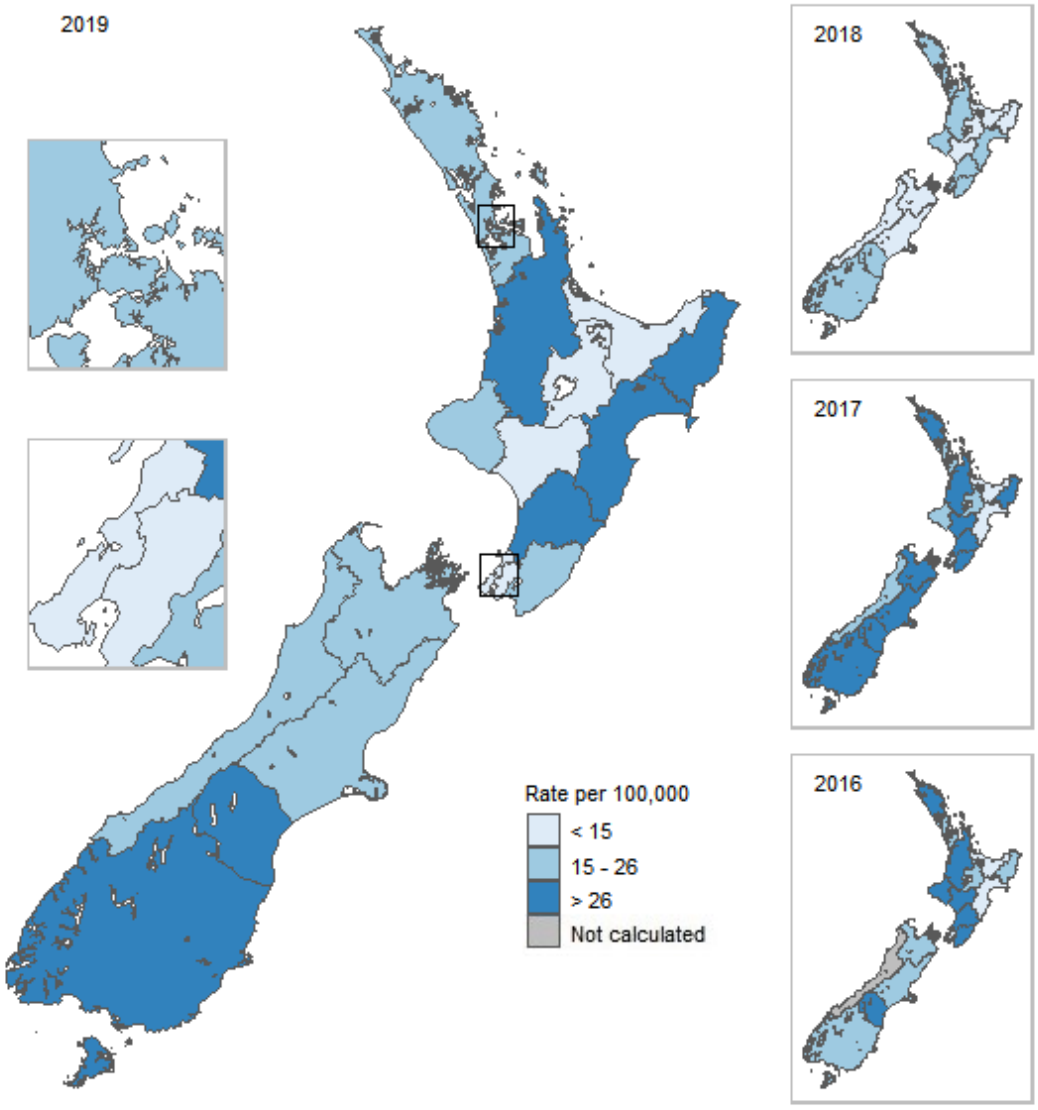
Age group (years)	EpiSurv notifications		Hospitalisations[a]	
	No.	Rate[b]	No.	Rate[b]
<1	20	33.5	2	-
1 to 4	250	101.6	21	8.5
5 to 9	100	30.3	9	2.7
10 to 14	69	21.4	3	-
15 to 19	55	17.4	0	-
20 to 29	179	25.7	6	0.9
30 to 39	141	21.7	7	1.1
40 to 49	89	14.3	5	0.8
50 to 59	56	8.9	4	-
60 to 69	41	7.9	3	-
70+	35	6.6	7	1.3
Total	**1035**	**21.0**	**67**	**1.4**

[a] MoH NMDS data for hospital admissions

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

Cryptosporidiosis rates varied throughout the country in 2019 as shown in Figure 15. The highest rates of cryptosporidiosis were reported for the DHBs Southern (40.7 per 100,000, 138 cases) and South Canterbury (26.2 per 100,000, 16 cases) in the South Island and MidCentral (33.8 per 100,000, 62 cases) and Tairawhiti (30.4 per 100,000, 15 cases) in the North Island.

Figure 15. Geographic distribution of cryptosporidiosis notifications, 2016–2019



Note: Since 2015 laboratories across New Zealand have gradually changed the methodology for testing faecal specimens. It is unclear at this stage how laboratory changes have affected the notification rates for cryptosporidiosis. Refer to report Introduction for details.

For cases where information on travel was provided in 2019, 9% had travelled overseas during the incubation period. Assuming that the cases for which travel information was provided were representative of all cryptosporidiosis cases, a Poisson distribution can be used to estimate the total number of potentially travel-related cases of cryptosporidiosis in 2019. The resultant distribution has a mean of 92 cases (95% CI 74-113).

If data from the last four years are considered the estimated proportion of cases travelling overseas within the incubation period of the organism was 10% (95% CI 9-11%).

Outbreaks reported as caused by *Cryptosporidium* spp.

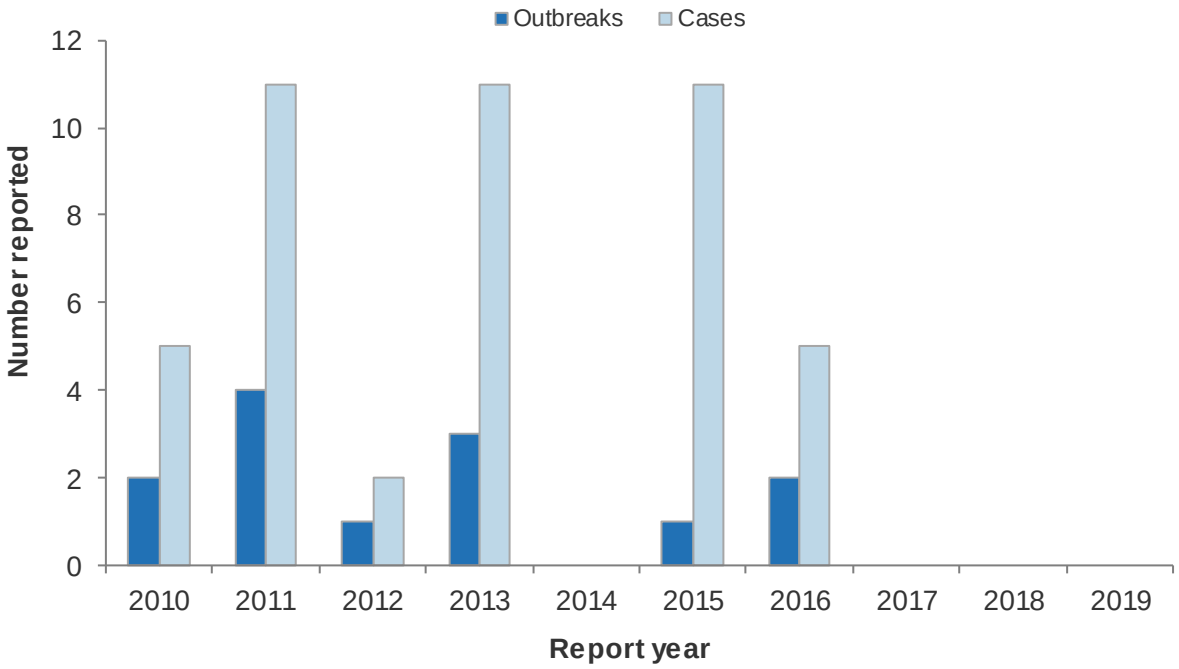
In 2019, none of the 15 cryptosporidiosis outbreak notifications reported food as a possible mode of transmission (Table 19). It is important to note that a single outbreak may have multiple pathogens, modes of transmission, settings where exposure occurred, or settings where preparation of food was conducted. Outbreaks of cryptosporidiosis accounted for 3.0% (15/499) of all enteric outbreaks and 1.2% (93/7824) of all associated cases.

Table 19. Cryptosporidiosis outbreaks reported, 2019

Measure	Cryptosporidiosis outbreaks	
	Possible foodborne transmission	All
Outbreaks	0	15
Cases	0	93
Hospitalised Cases	0	4

Foodborne transmission has rarely been reported for cryptosporidiosis outbreaks, with not more than four outbreaks with food reported as a possible mode of transmission reported each year between 2009 and 2018. The outbreak in 2015 had the largest number of cases (11) associated with a single outbreak (Figure 16).

Figure 16. Cryptosporidiosis outbreaks with food reported as a possible mode of transmission and associated cases reported by year, 2010–2019



Recent surveys

Nil.

Relevant New Zealand studies and publications

Nil.

Relevant regulatory developments

Nil.

Giardiasis

Summary data for giardiasis in 2019 are given in Table 20.

Table 20. Summary of surveillance data for giardiasis, 2019

Parameter	Value in 2019	Source
Number of notified cases	1749	EpiSurv
Notification rate (per 100,000)	35.6	EpiSurv
Hospitalisations[a]	88	MoH NMDS
Deaths	0	EpiSurv
Estimated travel-related cases (%)[b]	330 (19%)	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

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

Since 2015 laboratories across New Zealand have gradually changed the methodology for testing faecal specimens. In 2019, community faecal specimens in all DHBs with the exception of Canterbury, MidCentral, South Canterbury, Tairawhiti, Taranaki, West Coast and Whanganui were screened by multiplex PCR for a range of pathogens, including *Giardia*. It is unclear at this stage if laboratory changes have affected the notification rates for giardiasis as a decrease in disease rate may be masked by the increased frequency of testing. Prior to the change in methodology *Giardia* spp. were only screened for in those specimens where parasite screening was requested. There does not seem to be a large difference in sensitivity between EIA (used by most laboratories prior to enteric PCR introduction) and PCR for the detection of *Giardia* spp.

Giardiasis cases reported in 2019 by data source

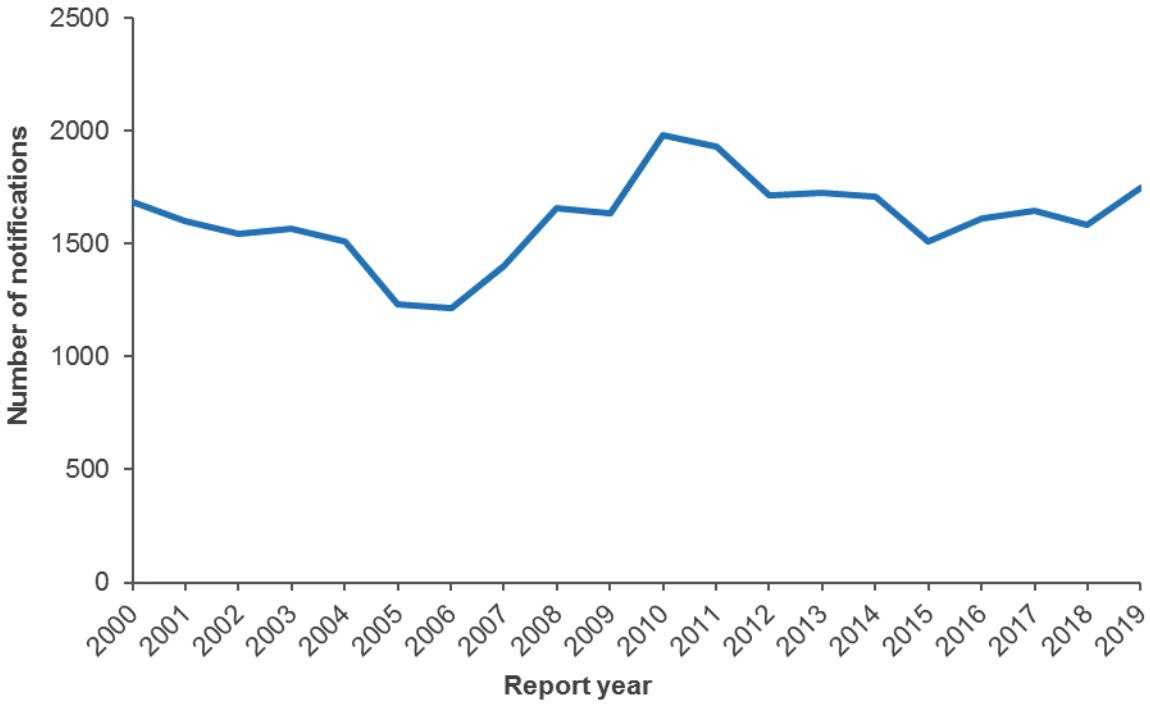
During 2019, 1749 cases (35.6 per 100,000 population) of giardiasis and no resulting deaths were reported in EpiSurv. Less than 3% of cases notified in EpiSurv were recorded as being hospitalised in 2019.

The ICD-10 code A07.1 was used to extract giardiasis hospitalisation data from the MoH NMDS database. Of the 88 hospital admissions (1.8 admissions per 100,000 population) recorded in 2019, 42 cases were reported with giardiasis as the primary diagnosis and 46 were reported with giardiasis as another relevant diagnosis.

Notifiable disease data

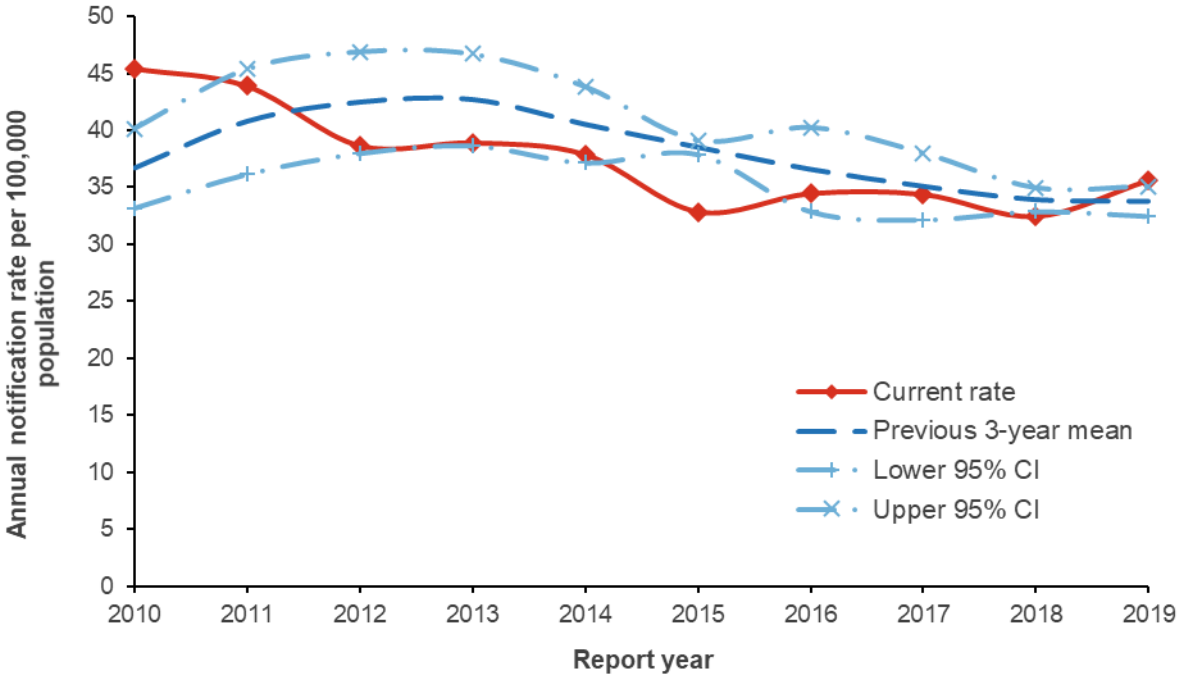
There was a steady decrease in the number of giardiasis cases reported each year from 1998 to 2006. An increasing trend in the number of notifications was observed from 2006 until 2010 followed by decreasing trend in the number of notifications. Since 2012, the number of giardiasis cases reported each year has been in the range of 1510 to 1750 cases (Figure 17).

Figure 17. Giardiasis notifications by year, 2000–2019



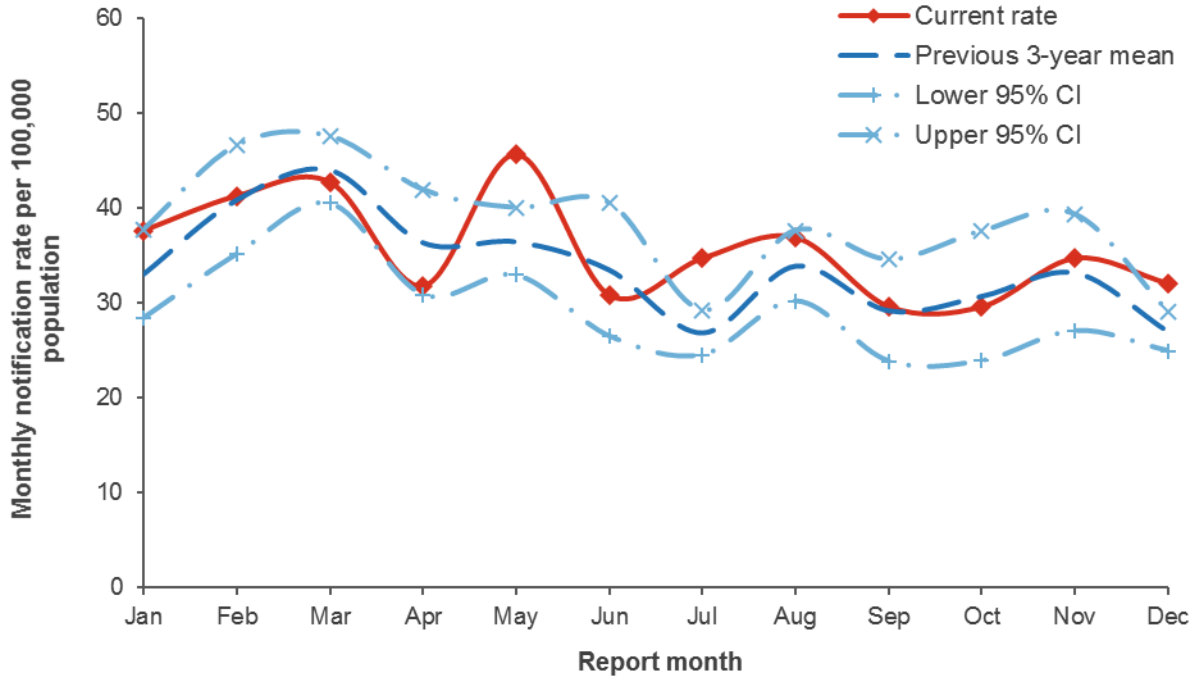
The notification rate in 2019 was similar (35.6 cases per 100,000) to the previous three-year average (33.9 cases per 100,000) (Figure 18).

Figure 18. Giardiasis notification rate by year, 2010–2019



The number of notified cases of giardiasis reported per 100,000 population by month for 2019 is shown in (Figure 19). The monthly number of notifications in 2019 ranged from 121 notifications (September and October) to 187 notifications (May).There was no distinct seasonal pattern in the population rate of giardiasis notifications reported by month when considering the previous three years (2016–2018). In 2019, a peak in cases was observed in May compared to the previous three years.

Figure 19. Giardiasis monthly rate (annualised), 2019



In 2019, the rate of notifications and hospital admissions for giardiasis was higher for males (37.0 cases, 2.0 admissions per 100,000 population) than females (34.2 cases, 1.6 admissions per 100,000 population) (Table 21).

Table 21. Giardiasis cases by sex, 2019

Sex	EpiSurv notifications		Hospitalisations[a]	
	No.	Rate[b]	No.	Rate[b]
Male	895	37.0	48	2.0
Female	853	34.2	40	1.6
Total[c]	**1749**	**35.6**	**88**	**1.8**

[a] MoH NMDS data for hospital admissions

[b] per 100,000 population

[c] total includes notifications where gender is unknown

In 2019, the highest notification rate was for the 1 to 4 years age group (126.0 per 100,000 population, 310 cases), followed by the 30 to 39 years age group (59.2 per 100,000, 384 cases) (Table 22). The highest hospitalisation rate was also for the 1 to 4 years age group (4.1 admissions per 100,000 population).

Table 22. Giardiasis cases by age group, 2019

Age group (years)	EpiSurv notifications		Hospitalisations[a]	
	No.	Rate[b]	No.	Rate[b]
<1	18	30.2	1	-
1 to 4	310	126.0	10	4.1
5 to 9	119	36.1	5	1.5
10 to 14	40	12.4	2	-
15 to 19	37	11.7	2	-
20 to 29	203	29.1	17	2.4
30 to 39	384	59.2	13	2.0
40 to 49	224	36.1	5	0.8
50 to 59	168	26.7	11	1.7
60 to 69	171	32.9	7	1.3
70+	75	14.2	15	2.8
Total	**1749**	**35.6**	**88**	**1.8**

[a] MoH NMDS data for hospital admissions

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

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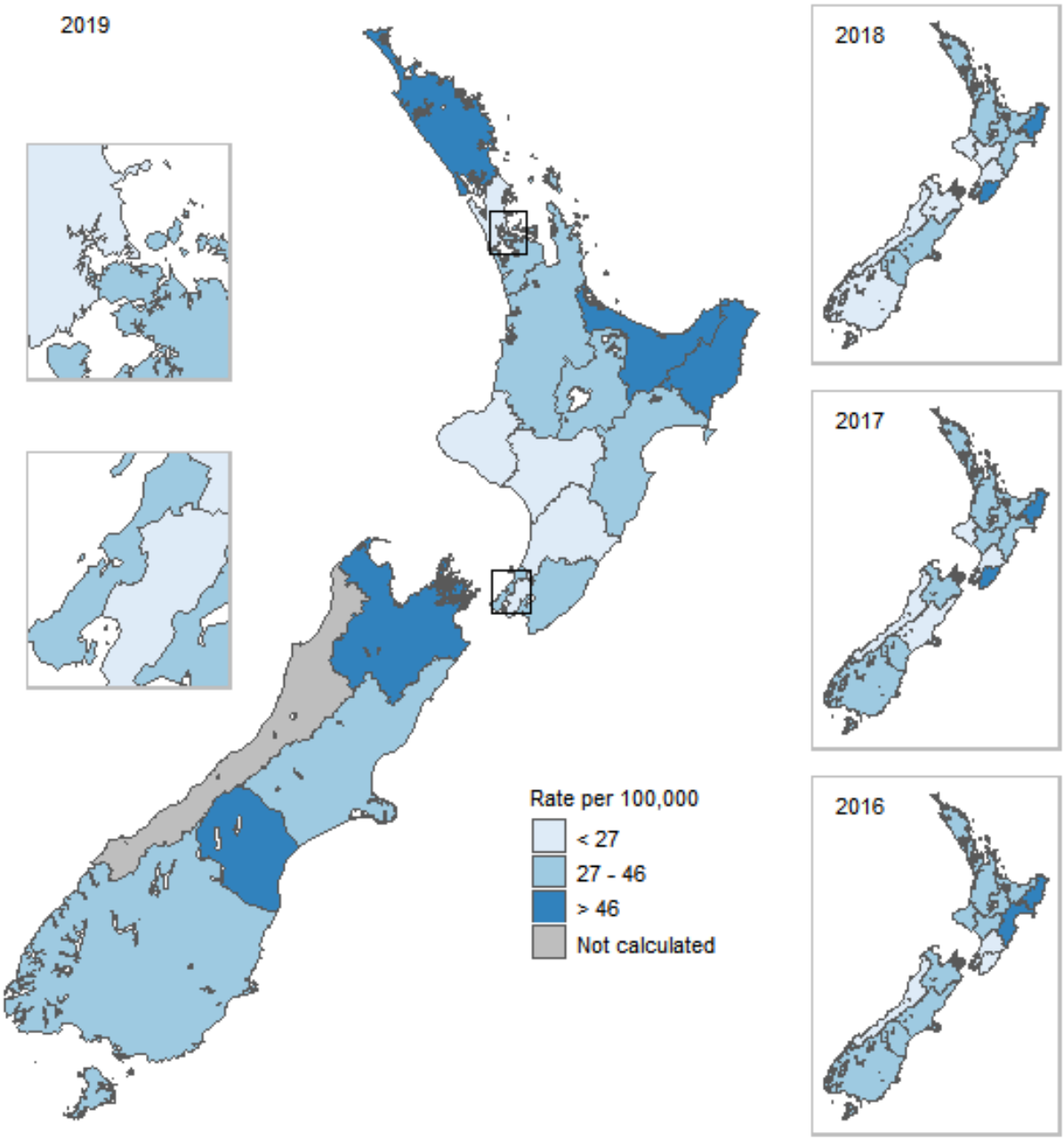
Giardiasis rates varied throughout the country during 2019 (Figure 20) and across 2016 to 2018. The highest rate was reported for Tairawhiti DHB (75.1 per 100,000 population, 37 cases), followed by Bay of Plenty (51.4 per 100,000, 130 cases), Nelson Marlborough (51.6 per 100,000, 81 cases), Northland (49.8 per 100,000, 94 cases), and South Canterbury (47.5 per 100,000, 29 cases) DHBs. The lowest rate was reported for Whanganui DHB (13.3 per 100,000 population, 9 cases).

Figure 20. Geographic distribution of giardiasis notifications, 2016–2019



Note: Since 2015 laboratories across New Zealand have gradually changed the methodology for testing faecal specimens. It is unclear at this stage how laboratory changes have affected the notification rates for giardiasis. Refer to report Introduction for details.

For cases where information on travel was provided in 2019, 19% had travelled overseas during the incubation period. Assuming that the cases for which travel information was provided were representative of all giardiasis cases, a Poisson distribution can be used to estimate the total number of potentially travel-related cases of giardiasis in 2019. The resultant distribution has a mean of 330 cases (95% CI 295-368).

If data from the last four years are considered the estimated proportion of cases travelling overseas within the incubation period of the organism was 23% (95% CI 21-24%).

Outbreaks reported as caused by *Giardia spp.*

In 2019, there were 24 giardiasis outbreak notifications in EpiSurv, two (8.3%) 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. Of the two outbreaks and 18 associated cases where food was reported as a possible mode of transmission, there were no hospitalisations.

Giardiasis outbreaks accounted for 4.8% (24/499) of all enteric outbreaks and 1.8% (141/7824) of all associated cases.

Table 23. Giardiasis outbreaks reported, 2019

Measure	Giardiasis outbreaks		
	Possible foodborne transmission with a suspected or confirmed source	Possible foodborne transmission but no suspected source	All
Outbreaks	1	1	24
Cases	18	4	141
Hospitalised Cases	0	0	2

Table 24 contains details of the two giardiasis outbreaks reported in 2019 with food as a possible mode of transmission.

