New Zealand Food Safety
Haumaru Kai Aotearoa

ANNUAL REPORT CONCERNING FOODBORNE DISEASE IN NEW ZEALAND 2018

New Zealand Food Safety Technical Paper No: 2019/03

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Cover Image: Computer-generated image of *Salmonella* serotype Typhi bacteria.
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Scientific Interpretative Summary

This SIS is prepared by New Zealand Food Safety (NZFS) risk assessors to provide context to the following report for MPI risk managers and external readers

Annual report concerning Foodborne Disease in New Zealand 2018

ESR Report FW19021

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. The series since 2006 can be found here.

Campylobacter remained our top priority foodborne pathogen of concern in 2018, and NZFS has a performance target to reflect this. The current performance target is to reduce the number of human cases of foodborne campylobacteriosis by 10% by 2020. Progress to meeting this target can be viewed in the section entitled Reporting against Targets.

Shiga toxigenic *Escherichia coli* (STEC), *Yersinia* and Hepatitis A also remain a focus for NZFS although foodborne transmission is only one of the routes by which humans are exposed to these pathogens; other routes include water, animal contact and person to person. Nevertheless, NZFS supported research programmes are continuing to identify optimal methods for detection and characterisation from foods to facilitate robust attribution studies, especially from fresh produce.

The gradual shift to culture-independent diagnostic tests (CIDT) using molecular polymerase chain reaction (PCR) methodology for detection of pathogens by medical laboratories in New Zealand continued through 2018. Laboratories using PCR screen all community faecal specimens for *Campylobacter*, *Shigella*, *Salmonella*, STEC, *Giardia* and *Cryptosporidium*, and the implication of CIDT for notification rates and attribution is well described in the introduction to the 2018 report.

STEC infection, shigellosis and cryptosporidiosis notification rates continue to increase sharply as more laboratories implement CIDT, despite no evidence that foodborne sources are increasing, and baseline prevalence in persons without illness or unrelated illness poorly understood. In contrast, rates for campylobacteriosis and salmonellosis remain constant, which may reflect a balance between a possible increase in detection sensitivity using CIDT and reduction in foodborne illness as NZFS and industry implement additional pathogen control measures.

ESR's current assumption is that the majority of diagnostic laboratories will have transitioned to CIDT for enteric pathogens by 2020, and MPI will continue to monitor the increase in notified illnesses and work with public health units to be assured that there is not an underlying increase in foodborne illness.

Robust foodborne disease reports are necessary to ensure that the NZFS science programme, and risk management and risk communications programmes are optimised to minimise foodborne illness in New Zealand and to ensure that industry and consumer stakeholders are adequately informed. To this end, ESR and NZFS will continue to improve the analysis of risk factors and develop contemporary strategies for presentation of this information for the 2019 report.

Science for Communities

ANNUAL REPORT CONCERNING FOODBORNE DISEASE IN NEW ZEALAND 2018

Prepared for New Zealand Food Safety under
Project MRP/18/01 – Systematic reporting of epidemiology of potentially foodborne disease in New Zealand for year 2018,
as part of an overall contract for scientific services

by

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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 2018 is intended to be 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 in 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. However, only a small proportion of outbreaks are reported, and experience shows that outbreaks associated with foodservice premises are more likely to be reported and investigated than outbreaks associated with other settings.
    - 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 similar food supplies to New Zealand can be helpful, especially for illnesses where a foodborne estimate was not developed from other 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 2018 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 2018 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]
Histamine (scombroid) fish poisoning	Toxin	N, O, H	T61.1 Toxic effect: scombroid fish poisoning
Hepatitis A infection	Virus	N, O, H	B15 Acute hepatitis A
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
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*, 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 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. To further complicate matters, some laboratories have changed testing criteria for some enteric pathogens in the process of moving over to CIDT. This may also impact on the numbers of positive results and subsequently notification rates. All community faecal specimens in the DHBs listed below are now screened for STEC when previously only those specimens from patients aged less than 5 years of age and those with haemolytic uraemic syndrome (HUS) or bloody diarrhoea recorded in the laboratory request were tested. Also all community faecal specimens are now screened for *Giardia* spp. and *Cryptosporidium* spp. when previously only those specimens where parasite screening was requested were tested. 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.

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	
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[b]	November 2018	November 2018	
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	n/a	
Waikato	n/a	November 2018	
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: ESR's NZMN CIDT survey, updated November 2018

CIDT = Culture-indipendent diagnostic tests, n/a = not applicable (In 2018 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.

[b] From January to July 2017 Lakes DHB changed to PCR panels for enteric pathogens; from July 2017 to October 2018, enteric testing was again done by traditional culture-based methods (due to using a different diagnostic laboratory).

Where STEC is detected by screening PCR, specimens are referred to the reference laboratory at ESR where confirmatory testing is performed using PCR, culture and serotyping. All community faecal specimens in the DHBs listed above are now screened for STEC when previously only those specimens from patients aged less than 5 years of age and those with haemolytic uraemic syndrome (HUS) or bloody diarrhoea recorded in the laboratory request were tested.

Also all community faecal specimens are now screened for *Giardia* spp. and *Cryptosporidium* spp. when previously only those specimens where parasite screening was requested were tested.

REPORTING

SUMMARY OF MAIN FOODBORNE DISEASES

The incidence of the main foodborne diseases is summarised for 2018 in Table 5 below.

Table 5. Estimated proportion and incidence of the main foodborne diseases for 2018

	Total notified		Estimated foodborne transmission[a]		
	Cases	Rate[b]	Cases	Proportion (%)[c]	Rate[d]
Campylobacteriosis	6957	142.4	3826	63.8 (44.1-83.2)	78.3 (54.1-102.1)
Cryptosporidiosis	1611	33.0	NE	-	-
Giardiasis	1585	32.4	NE	-	-
Hepatitis A	68	1.4	NE	-	-
Listeriosis	30	0.6	25	87.8 (57.9-98.5)	0.5 (0.3-0.6)
Salmonellosis	1100	22.5	417	62.1 (35.2-86.4)	8.5 (4.8-11.9)
Shigellosis	219	4.5	NE	-	-
STEC infection	925	18.9	236	29.9 (3.5-60.7)	4.8 (0.6-9.8)
Yersiniosis	1202	24.6	718	63.2 (29.0-91.5)	14.7 (6.7-21.3)

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.