Table 24. Details of giardiasis outbreaks with food reported as a possible mode of transmission, 2019

PHU	Month	Suspected source	Evidence	Setting	No. Ill
Tairawhiti	Jun	Unknown	Household cluster	-	4C
Hawke's Bay	Dec	Garden salad	Common meal and epidemiological investigation	Restaurant/cafe/bakery	1C 17P

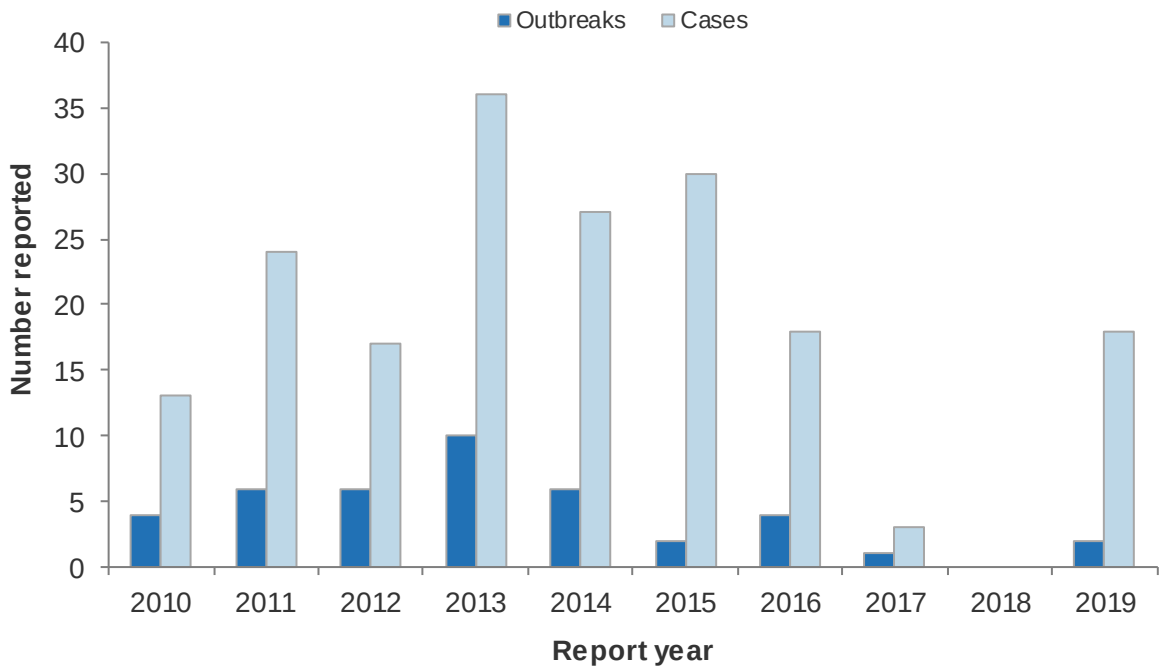
PHU: Public health unit, Tairawhiti: Tairawhiti DHB, Hawke's Bay: Hawke's Bay Public Health Unit

Number ill: C: confirmed, P: probable

The evidence was strong for the suspected food vehicle for one outbreak related to consumption of garden salad in December. For the second household based outbreak no suspected food vehicle was identified.

Over the 10 year period 2010 and 2019, between zero and 10 giardiasis outbreaks with food reported as a possible mode of transmission were reported each year with between three and 36 annual outbreak-associated cases (Figure 21).

Figure 21. Giardiasis outbreaks with food reported as a possible mode of transmission and associated cases reported by year, 2010–2019



Recent surveys

Nil.

Relevant New Zealand studies and publications

Nil.

Relevant regulatory developments

Nil.

Hepatitis A

Summary data for hepatitis A in 2019 are given in Table 25.

Table 25. Summary of surveillance data for hepatitis A, 2019

Parameter	Value in 2019	Source
Number of notified cases	58	EpiSurv
Notification rate (per 100,000)	1.2	EpiSurv
Hospitalisations[a]	76	MoH NMDS
Deaths	0	EpiSurv
Travel-related cases (%)[b]	34 (59%)	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

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 cases reported in 2019 by data source

During 2019, 58 cases (1.2 per 100,000 population) of hepatitis A and no resulting deaths were reported in EpiSurv. Hospitalisation rates are usually high for hepatitis A with 62 % of notified cases recorded as hospitalised in 2019.

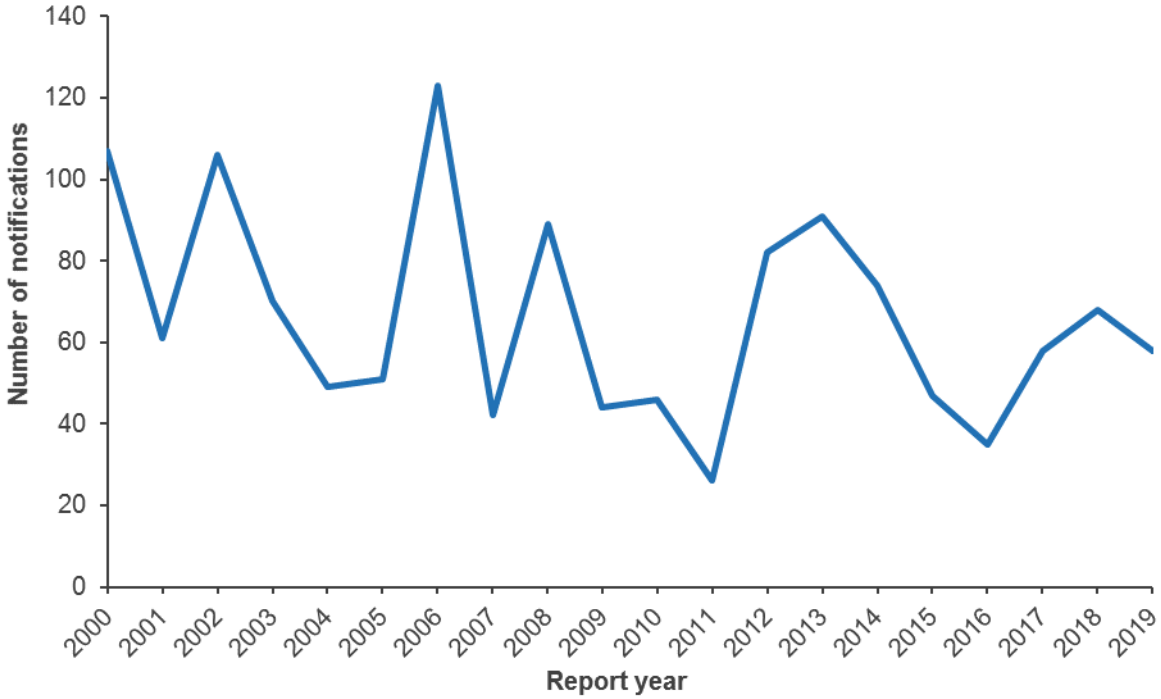
The ICD-10 code B15 was used to extract acute Hepatitis A hospitalisation data from the MoH NMDS database. Of the 76 hospital admissions (1.5 admissions per 100,000 population) recorded in 2019, 31 cases were reported with acute hepatitis A as the primary diagnosis and 45 with acute hepatitis A as another relevant diagnosis.

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 Hepatitis A in hospital are reported in EpiSurv.

Notifiable disease data

Between 2000 and 2019, the annual number of notifications has remained in the range of 26 (2011) to 123 (2006) (Figure 22). Due to the small number of notifications per year, plots of case notification rates by year and month are not presented for hepatitis A.

Figure 22. Hepatitis A notifications by year, 2000–2019



In 2019, hepatitis A notification and hospitalisation rates were similar for males and females (Table 26).

Table 26. Hepatitis A cases by sex, 2019

Sex	EpiSurv notifications		Hospitalisations[a]	
	No.	Rate[b]	No.	Rate[b]
Male	31	1.3	16	0.7
Female	27	1.1	15	0.6
Total	**58**	**1.2**	**31**	0.6

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

[b] per 100,000 population

In 2019, the hepatitis A cases were spread over the age range 1 to 69 years old. The rate of notification was slightly higher in the 1 to 4, and 15 to 29 age ranges (~2.0 cases per 100,000 population) (Table 27).

Table 27. Hepatitis A cases by age group, 2019

Age group (years)	EpiSurv notifications		Hospitalisations[a]	
	No.	Rate[b]	No.	Rate[b]
<1	0	-	0	-
1 to 4	5	2.0	3	-
5 to 9	5	1.5	2	-
10 to 14	4	-	0	-
15 to 19	7	2.2	3	-
20 to 29	14	2.0	9	1.3
30 to 39	10	1.5	8	1.2
40 to 49	5	0.8	4	-
50 to 59	6	1.0	1	-
60 to 69	2	-	1	-
70+	0	-	0	-
Total	**58**	**1.2**	**31**	**0.6**

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

For cases where information on travel was provided in 2019, 59% had travelled overseas during the incubation period. Assuming that the cases for which travel information was provided were representative of all hepatitis A cases, a Poisson distribution can be used to estimate the total number of potentially travel-related cases of hepatitis A in 2019. The resultant distribution has a mean of 34 cases (95% CI 24-48).

If data from the last four years are considered the estimated proportion of cases travelling overseas within the incubation period of the organism was 59% (95% CI 52-66%).

Outbreaks reported as caused by hepatitis A virus

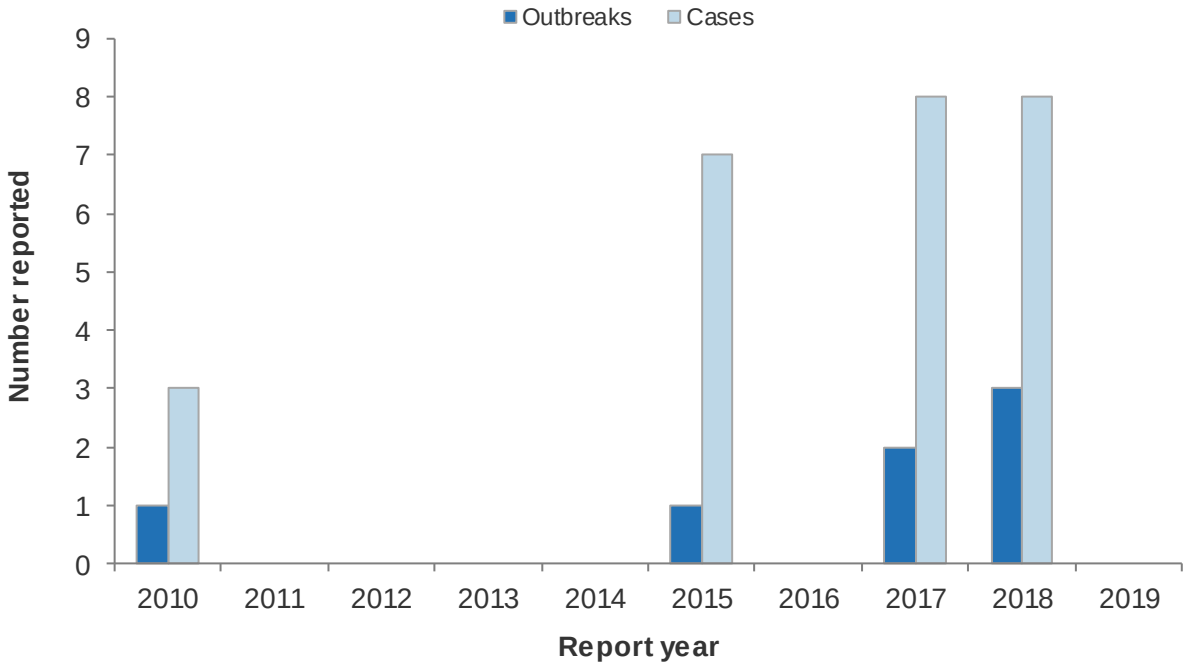
In 2019, neither of the two hepatitis A outbreaks reported food as a possible mode of transmission (Table 28). It is important to note that a single outbreak may have multiple pathogens, modes of transmission, settings where exposure occurred, or settings where preparation of food was conducted. Outbreaks caused by hepatitis A virus accounted for 0.4% (2/499) of all enteric outbreaks and 0.1% (10/7824) of all associated cases.

Table 28. Hepatitis A outbreaks reported, 2019

Measure	Hepatitis A outbreaks	
	Possible foodborne transmission	All
Outbreaks	0	2
Cases	0	10
Hospitalised Cases	0	3

Over the 10 year period 2010 to 2019, hepatitis A outbreaks with food reported as a possible mode of transmission were rare, with only seven outbreaks reported (Figure 23). Although occurring infrequently, foodborne outbreaks of hepatitis A can be associated with many cases (34 cases for an outbreak reported in 2006).

Figure 23. Hepatitis A outbreaks with food reported as a possible mode of transmission and associated cases reported by year, 2010–2019



Hepatitis A virus genotypes commonly reported

Hepatitis A virus typing data from ESR's Enteric, Environmental and Food Virology Laboratory are shown in Table 29. Faecal and/or serum/plasma specimens from notified hepatitis A cases are submitted to ESR for hepatitis A virus genotyping. The data relate to individual notified cases where a specimen has been submitted. The data include those cases not associated with foodborne transmission.

In 2019, hepatitis A virus positive specimens from 44 hepatitis A cases were submitted to ESR for genotyping. Hepatitis A virus IA was the most commonly identified sub-genotype, similar to 2016 to 2018.

Table 29. Hepatitis A genotypes identified by the Enteric, Environmental and Food Virology Laboratory, 2016–2019

Hepatitis A virus genotypes	2016	2017	2018	2019
IA	16	20	20	24
IIIA	1	4	14	8
IB	0	1	0	1
Unable to genotype	0	2	3	1
Total	**17**	**27**	**37**	**44**

Recent surveys

Nil.

Relevant New Zealand studies and publications

Reports

This preliminary study assessed the heat stability of the HAV HM-175 strain in strawberry puree using an approach adopted elsewhere for norovirus and viral surrogates, and in accordance with recommendations for heat inactivation studies [20]. The study showed that while exposure of HAV/strawberry puree to high temperatures (72^{o}C for 30 minutes or ≥85^{o}C for 1 minute) reduced the titre by more than 3 $\log_{10}$, heat treatment at 65^{o}C for only 1 minute had a minimal effect (<0.4 $\log_{10}$ reduction). From extrapolations from the linear portion of an inactivation model, it was determined that for strawberries at pH 3.35, the time required to achieve a 6 $\log_{10}$ reduction at 65^{o}C was 18 minutes, and 9 and 6 minutes at 70^{o}C and 75^{o}C respectively.

Relevant regulatory developments

Nil.

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 2019 by data source

During 2019, ten cases (0.2 per 100,000 population) of histamine (scombroid) fish poisoning were reported in EpiSurv. Note that not every case of histamine (scombroid) fish poisoning is necessarily notifiable; only those where there is a suspected common source.

The ICD-10 code T61.1 was used to extract histamine (scombroid) fish poisoning hospitalisation data from the MoH NMDS database. Of the nine hospital admissions (0.2 admissions per 100,000 population) recorded in 2019, nine cases were reported with histamine (scombroid) fish poisoning as the primary diagnosis and no cases were reported with histamine (scombroid) fish poisoning as another relevant diagnosis.

Outbreaks reported as caused by histamine (scombroid) fish poisoning

Three histamine (scombroid) fish poisoning outbreaks were reported in 2019 involving nine associated cases. No cases were reported as having been hospitalised (Table 30). 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 30. Histamine (scombroid) fish poisoning outbreaks reported, 2019

Measure	Histamine (scombroid) fish poisoning outbreaks	
	Foodborne	All
Outbreaks	3	3
Cases	9	9
Hospitalised Cases	0	0

Table 31 contains details of the three histamine poisoning outbreaks reported in 2019.

Table 31. Details of histamine (scombroid) fish poisoning outbreaks, 2019

PHU	Month	Suspected source	Evidence	Setting	No. Ill
Nelson Marlborough	Mar	Seafood chowder	Common meal	Restaurant/cafe/bakery	2P
Auckland	May	Unknown	Common food premise	Takeaway	5P
Auckland	Dec	Gurnet Fish	Common meal	Restaurant/cafe/bakery	2P

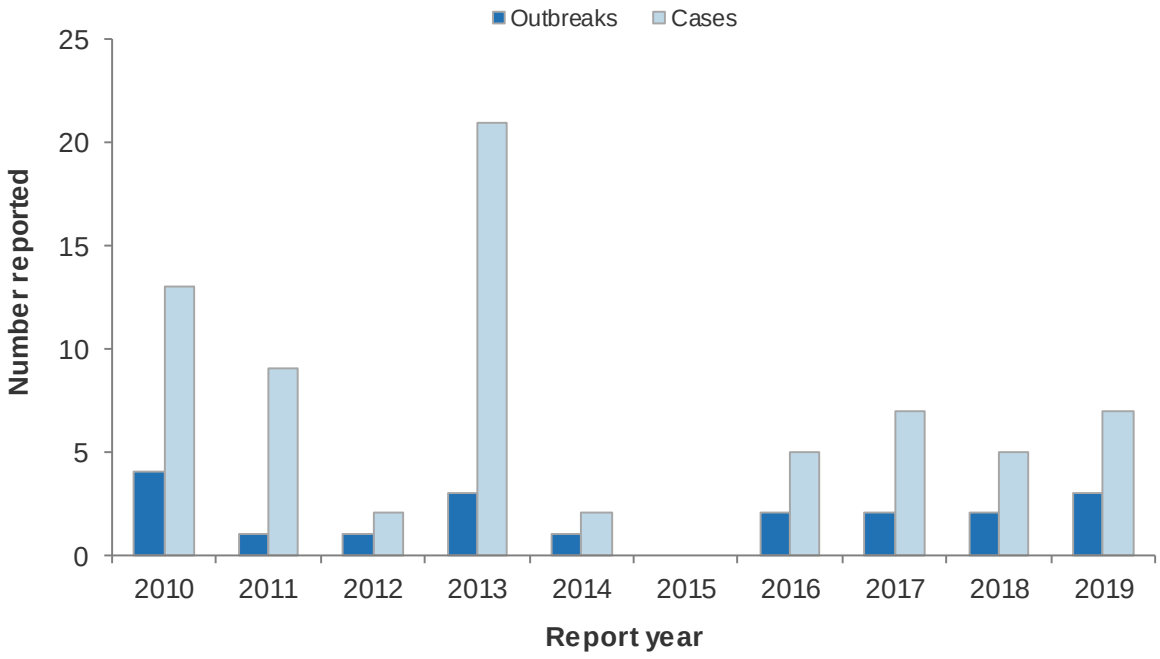
PHU Public health unit, Nelson Marlborough: Nelson Marlborough Public Health Service, Auckland: Auckland Regional Public Health Service

Number ill: C: confirmed, P: probable. Histamine (scombroid) fish poisoning cases are classified as probable if no sample of suspect fish is able to be analysed

The level of evidence for the suspected foods was recorded as weak in EpiSurv. A sample of pizza topping associated with the May outbreak was submitted to ESR's Public Health Laboratory, but nothing significant was detected and the topping did not include fish.

Over the 10 year period 2010 and 2019, the number of histamine (scombroid) fish poisoning outbreaks reported each year ranged from one to four, except for 2015 when no outbreaks were reported (Figure 24). The highest total number of outbreak-associated cases was reported in 2013 (3 outbreaks, 21 cases).

Figure 24. Histamine (scombroid) fish poisoning outbreaks and associated cases reported by year, 2010–2019



Recent surveys

Nil.

Relevant New Zealand studies and publications

Nil.

Relevant regulatory developments

Nil.

Listeriosis

Summary data for listeriosis in 2019 are given in Table 32.

Table 32. Summary of surveillance data for listeriosis, 2019

Parameter	Value in 2019	Source
Number of notified cases[a]	31	EpiSurv
Notification rate (per 100,000)	0.6	EpiSurv
Hospitalisations [b]	46	MoH NMDS
Deaths	1[e]	EpiSurv
Travel-related cases (%)[c]	1 (3%)	EpiSurv
Estimated food-related cases (%)[d]	26 (87.8%)	Expert consultation

[a] Includes non-perinatal (25) and perinatal cases (6)
[b] Cases hospitalised may not be notified on EpiSurv
[c] Percentage of the number of notified cases
[d] For estimation of food-related cases the proportions derived from expert consultation [2] exclude travel-related cases
[e] One perinatal case died. Another case notified with listeriosis died, but the death was not associated with listeriosis disease

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 cases reported in 2019 by data source

During 2019, 31 cases (0.6 per 100,000 population) of listeriosis with 1 resulting perinatal death were reported in EpiSurv. Six of those cases were perinatal listeriosis. Hospitalisation rates are usually very high for listeriosis with all 31 notified cases hospitalised in 2019 (100%).

The ICD-10 code A32 was used to extract listeriosis hospitalisation data from the MoH NMDS database. Of the 46 hospital admissions (0.9 admissions per 100,000 population) recorded in 2019, 22 were reported with listeriosis as the principal diagnosis and 24 with listeriosis as another relevant diagnosis.

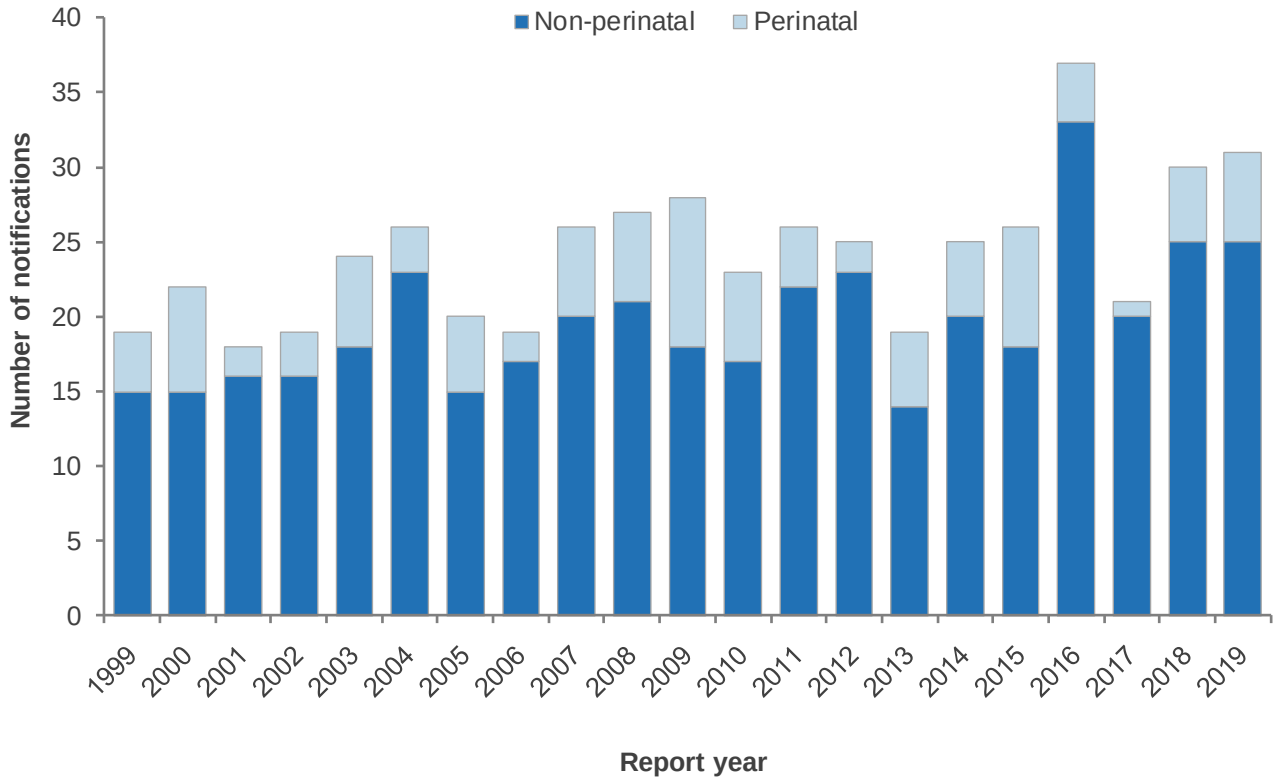
EpiSurv and the MoH NMDS database are separate systems and hospital admission can occur without cases being notified in EpiSurv. This means that not all cases diagnosed with listeriosis in hospital are reported in EpiSurv.

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. It was further estimated that approximately 55% of foodborne transmission was due to consumption of ready-to-eat meats.

Notifiable disease data

Between 1999 and 2019, the annual number of listeriosis notifications has fluctuated between 18 (2001) and 37 (2016) (Figure 25). Because of the low numbers of listeriosis cases, the rates calculated in this report may be highly variable from year to year and it is necessary to interpret trends with caution. The notification rate has been relatively stable for the past 20 years at around 0.6 per 100,000 population.

Figure 25. Listeriosis non-perinatal and perinatal notifications by year, 1999–2019



In 2019, the rate and number of notifications for listeriosis was similar for females (0.6 per 100,000 population, 15 cases) and males (0.7 per 100,000, 16 cases). The rate of hospitalisations was similar for males and females number, while the number of hospitalisations was higher for females (26 cases) compared to males (20 cases) (Table 33). It should be noted that notification case details for perinatal cases are those for the mother, so the female cases will include the six perinatal cases.

Table 33. Listeriosis cases by sex, 2019

Sex	EpiSurv notifications		Hospitalisations[a]	
	No.	Rate[b]	No.	Rate[b]
Male	16	0.7	20	0.8
Female	15	0.6	26	1.0
Total	**31**	**0.6**	**46**	**0.9**

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

In 2019, rates for listeriosis were highest in the 70 years and over age group for both the notifications (2.5 per 100,000 population, 13 cases) and hospitalisations (3.0 per 100,000, 16 admissions) (Table 34).

Table 34. Listeriosis cases by age group, 2019

Age group (years)	EpiSurv notifications		Hospitalisations[a]	
	No.[b]	Rate[c]	No.	Rate[c]
<1	0	-	2	-
1 to 4	0	-	0	-
5 to 9	0	-	0	-
10 to 14	0	-	0	-
15 to 19	1	-	0	-
20 to 29	5	0.7	11	1.6
30 to 39	3	-	2	-
40 to 49	3	-	3	-
50 to 59	3	-	9	1.4
60 to 69	3	-	3	-
70+	13	2.5	16	3.0
Total	**31**	**0.6**	**46**	**0.9**

[a] MoH NMDS data for hospital admissions (ICD-10 code A32)
[b] For perinatal cases the age reported is the mother's age
[c] per 100,000 population (rate not calculated when fewer than five cases reported)

Outbreaks reported as caused by *Listeria* spp.

There were no listeriosis outbreaks reported in 2019. Since 2006 there have been two listeriosis outbreaks reported. There was an outbreak with two associated cases in 2009 and an outbreak with food reported as a possible 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 30 isolates of *L. monocytogenes* during 2019. Table 35 shows the number of isolates and percentage of *L. monocytogenes* serotypes reported by the Special Bacteriology Laboratory at ESR between 2015 and 2019. The annual number of isolates identified to be serotype O4 or serotype O1/2 has been in the range of seven to 20 isolates over the 5-year period.

Table 35. *L. monocytogenes* serotypes identified by the Special Bacteriology Laboratory, 2015–2019

Serotype	2015		2016		2017		2018		2019	
	No.	%	No.	%	No.	%	No.	%		
O1/2	11	42.3	17	44.7	13	65.0	12	37.5	14	46.7
O4	15	57.7	20	52.6	7	35.0	19	59.4	16	53.3
Untypable	0	-	1	2.6	0	-	1	3.1	0	-
Total	**26**		**38**		**20**		**32**		**30**	

Recent surveys

Nil.

Relevant New Zealand studies and publications

Four cases of listeriosis in a hospital (A) in New Zealand were identified in 2012 [21]. Pulsed-field gel electrophoresis (PFGE) analyses used at the time matched clinical isolates to *Listeria monocytogenes* isolates obtained from ready-to-eat (RTE) meat samples. The outbreak investigation confirmed that the RTE producer had supplied product to the hospital and additional testing confirmed the presence of *L. monocytogenes* in RTE meats from the hospital kitchen Retrospective whole-genome sequencing confirmed that epidemiologically linked isolates belonging to three different genotypes for clinical cases from hospital A and RTE meat samples from the hospital kitchen differed by 0-1 core-genome locus or single nucleotide polymorphisms (SNP).

Relevant regulatory developments

Nil.

Norovirus infection

Case definition

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

Norovirus infection cases reported in 2019 by data source

During 2019, 20 cases (0.4 per 100,000 population) of norovirus infection with no associated deaths were reported in EpiSurv. It should be noted that not every case of norovirus infection is notifiable; only those that are part of a common source outbreak or from a person in a high risk category. In contrast to case reports of norovirus, outbreaks of norovirus infection are reported separately and involve significant numbers of cases. In 2019 there were 4209 cases associated with 181 notified outbreaks.

The ICD-10 code A08.1 was used to extract norovirus infection hospitalisation data from the from the MoH NMDS database. Of the 425 hospital admissions (8.6 admissions per 100,000 population) recorded in 2019, 240 cases were reported with norovirus infection as the primary diagnosis and 185 were reported with norovirus infection as another relevant diagnosis. Of the 425 hospital admissions, 126 were in the 0 to 5 age group and 84 were in the 70+ age group.

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 norovirus infections due to foodborne transmission were due to consumption of seafood.

Outbreaks reported as caused by norovirus

In 2019, there were 181 norovirus infection outbreak notifications, 9 (5.0%) of which reported food or a food handler as one of the possible modes of transmission (Table 36). There were no hospitalisations reported for these 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.

Norovirus infection outbreaks accounted for 36.3% (181/499) of all enteric outbreaks and 53.8% (4209/7824) of all outbreak-associated enteric cases reported in 2019.

Table 36. Norovirus infection outbreaks reported, 2019

Measure	Norovirus infection outbreaks		
	Possible foodborne transmission with a suspected or confirmed source	Possible foodborne transmission but no suspected source	All
Outbreaks	6	3	181
Cases	100	19	4209
Hospitalised Cases	0	0	22

Table 37 contains details of the nine norovirus infection outbreaks with food reported as a possible mode of transmission reported in 2019.

Table 37: Details of norovirus infection outbreaks with food or food handling reported as a possible mode of transmission, 2019

PHU	Month	Suspected source	Evidence	Setting	No. Ill
MidCentral	Jan	Unknown	Common event	Marae	1C 3P
Auckland	Jan	Unknown	Common meal and household cluster	Restaurant/cafe/bakery	3C 3P
Auckland	Jan	Flavoured water with cucumber, strawberry and mint or person to person	Common event and epidemiological investigation	Community event	4C 30P
Auckland	Jan	Food handler	Common food premise and food handler confirmed with norovirus GI/GII	Restaurant/cafe/bakery	1C 4P
Waikato	Feb	Sandwiches with ham/ chicken, hamburgers or food handler	Common meals	Camp	2C 28P
C and PH	Apr	Food handler	Common event	Restaurant/cafe/bakery	4C 1P
MidCentral	Apr	Unknown	Common meal	Restaurant/cafe/bakery	2C 7P
Toi Te Ora	Oct	Food handler	Common food premise	Restaurant/cafe/bakery	1C 13P
Auckland	Oct	Food handler	Common meal	Restaurant/cafe/bakery	1C 11P

PHU: Public Health Unit, MidCentral: MidCentral Public Health Service, Auckland: Auckland Regional Public Health Service, Waikato: Population Health Service Waikato, C and PH: Community and Public Health, Toi Te Ora: Toi Te Ora - Public Health

Number ill: C: confirmed, P: probable

A suspected food source was not identified in seven of these outbreaks. For two January outbreaks in Auckland the level of evidence for the suspected source was strong; an infected foodhandler in one outbreak and flavoured water in the other outbreak. The level of evidence for suspected foods was recorded as weak for one outbreak related to ham sandwiches or chicken hamburgers (Waikato in February).

During investigation of suspected foodborne illness outbreaks by ESR's Public Health Laboratory and the Enteric, Food and Environmental Virology/Norovirus Reference Laboratory in 2019, faecal specimens relating to eight of the nine outbreaks (Table 37) were received for norovirus testing. Norovirus was detected in faecal samples from all of those outbreaks.

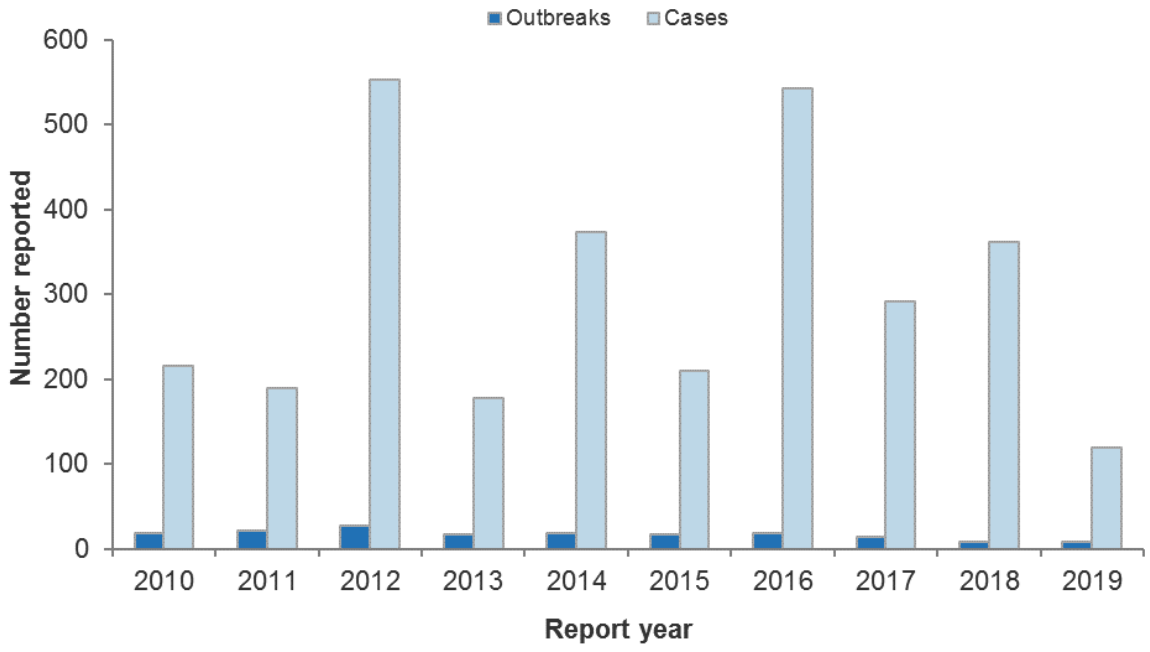
Table 38 shows the total cases by genotype for the eight tested outbreaks. For one outbreak (April, Community and Public Health), no sample was received for genotyping. The outbreaks are due to a variety of genotypes, with each outbreak being attributed to one genotype.

Table 38. Norovirus genotypes reported in foodborne outbreaks, 2019

Norovirus genotype	Outbreaks	Total cases
GI.4[P4]	1	4
GI.6[P6]	1	14
GII.12[P16]	1	5
GII.2[P16]	1	12
GII.3[P12]	1	9
GII.4 Sydney[P16]	1	34
GII.4 Sydney[P31]	1	6
GII.6[P7]	1	30
Total	**8**	**114**

Over the 10 year period 2010 and 2019, the annual number of norovirus infection outbreaks with food reported as a possible mode of transmission reported each year ranged from 8 (2018) to 30 (2009) (Figure 26). The total number of cases associated with these outbreaks ranged from 159 (2019) to 552 cases (2012) per year.

Figure 26. Norovirus infection outbreaks with food reported as a possible mode of transmission and associated cases reported by year, 2010–2019



Norovirus types commonly reported

Norovirus genotyping data from ESR's Norovirus Reference Laboratory (NRL) are shown in Table 39. The data relate to outbreaks not individual cases and includes 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 2019, 182 norovirus outbreaks were ESR laboratory-confirmed. Norovirus genogroup II (GII) was identified in 147/182 (80.8%) outbreaks. In the previous four years GII was identified in between 77.8% (2017) and 90.8% (2015) of outbreaks. In 2019, norovirus genogroup I (GI) was identified in 32/182 (17.6%) outbreaks. Both GI and GII were identified in 3/182 (1.6%) ESR laboratory-confirmed norovirus outbreaks.

The norovirus genotype was determined for 181/182 (99.5%) of ESR laboratory-confirmed norovirus outbreaks. As in previous years, GII.4 variants were the predominant norovirus genotype identified (85/181, 47.0% of outbreaks), however, this was not the case for foodborne norovirus outbreaks (see Table 38).

Table 39. Norovirus genotypes identified in outbreaks by the Norovirus Reference Laboratory, 2015–2019

Norovirus genotypes[a]	2015	2016	2017	2018	2019
Genogroup I	**13**	**29**	**51**	**15**	**32**
GI untyped	-	1	-	-	1
GI.1[P1]	-	2	2	1	-
GI.2[P2]	7	3	-	1	1
GI.3[P3]	2	15	19	4	9
GI.3[P13]			10	2	4
GI.4[P4]	-	-	1	3	5
GI.5[P4]				2	5
GI.5[P5]	2	-	1	-	1
GI.6[P6]	2		2	1	4
GI.6[P11]		6	13	-	1
GI.7[P7]	-	-	1	-	-
GI.8[P8]	-	-	2	-	-
GI.9[P9]	-	2	-	1	1
Genogroup II	**167**	**159**	**186**	**158**	**147**
GII.2[P16]	-	27	18	38	17
GII.3[P12]	18	19	2	8	20
GII.4 Sydney [P16][b]	1	19	103	70	49
GII.4 Sydney[P31][b]	87	30	13	3	21
GII.4 Sydney[P4 New Orleans][b]	2	35	13	2	13
GII.6[P7]	19	2	1	10	13
GII.9[P7]	-	-	-	-	2
GII.10[P16]	-	-	-	-	3
GII.14[P7]	1	-	4	7	2
GII.17[P17]	6	19	5	4	1
Other[c]	33	8	27	16	6
Mixed GI and GII	**4**	**-**	**2**	**1**	**3**
Total outbreaks[d]	**184**	**188**	**239**	**174**	**182**

[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 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

Papers

Filter feeding bivalve molluscan shellfish such as oysters, mussels and clams can readily accumulate norovirus present in growing water contaminated by human faecal material from point and non-point sources [22]. While pre-harvest preventative interventions are preferable, post-harvest interventions such as depuration, relaying and thermal treatment have been used to mitigate the risk of norovirus infection associated with shellfish consumption. Post-harvest depuration treatment does not necessarily remove norovirus from shellfish tissue, and freezing has little or no effect on norovirus infectivity in shellfish. Thermal treatments can inactivate norovirus but they also change the organoleptic characteristics of shellfish which makes them unacceptable to some consumers. High pressure processing is an alternative post-harvest intervention that has potential to inactivate norovirus effectively with a reduction of 2.8–4.0 $\log_{10}$ genome copies at 300–450 MPa. However, a human challenge showed that less than 600 MPa are not sufficient to prevent norovirus infection when people consume artificially-contaminated shellfish.

Relevant regulatory developments

Nil.

Salmonellosis

Summary data for salmonellosis in 2019 are given in Table 40. Note that in the following sections the term *Salmonella* refers to non-typhoidal serotypes of *Salmonella enterica* subspecies *enterica*.

Table 40. Summary of surveillance data for salmonellosis, 2019

Parameter	Value in 2019	Source
Number of notified cases	1188	EpiSurv
Notification rate (per 100,000)	24.2	EpiSurv
Hospitalisations[a]	230	MoH NMDS
Deaths	0	EpiSurv
Estimated travel-related cases (%)[a]	409 (34%)	EpiSurv
Estimated food-related cases (%)[c]	484 (62.1%)	Expert consultation

[a] Cases hospitalised may not be notified on EpiSurv
[b] Percentage of the number of notified cases
[c] 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

Since 2015 laboratories across New Zealand have gradually changed the methodology for testing faecal specimens. In 2019, community faecal specimens in all DHBs with the exception of Canterbury, MidCentral, South Canterbury, Tairawhiti, Taranaki, West Coast and Whanganui were screened by multiplex PCR for a range of pathogens, including *Salmonella* spp.. The introduction of these more sensitive assays may have triggered an increase in notifications for some enteric diseases. It is unclear at this stage if laboratory changes have affected the notification rates for salmonellosis.

Salmonellosis cases reported in 2019 by data source

During 2019, 1188 cases (24.2 per 100,000 population) of salmonellosis and no resulting deaths were reported in EpiSurv. Approximately 23% of cases notified in EpiSurv were recorded as hospitalised in 2019.

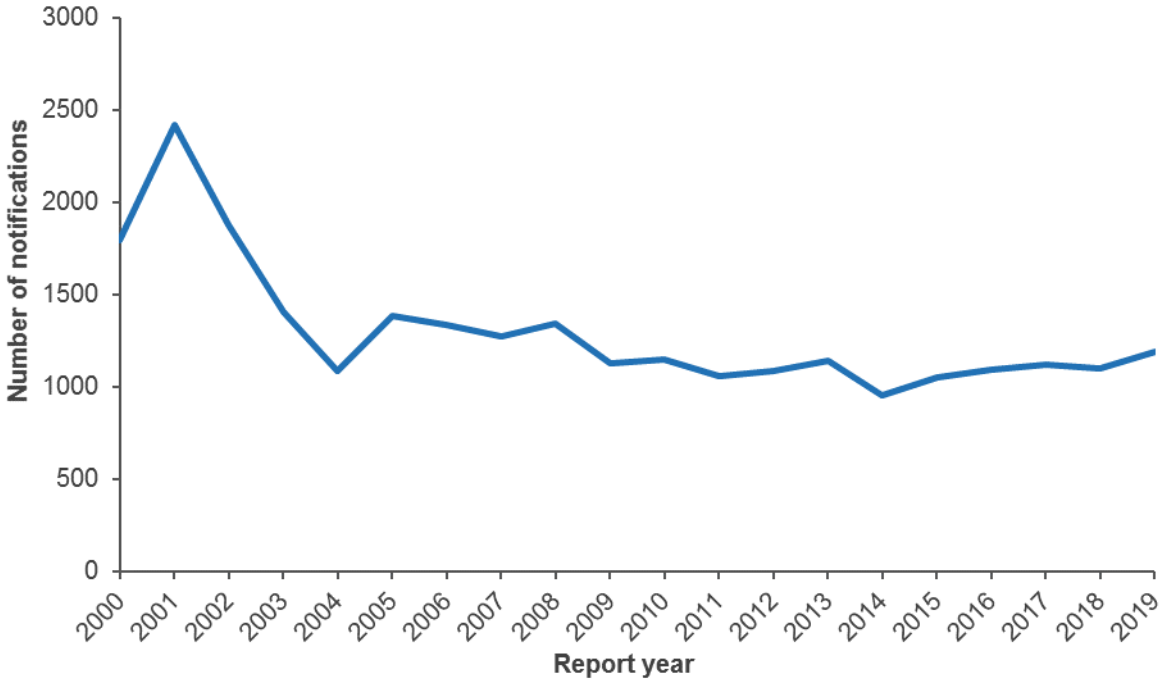
The ICD-10 code A02.0 (*Salmonella* enteritis) was used to extract salmonellosis hospitalisation data from the MoH NMDS database. Of the 230 hospital admissions (4.7 admissions per 100,000 population) recorded in 2019, 203 cases were reported with salmonellosis as the primary diagnosis and 27 were reported with salmonellosis as another relevant diagnosis.

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 transmission was due to transmission via poultry.

Notifiable disease data

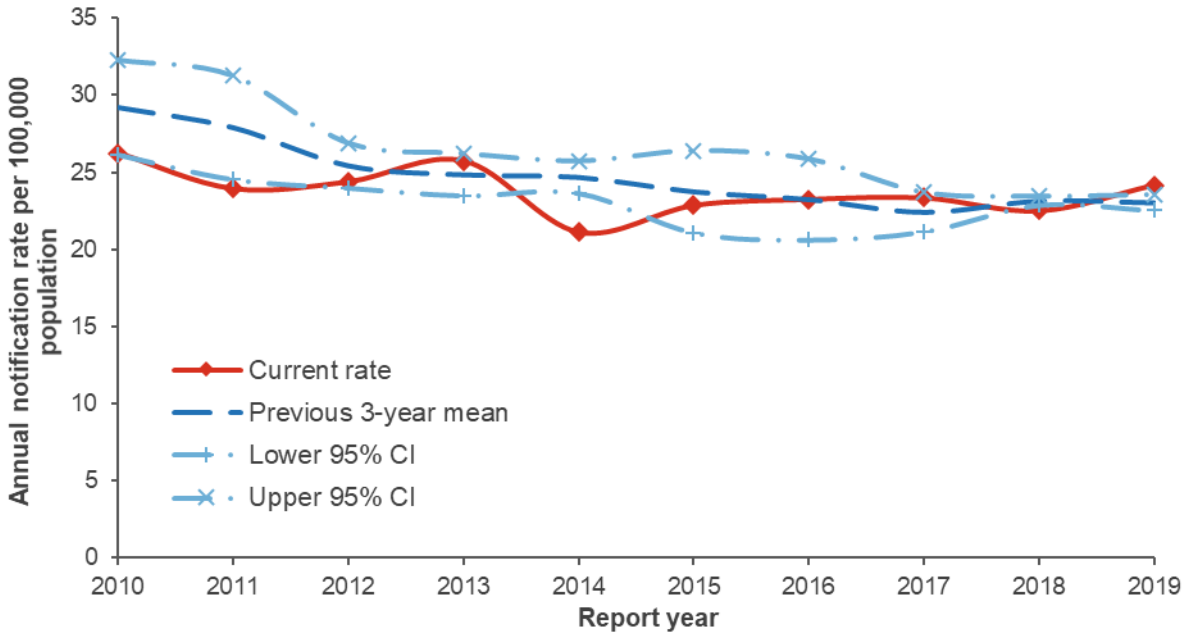
A sharp fall in notifications was observed between 2001 and 2004, followed by a more gradual decline from 2005 to 2009. Since 2010, the number of notifications has ranged between 955 and 1188 notified cases per year (Figure 27), and between 21.2 and 26.2 cases of salmonellosis per 100,000 population per year (Figure 28).

Figure 27. Salmonellosis notifications by year, 2000–2019



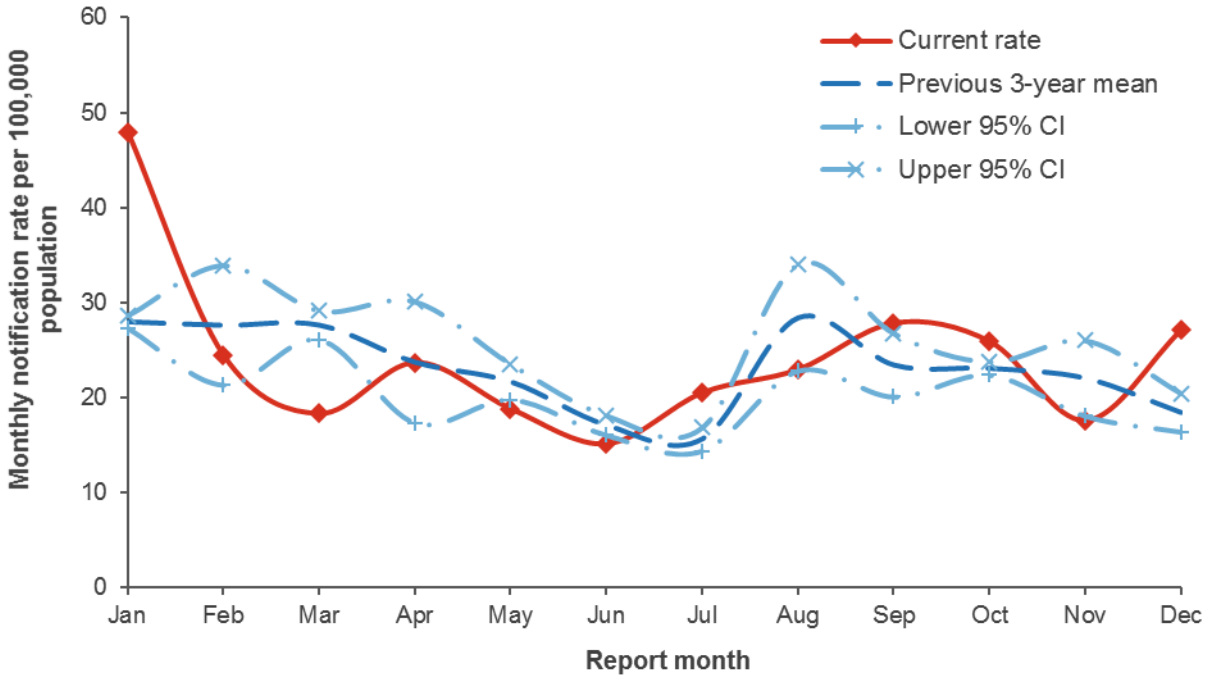
The notification rate in 2019 was similar (24.2 cases per 100,000 population) to the previous three-year average (23.1 cases per 100,000) (Figure 28).

Figure 28. Salmonellosis notification rate by year, 2010–2019



The number of notified cases of salmonellosis per 100,000 population by month for 2019 is shown in Figure 29. The monthly number of notifications in 2019 ranged from 62 notifications (June) to 196 notifications (January). The peak in January above the previous 3-year mean is associated with two known salmonellosis outbreaks (Table 44).

Figure 29. Salmonellosis monthly rate (annualised), 2019



In 2019, the rate of notifications and hospital admissions is similar for males and females (Table 41).

Table 41. Salmonellosis cases by sex, 2019

Sex	EpiSurv notifications		Hospitalisations[a]	
	No.	Rate[b]	No.	Rate[b]
Male	584	24.1	115	4.8
Female	603	24.1	115	4.6
Total	**1188**	**24.2**	**230**	**4.7**

[a] MoH NMDS data for hospital admissions

[b] per 100,000 population

[c] total includes notifications where gender is unknown

In 2019, notification rates and hospitalisation rates of salmonellosis were highest for infants aged less than 1 year (122.4 cases and 30.2 admissions per 100,000 population) and the 1 to 4 age group (64.2 cases and 8.1 admissions per 100,000 population) (Table 42).

Table 42. Salmonellosis cases by age group, 2019

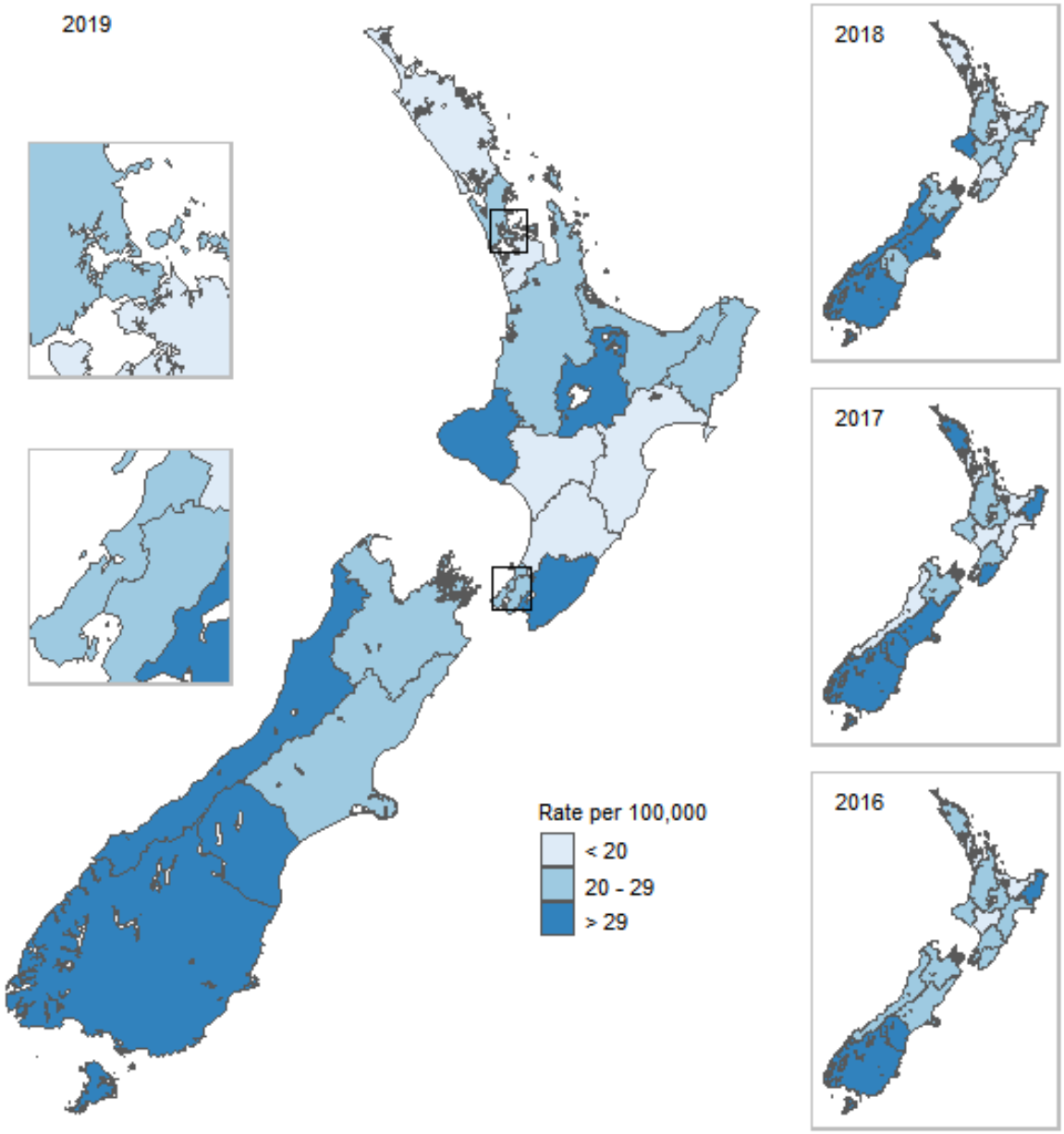
Age group (years)	EpiSurv notifications		Hospitalisations[a]	
	No.	Rate[b]	No.	Rate[b]
<1	73	122.4	18	30.2
1 to 4	158	64.2	20	8.1
5 to 9	64	19.4	9	2.7
10 to 14	38	11.8	11	3.4
15 to 19	44	13.9	7	2.2
20 to 29	151	21.7	21	3.0
30 to 39	146	22.5	32	4.9
40 to 49	117	18.8	16	2.6
50 to 59	149	23.7	29	4.6
60 to 69	149	28.7	33	6.3
70+	99	18.8	34	6.4
Total	**1188**	**24.2**	**230**	**4.7**

[a] MoH NMDS data for hospital admissions

[b] per 100,000 population

In 2019, rates of salmonellosis varied throughout the country as illustrated in Figure 30. The highest salmonellosis notification rate was reported for Southern DHB (41.9 per 100,000, 142 cases), West Coast DHB (36.8 per 100,000, 12 cases), followed by South Canterbury (34.4 per 100,000 population, 21 cases), Taranaki (31.8 per 100,000 population, 39 cases) and Lakes (29.7 per 100,000 population, 34 cases) DHBs. Southern DHB had consistently high salmonellosis notification rates between 2016 and 2019 compared to the rest of the country.

Figure 30. Geographic distribution of salmonellosis notifications, 2016–2019



Note: Since 2015 laboratories across New Zealand have gradually changed the methodology for testing faecal specimens. It is unclear at this stage how laboratory changes have affected the notification rates for salmonellosis. Refer to report Introduction for details.

For cases where information on travel was provided in 2019, 34% had travelled overseas during the incubation period. Assuming that the cases for which travel information was provided were representative of all salmonellosis cases, a Poisson distribution can be used to estimate the total number of potentially travel-related cases of salmonellosis in 2019. The resultant distribution has a mean of 409 cases (95% CI 370-451).

If data from the last four years are considered the estimated proportion of cases travelling overseas within the incubation period of the organism was 35% (95% CI 33-36%).

Outbreaks reported as caused by *Salmonella*

In 2019, there were 27 salmonellosis outbreak notifications in EpiSurv, 15 (56%) of which reported food as a possible mode of transmission (Table 43). These 15 outbreaks included 186 cases, of which 26 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, 2019

Measure	Salmonellosis outbreaks		
	Possible foodborne transmission with a suspected or confirmed source	Possible foodborne transmission but no suspected source	All
Outbreaks	11	4	27
Cases	171	15	226
Hospitalised Cases	22	4	30

Table 44 contains details of the 15 salmonellosis outbreaks with food reported as a possible mode of transmission reported in 2019.