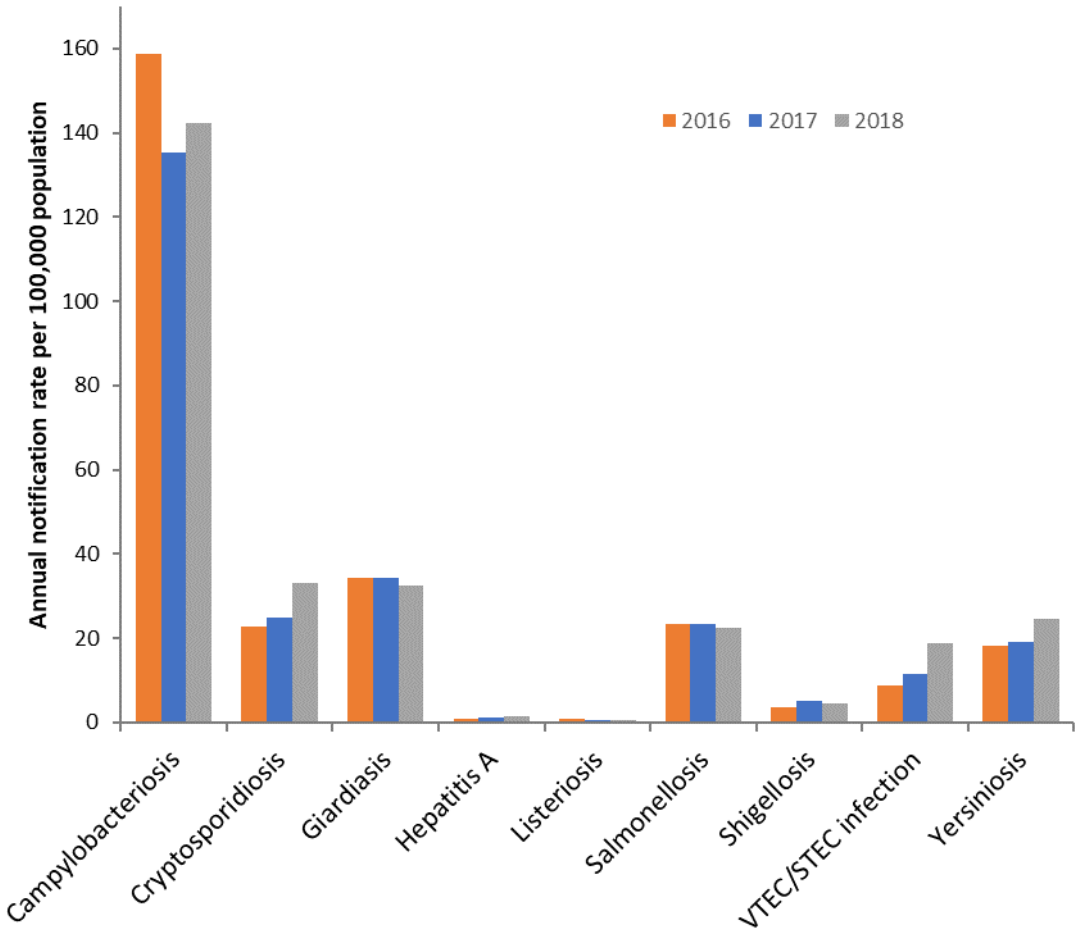
[b] Rate per 100,000, mid-year estimated population.

[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.

In 2018, a continued increase in notification rates was apparent for cryptosporidiosis, STEC infection, and yersiniosis compared to 2016 and 2017 (Figure 1). This increase might be partially due to additional laboratories changing their methodology to molecular methods and to the increased numbers of specimen routinely being tested (see section on Changes in laboratory testing methodology).

Figure 1. Notification rates of the main foodborne diseases, 2016–2018



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 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 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 routes for STEC and norovirus are outside of 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 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*. The estimate of the foodborne proportion of campylobacteriosis determined by the expert elicitation is approximately 0.6.

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) number (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 2018 is given in Table 6.

Table 6. Estimated proportion and incidence of foodborne campylobacteriosis for 2018

	Cases	Proportion (%)	Rate (per 100,000, mid-year estimated population)
Total notified	6957		142.4
Estimated not related to overseas travel[a]	5997	86.2	122.8
Estimated foodborne transmission	3826	63.8 (44.1-83.2)[b]	78.3 (54.1-102.1)[c]

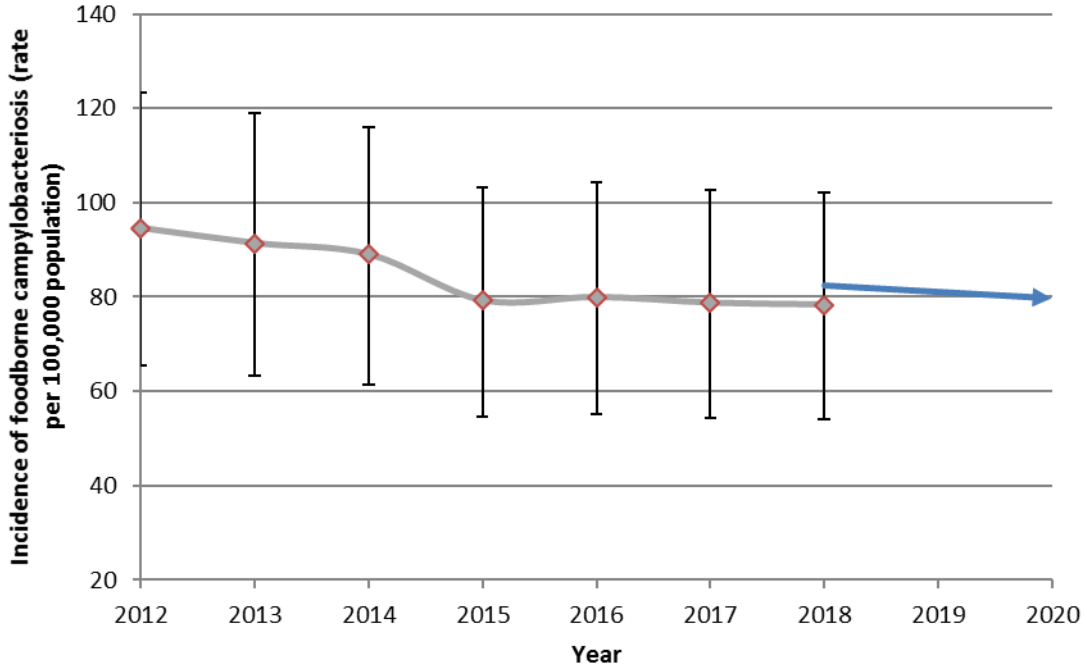
[a] The estimated percentage of cases relating to overseas travel is 13.8%.
[b] Most likely (95th percentile credible interval) estimates of proportion foodborne, from expert consultation.
[c] Most likely (95th percentile credible interval) estimates of foodborne rate.

* 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 2018 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 2018 to 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.

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 2018 by data source

During 2018, one case of *B. cereus* intoxication was reported in EpiSurv. Note that not all cases of *B. cereus* intoxication are necessarily notifiable; only those where there is a suspected common source.

The ICD-10 code A05.4 was used to extract *B. cereus* intoxication hospitalisation data from the MoH National Minimum Dataset (NMDS). Of the three hospital admissions recorded in 2018, two were reported with *B. cereus* intoxication as the primary diagnosis and one was reported as another relevant diagnosis.