Table 44. Details of salmonellosis outbreaks with food reported as a possible mode of transmission, 2019

PHU	Month	Suspected source	Evidence	Setting	No. Ill	Serotype[a]
Auckland	Jan	Unknown	Common meal	Restaurant/cafe/bakery	1C 1P	-
Auckland	Jan	Flavoured water- with cucumber, strawberry and mint	Common event and epidemiological investigation	Community Event	4C 30P	*S.* Infantis
Regional	Jan	Unknown	Common food premises	Restaurant/cafe/bakery	2C 1P	*S.* Typhimurium
MidCentral	Jan	Shredded cooked chicken	Common food type	Supermarket/delicatessen	2C	*S.* Typhimurium phage type 108/170
Toi Te Ora	Jan	Leftover Christmas dinner (most likely the ham)	Common meal	Home	1C 6P	-

PHU	Month	Suspected source	Evidence	Setting	No. Ill	Serotype[a]
Auckland	Jan	Alfalfa sprouts	Common organism type/strain in cases and epidemiological investigation	Home or café consumption of commercially grown sprouts	68C 2P	*S.* Typhimurium phage type 108/170
South	Feb	Undercooked old eggs	Common meal	Home	2C	*S.* Typhimurium phage type 56 variant
Auckland	Feb	Unknown	Common event	Home	1C 3P	*Salmonella enterica* subsp. *enterica* (I) ser. 4,5,12 : i : -
MidCentral	Mar	Chicken / Untreated drinking water	Household cluster	Home	4C	*S.* Typhimurium phage type 60
Auckland	May	Homemade chicken sushi	Household cluster	Home	2C 1P	*S.* Enteritidis phage type 8
Auckland	Aug	Unknown	Common event	Home	6C	*S.* Enteritidis phage type 8
Auckland	Sep	Eggs Benedict	Consumption of same food type	Overseas Restaurant/cafe/bakery	7C 2P	*S.* Enteritidis phage type 21
Auckland	Oct	Desserts prepared by infected food handler	Common food premise and food type, epidemiological investigation	Restaurant/cafe/bakery	17C 21P	*S.* Enteritidis ST11
Auckland	Dec	Cross-contamination from raw chicken	Household cluster	Home	1C 1P	*S.* Typhimurium ST19
Auckland	Dec	Leftover chicken meals	Household cluster, common food	Home	2C	-

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

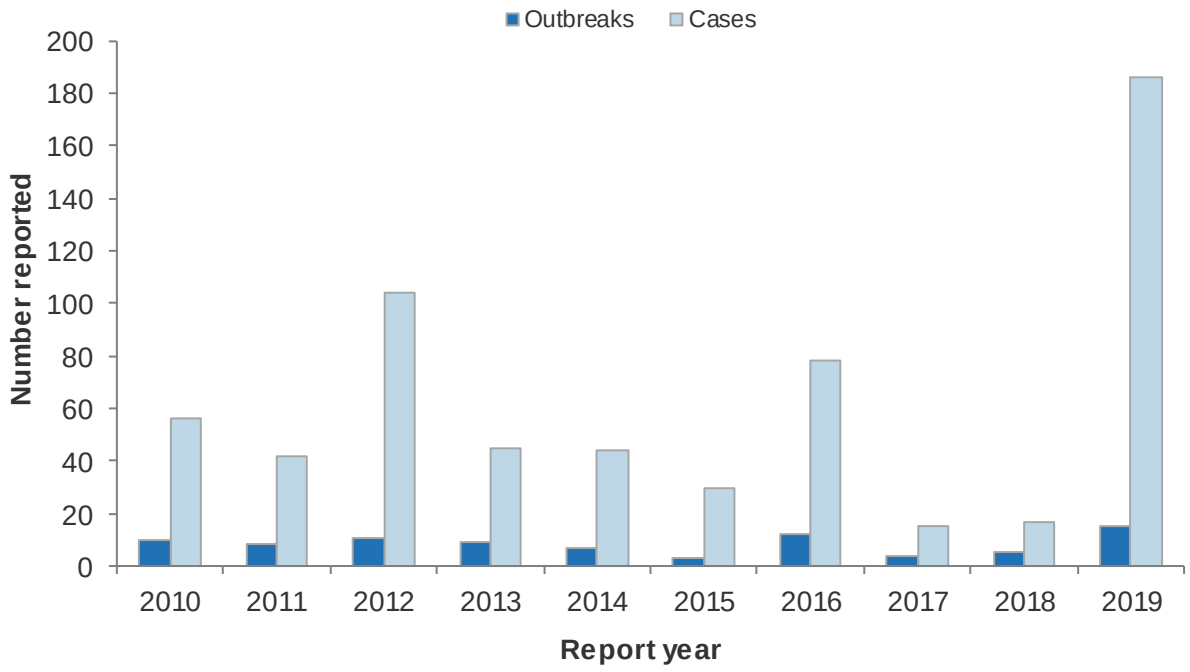
Number ill: C: confirmed, P: probable

[a] Serotypes were identified in clinical samples from outbreak cases; - no isolates were received for typing

For two outbreaks in January in Auckland the evidence linking the outbreak to a suspected food source was strong (alfalfa sprouts and flavoured water, respectively). For five other outbreaks with a suspected food source the evidence was weak. For four outbreaks, no suspected food source was identified. One outbreak (Auckland reported in September) was associated with overseas travel to Tonga.

Over the 10 year period 2010 and 2019, the number of salmonellosis outbreaks with food reported as a possible mode of transmission ranged from three (2015) to 15 (2019) (Figure 31). The total number of cases associated with the outbreaks over the same period ranged between 15 (2017) and 186 (2019).

Figure 31. Salmonellosis outbreaks with food reported as a possible mode of transmission and associated cases reported by year, 2010–2019



Salmonella types commonly reported

Human isolates

In 2019, 1055 isolates from cases with non-typhoidal *Salmonella* were typed by the ESR Enteric Reference Laboratory (Table 45). *S.* Typhimurium and *S.* Enteritidis were the most common serotypes identified, of which *S.* Typhimurium 108/170 (83 isolates), *S.* Typhimurium phage type 56 variant (49 isolates), *S.* Typhimurium phage type 101 (36 isolates) and *S.* Enteritidis phage type 11 (31 isolates) were most commonly detected.

Other serotypes most commonly reported were *S.* Bovismorbificans (50 isolates), *S*. enterica (I) ser. 4,[5],12 : i : - (48 isolates),*S.* Brandenburg (42 isolates) and *S.* Stanley (41 isolates).

Note: From 1st November 2019, all phage typing ceased. From this time serotypes that were historically phage typed, Typhimurium and Enteritidis, have all been fine typed using whole genome sequencing. Therefore, the data for 2019 only discriminates at phage level for the months of January to October. Typing of *S*. Typhimurium and *S*. Enteritidis completed in November and December 2019 will be included in 'Other or unknown' column for these types and *Salmonella* Subsp. (I) ser. 4,5,12 : i : - is being reported as monophasic *Salmonella* Typhimurium.

Table 45. *Salmonella* isolate serotypes and subtypes identified by the Enteric Reference Laboratory, 2016–2019

Serotype[a]	2016	2017	2018	2019[b]	% of cases with overseas travel history, 2019[c]	% of cases with unknown travel history, 2019[d]
S. Typhimurium	**389**	**429**	**345**	**418**	**10.0**	**17.0**
108/170	22	13	4	83	0	7.2
56 variant	64	115	70	49	0	14.3
101	47	65	61	36	0	11.1
135	30	34	39	21	9.5	19.0
2	2	7	0	18	22.2	33.3
23	8	6	16	17	0	11.8
9	42	14	21	13	38.5	23.1
42	12	27	13	11	9.1	27.3
Other or unknown	162	148	121	268	6.0	15.3
S. Enteritidis	**114**	**151**	**130**	**167**	**37.7**	**19.8**
11	46	55	30	31	3.2	25.8
26	1	7	6	21	28.6	52.4
8	1	6	5	19	36.8	0
Other or unknown	66	83	89	96	51.0	14.6
Other serotypes	**570**	**523**	**575**	**470**	**37.4**	**19.6**
S. Bovismorbificans	39	52	83	50	2	16
S. Brandenburg	67	54	45	42	0	28.6
S. Stanley	60	39	35	41	39	36.6
S. Infantis	14	18	16	26	30.8	30.8
S. Saintpaul	35	27	39	22	18.2	13.6
S. Weltevreden	18	21	21	20	60	20
S. Mississippi	21	15	15	15	20	20
S. Agona	18	16	27	14	71.4	21.4
S. enterica (I) ser. 4,[5],12 : i : -	23	28	26	48	35.4	10.4
Other or unknown	275	253	268	192	54.7	16.1
Total	**1073**	**1103**	**1050**	**1055**	**27.6**	**18.7**

Please note that some cases had mixed infections, i.e. an individual case might be represented by two *Salmonella* serotypes

[a] Excludes *S.* Paratyphi and *S.* Typhi

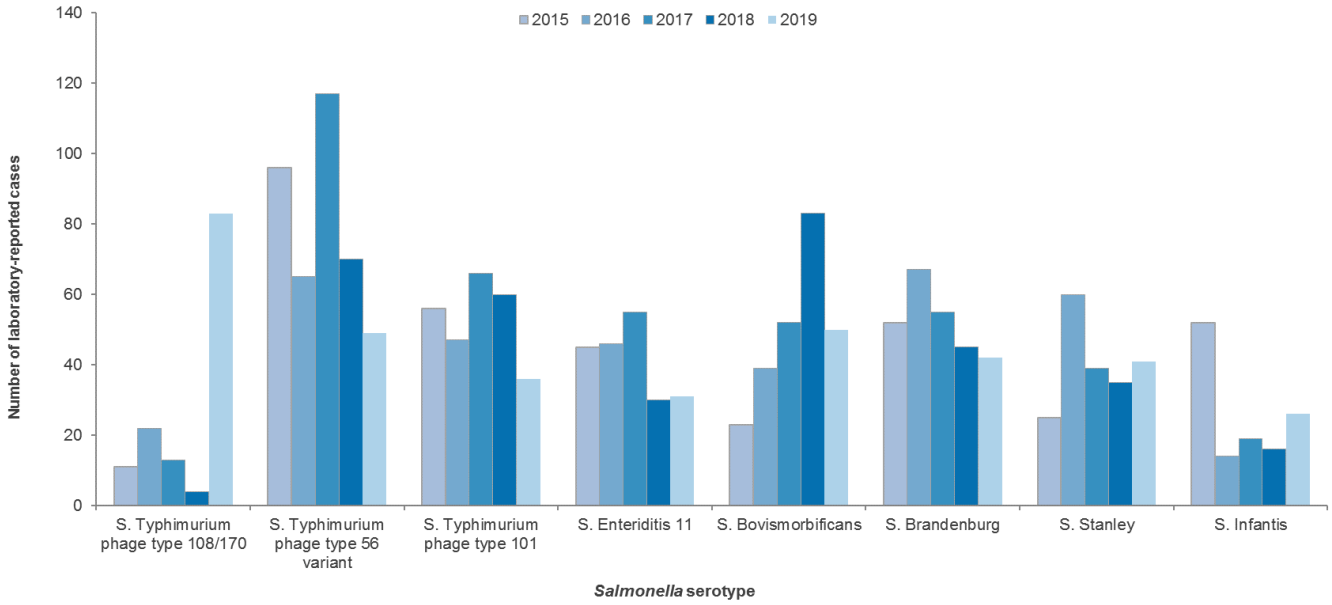
[b] From 1st November 2019, all phage typing ceased. From this time serotypes that were historically phage typed (Typhimurium and Enteritidis) have all been fine typed using whole genome sequencing. Therefore the data for 2019 only discriminate at phage level for the months of January to October. Typing of *S.* Typhimurium and *S.* Enteritidis completed in November and December will be included in Other or unknown column for these types and *Salmonella* Subsp. (I) ser. 4,5,12 : i : - is being reported as monophasic *Salmonella* Typhimurium

[c] Percentage refers to the number of cases that answered "yes" for overseas travel during the incubation period out of the total number of cases for which travel information was recorded. However, even if a person has travelled within the incubation period it does not necessarily imply the infection has been acquired in the respective country. Incubation periods for salmonellosis typically range between 6-72 hours [11], for atypical cases incubation periods of up to 16 days have been reported

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

Figure 32 shows the annual trend for selected *Salmonella* serotypes during 2015 to 2019. For the types shown, there is within type variation year to year, but no one type is more prevalent overall. *S*. Typhimurium phage type 108/170 has much higher prevalence in 2019 compared to previous years due to outbreak involving alfalfa sprouts (Table 44).

Figure 32. Number of laboratory-reported case related isolates for selected *Salmonella* serotypes by year, 2015–2019



Non-human isolates

A total of 861 non-human *Salmonella* isolates were typed by the Enteric Reference Laboratory during 2019. *S.* Typhimurium and *S.* Bovismorbificans were the most commonly isolated serotypes in non-human samples in 2019. *Salmonella* Typhimurium phage type 101 (47 isolates) and phage type 56 variant (36 isolates) were the most commonly detected phage types. Fourty one *S.* Typhimurium isolates were classified as reacts but does not conform (RDNC). The most common of the other serotypes were *S*. Bovismorbificans and *S.* Brandenburg with 288 and 131 isolates, respectively (Table 46). Some caution should be exercised with respect to trends in non-human typing data as the basis for sample selection may differ from year to year.

Table 46. *Salmonella* serotypes and subtypes from non-human sources identified by the Enteric Reference Laboratory, 2015–2019

Serotype	2015	2016	2017	2018	2019[c]	Major sources, 2019
S. Typhimurium	**258**	**249**	**372**	**282**	**291**	
9	9	12	20	28	27	Bovine (24)
23	3	7	17	19	27	Bovine (27)
56 variant[a]	56	43	59	36	36	Feline (12), bovine (7), canine(6), equine (6)
101	32	45	92	62	47	Bovine (40), canine (4)
108/170	3	21	34	3	25	Bovine (14), poultry environmental (6)
135	18	10	11	25	28	Bovine (27)
RDNC	41	31	42	35	41	Bovine (36)
Unknown or other	96	80	97	74	60	-
Other serotypes	**379**	**435**	**600**	**566**	**570**	
S. Bovismorbificans	71	135	292	297	288	Bovine (263), avian (7), canine (5)
S. Brandenburg	102	127	137	106	131	Bovine (75), ovine (36), food[b] (10) , canine(6)

Serotype	2015	2016	2017	2018	2019[c]	Major sources, 2019
S. Hindmarsh	49	48	27	26	27	Ovine (24)
S. Mbandaka	10	6	9	4	16	Poultry environmental (5)
S. Saintpaul	12	9	12	12	14	-
S. Give	0	0	0	0	11	Bovine(14)
Other or unknown serotypes	135	110	123	121	83	-
Total	**637**	**684**	**972**	**848**	**861**	

RDNC = reaction does not conform

[a] *Salmonella* Typhimurium phage type 56 variant was previously known as *S*. Typhimurium phage type RDNC-May 06. Further characterisation by the *Salmonella* Reference Unit at Colindale (Public Health England) identified this phage type to be a 56 variant

[b] Includes animal carcasses from meat works

[c] In 2019, typing for non-human *Salmonella* isolates was not conducted in November and December

Recent surveys

A baseline survey of *Salmonella* prevalence in the egg production environment was performed [23]. The survey included 28 commercial chicken egg layer farms throughout New Zealand that comprised different production sizes and practices. Samples of feed, the environment and egg contact surfaces were taken for microbiological testing. A total of 12/28 farms had at least one *Salmonella*-positive sample. Four of the 12 positive farms had only one *Salmonella* positive sample, three of them were pooled dust samples. Of the farm environments, 21/67 farm sheds and 3/26 packhouses had at least one *Salmonella*-positive sample. Of the 43/323 *Salmonella*-positive samples, pooled dust samples had the highest prevalence (19/67), followed by boot/manure belt swabs (11/67), pooled faeces (7/67), and packhouse egg contact surfaces (5/87). One feed sample tested positive (which may have been contaminated from the shed) (1/33). A significantly higher prevalence of *Salmonella*-positive layer shed samples was observed from caged (colony and conventional cages) systems (33/75), compared with cage-free (free-range and barn) systems (4/126). Farms with *Salmonella*-positive packhouse samples also had the highest numbers of positive layer shed samples, consistent with a high laying shed prevalence increasing the likelihood of egg surface contamination. This suggests that cross contamination between contaminated and uncontaminated eggs via packhouse surfaces may occur, although eggs were not analysed. Five serotypes were identified among the isolates, including *S*. Infantis, *S*. Thompson, *S*. Typhimurium, *S*. Anatum and *S*. Mbandaka.

Relevant New Zealand studies and publications

Reports

Documentation and experimental findings regarding survival on the shell and internalisation of *Salmonella* in chicken eggs, in the context of the New Zealand processing and retail environment were reviewed [24]. Experimental studies were undertaken to fill the identified knowledge gaps and better inform the question of whether storage at 15°C or less for a shelf life of 35 days is necessary to protect consumers of New Zealand eggs from salmonellosis. Key experimental findings of the study were:

- Survival of *Salmonella* on egg surfaces was higher following incubation at 15°C (31% relative humidity [RH]) compared with 22°C (45% RH) after both 21 and 35 days of incubation. Reduced survival of New Zealand egg-associated *Salmonella* isolates on egg surfaces at the higher storage temperature and higher RH is consistent with some earlier reports from non-Enteritidis serotypes in international studies.
- *Salmonella* present on visibly clean eggshell surfaces declined in viability over time at both storage temperatures, and was virtually undetectable from eggs stored at 22°C for 35 days.
- A substantially higher concentration of viable *Salmonella* was recovered from eggs contaminated with chicken faeces. The contribution of faeces to *Salmonella* survival on eggs was particularly high on eggs stored at 15°C for 35 days (2.38 log higher CFU recovery on eggs contaminated with faeces than those without).

- No *Salmonella* was detected in egg contents (albumen or yolk) at any incubation temperature or time point, regardless of the presence of faeces.

Papers

Data on isolates of *Salmonella enterica* serovars Mississippi and Typhimurium definitive type 160 (DT160) collected from human, animal, and environmental sources were used to elucidate their epidemiology and disease reservoirs in Australia and New Zealand [25]. Phylogenomic data identified plausible sources of human infection from wildlife and environmental reservoirs and provided evidence supporting New Zealand-acquired DT160 in a group of travellers returning to Australia.

The studies reported above on *Salmonella* in the egg laying environment and the survival of *Salmonella* on eggs were also published in the scientific literature [26, 27].

Relevant regulatory developments

Nil.

Sapovirus infection

Case definition

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

Sapovirus infection cases reported in 2019 by data source

During 2019, no cases of sapovirus infection were reported in EpiSurv. Note that not every case of sapovirus infection is necessarily notifiable; only those that are part of a common source outbreak or from a person in a high risk category.

Outbreaks reported as caused by sapovirus

In 2019, 10 sapovirus infection outbreaks were reported in EpiSurv with 223 associated cases and no deaths. None of the outbreaks reported food as a possible mode of transmission. It is important to note that a single outbreak may have multiple pathogens, modes of transmission, settings where exposure occurred, or settings where preparation of food was conducted.

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.

There have been no sapovirus infection outbreaks with food reported as a possible mode of transmission in the last three years. The last outbreaks were in 2016 (three outbreaks, 72 cases) and 2015 (one outbreak, 3 cases).

Recent surveys

Nil.

Relevant New Zealand studies and publications

Nil.

Relevant regulatory developments

Nil.

Shigellosis

Summary data for shigellosis in 2019 are given in Table 47.

Table 47. Summary of surveillance data for shigellosis, 2019

Parameter	Value in 2019	Source
Number of notified cases	222	EpiSurv
Notification rate (per 100,000)	4.5	EpiSurv
Hospitalisations[a]	66	MoH NMDS
Deaths	0	EpiSurv
Estimated travel-related cases (%)[b]	135 (61%)	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

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

Since 2015 laboratories across New Zealand have gradually changed the methodology for testing faecal specimens. In 2019, community faecal specimens in all DHBs with the exception of Canterbury, MidCentral, South Canterbury, Tairawhiti, Taranaki, West Coast and Whanganui were screened by multiplex PCR for a range of pathogens, including *Shigella* spp.. The introduction of these more sensitive assays may have triggered an increase in notifications for some enteric diseases. It is likely that laboratory changes have affected the notification rates for shigellosis, i.e. the increase in shigellosis notifications is likely due to the increased sensitivity of the PCR methodology. However, one potential caveat is that many of the PCR assays in use cannot differentiate between *Shigella* spp. and enteroinvasive *E. coli*. Work is ongoing to try and resolve this issue.

Shigellosis cases reported in 2019 by data source

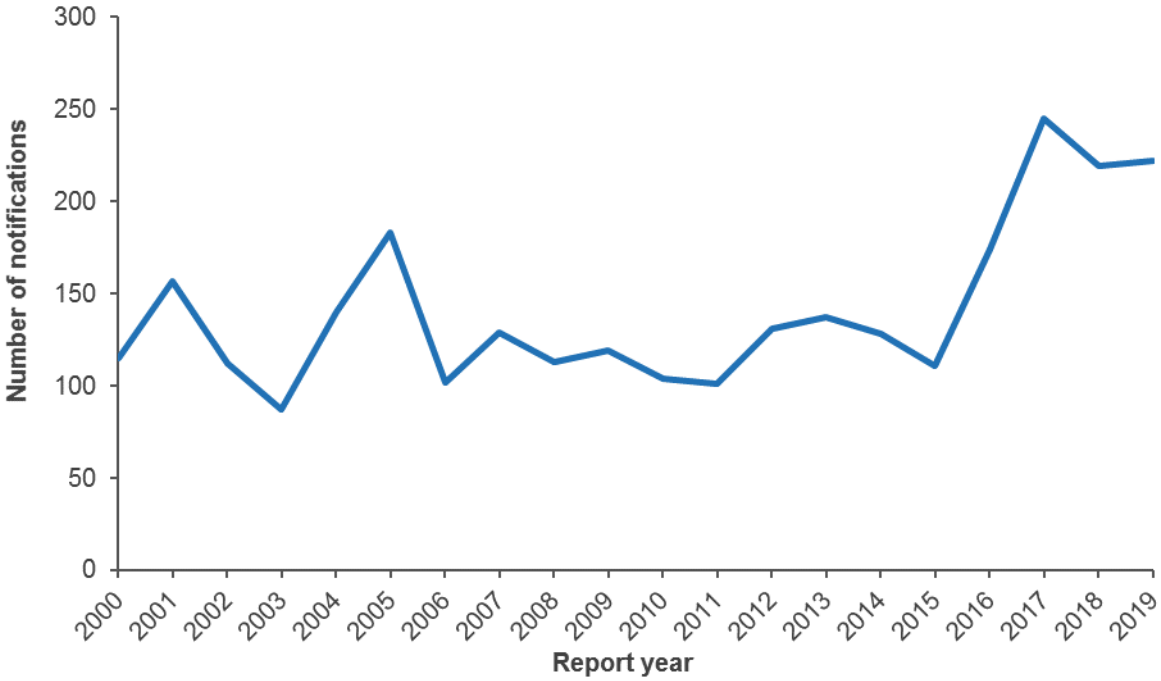
In 2019, 222 cases (4.5 per 100,000 population) of shigellosis and no resulting deaths were reported in EpiSurv. Approximately 30% of cases notified in EpiSurv in 2019 were recorded as hospitalised.

The ICD-10 code A03 was used to extract shigellosis hospitalisation data from the MoH NMDS database. Of the 66 hospital admissions (1.3 admissions per 100,000 population) recorded in 2019, 44 were reported with shigellosis as the principal diagnosis and 22 with shigellosis as another relevant diagnosis.

Notifiable disease data

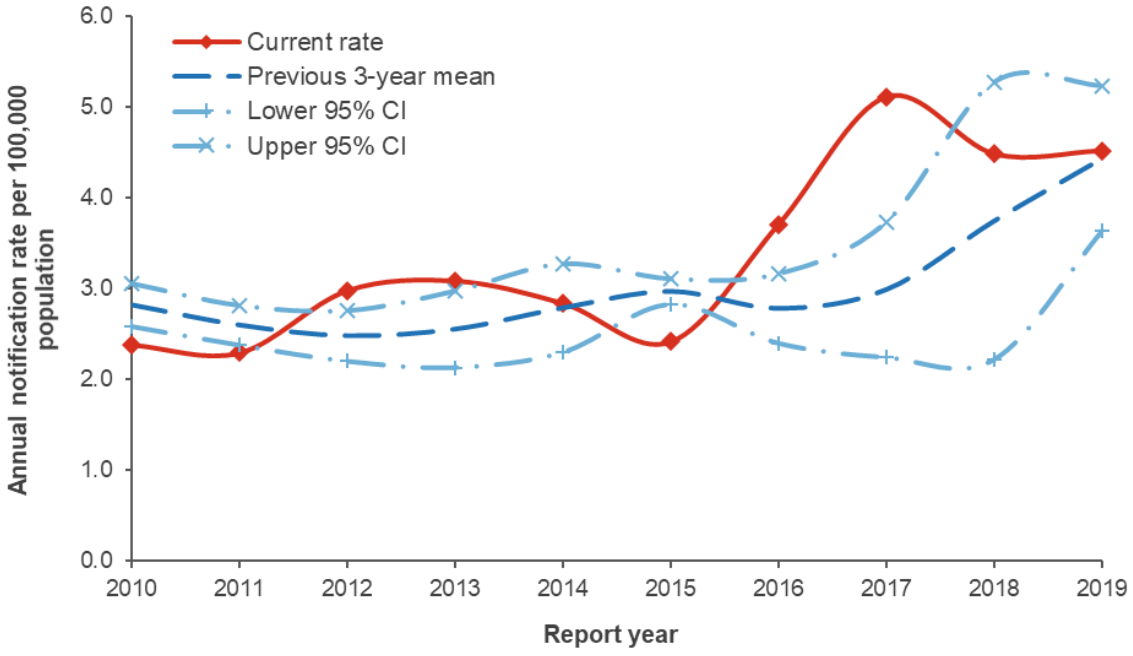
Between 2006 and 2015 the number of notifications has been in the range of 101 to 137 cases. In 2016 to 2017 there was an increase in notifications and the notification rate per 100,000 population, which has been sustained in 2018 (219 cases) and 2019 (222 cases) (Figure 33 and Figure 34). This may be due to the change in laboratory methods as described above.

Figure 33. Shigellosis notifications by year, 2000–2019



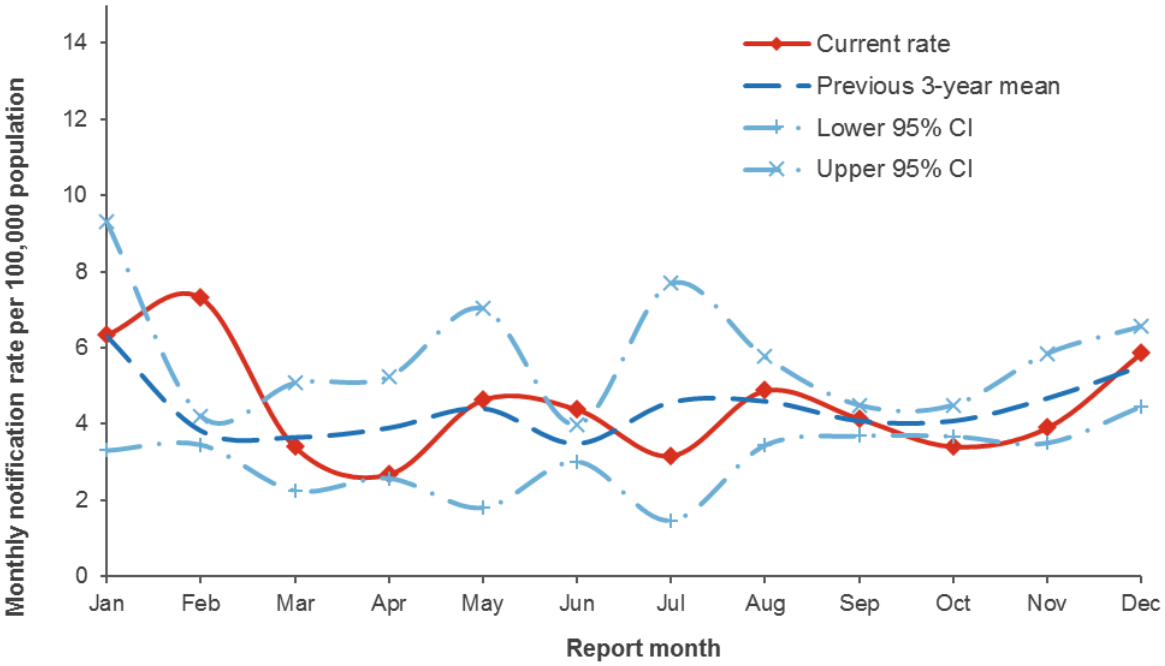
Between 2010 and 2015, the shigellosis notification rate has consistently been in the range of 2.3 to 3.1 notifications per 100,000 population (Figure 34). Higher rates have been noted in 2016 (3.7 per 100,000 population), 2017 (5.1 per 100,000 population), 2018 and 2019 (4.5 per 100,000 population). The notification rate in 2019 was similar to the previous three-year average (4.4 cases per 100,000).

Figure 34. Shigellosis notification rate by year, 2010–2019



The number of notified cases of shigellosis per 100,000 population by month for 2019 is shown in Figure 35. The number of notifications per month was small, ranging from 11 in April to 30 in January, and shows no strong seasonal differences.

Figure 35. Shigellosis monthly rate (annualised), 2019



In 2019, the rates for notification and hospitalisation were similar for males (4.8 and 1.3 per 100,000 population, respectively) and females (4.3 and 1.4 per 100,000, respectively) (Table 48).