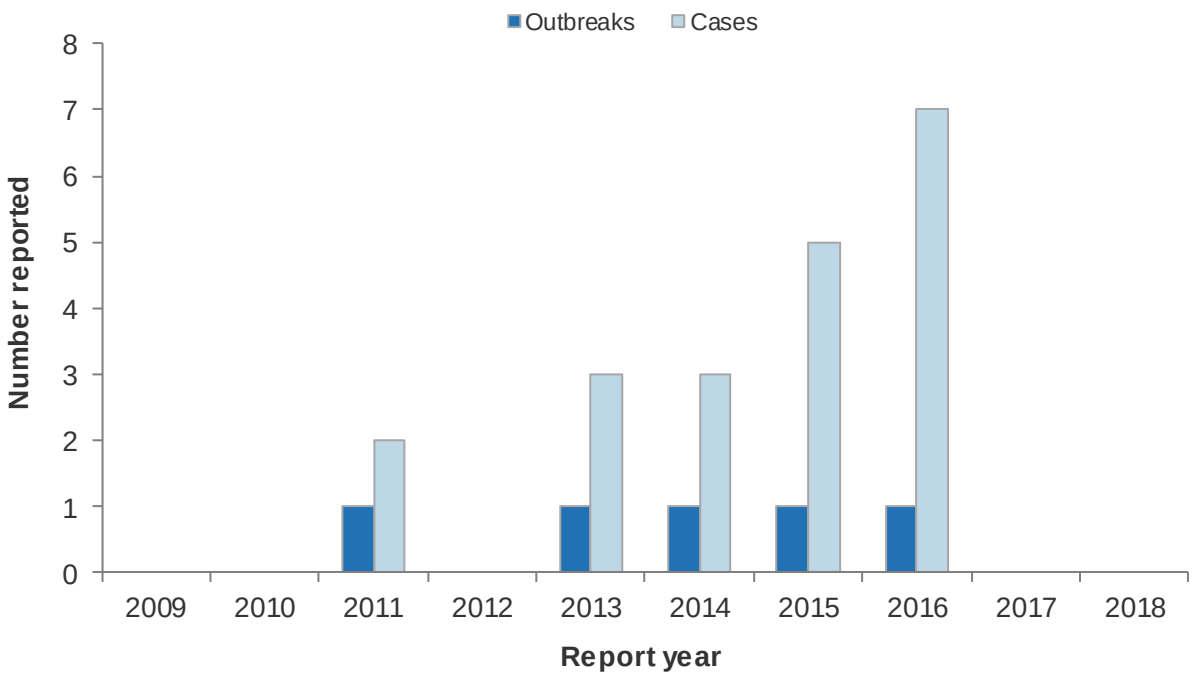
Expert consultation estimated that 97% (minimum = 90%, maximum = 100%) of *B. cereus* intoxication will be due to foodborne transmission [14]. The expert consultation also estimated that approximately 60% of the foodborne transmission would be due to consumption of rice.

Outbreaks reported as caused by *Bacillus cereus*

During 2018, no outbreaks caused by *B. cereus* intoxication were reported in EpiSurv.

Outbreaks of *B. cereus* intoxication are rare, with only five outbreaks reported since 2009 (Figure 3). The number of cases associated with the outbreaks ranged between two and seven cases.

Figure 3. Foodborne *B. cereus* outbreaks and associated cases reported by year, 2009−2018



Recent surveys

Nil.

Relevant New Zealand studies and publications

Nil.

Relevant regulatory developments

Nil.

Campylobacteriosis

Summary data for campylobacteriosis in 2018 are given in Table 7.

Table 7. Summary of surveillance data for campylobacteriosis, 2018

Parameter	Value in 2018	Source
Number of notified cases	6957	EpiSurv
Notification rate (per 100,000)	142.4	EpiSurv
Hospitalisations[a]	780	MoH NMDS
Deaths	0	EpiSurv
Estimated travel-related cases (%)[b]	960 (13.8%)	EpiSurv
Estimated food-related cases (%)[c]	3826 (63.8%)	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 several laboratories across New Zealand changed the methodology for testing faecal specimens. All community faecal specimens in Northland, Waitemata, Auckland and Counties Manukau DHBs (June 2015), Southern DHB (January 2017), Lakes DHB (January 2017–June 2017), Capital & Coast, Hawke's Bay, Hutt Valley, Nelson & Marlborough, Wairarapa DHBs (January 2018) and Bay of Plenty, Lakes, and Waikato DHBs (November 2018) 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 2018 by data source

During 2018, 6957 cases (142.4 per 100,000 population) of campylobacteriosis and no resulting deaths were reported in EpiSurv. Approximately 15% of cases notified in EpiSurv were hospitalised in 2018.

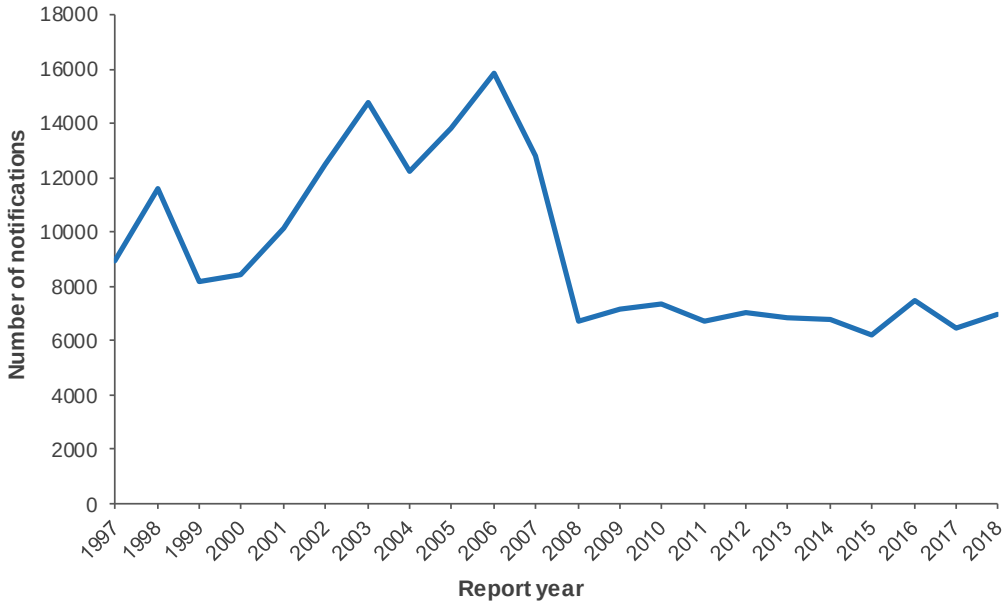
The ICD-10 code A04.5 was used to extract campylobacteriosis hospitalisation data from the MoH NMDS database. Of the 780 hospital admissions (16.0 admissions per 100,000 population) recorded in 2018, 630 were reported with campylobacteriosis as the principal diagnosis and 150 with campylobacteriosis 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