Table 48. Shigellosis cases by sex, 2019

Sex	EpiSurv notifications		Hospitalisations[a]	
	No.	Rate[b]	No.	Rate[b]
Male	115	4.8	31	1.3
Female	107	4.3	35	1.4
Total	**222**	**4.5**	**66**	**1.3**

[a] MoH NMDS data for hospital admissions

[b] per 100,000 population

In 2019, high shigellosis notification rates are spread throughout the age groups. The lowest notification rates are for those in the 5 to 19 years and 70+ age groups. The hospital admissions rate was highest for the 1 to 4 years of age-group (3.7 admissions per 100,000 population) and the 70+ age group (2.3 admissions per 100,000 population) (Table 49).

Table 49. Shigellosis cases by age group, 2019

Age group (years)	EpiSurv notifications		Hospitalisations[a]	
	No.	Rate[b]	No.	Rate[b]
<1	2	-	0	-
1 to 4	15	6.1	9	3.7
5 to 9	11	3.3	4	-
10 to 14	7	2.2	1	-
15 to 19	5	1.6	2	-
20 to 29	46	6.6	12	1.7
30 to 39	37	5.7	3	-
40 to 49	24	3.9	8	1.3
50 to 59	36	5.7	9	1.4
60 to 69	25	4.8	6	1.2
70+	14	2.7	12	2.3
Total	**222**	**4.5**	**66**	**1.3**

[a] MoH NMDS data for hospital admissions

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

For cases where information on travel was provided in 2019, 61% had travelled overseas during the incubation period. Assuming that the cases for which travel information was provided were representative of all shigellosis cases, a Poisson distribution can be used to estimate the total number of potentially travel-related cases of shigellosis in 2019. The resultant distribution has a mean of 135 cases (95% CI 113-160).

If data from the last four years are considered the estimated proportion of cases travelling overseas within the incubation period of the organism was 61.1% (95% CI 57.6-64.5%).

Outbreaks reported as caused by *Shigella spp.*

In 2019, there were nine shigellosis outbreaks reported in EpiSurv, four (44%) of which reported food as a possible mode of transmission (Table 50). 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 50. Shigellosis outbreaks reported, 2019

Measure	Shigellosis outbreaks	
	Possible foodborne transmission	All
Outbreaks	4[a]	9
Cases	9	27
Hospitalised Cases	4	5

[a] Three outbreaks are associated with overseas travel

Table 51 contains details of the four shigellosis outbreaks with food reported as a possible mode of transmission reported in 2019.

Table 51. Details of shigellosis outbreaks with food reported as a possible mode of transmission, 2019

PHU	Month	Suspected source	Evidence	Setting	No. Ill
Auckland	Feb	Unknown	Household cluster	Other setting, overseas (Tonga)	2C
Auckland	Feb	Unknown	Household cluster	Overseas (India)	2C
Auckland	Jul	Unknown	Travelled together	Other setting, overseas (Samoa)	1C 1P
Auckland	Aug	Fish from Tonga	Household cluster	Home	1C 2P

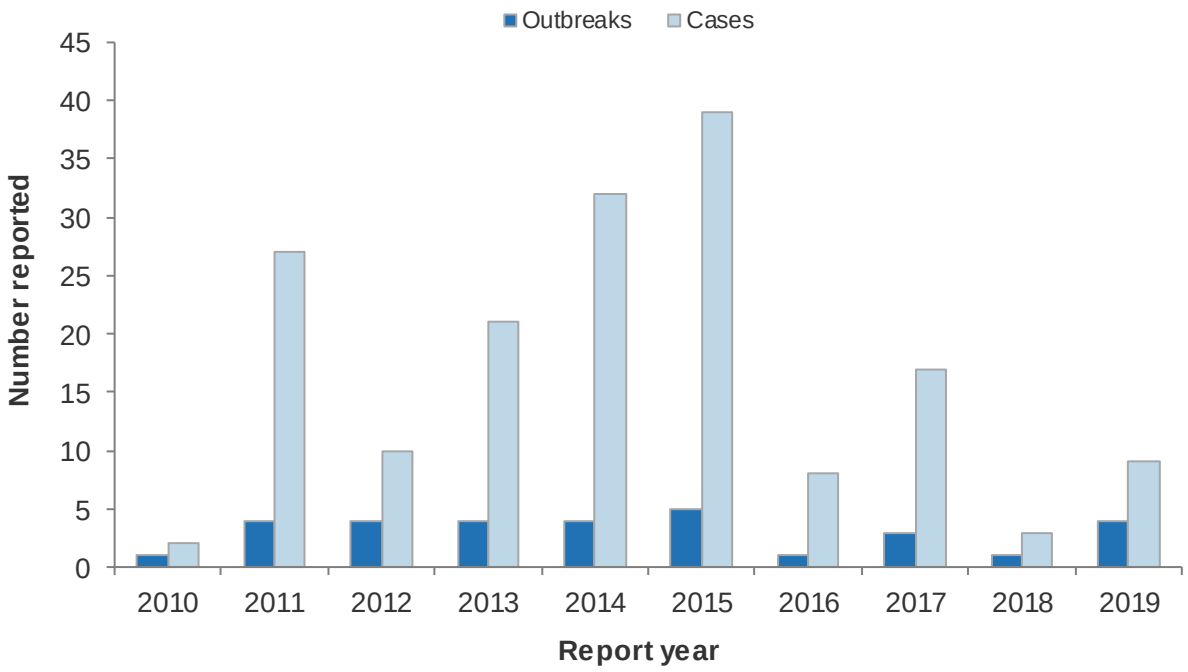
PHU Public Health Unit, Auckland: Auckland Regional Public Health Service

Number ill: C: confirmed, P: probable

Of the four outbreaks where food was reported as a possible mode of transmission, three outbreaks (6 cases and 1 hospitalisation) were associated with overseas travel and one outbreak (3 cases, all hospitalised) involved a household cluster (Table 51). The evidence for the Tongan fish as a source for the household cluster was weak, and it was not known if the cases ate the fish.

Over the 10 year period 2010–2019, the 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 36).

Figure 36. Shigellosis outbreaks with food reported as a possible mode of transmission and associated cases reported by year, 2010–2019



Shigella species commonly reported

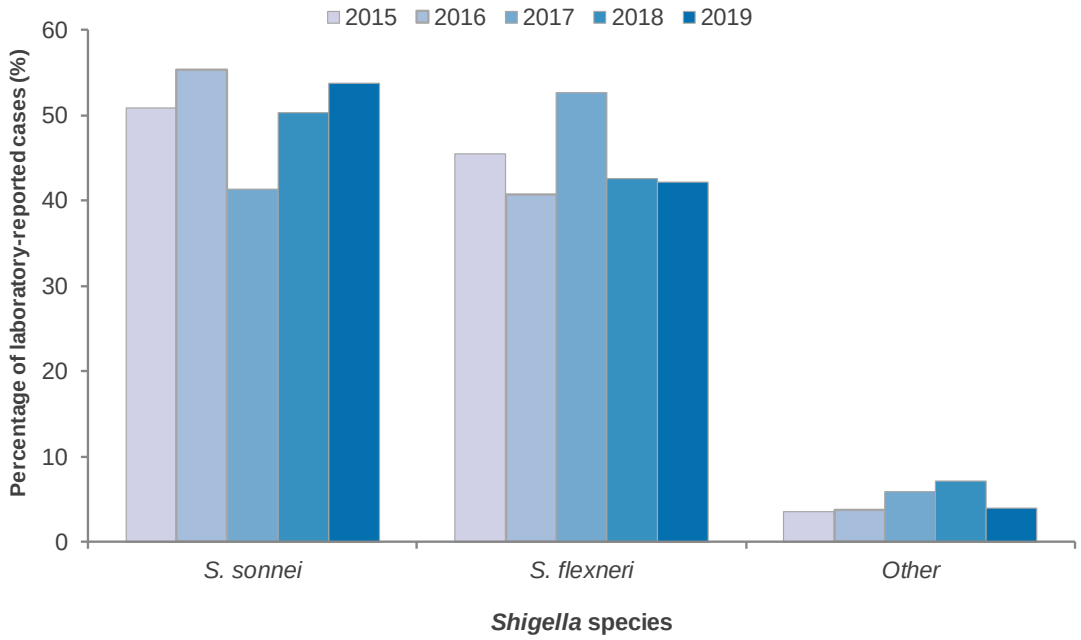
In 2019, isolates from 199 cases infected with *Shigella* spp. were typed by the Enteric Reference Laboratory at ESR. *S. sonnei* and *S. flexneri* were the species most often identified. Of these, *S. sonnei* biotype g was most common in 2019 (Table 52).

Table 52. *Shigella* species and subtypes identified by the Enteric Reference Laboratory, 2015–2019

Species	2015	2016	2017	2018	2019
S. sonnei	**57**	**87**	**99**	**99**	**107**
biotype a	20	31	30	37	33
biotype f	0	1	1	1	1
biotype g	37	55	68	61	73
S. flexneri	**51**	**64**	**126**	**84**	**84**
1b	4	16	31	36	14
2a	14	18	18	15	19
6 biotype Boyd 88	0	10	43	13	12
Other	33	20	34	20	39
Other	**4**	**6**	**14**	**14**	**8**
S. boydii	4	3	13	10	3
S. dysenteriae	0	2	1	4	4
Shigella species not identified	0	1	0	0	1
Total	**112**	**157**	**239**	**197**	**199**

The percentage of shigellosis cases infected with *S. sonnei* in 2019 (53.8%) was within the range of values observed between 2015 and 2018 (between 41.4% and 55.4%). The percentage of shigellosis cases with *S. flexneri* in 2019 (42.2%) was also within the range of values observed between 2015 and 2018 (between 40.8% and 52.7%) (Figure 37).

Figure 37. Percentage of laboratory-reported cases by *Shigella* species and year, 2015–2019



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 cases reported in 2019 by data source

During 2019, no cases of *S. aureus* intoxication were reported in EpiSurv. Note that not every case of *S. aureus* intoxication is necessarily notifiable; only those where there is a suspected common source.

The ICD-10 code A05.0 was used to extract foodborne staphylococcal intoxication hospitalisation data from the MoH NMDS database. One hospital admission was recorded in 2019 with *S. aureus* intoxication as the primary diagnosis and no cases were reported with *S. aureus* intoxication as another relevant diagnosis.

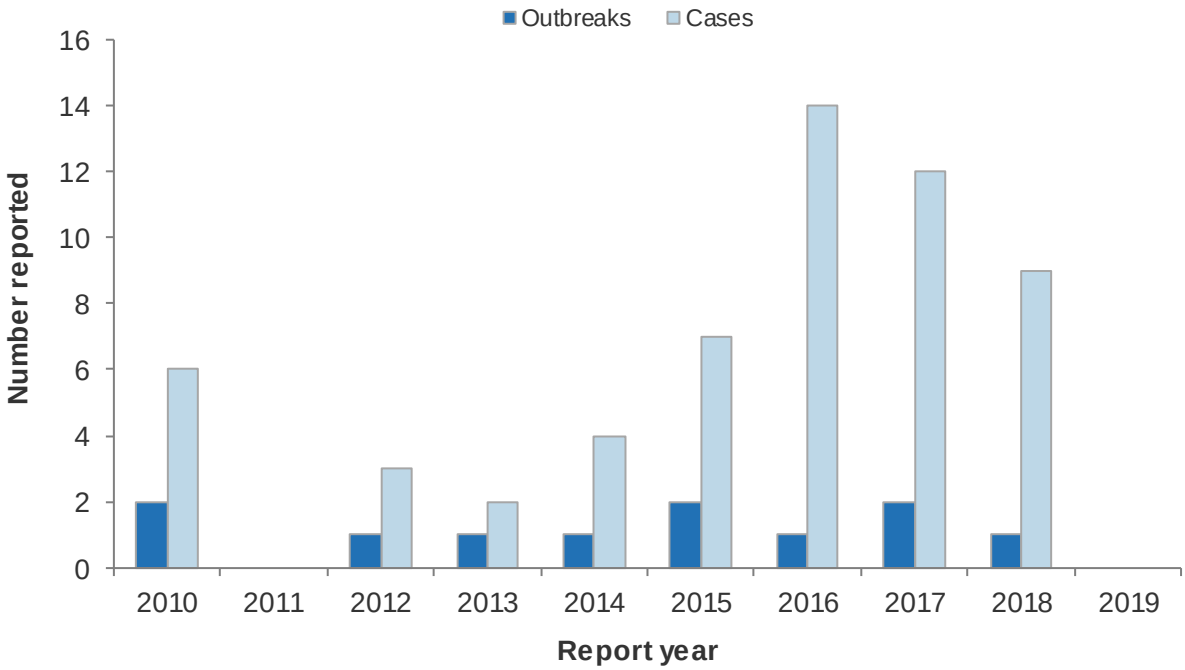
It should be noted that EpiSurv and MoH NMDS database are separate systems and hospital admission can occur without cases being notified in EpiSurv. This means that not all cases diagnosed with staphylococcal intoxication in hospital are reported in EpiSurv.

Outbreaks reported as caused by *Staphylococcus aureus*

During 2019, no outbreaks of *S. aureus* intoxication were reported in EpiSurv.

Over the 10 year period 2010 to 2019, the number of *S. aureus* intoxication outbreaks with food reported as a possible mode of transmission ranged from zero to two, with between two and 14 associated cases (Figure 38).

Figure 38. *S. aureus* intoxication outbreaks with food reported as a possible mode of transmission and associated cases reported by year, 2010–2019



Recent surveys

Nil.

Relevant New Zealand studies and publications

Nil.

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 regulatory limit in shellfish obtained from near or same site (not leftovers) within seven days of collection of shellfish consumed by case. Current levels are as follows:

ASP: 20 ppm domoic acid/100 g shellfish
DSP: 20 g/100 g or 5 MU/100 g shellfish
(MU = mouse units)
NSP: 20 MU/100 g shellfish
PSP: 80 g/100 g 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 2019 by data source

During 2019, two cases (0.04 per 100,000 population) of toxic shellfish poisoning and no resulting deaths were reported in EpiSurv. The toxin type was not specified for any of the cases.

One case was of Pacific Peoples ethnicity and had eaten cooked squid from a food outlet. The other case of European ethnicity had eaten raw and cooked recreationally collected tuatua. In EpiSurv, the two cases were not reported as hospitalised.

The ICD-10 code T61.2 was used to extract hospitalisation data for 'other fish and shellfish poisoning' from the MoH NMDS database. Of the seven hospital admissions (0.1 admissions per 100,000 population) recorded in 2019, seven cases were reported with 'other fish and shellfish poisoning' as the primary diagnosis and no cases were reported with 'other fish and shellfish poisoning' as another relevant diagnosis. Note that this ICD-10 code includes shellfish and other fish.

EpiSurv and 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 2019, no toxic shellfish poisoning outbreaks were reported in which cases had symptoms consistent with PSP. It should be noted that all cases of toxic shellfish poisoning will be categorised as foodborne as consumption of contaminated fish is the only recognised transmission route for this disease.

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

Recent surveys

Nil.

Relevant New Zealand studies and publications

Blooms of the dinoflagellate *Dinophysis acuminata* occur every year in an important mussel cultivation area in Port Underwood, Marlborough Sounds, New Zealand [28]. Annual maximum cell numbers range from 1500-75,000 cells/L and over 25 years of weekly monitoring the *D. acuminata* bloom has never failed to exhibit peaks in abundance at some time between spring and autumn. During winter (June-August) the dinoflagellate is often undetectable, or at low levels (100 cells/L), and the risk of diarrhetic shellfish poisoning (DSP)-toxin contamination over this period is negligible. The toxin profile of *D. acuminata* is dominated by pectenotoxin-2 (PTX-2) and dinophysistoxin-1 (DTX-1), but the cellular toxin content is low. In only five out of >2500 mussel samples over 16 years have the levels of total DTX-1 marginally exceeded the regulated level of 0.16 mg/kg. The *D. acuminata* alert level of 1000 cells/L is often exceeded without DTX-1 residues increasing appreciably, and this level is considered too conservative.

Relevant regulatory developments

Nil.

VTEC/STEC infection

Important note: Shiga toxin-producing *E. coli* (STEC) may also be referred to as verotoxin-producing *E. coli* (VTEC). STEC is now the preferred term and will be used throughout this document.

Summary data for STEC infection in 2019 are given in Table 53.

Table 53. Summary of surveillance data for STEC infection, 2019

Parameter	Value in 2019	Source
Number of notified cases	1101	EpiSurv
Notification rate (per 100,000)	22.4	EpiSurv
Hospitalisations[a]	52	MoH NMDS
Deaths	1	EpiSurv
Estimated travel-related cases (%)[b]	128 (12%)	EpiSurv
Estimated food-related cases (%)[c]	331 (34%)	Expert consultation

[a] Cases hospitalised may not be notified on EpiSurv

[b] Percentage of the number of notified cases

[c] For estimation of food-related cases the proportions derived from expert consultation [2] exclude travel-related cases. The expert elicitation derived separate estimates of the foodborne proportion for O157 STEC and non-O157 STEC. 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 Not applicable. 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.

Terminology

In 2016, a joint FAO/WHO consultation on STEC reviewed the terminology related to these organisms and "the expert group agreed to only use the term STEC, as it includes EHEC (enterohaemorrhagic *E. coli*) and because the interaction between known and putative virulence factors of STEC and the pathogenic potential of individual strains is not fully resolved" [29].

Changes to laboratory methods since 2015

Since 2015 laboratories across New Zealand have gradually changed the methodology for testing faecal specimens. In 2019, community faecal specimens in all DHBs with the exception of Canterbury, MidCentral, South Canterbury, Tairawhiti, Taranaki, West Coast and Whanganui were screened by multiplex PCR for a range of pathogens, including STEC. The introduction of these more sensitive assays may have triggered an increase in notifications for some enteric diseases. Prior to the change in methodology only faecal samples with blood, or those from under 5-year-olds were tested for STEC infection. The increased sensitivity of the PCR methodology and the increased frequency in testing is contributing to the increase in notifications since 2015 [30].

VTEC/STEC infection cases reported in 2019 by data source

During 2019, 1101 cases (22.4 per 100,000 population) of STEC infection and one resulting death were reported in EpiSurv. While the case died while infected with STEC, it is suspected that they died of other causes. Approximately 20% of cases notified in EpiSurv in 2019 were recorded as hospitalised.

The ICD-10 code A04.3 was used to extract enterohaemorrhagic *E. coli* infection hospitalisation data from the MoH NMDS database. Of the 52 hospital admissions (1.1 admissions per 100,000 population) recorded in 2019, 29 cases were reported with enterohaemorrhagic *E. coli* infection as the primary diagnosis and 23 were reported with enterohaemorrhagic *E. coli* infection as another relevant diagnosis.

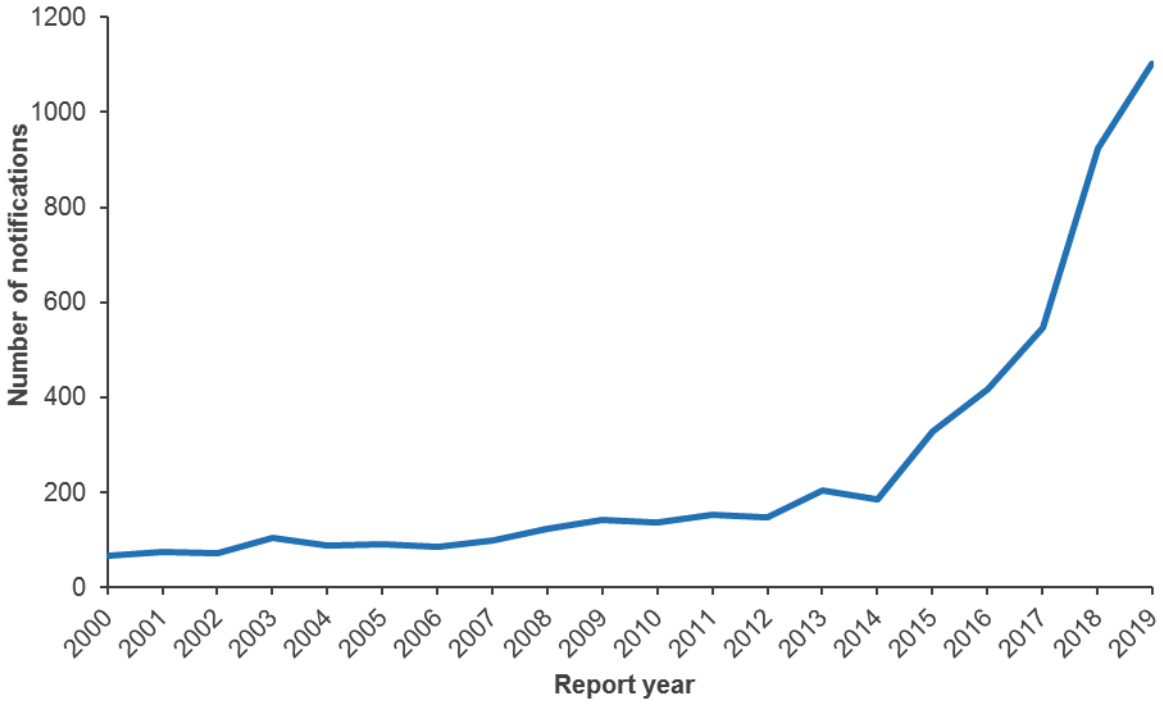
It has been estimated by expert consultation that 29.9% (95th percentile credible interval; 3.5% to 60.7%) of O157 STEC incidence and 34.0% (95th percentile credible interval: 3.5% to 63.5%) of non-O157 incidence is due to foodborne transmission. The expert consultation also estimated that approximately 30% of foodborne STEC transmission was due to red meat*, irrespective of serotype.

Notifiable disease data

In 2015, there was a large increase in STEC notifications compared to previous years with further yearly increases since 2015 (Figure 39 and Figure 40). The start in increase in annual notifications occurs at the same time as changed laboratory methods and screening are introduced, and the increase is compounded with each new lab changing to the new methodology [30].

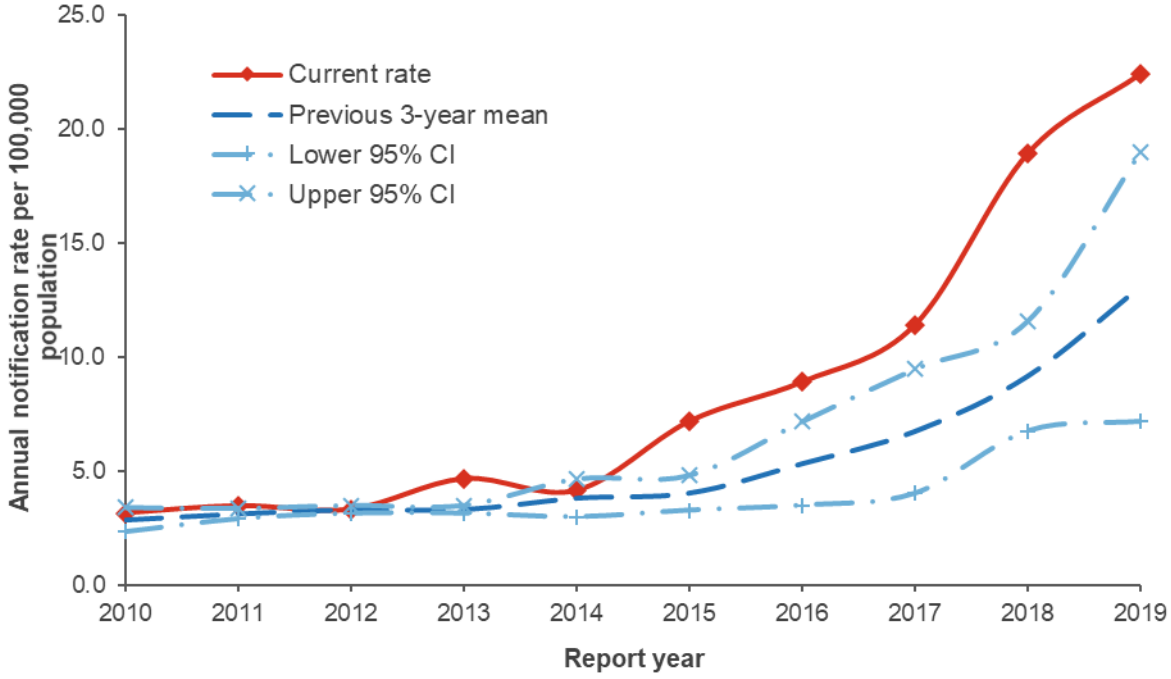
* In NZ, however, no outbreaks of STEC have been conclusively linked to consumption of red meat.

Figure 39. STEC infection notifications by year, 2000–2019



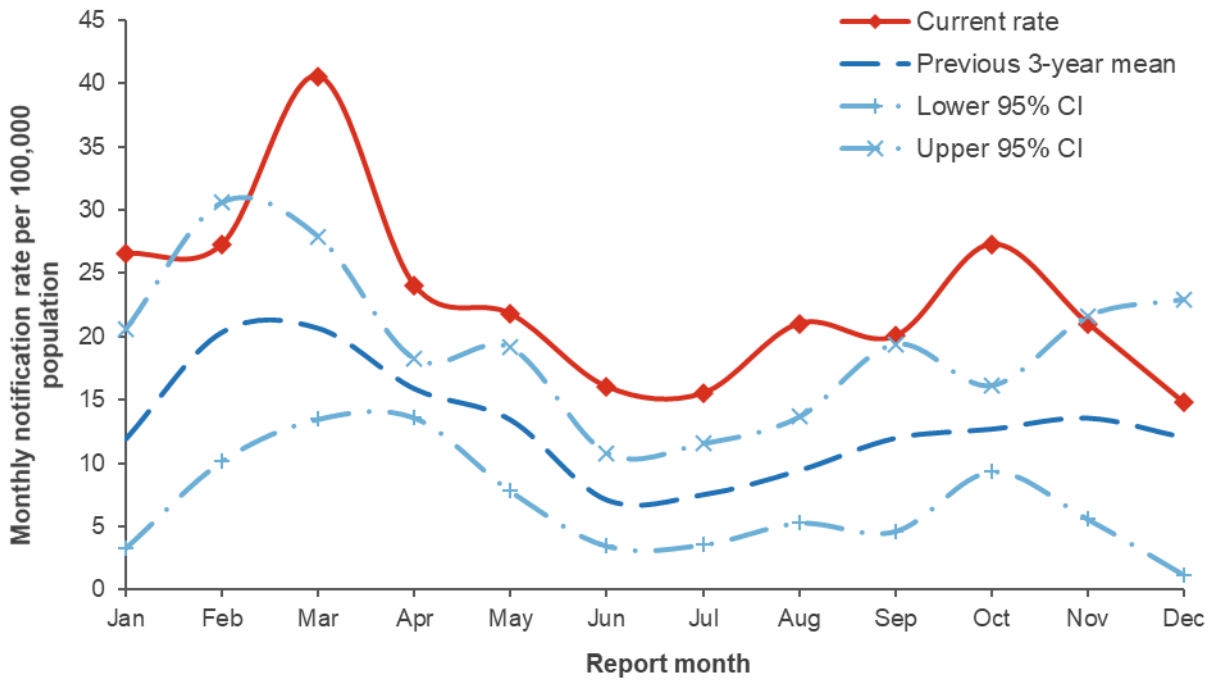
Between 2010 and 2014, the notification rate of STEC infection was in the range of 3.2 to 4.7 notifications per 100,000 population (Figure 40). Increasing rates have been noted every year since 2015 with the highest notification rate in 2019 (22.4 cases per 100,000 population). The previous three-year average was 13.1 cases per 100,000 population.

Figure 40. STEC infection notification rate by year, 2010–2019



The number of notified cases of STEC infection per 100,000 population by month for 2019 are shown in Figure 41. In 2019, monthly notification rates were generally higher compared to the previous three-year mean monthly rates. The monthly number of notifications in 2019 ranged from 59 notifications (December) to a peak of 162 notifications (March). The trend in monthly notification rates in 2019 was similar to recent years (2016-2018) with a small increase in spring, and a higher peak from January to March.

Figure 41. STEC infection monthly rate (annualised), 2019



In 2019 notification rates were slightly higher for females than males (23.3 and 21.5 notifications per 100,000 population, respectively), however, hospitalisation admission rates for cases were similar (Table 54).

Table 54. STEC cases by sex, 2019

Sex	EpiSurv notifications		Hospitalisations[a]	
	No.	Rate[b]	No.	Rate[b]
Male	520	21.5	23	1.0
Female	581	23.3	29	1.2
Total	**1101**	**22.4**	**52**	**1.1**

[a] MoH NMDS data for hospital admissions

[b] per 100,000 population

In 2019, the STEC infection notification rate was highest for the less than 1 year age group (85.5 per 100,000 population, 51 cases) and the 1 to 4 years age group (76.5 per 100,000, 188 cases). The number of hospitalisations was highest in the 70+ age group (13 hospital admissions) and ranged between one and seven in all other age groups. The hospital admission rate was highest for the 1 to 4 years age group and the 70+ age group (2.4 and 2.5 hospital admissions per 100,000) (Table 55).

Table 55. STEC cases by age group, 2019

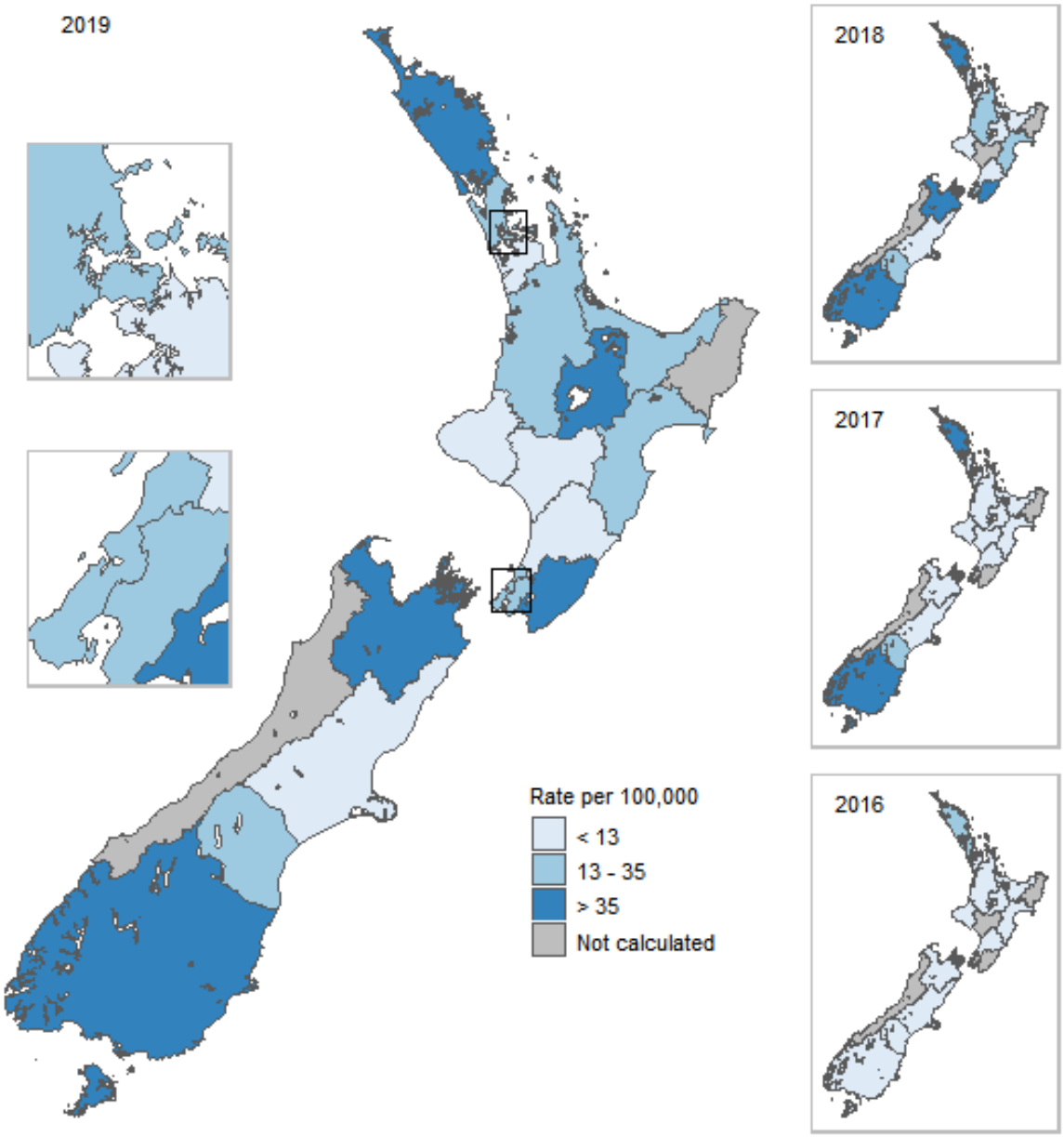
Age group (years)	EpiSurv notifications		Hospitalisations[a]	
	No.	Rate[b]	No.	Rate[b]
<1	51	85.5	1	-
1 to 4	188	76.4	6	2.4
5 to 9	52	15.8	4	-
10 to 14	39	12.1	2	-
15 to 19	48	15.2	2	-
20 to 29	122	17.5	7	1.0
30 to 39	87	13.4	2	-
40 to 49	78	12.6	4	-
50 to 59	124	19.7	4	-
60 to 69	143	27.5	7	1.3
70+	169	32.0	13	2.5
Total	**1101**	**22.4**	**52**	**1.1**

[a] MoH NMDS data for hospital admissions

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

Rates of STEC infection varied throughout the country as illustrated in Figure 42. In 2019, the highest rates of STEC infection were reported for the DHBs Wairarapa (63.0 per 100,000, 30 cases) and Southern (59.3 per 100,000, 201 cases), followed by Lakes DHB (40.2 per 100,000, 46 cases), Northland DHB (36.6 per 100,000, 69 cases) and Nelson Marlborough DHB (35.7 per 100,000, 56 cases). Note that rates were not calculated for two DHBs where there were less than five cases notified in 2019.

Figure 42. Geographic distribution of STEC infection notifications, 2016–2019



Note: Since 2015 laboratories across New Zealand have gradually changed the methodology for testing faecal specimens. The increase in STEC infection notifications is likely due to the changes in detection methods, i.e. the increased sensitivity and frequency of the PCR methodology. Refer to report Introduction for details.

For cases where information on travel was provided in 2019, 12% had travelled overseas during the incubation period. Assuming that the cases for which travel information was provided were representative of all STEC cases, a Poisson distribution can be used to estimate the total number of potentially travel-related cases of STEC in 2019. The resultant distribution has a mean of 128 cases (95% CI 107-152).

If data from the last four years are considered the estimated proportion of cases travelling overseas within the incubation period of the organism was 12% (95% CI 11-13%).

Outbreaks reported as caused by STEC

Of the 15 outbreaks (63 cases) of STEC infection during 2019, one outbreak (three cases) was reported with food as a possible mode of transmission (Table 56). 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 56. STEC outbreaks reported, 2019

Measure	STEC outbreaks	
	Possible foodborne transmission	All
Outbreaks	1	15
Cases	3	80
Hospitalised Cases	0	5

Table 57 gives the details of the single outbreak of STEC infection with food reported as a possible mode of transmission.

Table 57. Details of the STEC outbreak with food reported as a possible mode of transmission, 2019

PHU	Month	Suspected Vehicle	Evidence	Setting	No. Ill
Toi Te Ora	Aug	Raw Milk	Consumption of milk from same source	Home	3C

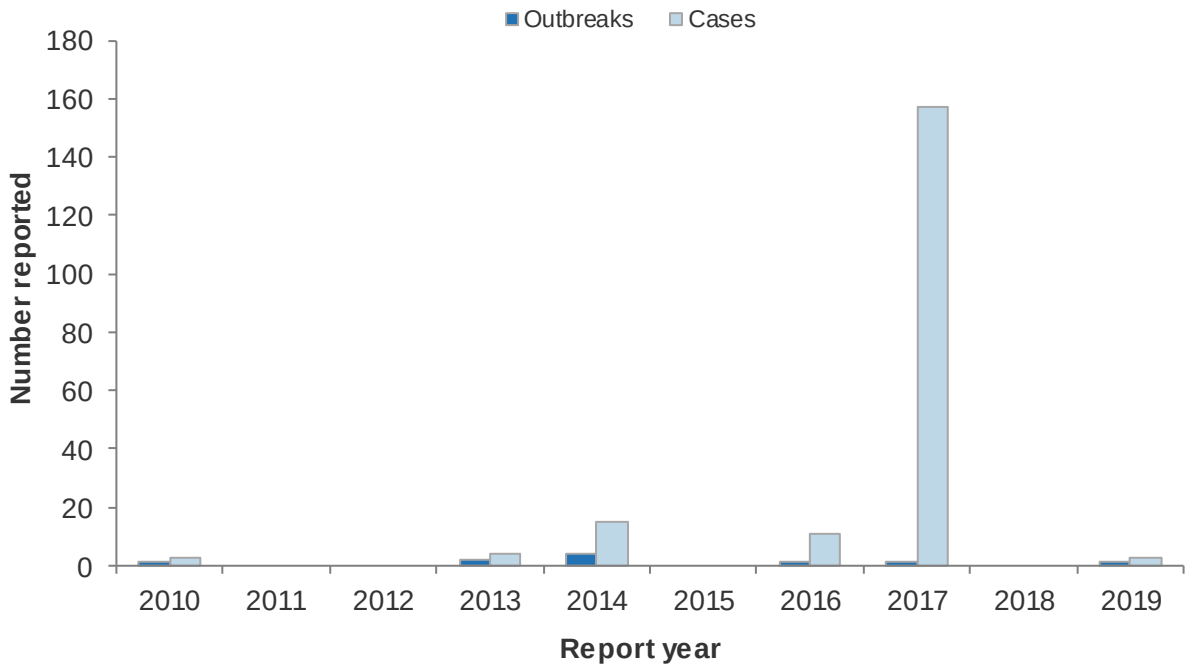
PHU Public Health Unit, Toi Te Ora: Toi Te Ora - Public Health

Number ill: C: confirmed, P: probable

The suspected vehicle for this outbreak was raw milk from a farm. The level of evidence recorded for this vehicle was weak. The cases in this outbreak were also found to be infected with *Campylobacter*.

Over the 10 year period 2010 to 2019, the number of STEC outbreaks with food reported as a possible mode of transmission ranged from one to four per year, with no outbreaks reported for four of the ten years (Figure 43). The total number of cases associated with the outbreaks has varied over the same period with peaks in 2014 (15 cases) and 2017 (157 cases).

Figure 43. STEC outbreaks with food reported as a possible mode of transmission and associated cases reported by year, 2010–2019



STEC types commonly reported

Isolates from 781 cases infected with STEC were reported by the ESR Enteric Reference Laboratory in 2019. Of the 791 associated isolates, 203 (25.7%) were identified as *E. coli* O157:H7, 484 (61.2%) as non-O157 and for 104 (13.1%) isolates the serotype was not able to be determined.

Of the 484 non-O157 isolates, 119 were typed as O26:H11, 55 as O128:H2 and 27 as O38:H26 (Table 58 and Figure 44). The percentage of non-O157 STEC cases has been increasing every year (2015: 25.1%, 2016: 34.8%, 2017: 38.6%, 2018: 52.7%, 2019: 61.2%) possibly due to mentioned previously changes in laboratory methods and the screening* of all submitted faecal samples for STEC infection (Figure 44).

* See the Introduction for the description of changes

Figure 44. Number of *E. coli* O157 and non-O157 laboratory reported isolates by year, 2015–2019

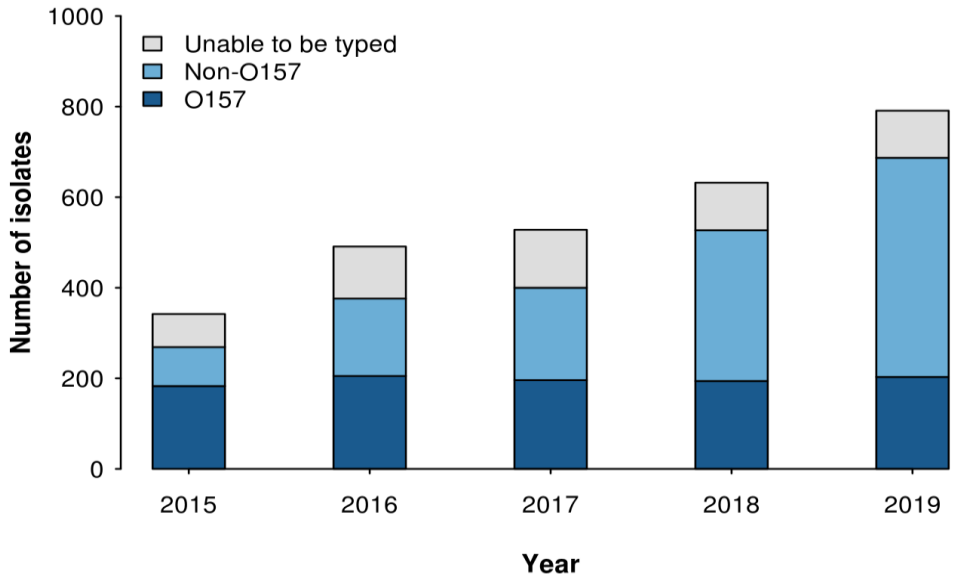


Table 58. Case STEC subtypes identified by the Enteric Reference Laboratory, 2015–2019

Serotype	2015	2016	2017	2018	2019
O157	**183**	**205**	**196**	**194**	**203**
O157:H7[a]	183	205	196	194	203
Non-O157	**86**	**171**	**204**	**333**	**484**
O26:H11	14	46	44	76	119
O128:H2	4	25	7	22	55
O38:H26	5	10	7	19	27
O146:H21	2	4	13	17	15
O103:H25	2	1	1	4	12
O176:H4	0	0	0	0	12
O91:H14	0	0	0	0	12
ONT:H2	9	3	22	17	11
O103:H2	2	2	3	7	11
O153:H2	4	2	0	3	10
O174:H8	1	0	1	4	10
O5:HNT	0	0	0	0	8
O64:H20	0	3	2	4	7
O117:H7	2	0	1	2	7
O26:HNT	0	0	2	1	7
O163:H19	1	0	0	1	7
O88:H8	0	0	0	0	7
ONT:H7	0	3	7	6	6

Serotype	2015	2016	2017	2018	2019
ONT:H21	0	1	4	4	5
O174:H21	0	0	0	1	5
O130:H11	1	2	1	1	4
O176:HNM	10	2	4	9	0
ORough:H2	1	6	4	7	0
O91:HNM	5	2	2	5	0
O123/O186:HNM	0	0	0	13	0
O128:HNM	1	5	1	6	0
Other types[b]	22	54	78	104	127
Unable to be typed[c]	**73**	**115**	**128**	**105**	**104**
Total	**342**	**491**	**528**	**632**	**791**

NM: Non-Motile. NT: Non-typable

[a]Whole genome sequencing of human O157:H7 isolates from 2017 to 2019 revealed a wide diversity of genotypes present, with most of the isolates quite distinct from any other. A total of 564 isolates from 2017 to 2019 were analysed, resulting in 428 different genotypes.

[b] Isolates with identifiable serotypes, not listed in table. Full list available in Appendix

[c] Isolates unable to be typed, includes ONT:HNT or HNM, ONM:HNT or HNM, ORough:HNT or HNM

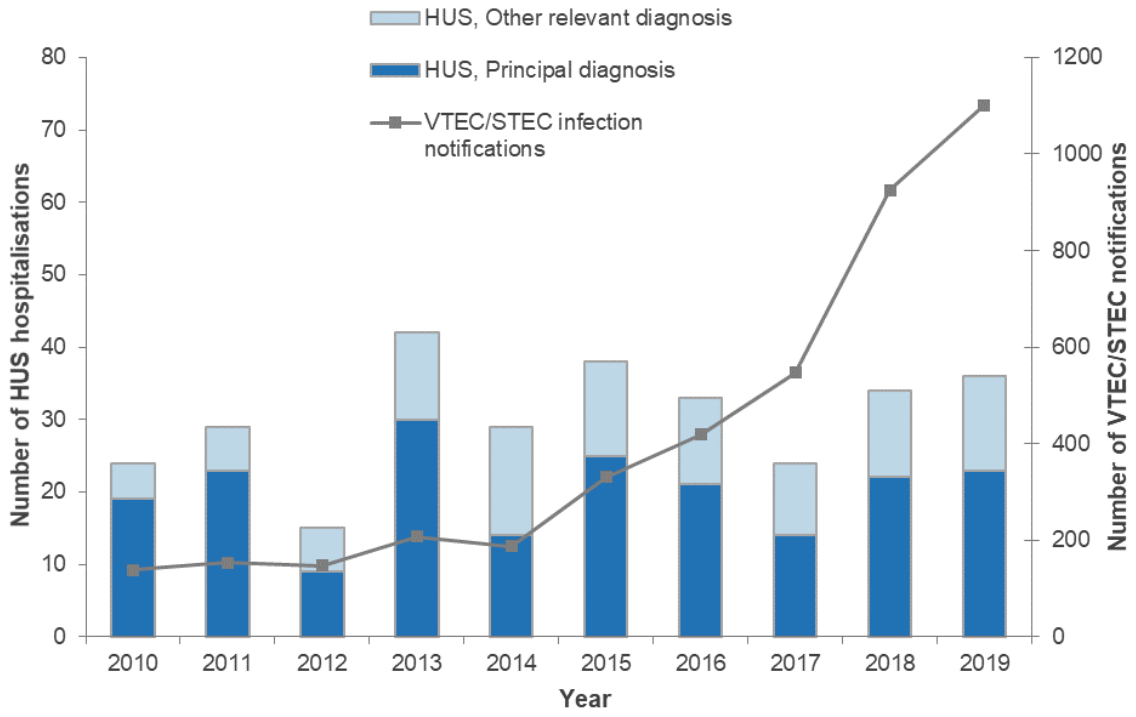
Disease sequelae – haemolytic uraemic syndrome (HUS)

HUS is a serious sequela that may result from a STEC infection. HUS is usually preceded by a STEC infection [31]. 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 [32], the most recent European data report that *E. coli* O26 was most frequently associated with HUS cases [33]. In 2019, 21 STEC cases notified in EpiSurv were reported to have developed HUS. The associated serotypes were O157 (11), O26:H11 (3), O38:H25 (1), O88:H8 (1) and not reported (5).

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 2019 year were considered, rather than all cases that were hospitalised in that year. That is, if a HUS case hospitalised in 2019 had been hospitalised with HUS in a previous year, the 2019 admission was considered to be a readmission, rather than an incident case. Of the 36 incident hospital admissions recorded in 2019 (0.7 per 100,000 population), 23 were reported with HUS as the primary diagnosis and 13 with HUS as another relevant diagnosis.

Between 2010 and 2019, the number of incident hospitalised cases (any diagnosis code) of HUS each year ranged from 15 to 42 (Figure 45). In 2019, the number of incident hospitalised cases increased slightly to 36 from 34 in 2018. STEC notifications have increased steadily over this period (Figure 39). That HUS cases have not increased over this period supports the conclusion that the increase in STEC infection notifications remains predominantly due to the changes in detection methods.

Figure 45. Haemolytic-uraemic syndrome (HUS) hospitalised cases, 2010–2019



In 2019, the number of female cases hospitalised due to HUS was greater than the number of male cases (Table 59). This is the same as the pattern seen in 2018, but the reverse of the pattern seen in 2017, when more males were hospitalised with HUS than females.

Table 59. Haemolytic uraemic syndrome hospitalised cases by sex, 2019

Sex	Hospitalised cases[a]	
	No.	Rate[b]
Male	14	0.6
Female	22	0.9
Total	**36**	**0.7**

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

In 2019, the highest age-specific rates of incident hospitalised cases due to HUS were in the less than 5 years age group (Table 60).

Table 60. Haemolytic uraemic syndrome hospitalised cases by age group, 2019

Age group (years)	Hospitalised cases [a]	
	No.	Rate[b]
<5	17	5.6
5 to 9	6	1.8
10 to 14	0	-
15 to 19	1	-
20 to 29	4	-
30 to 39	1	-
40 to 49	0	-
50 to 59	1	-
60 to 69	3	-
70+	3	-
Total	**36**	**0.7**

[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)

During 2019, 15 cases of HUS were reported to the NZPSU, of which 12 had a diarrhoeal prodrome. The median age of cases was 2.7 years. All of the 12 diarrhoea-associated cases had STEC isolated from their stools. Ten of these cases were from the North Island. One death was reported, with *E. coli* O26 isolated. Risk factors were identified for 7 cases, including consumption of unpasteurised milk (2), contact with flood run-off (1), living on farm/lifestyle block (2), drinking tank water (1) and swimming in a public swimming pool (1).

Note: the details given above are from an advance excerpt from the NZPSU Annual Report, which had not been published at the time of finalisation of the current report. The source reference provided here is the website where NZPSU Annual Reports are published: http://dnmeds.otago.ac.nz/departments/womens/paediatrics/research/nzpsu/about/annual-reports.html

Recent surveys

Nil.

Relevant New Zealand studies and publications

Journal papers

Phylogenetic bacterial lineages in a country of Shiga toxin-producing *Escherichia coli* serogroup O26 can be associated with the level and timing of international imports of live cattle, the main reservoir [34]. Genomes of 152 *E. coli* O26 isolates from New Zealand were sequenced and compared with 252 *E. coli* O26 genomes from 14 other countries. Gene variation among isolates from humans, animals, and food was strongly associated with country of origin and stx toxin profile but not isolation source. Time of origin estimates indicate serogroup O26 sequence type 21 was introduced at least 3 times into New Zealand from the 1920s to the 1980s, whereas nonvirulent O26 sequence type 29 strains were introduced during the early 2000s.

Shiga toxin-producing *Escherichia coli* strains (STEC) are food-borne pathogens [35]. While *E. coli* O157:H7 is commonly associated with cattle, less is known about the prevalence of non-O157 STEC serogroups in bovines. This study evaluated the prevalence and virulence status of O157:H7 and six *E. coli* O-serogroups (O26, O103, O45, O145, O121, O111) in New Zealand dairy farms using molecular as well as culture-based methods. Fresh farm dairy effluent (FDE) (n = 36) and composite calf faeces (n = 12) were collected over three samplings from 12 dairy farms. All seven target serogroups were detected through molecular techniques. Of the 202 isolates which were serologically confirmed following traditional culturing and immunomagnetic separation (IMS), O103, O26, O45 and O121 were the most common serogroups, being found in 81, 47, 42 and 32% of the FDE and in 17, 33, 25 and 9% of the calf faeces respectively. The majority (157/202) of the isolates were negative for *stx* and *eae* virulence genes. The prevalence of the seven target STEC was low, and only nine O26 isolates (4%) were recovered from four of the farms.

Relevant regulatory developments

Nil.

Vibrio parahaemolyticus infection

Case definition

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

Vibrio parahaemolyticus infection cases reported in 2019 by data source

During 2019, 50 cases (1 per 100,000 population) of *V. parahaemolyticus* infection and no resulting deaths 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 five hospital admissions (0.1 admissions per 100,000 population) recorded in 2019, three cases were reported with *V. parahaemolyticus* infection as the primary diagnosis and two were reported with *V. parahaemolyticus* infection as another relevant diagnosis.

Outbreaks reported as caused by *Vibrio parahaemolyticus*

One outbreak of *V. parahaemolyticus* infection with food as a possible mode of transmission was reported in 2019 involving 24 associated cases, two of whom were hospitalised (Table 61). This is the first foodborne outbreak caused by *V. parahaemolyticus* that has been recorded since 2009, when there were two outbreaks with three and four cases, respectively.

Table 61. *V. parahaemolyticus* infection outbreaks reported, 2019

Measure	*V. parahaemolyticus* infection outbreaks	
	Possible foodborne transmission	All
Outbreaks	1	1
Cases	24	24
Hospitalised cases	2	2

Table 62 provides details of the *V. parahaemolyticus* outbreak with food reported as a possible mode of transmission reported in 2019.

Table 62. Details of the *V. parahaemolyticus* infection outbreak with food reported as a possible mode of transmission, 2019

PHU	Month	Suspected source	Evidence	Setting	No. Ill
Toi Te Ora	May	Mussels	Common food type eaten by cases	Home consumption of commercially grown mussels	23C, 1P

PHU Public Health Unit, Toi Te Ora: Toi Te Ora - Public Health
Number ill: C: confirmed, P: probable

The level of evidence for the suspected source (mussels) was categorised as reasonably weak. The outbreak cases were not part of a defined exposure group but had consumed the suspected mussels. No leftover mussels where available for testing.

Recent surveys

Nil.

Relevant New Zealand studies and publications

Nil.

Relevant regulatory developments

Nil.

Yersiniosis

Summary data for yersiniosis in 2019 are given in Table 63.

Table 63. Summary of surveillance data for yersiniosis, 2019

Parameter	Value in 2019	Source
Number of notified cases	1186	EpiSurv
Notification rate (per 100,000)	24.1	EpiSurv
Hospitalisations[a]	138	MoH NMDS
Deaths	0	EpiSurv
Estimated travel-related cases (%)[b]	110 (9%)	EpiSurv
Estimated food-related cases (%)[c]	680 (63.2%)	Expert consultation

[a] Cases hospitalised may not be notified on EpiSurv
[b] Percentage of the number of notified cases
[c] For estimation of food-related cases the proportions derived from expert consultation [2] 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.

Changes to laboratory methods since 2015

Since 2015 laboratories across New Zealand have gradually changed the methodology for testing faecal specimens for *Yersinia spp.*. For 2019, all community faecal specimens in Auckland, Bay of Plenty, Capital & Coast, Counties Manukau, Hawke's Bay, Hutt Valley, Lakes, Nelson Marlborough, Northland, Southern, Waikato, Wairarapa, and Waitemata were screened by multiplex PCR for *Y. enterocolitica,* in addition to a range of other pathogens. However, due to the changes in methodology laboratories servicing about 50% of the New Zealand population are no longer testing for *Yersinia pseudotuberculosis* [36].

Yersiniosis cases reported in 2019 by data source

During 2019, 1186 cases (24.1 per 100,000 population) of yersiniosis and no resulting deaths were reported in EpiSurv. Approximately 8% of cases notified in EpiSurv in 2019 were recorded as hospitalised.

* 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 as of July 2017 [11].

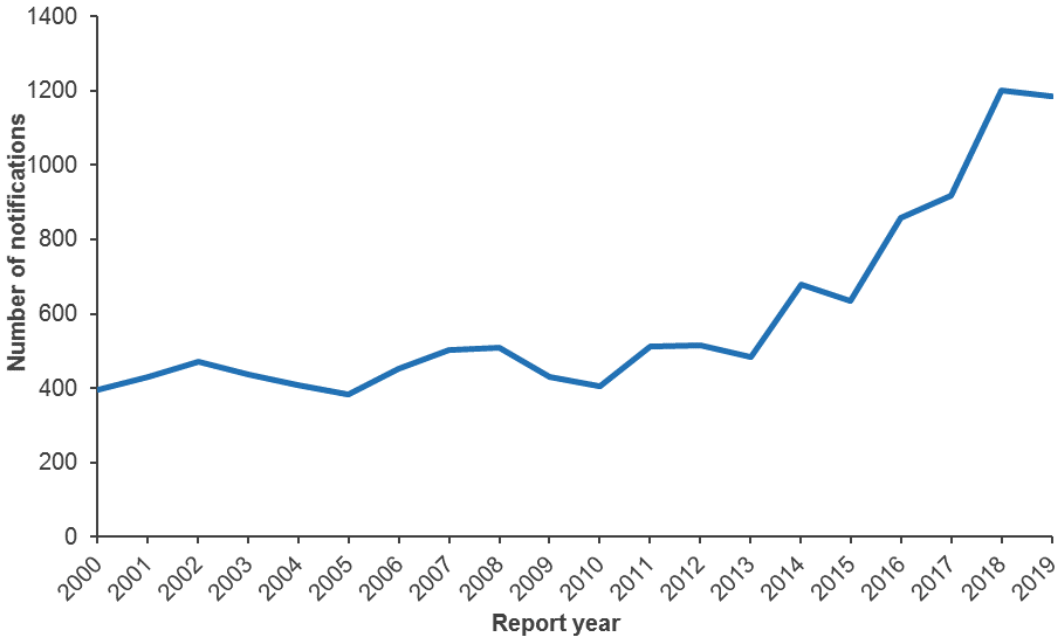
The ICD-10 code A04.6 was used to extract yersiniosis (enteritis due to *Y. enterocolitica)* hospitalisation data from the MoH NMDS database. Of the 138 hospital admissions (2.8 admissions per 100,000 population) recorded in 2019, 69 cases were reported with yersiniosis as the primary diagnosis and 69 were reported with yersiniosis as another relevant diagnosis.