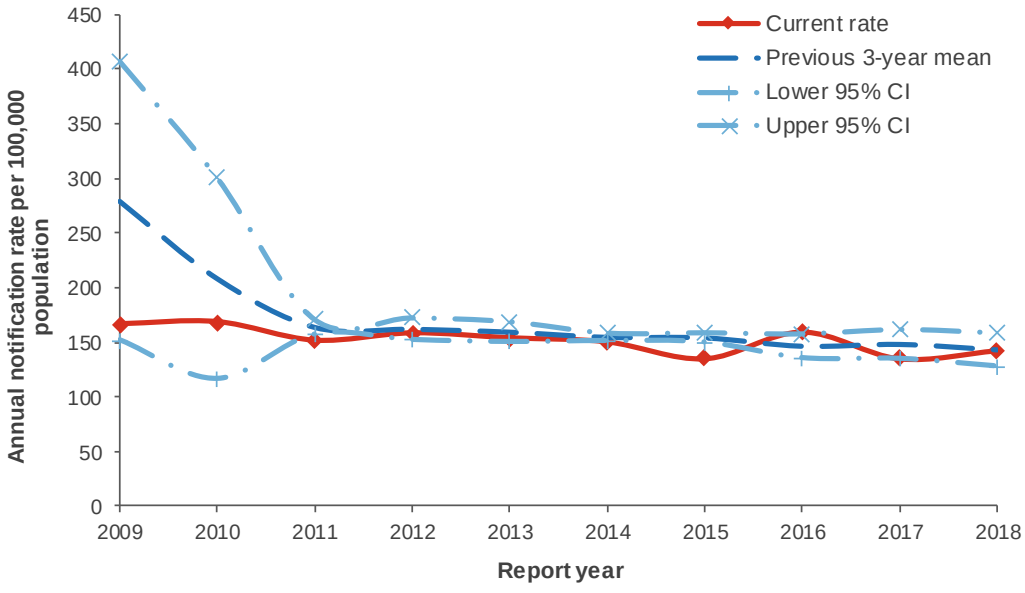
The number of campylobacteriosis notifications reported each year generally increased from 1997, up to the highest number recorded in 2006 (15,873 cases). During 2007 and 2008, there was a significant decrease in the number of cases reported (Figure 4). The number of notifications each year has remained stable from 2008 to 2018, with the exception of 2016, due to an outbreak in Hawke's Bay attributed to contaminated drinking water [15].

Figure 4. Campylobacteriosis notifications by year, 1997–2018



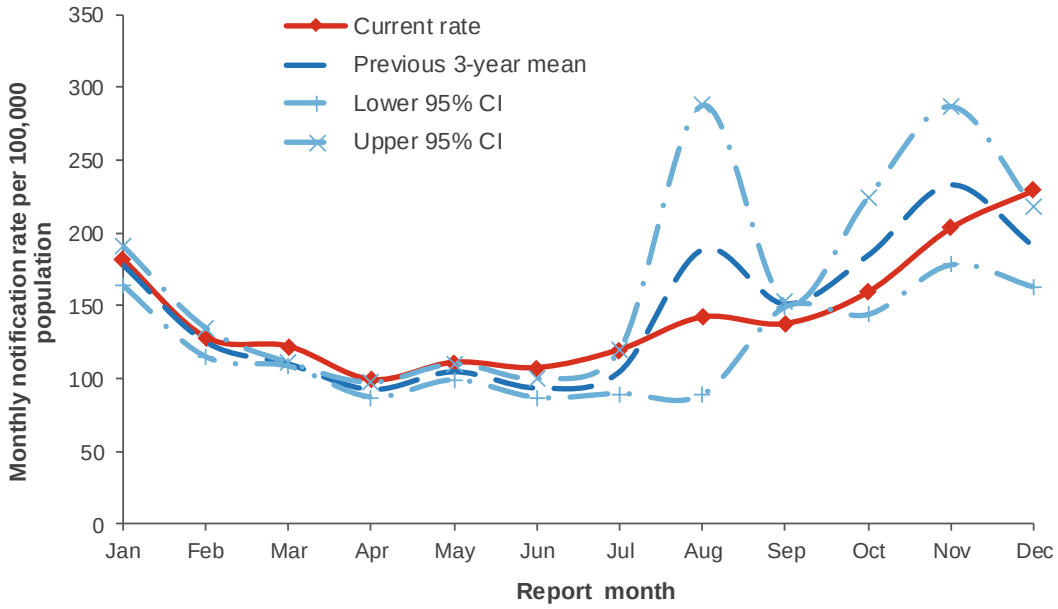
The campylobacteriosis annual rate trend (Figure 5) was very similar to the corresponding annual notification trend (Figure 4); with the notification rate remaining stable between 2009 and 2018. The notification rate was significantly higher in 2016 (158.9 cases per 100,000 population) than the previous 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, 2009–2018



The number of notified cases of campylobacteriosis per 100,000 population by month for 2018 is shown in Figure 6. The monthly number of notifications in 2018 ranged from 395 notifications (April) to 918 notifications (December). In 2018, the lowest notification rates occurred between March and July. Rates by month followed a similar pattern as seen in previous years prior to 2016 and in 2017. The current previous three-year mean is influenced by a 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), 2018



In 2018, the rate of notifications and hospitalisations for campylobacteriosis was higher for males (160.7 and 17.7 per 100,000 population) compared with females (124.6 and 14.3 per 100,000 population; Table 8).