It has been estimated by expert consultation that 63.2% (95th percentile credible interval: 29.0% to 91.5%) of yersiniosis incidence is due to foodborne transmission. Approximately 70% of foodborne transmission was estimated to be due to consumption of pork.

Notifiable disease data

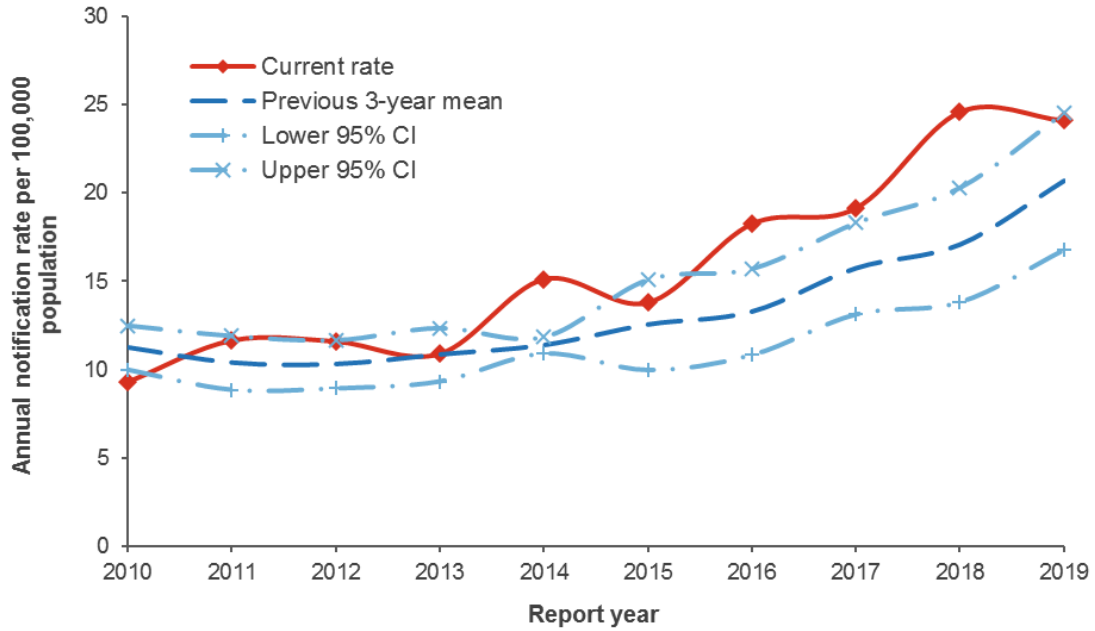
Between 1998 and 2013 the annual number of notifications reported ranged between 383 and 546. Since 2015, the number of notifications for yersiniosis and the rate of yersiniosis notifications per 100,000 population has been increasing sharply, with the highest number of cases reported in 2018 (1202 cases) and 2019 (1186) (Figure 46 and Figure 47).

Figure 46. Yersiniosis notifications by year, 2000–2019



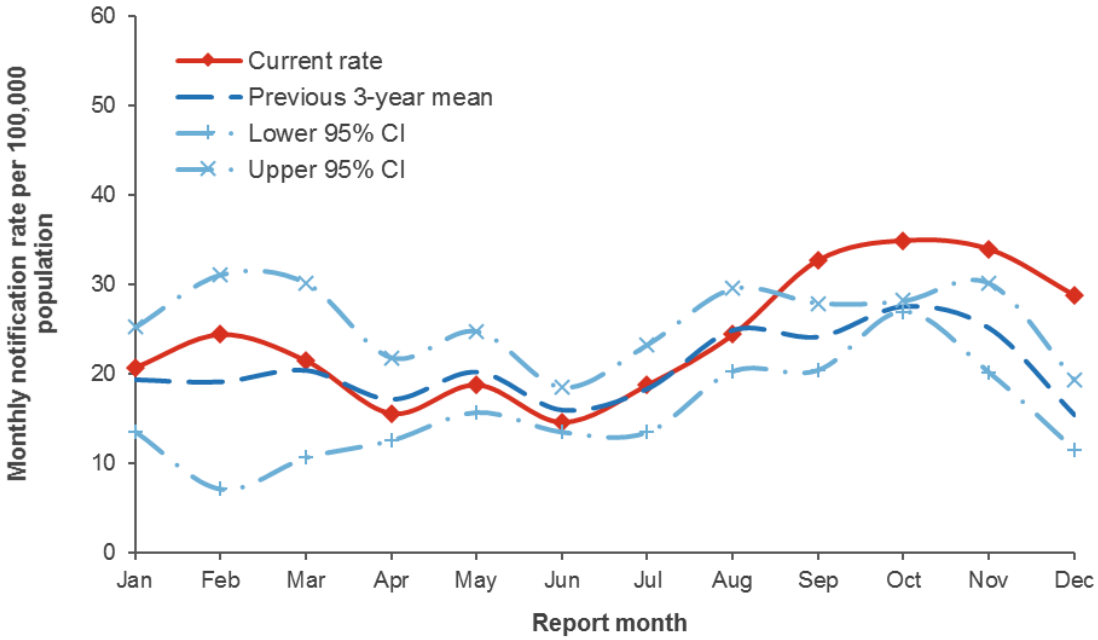
The yersiniosis annual notification rate remained stable between 2000 and 2013 (ranging from 9.3 to 11.6 per 100,000) and has increased steadily since then (Figure 47). The 2019 notification rate was 24.1 per 100,000 population, higher than the previous three-year average (20.7 cases per 100,000).

Figure 47. Yersiniosis notification rate by year, 2010–2019



The number of notified cases of yersiniosis per 100,000 population by month for 2019 is shown in Figure 48. In 2019, the monthly number of notifications ranged from 60 notifications (June) to 143 notifications (October). The seasonal trend in 2019 followed a similar pattern to 2015 to 2017, with increased notification rates from September to November. In contrast, in 2018 no seasonal trend in monthly notification rates was apparent. During September to November, the notification rates in 2019 (~34 cases per 100,000) were above the three year average rate (~26 cases per 100,000).

Figure 48. Yersiniosis monthly rate (annualised), 2019



In 2019, the yersiniosis notification and hospitalisation rates were similar for males and females (Table 64).

Table 64. Yersiniosis cases by sex, 2019

Gender	EpiSurv notifications		Hospitalisations[a]	
	No.	Rate[b]	No.	Rate[b]
Male	571	23.6	72	3.0
Female	615	24.6	66	2.6
Total	**1186**	**24.1**	**138**	**2.8**

[a] MoH NMDS data for hospital admissions

[b] per 100,000 population

In 2019, the highest yersiniosis notification rates were for the less than 1 year (100.6 per 100,000 population, 60 cases) and 1 to 4 years (60.6 per 100,000, 149 cases) age groups (Table 65). The highest hospitalisation rate was reported for the under 1 year age group (20.1 per 100,000 population, 12 cases).

Table 65. Yersiniosis cases by age group, 2019

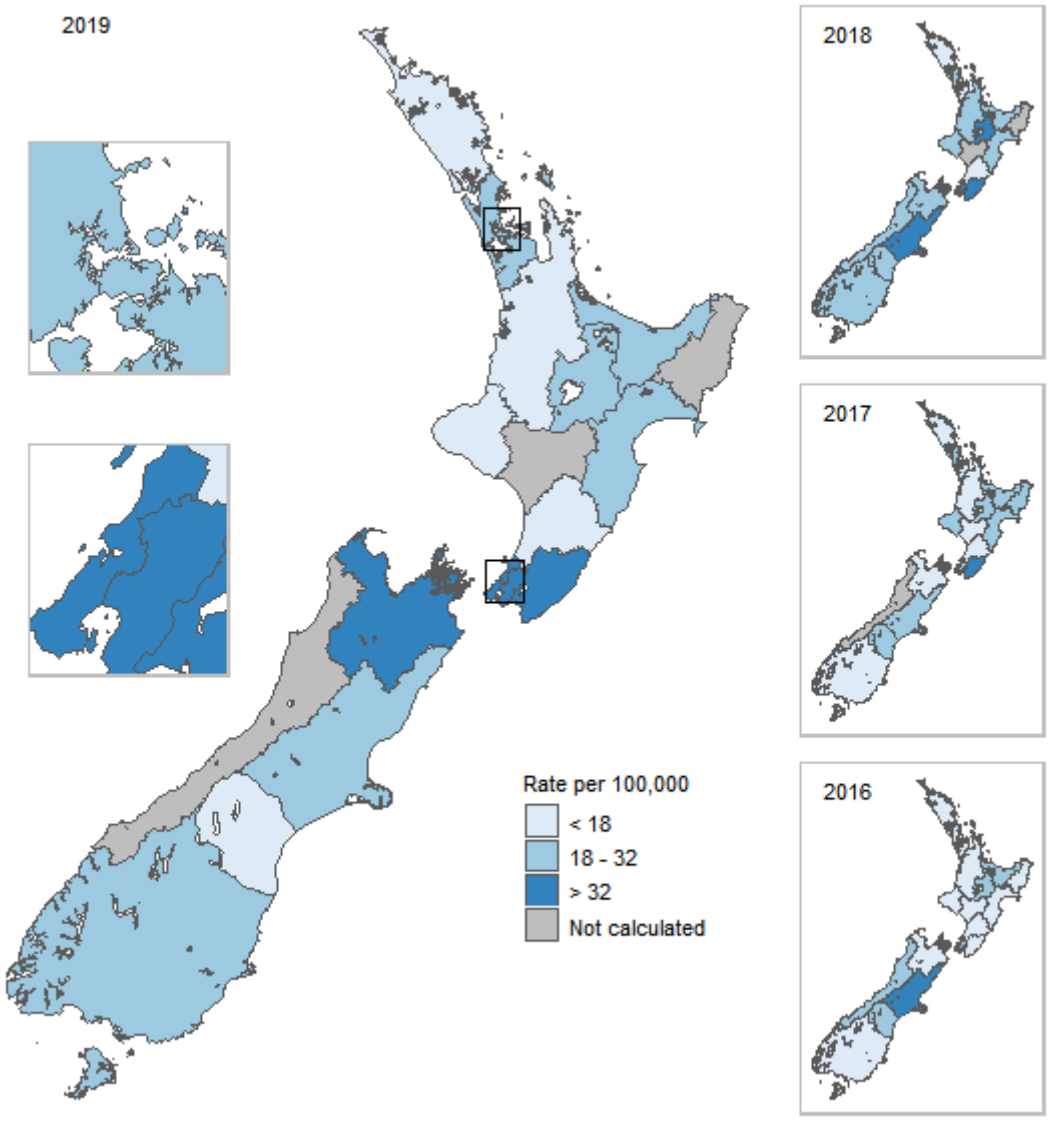
Age group (years)	EpiSurv notifications		Hospitalisations[a]	
	No.	Rate[b]	No.	Rate[b]
<1	60	100.6	12	20.1
1 to 4	149	60.6	6	2.4
5 to 9	50	15.2	1	-
10 to 14	48	14.9	5	1.5
15 to 19	45	14.3	2	-
20 to 29	131	18.8	8	1.1
30 to 39	159	24.5	17	2.6
40 to 49	133	21.4	16	2.6
50 to 59	127	20.2	17	2.7
60 to 69	139	26.7	17	3.3
70+	145	27.5	37	7.0
Total	**1186**	**24.1**	**138**	**2.8**

[a] MoH NMDS data for hospital admissions

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

Yersiniosis notification rates have varied spatially and temporally throughout New Zealand over the last four years as illustrated in Figure 49. In 2019, the highest rates were reported for the DHBs Wairarapa (63.0 per 100,000 population, 30 cases), Capital and Coast (41.8 per 100,000 population, 132 cases) and Nelson Marlborough (40.8 per 100,000 population, 64 cases). Note that rates were not calculated for DHB year combinations where there were less than five cases notified.

Figure 49. Geographic distribution of yersiniosis notifications, 2016–2019



Note: Changes in laboratory methods were introduced in Northland, Waitemata, Auckland and Counties Manukau DHBs. Since June 2017 a new assay is used to include *Y. enterocolitica.* This may have contributed to the increase in notifications for yersiniosis. Refer to report Introduction for details.

For cases where information on travel was provided in 2019, 9% had travelled overseas during the incubation period. Assuming that the cases for which travel information was provided were representative of all yersiniosis cases, a Poisson distribution can be used to estimate the total number of potentially travel-related cases of yersiniosis in 2019. The resultant distribution has a mean of 110 cases (95% CI 90-133).

If data from the last four years are considered the estimated proportion of cases travelling overseas within the incubation period of the organism was 8% (95% CI 6-9%).

Outbreaks reported as caused by *Yersinia* spp.

In 2019, there were four yersiniosis outbreaks reported in EpiSurv, two of which reported food as a possible mode of transmission (Table 66). 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 66. Yersiniosis outbreaks reported, 2019

Measure	Yersiniosis outbreaks		
	Possible foodborne transmission with a suspected or confirmed source	Possible foodborne transmission but no suspected source	All
Outbreaks	1	1	4
Cases	62	3	103
Hospitalised cases	3	2	5

Table 67 contains details of the two yersiniosis outbreaks with food reported as a possible mode of transmission reported in 2019.

Table 67. Details of yersiniosis outbreaks with food reported as a possible mode of transmission, 2019

PHU	Month	Suspected Vehicle	Evidence	Setting	No. Ill
Auckland	Oct	Unknown	Household cluster	Home	1C 2P
Waikato	Dec	Hot and cold chicken meals, also food is sometimes hoarded in rooms, so not in ideal storage conditions.	Increase in disease incidence, common meals	Prison	4C 58P

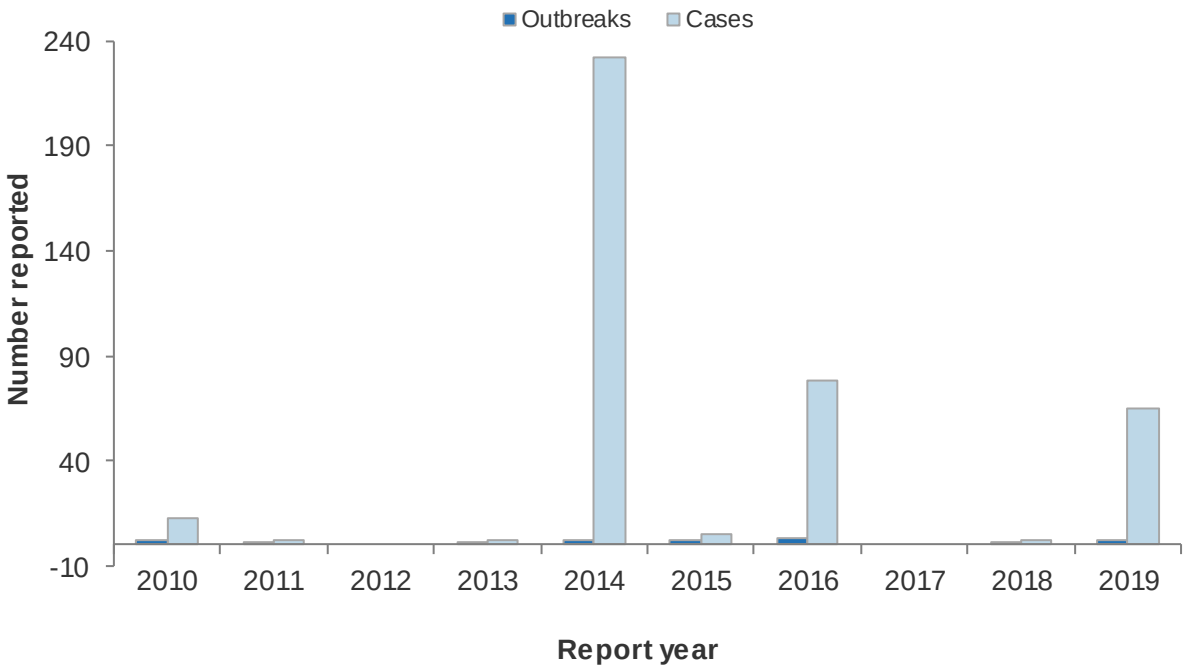
PHU Public Health Unit, Auckland: Auckland Regional Public Health Service, Waikato: Population Health Service Waikato

Number ill: C: confirmed, P: probable

Campylobacter was also isolated from case samples in the December outbreak and the level of evidence for the chicken meals being a cause of the outbreak was weak. *Y. pseudotuberculosis* was reported as the cause of the October outbreak in Auckland.

Over the 10 year period 2010 to 2019, very few yersiniosis outbreaks with food reported as a possible mode of transmission were reported in EpiSurv; three or less each year, with a total number of associated cases ranging from two to 232 (Figure 51). The number of outbreaks in 2014 (2 outbreaks) and 2016 (3 outbreaks) was not unusual, but the number of cases involved (232 and 78, respectively) was higher than has been previously seen in New Zealand. The increased number of outbreak cases in 2019 is due to the outbreak in a prison setting.

Figure 50. Yersiniosis outbreaks with food reported as a possible mode of transmission and associated cases reported by year, 2010–2019



Yersinia species and biotypes commonly reported

In 2019, the Enteric Reference Laboratory (ERL) at ESR confirmed 799 clinical case isolates as notifiable *Yersinia* spp. (i.e. *Y. enterocolitica* (YE) and *Y. pseudotuberculosis* (YTB)). Note that the case status in EpiSurv is changed to "not a case" for *Yersinia* isolates that are identified by ERL as non-notifiable (i.e. not YE or YTB) and these cases no longer appear in the reported notifications.

The number of notifiable *Yersinia* spp. cases identified by the Enteric Reference Laboratory at ESR each year is shown in Table 68 and the percentage of cases with different types is shown in Figure 51. 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 changed during this period and
c) successful isolation and identification of *Yersinia* spp. is influenced by the methods used by the laboratories – the newer methods have not been shown to be more sensitive than the historical ones, but >50% of NZ samples are no longer being tested for *Yersinia pseudotuberculosis* as the organism is not targeted by the commercial PCR some diagnostic laboratories have chosen to use.

Between 2015 and 2019, each year the largest proportion of cases was due to *Y. enterocolitica* (Table 68 and Figure 51). Since the number of isolates referred to ESR's Enteric Reference Laboratory has dropped markedly in 2019 trends need to be interpreted with caution. Since 2015 the number of cases reported with *Y. enterocolitica* biotype 2/3 has continued to increase. However, the percentage of cases reported with *Y. enterocolitica* biotype 2/3 compared to all typed cases was similar across 2016 to 2019 and ranged between 55.2% (2019) and 66.7% (2017).

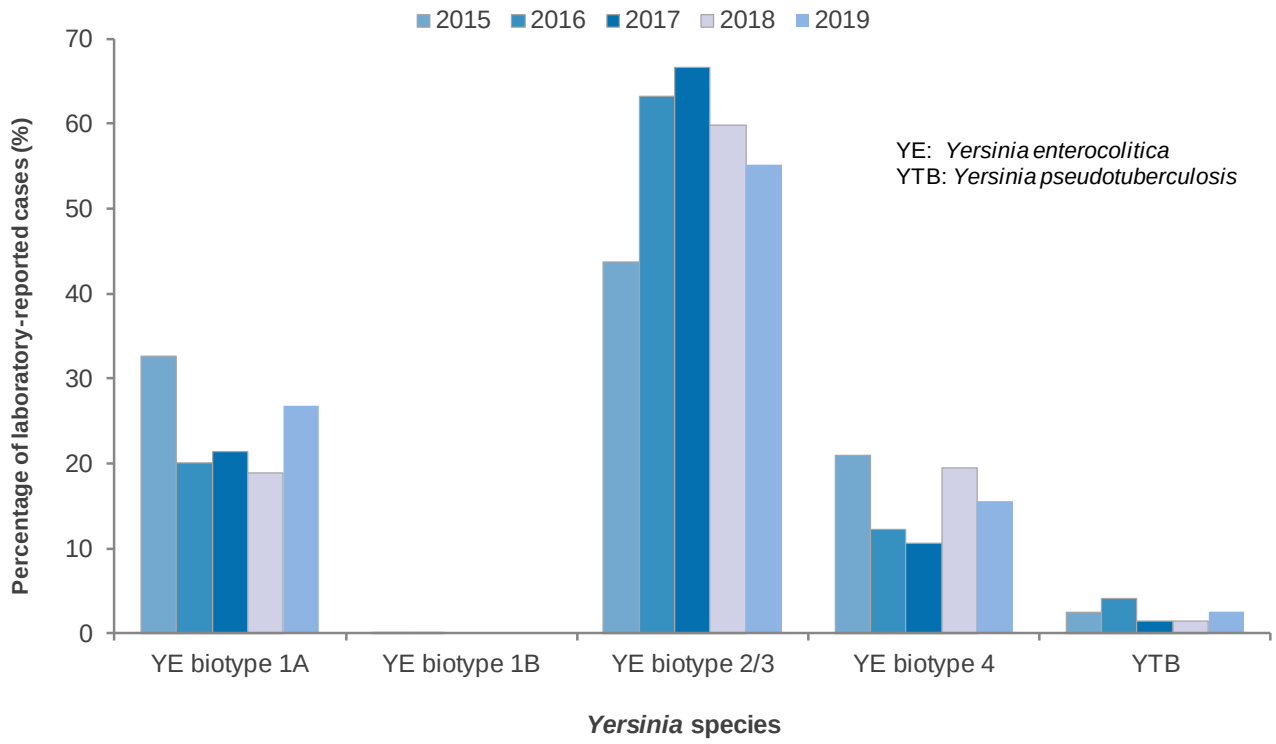
Since 2017 diagnostics of *Yersinia pseudotuberculosis* infection has been limited by clinical laboratories not testing for this organism therefore case notifications for this organism might be reduced.

Table 68. Notifiable *Yersinia* spp. identified by the Enteric Reference Laboratory, 2015–2019

Species	2015	2016	2017	2018	2019
Yersinia enterocolitica	**521**	**748**	**822**	**1049**	**779**
biotype 1A	173	157	178	201	214
biotype 1B	1	1	0	0	0
biotype 2/3[a]	232	493	556	637	441
biotype 4	111	96	88	207	124
biotype not identified	4	1	0	4	0
Yersinia pseudotuberculosis	**13**	**32**	**12**	**15**	**20**
Total	**534**	**780**	**834**	**1064**	**799**

[a] *Yersinia enterocolitica* biotypes 2 and 3 were shown to be genetically very similar and should not be separated [37]. The discriminating biochemical test, a delayed weak indole reaction, can be subjective [38]. From September 2017 onwards biotypes 2 and 3 were combined into biotype 2/3. For the purpose of presenting retrospective data in the same format, biotype 2 and 3 for previous years were also combined

Figure 51. Percentage of laboratory-reported cases of notifiable *Yersinia* spp. by species and year, 2015–2019



Recent surveys

Nil.

Relevant New Zealand studies and publications

Nil.

Relevant regulatory developments

Nil.

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 2018, 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 Public Health Units (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 2019* [13].

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).

Ministry of Health (MoH)

MoH 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 [12]. 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 actually 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 readmissions, have been reported for all primary diseases. For the disease sequelae (GBS and HUS), readmissions within the calendar year were removed with reported case numbers representing unique cases, rather than total admissions.

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* [39].

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 or PFGE 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 FSANZ were briefly summarized 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 are the experts in this area and the regulatory developments summarised in this report were confirmed with New Zealand Food Safety.

Risk attribution

Information from a project on risk ranking was used to estimate the proportion of disease due to specific pathogens that can be attributed to transmission by food [2]. Attributable proportions were determined by expert consultation, using a modified double-pass Delphi, with a facilitated discussion between passes. Each expert was asked to provide a minimum ('at least'), a most likely and a maximum ('not more than') estimate of the proportion of a number of microbial diseases that were due to transmission by food. Estimates presented in the current report are mean values from the second pass, incorporating a weighting scheme based on a self-assessment of expertise for each pathogen. The 2013 expert consultation did not consider *Bacillus cereus* intoxication. The estimate for the proportion of *Bacillus cereus* intoxication due to transmission by food is taken from the previous expert consultation which took place in 2005 [14].

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 21 February 2020. Outbreak data contained in this report are based on information recorded as an outbreak in EpiSurv as at 31 July 2020. 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. Laboratory results are reported according to the date the specimen was received.

Case status for notifications

All notifications recorded in EpiSurv that meet the case definitions [11] 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 2019 mid-year population estimates and are crude rates unless otherwise stated. At 30 June 2019, the New Zealand population was estimated to be 4,917,000. The population estimates for 2018 have been revised by Statistics New Zealand, taking into account new migration measures and 2018 Census distributions. Any cases rates given in this report for 2018 will be based on the revised population estimates.

Mid-year population estimates by ethnicity were not available from Statistics New Zealand for 2019 at the time of writing the report. Population estimates were provided by the Ministry of Health.

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.

Map classification scheme

The map classification break points for the disease have been selected to divide the data into three bands to show the range of rates among DHBs. 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). The map showing all DHBs and their boundaries is presented in Figure 53.

Figure 53. Map of District Health Boards

Statistical tests

Confidence intervals have been calculated for the disease rates and displayed on the graphs. The historical mean is calculated from the previous three years data (2016−2018).

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SUMMARY TABLES

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

Table 69. Number of cases and rate per 100,000 population of selected notifiable diseases in New Zealand, 2018–2019

Disease	2018[a]		2019		Change[b]
	Cases	Rate	Cases	Rate	
Campylobacteriosis	6957	143.7	6202	126.1	↓
Cryptosporidiosis	1613	33.3	1035	21.0	↓
Gastroenteritis[c]	231	4.7	489	9.9	↑
Giardiasis	1585	32.7	1749	35.6	↑
Hepatitis A	68	1.4	58	1.2	↓
Listeriosis	30	0.6	31	0.6	-
Salmonellosis	1100	22.7	1188	24.2	↑
Shigellosis	217	4.5	222	4.5	-
STEC infection	925	19.1	1101	22.4	↑
Yersiniosis	1201	24.8	1186	24.1	↓

[a] 2018 rates of disease may be different to those reported in the 2018 Annual report, due to revised population estimates as provided by Statistics New Zealand and implemented in this report

[b] Fisher's exact tests were used to determine statistical differences between the number of cases in the two years. Results are considered statistically significant when the P value is less than or equal to 0.05.