Table 8. Campylobacteriosis cases by sex, 2018

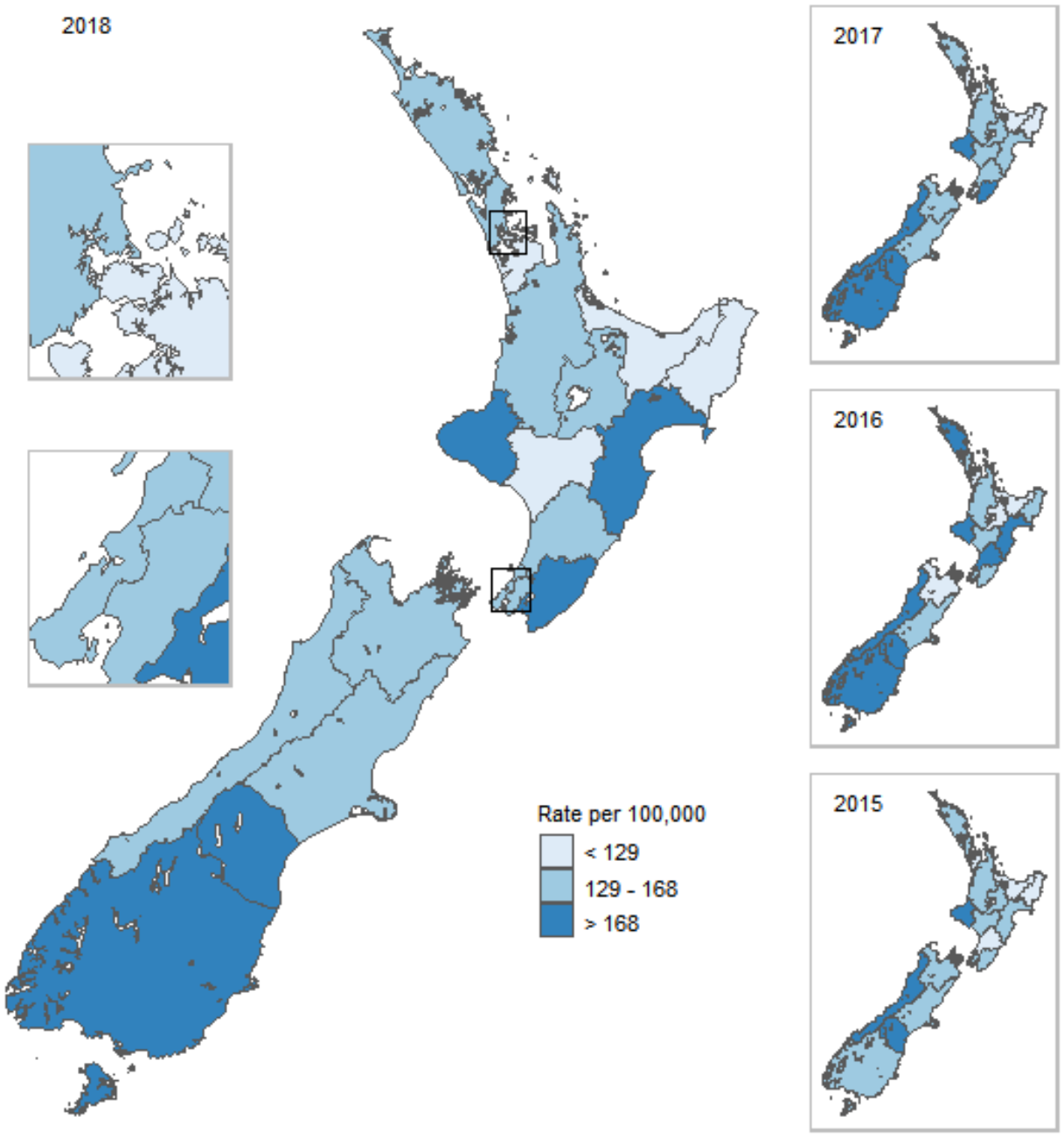
Sex	EpiSurv notifications		Hospitalisations[a]	
	No.	Rate[b]	No.	Rate[b]
Male	3871	160.7	427	17.7
Female	3085	124.6	353	14.3
Total	**6957**	**142.4**	**780**	**16.0**

[a] MoH NMDS data for hospital admissions.

[b] per 100,000 population.

Campylobacteriosis rates varied throughout the country in 2018 as shown in Figure 7. In the South Island, South Canterbury DHB (250.4 per 100,000 population, 150 cases), and Southern DHB (218.4 per 100,000 population, 721 cases) were higher than other DHBs (range 135.3-158.7 per 100,000 population). In the North Island, Taranaki DHB (185.3 per 100,000, 222 cases) had the highest rate, followed by Hawkes Bay DHB (177.3 per 100,000, 294 cases). The lowest rate in New Zealand was reported for Bay of Plenty DHB (102.1per 100,000, 242 cases). South Canterbury and Taranaki DHBs have consistently been in the highest quantile of notification rates in the last four years.

Figure 7. Geographic distribution of campylobacteriosis notifications, 2015–2018



Note: Changes in laboratory methods were introduced in Northland, Waitemata, Auckland and Counties Manukau DHBs (June 2015), Southern DHB (since January 2017) and Lakes DHB (January 2017 - June 2017), Capital & Coast, Hawke's Bay, Hutt Valley, Nelson & Marlborough, Wairarapa DHBs (January 2018) and Bay of Plenty, Lakes, and Waikato DHBs (November 2018). The new, more sensitive assays may have triggered an increase in notifications for some enteric diseases. Refer to text for details.

The highest age-specific notification rates for campylobacteriosis in 2018 were reported for children aged 1 to 4 years (302.9 per 100,000 population, 746 cases) and infants aged less than 1 year (229.2 per 100,000, 138 cases). The highest hospitalisation rates were for the 70 years and over age group (46.1 admissions per 100,000 population) and infants aged less than 1 year (33.2 admissions per 100,000 population) , which were noticeably higher than other age groups (Table 9).

Table 9. Campylobacteriosis cases by age group, 2018

Age group (years)	EpiSurv notifications		Hospitalisations[a]	
	No.	Rate[b]	No.	Rate[b]
<1	138	229.2	20	33.2
1 to 4	746	302.9	45	18.3
5 to 9	300	91.7	20	6.1
10 to 14	232	74.6	20	6.4
15 to 19	391	124.5	30	9.6
20 to 29	1057	143.2	88	11.9
30 to 39	761	121.1	81	12.9
40 to 49	775	125.9	64	10.4
50 to 59	877	140.2	77	12.3
60 to 69	799	156.9	100	19.6
70+	880	172.6	235	46.1
Unknown	1	-	0	1
Total	**6957**	**142.4**	**780**	**16.0**

[a] MoH NMDS data for hospital admissions (ICD-10 code: A04.5).

[b] per 100,000 of population.

For cases where information on travel was provided in 2018, 13.8% (95% CI 12.7-15.0%) 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 2018. The resultant distribution has a mean of 960 cases (95% CI 858-1065).

If data from the last four years are considered the estimated proportion of cases travelling overseas within the incubation period of the organism was 10.3% (95% CI 9.7-10.8%).

Outbreaks reported as caused by *Campylobacter* spp.

In 2018, seven (43.8%) of the outbreaks caused by *Campylobacter* spp. and 24 (26.1%) of the associated cases were reported as foodborne (Table 10). 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. *Campylobacter* outbreaks accounted for 3.6% (16/446) of all enteric outbreaks and 1.3% (92/7204) of all associated cases reported in 2018.

Table 10. *Campylobacter* spp. outbreaks reported, 2018

Measure	Foodborne *Campylobacter* spp. Outbreaks	All *Campylobacter* spp. outbreaks
Outbreaks	7	16
Cases	24	92
Hospitalised cases	1	3

Table 11 contains details of the seven foodborne outbreaks of campylobacteriosis reported in 2018. The evidence was strong for the suspected food vehicle for one raw milk-related outbreak in March, resulting in two notifications. Food and clinical samples related to this raw milk associated outbreak were submitted to ESR's Public Health Laboratory. *Campylobacter jejuni* was isolated from milk and clinical samples. Isolates were indistinguishable by whole genome sequencing. For the other four *Campylobacter* spp. outbreaks with a suspected food vehicle (Table 11), the evidence for the implicated food was weak. For two outbreaks the suspected vehicle was listed as unknown, however in one of these outbreaks raw milk was listed as one of the suspected risk factors for one of the three cases.

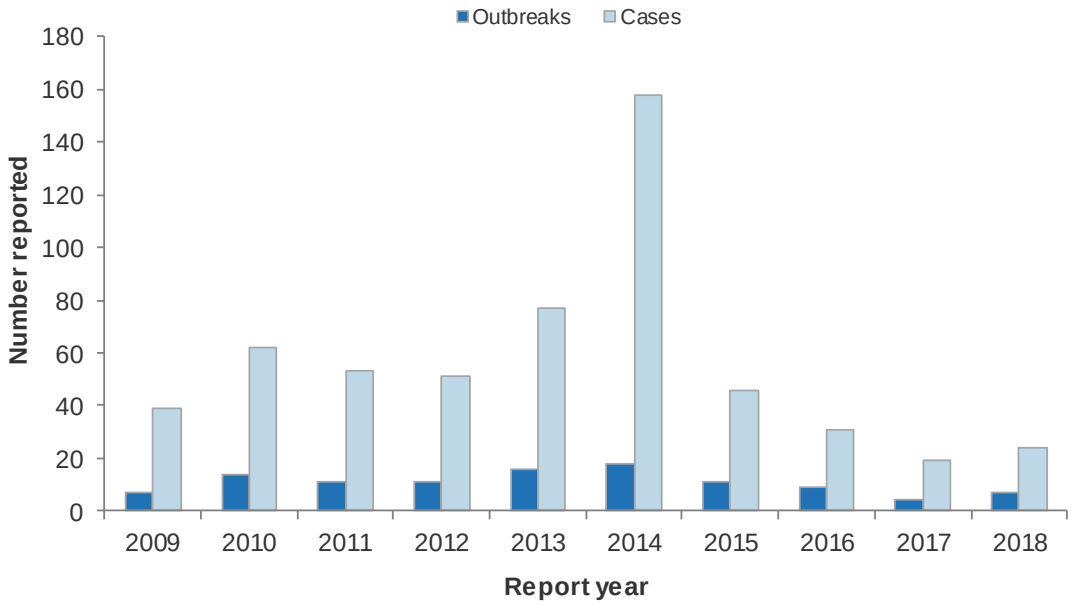
Table 11. Details of foodborne *Campylobacter* spp. outbreaks, 2018

PHU	Month	Suspected vehicle	Exposure setting	Preparation setting	No. ill
MidCentral	Mar	Raw milk	Other food outlet	Other food outlet	2C
Toi Te Ora	May	Raw milk	Hotel/motel	Hotel/motel	2C
Nelson Marlborough	Jun	Raw milk	Other food outlet	Other food outlet	4C
Regional	Sep	Unknown	Restaurant/cafe/bakery	Restaurant/cafe/bakery	4C, 1P
South	Oct	Raw milk	Farm	Farm	2C
South	Oct	Unknown	Farm / Home	Farm	3C
MidCentral	Dec	Duck rilette	Restaurant/cafe/bakery	Restaurant/cafe/bakery	1C, 5P

PHU: Public Health Unit, MidCentral: MidCentral Public Health Service, Nelson Marlborough: Nelson Marlborough Public Health Service, Regional: Regional Public Health, South: Public Health South, Toi Te Ora: Toi Te Ora - Public Health, C: confirmed, P: probable.

During 2009 to 2018, excluding 2014, the number of reported foodborne outbreaks of campylobacteriosis has ranged between four and 16 outbreaks reported each year with between 19 and 77 annual outbreak-associated cases (Figure 8). The increased number of cases in 2014 was due to three foodborne outbreaks with high numbers of associated cases (51, 32 and 17).

Figure 8. Foodborne *Campylobacter* spp. outbreaks and associated cases reported by year, 2009–2018



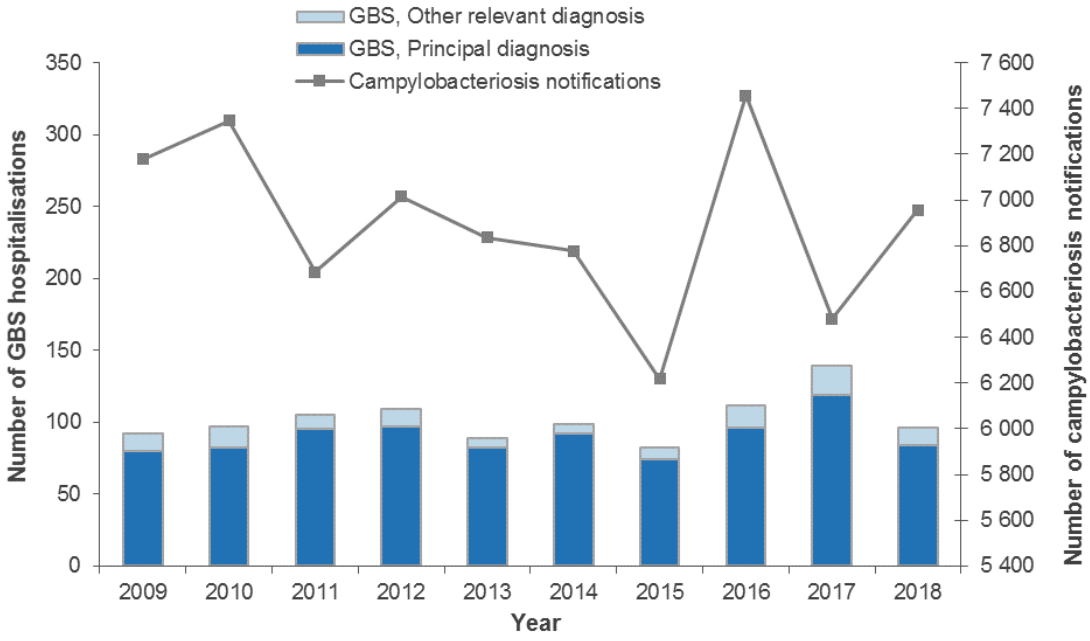
Disease sequelae - Guillain-Barré syndrome

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 2018 were considered, rather than all cases that were hospitalised in 2018. That is, if a GBS case hospitalised in 2018 had been hospitalised with GBS in a previous year, the 2018 admission was considered to be a readmission, rather than an incident case. There were 96 incident hospitalised cases recorded in 2018 (2.0 admissions per 100,000 population), 84 were reported with GBS as the primary diagnosis and 12 with GBS as another relevant diagnosis.

Between 2009 and 2018, 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, 2009–2018



In 2018, the number of incident hospitalised cases due to GBS was higher for males than for females (Table 12). This is consistent with the pattern seen for GBS in most previous years, except 2016 when case numbers for males and females were almost identical. It is also consistent with the gender differences seen in notification rates for campylobacteriosis in males and females in 2018 (Table 8).

Table 12. Guillain-Barré syndrome hospitalised cases by sex, 2018

Sex	Hospitalised cases[a]	
	No.	Rate[b]
Male	55	2.3
Female	41	1.7
Total	**96**	**2.0**

[a] MoH NMDS data for hospital admissions.