↓ = Significant decrease, ↑ = Significant increase, ↓ = Not significant decrease, ↑ = Not significant increase, - = No change

[c] Cases of acute gastroenteritis are notifiable if; there is a suspected common source, it is a person with an increased risk of spreading the disease or it is an infectious gastroenteritis of public health significance such as botulism, histamine poisoning and toxic shellfish poisoning

Table 70. Deaths due to selected notifiable diseases recorded in EpiSurv, 2000–2019

Disease	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019
Campylobacteriosis	3	1	1	0	0	1	1	1	0	0	0	0	0	1	0	0	0	0	0	0
Gastroenteritis[a]	0	0	1	0	0	0	0	0	0	0	0	0	0	0	2	0	1	0	0	0
Giardiasis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Listeriosis - non-perinatal	2	1	0	2	3	1	0	2	3	2	3	4	4	2	3	1	0	0	2	0
Listeriosis - perinatal	4	1	3	2	2	4	1	2	2	2	4	0	2	3	2	3	2	0	0	1
Salmonellosis	7	2	1	0	0	1	1	1	1	1	0	0	0	0	0	0	0	1	0	0
Shigellosis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0
STEC infection	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0	2	0
Yersiniosis	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

[a] Cases of acute gastroenteritis are notifiable if; there is a suspected common source, it is a person with an increased risk of spreading the disease or it is an infectious gastroenteritis of public health significance such as botulism, histamine poisoning and toxic shellfish poisoning

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 71. MoH hospitalisations data for selected notifiable diseases, 2017–2019

Disease	ICD 10 Codes	2017		2018		2019	
		Principal diagnosis	Other relevant diagnosis	Principal diagnosis	Other relevant diagnosis	Principal diagnosis	Other relevant diagnosis
Campylobacteriosis	A04.5	591	142	631	151	582	120
Cryptosporidiosis	A07.2	46	21	82	53	43	24
Giardiasis	A07.1	38	33	38	26	42	46
Hepatitis A	B15	40	42	47	49	31	45
Listeriosis	A32	7	12	17	24	22	24
Salmonellosis[a]	A02.0	144	26	184	44	203	27
Shigellosis	A03	33	12	37	22	44	22
STEC infection[b]	A04.3	11	9	19	22	29	23
Yersiniosis	A04.6	54	37	86	67	69	69

[a] *Salmonella* enteritis

[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 72. Number of cases and rate per 100,000 population of selected notifiable diseases by ethnic group, 2019

Disease	Ethnic group[a]											
	Maori		Pacific peoples		Asian		MELAA[b]		European or Other		Total[c]	
	Cases	Rate	Cases	Rate	Cases	Rate	Cases	Rate	Cases	Rate	Cases	Rate
Campylobacteriosis	544	67.4	141	43.8	359	49.6	48	93.3	4775	160.5	6202	126.1
Cryptosporidiosis	123	15.2	32	9.9	78	10.8	10	19.4	774	26.0	1035	21.0
Gastroenteritis[d]	73	9.0	14	4.4	34	4.7	5	9.7	350	11.8	487	9.9
Giardiasis	176	21.8	32	9.9	121	16.7	19	36.9	1357	45.6	1749	35.6
Hepatitis A	6	0.7	17	5.3	18	2.5	1	-	14	0.5	58	1.2
Listeriosis	7	0.9	2	-	2	-	1	-	18	0.6	31	0.6
Salmonellosis	133	16.5	72	22.4	116	16.0	15	29.1	839	28.2	1188	24.2
Shigellosis	20	2.5	51	15.9	31	4.3	5	9.7	115	3.9	222	4.5
STEC infection	137	17.0	30	9.3	56	7.7	17	33.0	849	28.5	1101	22.4
Yersiniosis	87	10.8	47	14.6	241	33.3	26	50.5	738	24.8	1186	24.1

[a] Ethnicity is prioritised in the following order: Maori, Pacific Peoples, Asian, MELAA, European or Other Ethnicity (including New Zealander)

[b] MELAA: Middle Eastern/Latin America/African

[c] Total includes cases where ethnicity was unknown

[d] Cases of acute gastroenteritis are notifiable if; there is a suspected common source, it is a person with an increased risk of spreading the disease or it is an infectious gastroenteritis of public health significance such as botulism, histamine poisoning and toxic shell fish poisoning

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

Table 73. Number of cases and rate per 100,000 population of selected notifiable diseases by sex, 2019

Disease	Sex					
	Male		Female		Total[a]	
	Cases	Rate	Cases	Rate	Cases	Rate
Campylobacteriosis	3550	146.7	2650	106.1	6202	126.1
Cryptosporidiosis	474	19.6	560	22.4	1035	21.0
Gastroenteritis[b]	229	9.4	257	10.3	489	9.9
Giardiasis	895	37.0	853	34.2	1749	35.6
Hepatitis A	31	1.3	27	1.1	58	1.2
Listeriosis[c]	16	0.7	15	0.6	31	0.6
Salmonellosis	584	24.1	603	24.1	1188	24.2
Shigellosis	115	4.8	107	4.3	222	4.5
STEC infection	520	21.5	581	23.3	1101	22.4
Yersiniosis	571	23.6	615	24.6	1186	24.1

[a] Total includes cases where sex was unknown

[b] Cases of acute gastroenteritis are notifiable if; there is a suspected common source, it is a person with an increased risk of spreading the disease or it is an infectious gastroenteritis of public health significance such as botulism, histamine poisoning and toxic shellfish poisoning

[c] Case details for perinatal cases are those for the mother, so the female cases will include all six perinatal cases

Table 74. Number of cases of selected notifiable diseases by age group, 2019

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	128	597	269	219	324	865	667	660	809	804	860	6202
Cryptosporidiosis	20	250	100	69	55	179	141	89	56	41	35	1035
Gastroenteritis[b]	11	34	11	8	19	56	81	69	67	72	54	489
Giardiasis	18	310	119	40	37	203	384	224	168	171	75	1749
Hepatitis A	0	5	5	4	7	14	10	5	6	2	0	58
Listeriosis[c]	0	0	0	0	1	5	3	3	3	3	13	31
Salmonellosis	73	158	64	38	44	151	146	117	149	149	99	1188
Shigellosis	2	15	11	7	5	46	37	24	36	25	14	222
STEC infection	51	188	52	39	48	122	87	78	124	143	169	1101
Yersiniosis	60	149	50	48	45	131	159	133	127	139	145	1186

[a] Total includes cases where age was unknown

[b] Cases of acute gastroenteritis are notifiable if; there is a suspected common source, it is a person with an increased risk of spreading the disease or it is an infectious gastroenteritis of public health significance such as botulism, histamine poisoning and toxic shellfish poisoning

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

Table 75. Rate per 100,000 population of selected notifiable diseases by age group, 2019

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	214.6	242.7	81.6	67.8	102.6	124.1	102.8	106.3	128.6	154.7	162.9	126.1
Cryptosporidiosis	33.5	101.6	30.3	21.4	17.4	25.7	21.7	14.3	8.9	7.9	6.6	21.0
Gastroenteritis[a]	18.4	13.8	3.3	2.5	6.0	7.9	12.3	11.1	10.6	13.9	10.2	9.9
Giardiasis	30.2	126.0	36.1	12.4	11.7	29.1	59.2	36.1	26.7	32.9	14.2	35.6
Hepatitis A	-	2.0	1.5	-	2.2	2.0	1.5	0.8	1.0	-	-	1.2
Listeriosis[c]	-	-	-	-	-	0.7	-	-	-	-	2.5	0.6
Salmonellosis	122.4	64.2	19.4	11.8	13.9	21.7	22.5	18.8	23.7	28.7	18.8	24.2
Shigellosis	-	6.1	3.3	2.2	1.6	6.6	5.7	3.9	5.7	4.8	2.7	4.5
STEC infection	85.5	76.4	15.8	12.1	15.2	17.5	13.4	12.6	19.7	27.5	32.0	22.4
Yersiniosis	100.6	60.6	15.2	14.9	14.3	18.8	24.5	21.4	20.2	26.7	27.5	24.1

[a] Cases of acute gastroenteritis are notifiable if; there is a suspected common source, it is a person with an increased risk of spreading the disease or it is an infectious gastroenteritis of public health significance such as botulism, histamine poisoning and toxic shellfish poisoning

[b] Total includes cases where age was unknown

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

Fewer than 5 cases in a cell or less than a national total of 100 cases for the year

First (lowest) band (lower than 25th percentile)

Second (middle) band

Third (highest) band (above 75th percentile)

Table 76. Number of cases of selected notifiable diseases by District Health Board, 2019

Disease	District Health Board																				
	Northland	Waitemata	Auckland	Counties Manukau	Waikato	Lakes	Bay of Plenty	Tairawhiti	Taranaki	Hawke's Bay	Whanganui	MidCentral	Hutt Valley	Capital and Coast	Wairarapa	Nelson Marlborough	West Coast	Canterbury	South Canterbury	Southern	Total
Campylobacteriosis	249	793	515	487	619	151	289	44	223	260	80	261	152	330	108	205	45	713	142	536	6202
Cryptosporidiosis	42	103	94	114	112	12	30	15	19	46	7	62	14	44	9	30	7	121	16	138	1035
Gastroenteritis[a]	22	9	14	18	124	41	119	1	2	1	11	1	19	38	14	11	1	28	4	11	489
Giardiasis	94	166	205	173	187	43	130	37	27	73	9	48	39	132	21	81	2	159	29	94	1749
Hepatitis A	0	11	9	19	6	1	0	0	0	2	0	2	0	2	0	0	0	4	0	2	58
Listeriosis	0	3	3	2	3	1	1	0	0	1	1	2	3	2	1	0	0	5	2	1	31
Salmonellosis	36	144	117	108	96	34	57	10	39	31	10	32	37	75	14	32	12	141	21	142	1188
Shigellosis	3	26	66	35	5	6	12	1	3	10	1	0	3	19	2	5	0	18	0	7	222
STEC infection	69	102	77	64	107	46	75	1	9	55	6	9	34	76	30	56	0	67	17	201	1101
Yersiniosis	12	143	155	108	75	21	59	4	12	38	3	19	57	132	30	64	0	153	8	93	1186

[a] Cases of acute gastroenteritis are notifiable if; there is a suspected common source, it is a person with an increased risk of spreading the disease or it is an infectious gastroenteritis of public health significance such as botulism, histamine poisoning and toxic shellfish poisoning

Table 77. Rate per 100,000 population of selected notifiable diseases by District Health Board, 2019

Disease	District Health Board																			
	Northland	Waitemata	Auckland	Counties Manukau	Waikato	Lakes	Bay of Plenty	Tairawhiti	Taranaki	Hawke's Bay	Whanganui	MidCentral	Hutt Valley	Capital and Coast	Wairarapa	Nelson Marlborough	West Coast	Canterbury	South Canterbury	Southern	Total
Campylobacteriosis	132.0	129.2	106.0	86.3	145.3	132.0	114.3	89.2	181.6	149.8	118.5	142.4	98.3	104.4	226.9	130.7	138.0	125.9	232.4	158.0	126.2
Cryptosporidiosis	22.3	16.8	19.3	20.2	26.3	10.5	11.9	30.4	15.5	26.5	10.4	33.8	9.0	13.9	18.9	19.1	21.5	21.4	26.2	40.7	21.1
Gastroenteritis[a]	11.7	1.5	2.5	3.2	29.1	35.8	47.1	-	-	-	16.3	-	12.3	12.0	29.4	7.0	-	4.9	-	3.2	9.9
Giardiasis	49.8	27.0	42.2	30.7	43.9	37.6	51.4	75.1	22.0	42.1	13.3	26.2	25.2	41.8	44.1	51.6	-	28.1	47.5	27.7	35.6
Hepatitis A	-	1.8	1.9	3.4	1.4	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1.2
Listeriosis	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0.9	-	-	0.6
Salmonellosis	19.1	23.5	24.1	19.1	22.5	29.7	22.5	20.3	31.8	17.9	14.8	17.5	23.9	23.7	29.4	20.4	36.8	24.9	34.4	41.9	24.2
Shigellosis	-	4.2	13.6	6.2	1.2	5.2	4.7	-	-	5.8	-	-	-	6.0	-	3.2	-	3.2	-	2.1	4.5
STEC infection	36.6	16.6	15.9	11.3	25.1	40.2	29.7	-	7.3	31.7	8.9	4.9	22.0	24.1	63.0	35.7	-	11.8	27.8	59.3	22.4
Yersiniosis	6.4	23.3	31.9	19.1	17.6	18.4	23.3	-	9.8	21.9	-	10.4	36.8	41.8	63.0	40.8	-	27.0	13.1	27.4	24.1

[a] Cases of acute gastroenteritis are notifiable if; there is a suspected common source, it is a person with an increased risk of spreading the disease or it is an infectious gastroenteritis of public health significance such as botulism, histamine poisoning and toxic shellfish poisoning

Fewer than 5 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 78. Number of cases of selected notifiable diseases by year, 1990–2019

Disease	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004
Campylobacteriosis	3850	4148	5144	8101	7714	7442	7635	8924	11,572	8161	8418	10,146	12,493	14,788	12,215
Cryptosporidiosis[a]	-	-	-	-	-	-	119	357	866	977	775	1208	975	817	611
Gastroenteritis[a b]	-	-	-	-	-	-	555	316	493	608	730	942	1088	1030	1362
Giardiasis[a]	-	-	-	-	-	-	1235	2127	2183	1793	1688	1604	1547	1570	1514
Hepatitis A	150	224	288	257	179	338	311	347	145	119	107	61	106	70	49
Listeriosis	16	26	16	11	8	13	10	35	17	19	22	18	19	24	26
Salmonellosis	1619	1244	1239	1340	1522	1334	1141	1177	2069	2077	1795	2417	1880	1401	1081
Shigellosis	197	152	124	128	185	191	167	117	122	147	115	157	112	87	140
STEC infection[c]	-	-	-	3	3	6	7	13	48	64	67	76	73	104	89
Yersiniosis[a]	-	-	-	-	-	-	330	488	546	503	396	429	472	436	407

Disease	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019
Campylobacteriosis	13,836	15,873	12,778	6692	7177	7346	6686	7016	6837	6782	6218	7457	6482	6957	6202
Cryptosporidiosis	888	737	924	765	854	954	610	877	1348	584	696	1062	1192	1613	1035
Gastroenteritis[a]	559	926	617	676	713	502	570	765	558	774	506	513	324	231	489
Giardiasis	1231	1214	1402	1660	1639	1985	1934	1714	1729	1709	1510	1616	1648	1585	1749
Hepatitis A	51	123	42	89	44	46	26	82	91	74	47	35	58	68	58
Listeriosis	20	19	26	27	28	23	26	25	19	25	26	36	21	30	31
Salmonellosis	1382	1335	1275	1337	1128	1146	1055	1081	1143	955	1051	1091	1119	1100	1188
Shigellosis	183	102	129	113	119	104	101	131	137	128	111	174	244	217	222
STEC infection	92	87	100	122	143	138	153	147	205	187	330	417	547	925	1101
Yersiniosis	383	453	502	508	430	406	513	514	483	680	634	858	917	1201	1186

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

[b] Cases of acute gastroenteritis from a common source or foodborne intoxication e.g. staphylococcal intoxication

[c] The first case of STEC infection confirmed in New Zealand was reported in October 1993 [40]. Note: cell marked "-" where data are unavailable

Table 79. Rate per 100,000 population of selected notifiable diseases in New Zealand and other selected countries

Disease	Country/Region (publication year of report)						
	New Zealand (2019)	Australia[a] (2019)	USA[b] (2019)	Canada[d] (2017)	UK[e] (2018)	EU Total[e] (2018)	Other high
Campylobacteriosis	126.1	143.5	19.5	28.4	98.4	64.1	215.8 (Czech Republic)[e] 153.2 (Slovakia)[e]
Cryptosporidiosis	21.0	10.7	3.8[c]	2.2	7.7[6]	3.2[f]	12.0 (Ireland)[f] 7.8 (Sweden)[f]
Giardiasis	35.6	NN	6.1[c]	10.0	7.9[f]	5.5[f]	17.6 (Belgium)[f] 12.2 (Estonia)[f]
Hepatitis A	1.2	1.0	3.8[c]	0.75	0.8[6]	2.4[f]	25.0 (Slovakia)[f] 22.7 (Bulgaria)[f]
Listeriosis	0.6	0.2	0.3	0.33	0.25	0.47	2.05 (Estonia)[e] 1.45 (Finland)[e]
Salmonellosis	24.2	58.8	17.1	19.5	14.3	20.1	124.8 (Slovakia)[e] 102.7 (Czech Republic)[e]
Shigellosis	4.5	12.6	4.8	2.3	2.9[f]	1.5[f]	4.1 (Bulgaria)[f] 3.7 (Denmark)[f]
STEC infection	22.4	2.6	6.3	2.2	2.8	2.3	20.0 (Ireland)[e] 8.8 (Sweden)[e]
Yersiniosis	24.1	NN	1.4	NN	0.3	1.7	9.6 (Finland)[e] 6.9 (Belgium)[e]

NN: Not notifiable

[a] National Notifiable Diseases Surveillance System (NNDSS) http://www9.health.gov.au/cda/source/CDA-index.cfm (data downloaded on 28 April 2020)

[b] FoodNet – Foodborne Diseases Active Surveillance Network http://www.cdc.gov/foodnet/. From 2017, FoodNet incidence rates are made up of a mixture of culture positive and culture-independent diagnostic test positive detections

[c] Centers for Disease Control and Prevention. Summary of notifiable disease https://wwwn.cdc.gov/nndss/infectious-tables.html (CDC data presented here relate to the 2018 year)

[d] Canadian Notifiable Disease Surveillance System (CNDSS) http://dsol-smed.phac-aspc.gc.ca/dsol-smed/ndis/index-eng.php

[e] European Food Safety Authority and European Centre for Disease Prevention and Control (ECDC). The European Union One Health 2018 Zoonoses Report https://www.ecdc.europa.eu/sites/default/files/documents/zoonoses-EU-one-health-2018-report.pdf

[f] European Centre for Disease Prevention and Control (ECDC). Annual epidemiological reports http://ecdc.europa.eu/en/publications/surveillance_reports/annual_epidemiological_report/Pages/epi_index.aspx (ECDC data presented here relate to the 2017 year for cryptosporidiosis and giardiasis and to the 2016 year for hepatitis A and shigellosis)

Table 80. Foodborne outbreaks and associated cases by pathogen/condition, 2019

Pathogen/Condition	Outbreaks (n = 63)		Cases (n = 588)	
	No.	%[a]	No.	%[b]
Salmonella	15	23.8	186	31.6
Norovirus	10	15.9	159	27.0
Campylobacter	8	12.7	81	13.8
Shigella	4	6.3	9	1.5
Clostridium perfringens	3	4.8	53	9.0
Giardia	2	3.2	18	3.1
Histamine (scombroid) fish poisoning	2	3.2	7	1.2
Yersinia	2	3.2	65	11.1
Ciguatera fish poisoning	1	1.6	4	0.7
Vibrio	1	1.6	24	4.1
Pathogen not identified[c]	17	27.0	78	13.3

Note: Two agents were reported in three outbreaks (99 cases), therefore percentage totals add to more than 100%

[a] Percentage of outbreaks for each pathogen/condition, calculated using the total number of foodborne outbreaks (63). 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 pathogen/condition, calculated using the total number of associated cases (588)

[c] All enteric outbreaks with no pathogen identified in 2019 were recorded as gastroenteritis

Table 81. Foodborne outbreaks and associated cases by exposure setting, 2019

Exposure setting	Outbreaks (n = 63)		Cases (n = 588)	
	No.	%[a]	No.	%[b]
Commercial food operators	**34**	**54.0**	**275**	**46.8**
Restaurant/café/bakery	25	39.7	168	28.6
Takeaway	4	6.3	9	1.5
Caterers	2	1.6	70	5
Other food outlet	1	1.6	6	1.0
Supermarket/delicatessen	1	1.6	2	0.3
Temporary or mobile service	1	1.6	23	3.9
Institutions	**8**	**12.7**	**133**	**22.6**
Camp	2	3.2	34	5.8
Long-term care facility	2	3.2	10	1.7
Hospital	1	1.6	3	0.5
Hostel / boarding house	1	1.6	20	3.4
Marae	1	1.6	4	0.7
Prison	1	1.6	62	10.5
Other	**16**	**25.4**	**82**	**13.9**
Private home	11	17.5	42	7.1
Community, church or sports gathering	2	4.8	6	1.0
Wedding	1	1.6	34	5.8
Overseas	2	3.2	4	0.7
Unknown exposure setting	**5**	**7.9**	**98**	**16.7**

Note: Two outbreaks had two exposure settings each (7 cases)

[a] Percentage of outbreaks for each exposure setting, calculated using the total number of foodborne outbreaks (63). 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 (588)

Table 82. Foodborne outbreaks and associated cases by preparation setting, 2019

Preparation setting	Outbreaks (n = 63)		Cases (n = 588)	
	No.	%[a]	No.	%[b]
Commercial food operators	**28**	**44.4**	**236**	**40.1**
Restaurant/café/bakery	18	28.6	126	21.4
Takeaway	4	6.3	9	1.5
Caterers	3	4.8	52	8.8
Commercial food manufacturer	1	1.6	24	4.1
Other food outlet	1	1.6	3	0.5
Supermarket/delicatessen	1	1.6	2	0.3
Temporary or mobile service	1	1.6	23	3.9
Institutions	**6**	**9.5**	**110**	**18.7**
Camp	2	3.2	34	5.8
Long term care facility	2	3.2	10	1.7
Marae	1	1.6	4	0.7
Prison	1	1.6	62	10.5
Other	**11**	**17.5**	**35**	**6.0**
Farm	7	11.1	7	1.2
Home	4	6.3	28	4.8
Unknown preparation setting	**21**	**33.3**	**211**	**35.9**

Note: Two outbreaks had two preparation settings each (7 cases)

[a] Percentage of outbreaks for each preparation setting, calculated using the total number of foodborne outbreaks (63). 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 (588)

Table 83. All Non-O157 STEC subtypes identified from cases by the Enteric Reference Laboratory, 2015–2019

Serotype	2015	2016	2017	2018	2019
O3:H21	0	0	0	0	1
O5:HNM	0	4	1	4	0
O5:HNT	0	0	0	0	8
O6:H34	0	0	0	0	1
O6:HNM	0	0	0	1	0
O8:H7	0	0	1	0	0
O8:H9	0	0	0	1	0
O8:H28	1	0	0	0	0
O8:HNM	0	1	1	1	0
O9:H2	0	0	1	0	0
O15:H2	0	1	0	1	2
O15:H14	0	0	1	0	0
O15:H16	0	0	0	0	1
O15:H21	0	0	1	0	0
O15:H27	0	0	0	0	1
O17:H18	0	0	0	0	2
O18:H7	0	0	1	0	0
O20:HNM	0	0	1	0	0
O22:H16	0	0	1	0	1
O23:H8	0	0	0	0	1
O23:H39	0	0	1	0	0
O25:H4	0	0	0	0	1
O26:H8	0	0	0	0	1
O26:H11	14	46	44	76	119
O26:HNT	0	0	2	1	7
O26:HNM	0	5	4	1	0
O29:H4	0	0	0	1	0
O38:H26	5	10	7	19	27
O38:HNT	0	0	1	0	2
O38:HNM	1	1	0	0	0
O41:H21	0	0	0	0	2
O43:H2	0	0	0	0	1
O45:H2	0	0	0	1	0
O51:H24	0	0	0	0	1
O55:H12	0	1	0	0	1

Serotype	2015	2016	2017	2018	2019
O55:HNT	1	0	0	0	0
O60:HNM	0	0	1	0	0
O61:H2	0	0	0	0	1
O63:H6	0	1	0	0	0
O64:H20	0	3	2	4	7
O65:H2	0	1	0	1	1
O69:H11	0	0	0	0	1
O71:H2	0	0	0	0	1
O74:H20	0	0	0	0	1
O75:H7	0	1	0	0	0
O75:H8	0	0	2	1	1
O75:HNT	0	0	0	1	0
O76:H19	0	2	1	0	1
O76:H20	0	1	0	0	0
O76:H21	0	0	0	1	0
O77:HNM	0	0	0	1	0
O78:HNT	0	0	1	0	0
O80:H2	0	1	1	0	0
O80:HNM	1	0	0	1	0
O81:H6	0	1	0	0	0
O81:H21	0	0	0	1	0
O82:H8	0	0	0	0	1
O84:H2	1	0	0	0	4
O84:HNM	0	2	6	2	0
O84:HNT	0	0	0	0	3
O85:H49	0	0	0	0	2
O87:H2	0	0	0	1	0
O88:H8	0	0	0	0	7
O88:HNT	0	0	1	2	2
O88:HNM	0	0	1	2	0
O91:H14	0	0	0	0	12
O91:H21	1	2	0	2	1
O91:HNM	5	2	2	5	0
O91:HNT	0	0	0	1	1
O95:H16	0	1	0	0	0

Serotype	2015	2016	2017	2018	2019
O96:H5	0	1	0	0	0
O99:H11, H35	0	0	0	0	1
O100:H20	0	0	0	0	1
O101:H2	0	1	0	0	0
O101:H19	0	0	0	1	0
O101:HNM	0	1	0	0	0
O103:H2	2	2	3	7	11
O103:H25	2	1	1	4	12
O103:HNT	0	0	0	1	1
O103:HRough	0	0	0	1	0
O104:H7	0	1	0	1	1
O107:H7	0	0	1	0	0
O108:H9	0	0	0	0	1
O108:H25	0	0	0	1	0
O111:H21	0	0	0	1	0
O111:HNM	0	1	2	3	0
O112:H8	0	0	0	0	1
O112:H9	0	0	0	0	4
O112:H19	0	0	0	0	1
O112:HNM	0	0	0	2	0
O113:H4	0	1	0	0	1
O113:H21	0	0	2	0	1
O114:HNT	0	0	0	0	1
O117:H4	0	0	0	2	3
O117:H7	2	0	1	2	7
O117:HNM	0	0	0	1	0
O118:H2	0	0	0	0	1
O119:H4	0	0	0	1	0
O121:H19	0	0	0	0	1
O123:H2	0	0	1	0	3
O123:H10	0	0	0	0	2
O128:H2	4	25	7	22	55
O128:H8	0	0	0	0	1
O128:H45	0	0	0	1	0
O128:HNM	1	5	1	6	0
O128:HNT	0	0	1	1	3
O130:H11	1	2	1	1	4

Serotype	2015	2016	2017	2018	2019
O130:H23	0	0	1	0	0
O136:H16	0	0	0	1	0
O141:H2	0	0	0	0	1
O141:HNT	0	0	0	0	1
O144:H2	0	0	0	0	1
O145:H2	0	3	0	1	0
O145:HNM	1	0	1	0	0
O146:H8	0	1	0	0	0
O146:H11	0	0	1	0	0
O146:H21	2	4	13	17	15
O146:H28	0	0	0	0	1
O146:HNM	0	0	3	2	0
O146:HNT	0	0	1	0	0
O148:H7	0	0	0	0	1
O148:H21	0	0	1	0	0
O149:H2	0	2	0	2	2
O149:H18	1	0	0	0	0
O152:H10	0	0	0	1	0
O152:H38	0	0	0	1	0
O153:H2	4	2	0	3	10
O153:HNT	0	0	2	0	1
O156:H19	0	0	1	0	0
O156:H25	0	0	0	0	2
O158:HNM	0	0	0	1	0
O159:HNT	0	0	0	0	1
O162:H7	0	1	0	0	0
O162:H10	0	0	0	1	0
O163:H19	1	0	0	1	7
O165:HNM	0	0	3	0	0
O165:HNT	0	0	0	0	2
O166:H15	0	0	0	0	1
O171:H2	0	0	0	1	1
O172:HNM	0	1	0	0	0
O174:H8	1	0	1	4	10
O174:H21	0	0	0	1	5
O174:HNM	1	1	0	3	0
O174:HNT	0	0	0	2	1
O176:H4	0	0	0	0	12

Serotype	2015	2016	2017	2018	2019
O176:HNM	10	2	4	9	0
O176:HNT	0	0	0	0	4
O176:HRough	0	0	1	0	0
O177:H25	0	0	0	0	2
O177:HNM	1	0	1	1	0
O177:HNT	0	0	0	0	1
O178:H7	1	1	0	1	0
O179:H8	1	0	2	0	0
O179:H26	0	0	0	0	1
O181:H16	0	0	0	1	1
O182:H25	0	0	0	0	3
O182:HNM	0	1	2	2	0
O183:H18	1	3	0	0	3
O183:HNM	0	1	0	0	0
O186:H10	1	0	2	0	2
O186:HNT	0	0	0	0	4
O186:HNM	0	0	4	0	0
O187:H7	0	0	0	1	0
O188:H7	0	0	0	1	0
O188:H14	0	0	0	5	0
ONT:H1	0	0	0	0	1
ONT:H2	9	3	22	17	11
ORough:H2	1	6	4	7	0
O123/O186:H2	0	0	0	2	0
ONT:H4	0	0	0	2	0
ORough:H5	0	0	0	1	0
ONT:H5	0	1	0	0	0
ONT:H6	0	0	0	0	1
ONT:H7	0	3	7	6	6
ORough:H7	1	1	0	0	0
ONT:H8	2	0	1	2	4
ONT:H9	0	0	1	2	1
ONT:H10	0	1	0	1	2
O123/O186:H10	0	0	0	2	0
Onovel32:H10	0	0	0	0	1

Serotype	2015	2016	2017	2018	2019
ORough:H10	0	0	0	1	0
ONT:H11	2	0	1	2	0
ONT:H12	0	0	0	1	0
ONT:H13	0	1	0	0	0
ONT:H14	0	1	2	1	1
Onovel21:H14	0	0	0	0	2
ONT:H15	0	0	0	1	0
ORough:H16	1	0	0	0	0
ONT:H18	0	0	0	0	2
ONT:H19	0	0	2	1	1
ORough:H19	0	0	0	2	0
ONT:H20	0	0	0	2	0
ONT:H21	0	1	4	4	5
ORough:H21	0	1	0	1	0
Onovel27:H21	0	0	0	0	1
ONT:H25	0	0	0	0	4
ORough:H25	0	0	1	0	0
ONT:H26	1	0	4	0	0
ORough:H26	0	0	0	1	0
ONT:H27	0	0	1	1	0
ONT:H28	0	1	0	0	0
ONT:H30	0	0	0	1	0
ONT:H31	0	0	1	1	0
ORough:H45	0	0	0	1	0
ONT:H45	0	0	1	0	0
ONT:H49	1	0	0	0	1
O123/O186:HNM	0	0	0	13	0
ORough:HRough	0	0	0	1	0
ONT:HRough	0	0	0	1	0
ONT:NHM	0	0	1	0	0

NM: Non-Motile. NT: Non-typable

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