[b] per 100,000 population.

In 2018, the highest rates of incident hospitalisation for GBS were in the 70 years and over age group, followed by the 60-69 years age group (Table 13).

Table 13. Guillain-Barré syndrome hospitalised cases by age group, 2018

Age group (years)	Hospitalised cases	
	No.	Rate[b]
<5	2	-
5 to 9	4	-
10 to 14	2	-
15 to 19	4	-
20 to 29	11	1.5
30 to 39	11	1.8
40 to 49	9	1.5
50 to 59	14	2.2
60 to 69	15	2.9
70+	24	5.7
Total	**138**	**2.0**

[a] MoH NMDS data for hospital admissions.

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

Recent surveys

A survey was carried out of the prevalence of *Campylobacter* (*C. jejuni* and *C. coli)* on ovine carcasses following slaughter and dressing [16]. A baseline survey was undertaken for carcass trim from "spring" lamb and mutton animals (*n* = 50 for each class), involving PCR detection post-enrichment and culture isolation. Nine processing plants (five from the North Island and four from the South Island) were sampled for the pilot survey. All lamb and mutton carcass trim samples that were PCR-positive for *Campylobacter* were confirmed by culture isolation. When all fresh and frozen trim samples are considered, the overall prevalence of *Campylobacter* for ovine trim nationally was 27% (40 out of 150 samples), with prevalences for hogget (pilot survey), lamb and mutton carcass trim (baseline survey) of 58% (29 out of 50), 8% (4 out of 50) and 14% (7 out of 50), respectively. When frozen lamb and mutton samples are excluded, the national prevalence increased to 36% (40 out of 110) with prevalences for lamb and mutton carcass trim increasing to 11% (4 out of 35) and 20% (7 out of 35), respectively.

Relevant New Zealand studies and publications
Journal papers

A study was carried out to assess consumers' knowledge of safe chicken handling practices and to assess whether consumers' expectations for food safety labelling of chicken were being met [17]. Most consumers were unaware of the level of *Campylobacter* contamination on fresh chicken and there is a significant, but unmet, consumer demand for information on safe chicken preparation on labels. It was concluded that labels on fresh chicken products are a potentially valuable but underused tool for campylobacteriosis prevention in New Zealand.

A New Zealand study was carried out to analyse the differences in the viable count and population genetic structure between *Campylobacter* isolated from chicken drumsticks and whole carcass meat for retail sale over a 1-year period and assess the genetic relatedness of human and chicken isolates collected concurrently [18]. Whole carcasses showed significantly higher *Campylobacter* counts than drumsticks, but were not different in population genetic structure.

Relevant regulatory developments

New Zealand Food Safety published an Animal Products Notice entitled *Specifications for National Microbiological Database Programme* in February 2018 [19]. The Notice includes details of sampling, analysis and assessment for *Campylobacter* in meat chickens.

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.

Ciguatera fish poisoning cases reported in 2018 by data source

During 2018, no cases of ciguatera fish poisoning were reported in EpiSurv. Note that not all cases of ciguatera fish poisoning are necessarily notifiable, only those where there is a suspected common source.

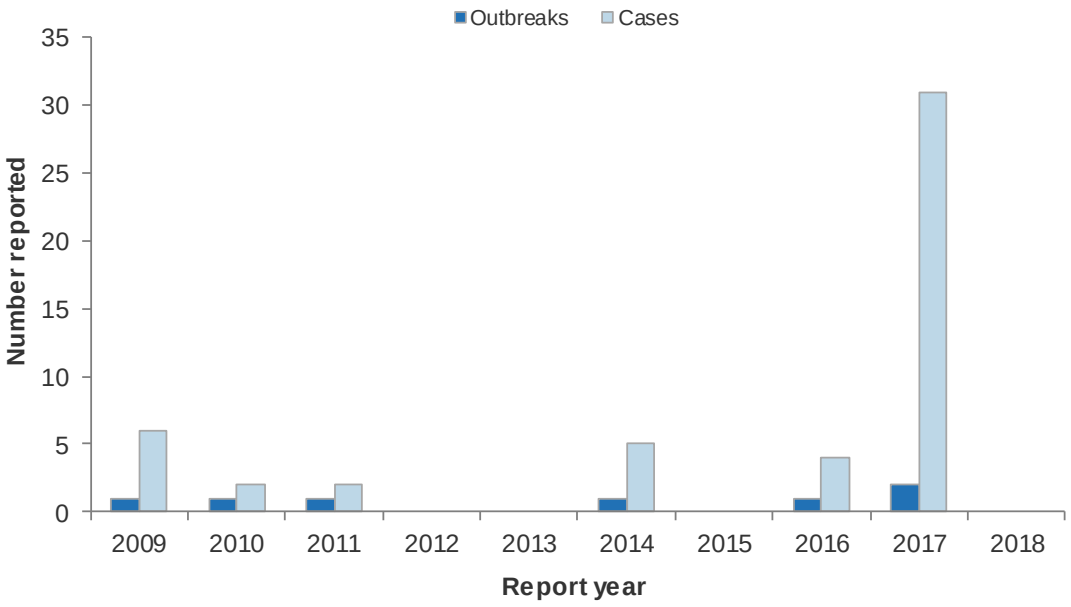
The ICD-10 code T61.0 was used to extract ciguatera fish poisoning hospitalisation data from the MoH NMDS database. Of the four hospital admissions (0.08 admissions per 100,000 population) recorded in 2018, all four were reported with ciguatera fish poisoning as the primary diagnosis. It should be noted that EpiSurv and the MoH NMDS database are separate systems and hospital admission can occur without cases being notified.

Outbreaks reported as caused by ciguatera fish poisoning

During 2018, no outbreaks of ciguatera fish poisoning were reported in EpiSurv. It should be noted that all ciguatera fish poisoning outbreaks will be categorised as foodborne, as consumption of contaminated seafood is the only currently recognised transmission route for this disease.

Over the 10-year period from 2009 to 2018, seven outbreaks of ciguatera fish poisoning were reported, with no more than two outbreaks of ciguatera fish poisoning reported in any year (Figure 10).

Figure 10. Ciguatera fish poisoning outbreaks and associated cases reported by year, 2009–2018



Recent surveys

Nil.

Relevant New Zealand studies and publications

Nil.

Relevant regulatory developments

Nil.

Clostridium perfringens intoxication

Case definition

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

Clostridium perfringens intoxication cases reported in 2018 by data source

During 2018, no cases of *C. perfringens* intoxication were reported in EpiSurv.

The ICD-10 code A05.2 was used to extract foodborne *C. perfringens* intoxication hospitalisation data from the MoH NMDS database. In 2018, there were no hospital admissions recorded with *C. perfringens* intoxication as diagnosis.

Outbreaks reported as caused by *Clostridium perfringens*

There was one *C. perfringens* intoxication outbreak reported in 2018, which was associated with a suspected or known foodborne source (Table 14). 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.

Table 14. *C. perfringens* intoxication outbreaks reported, 2018

Measure	Foodborne *C. perfringens* intoxication outbreaks	All *C. perfringens* intoxication outbreaks
Outbreaks	1	1
Cases	21	21
Hospitalised cases	0	0

Table 15 contains details of the foodborne *C. perfringens* intoxication outbreak reported in 2018. The suspected vehicle of infection for this outbreak was a pork mince meal with rice and vegetables. The level of evidence was strong.

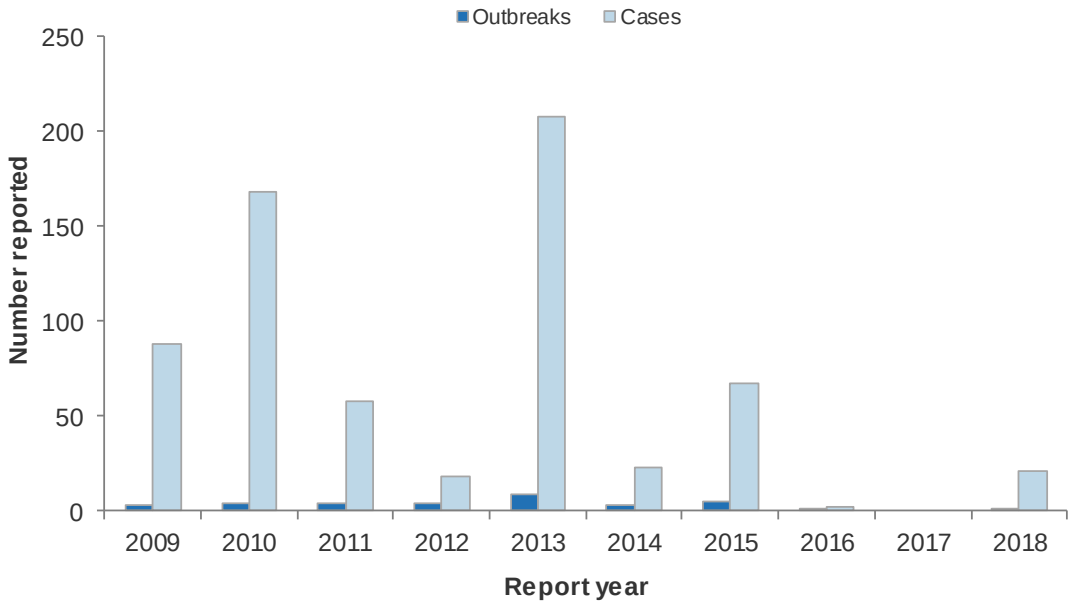
Table 15. Details of foodborne *C. perfringens* intoxication outbreaks, 2018

PHU	Month	Suspected vehicle	Exposure setting	Preparation setting	No. ill
C and PH	Jul	Pork mince, rice and vegetables	Other institution	Home	2C, 19P

PHU: Public Health Unit, C and PH: Community and Public Health, C: confirmed, P: probable.

Between 2009 and 2018, the number of foodborne outbreaks associated with *C. perfringens* 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 foodborne outbreaks due to *C. perfringens* occurred in 2013 (208 cases).

Figure 11. Foodborne *C. perfringens* outbreaks and associated cases reported by year, 2009–2018



Recent surveys

Nil.

Relevant New Zealand studies and publications

Nil.

Relevant regulatory developments

Nil.

Cryptosporidiosis

Summary data for cryptosporidiosis in 2018 are given in Table 16.

Table 16. Summary of surveillance data for cryptosporidiosis, 2018

Parameter	Value in 2018	Source
Number of notified cases	1611	EpiSurv
Notification rate (per 100,000)	33.0	EpiSurv
Hospitalisations[a]	135	MoH NMDS
Deaths	0	EpiSurv
Estimated travel-related cases (%)[b]	119 (7.4%)	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 several laboratories across New Zealand changed the methodology for testing faecal specimens. All community faecal specimens in Northland, Waitemata, Auckland and Counties Manukau DHBs (June 2015), Southern DHB (January 2017), Lakes DHB (January 2017–June 2017), Capital & Coast, Hawke's Bay, Hutt Valley, Nelson & Marlborough, Wairarapa DHBs (January 2018) and Bay of Plenty, Lakes, and Waikato DHBs (November 2018) were screened by multiplex PCR for a range of pathogens, including *Cryptosporidium*. All community faecal specimens are now screened for *Cryptosporidium* spp. when prior to the change in methodology *Cryptosporidium* spp. were only screened for in those specimens where parasite screening was requested. 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.

Cryptosporidiosis cases reported in 2018 by data source

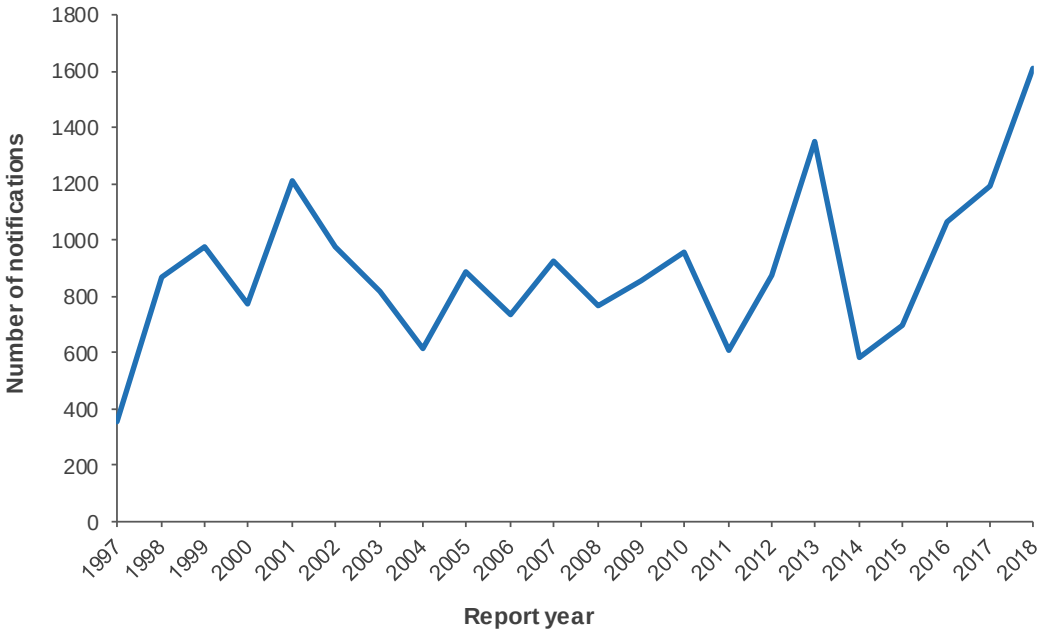
During 2018, 1611 cases (33.0 per 100,000 population) of cryptosporidiosis and no resulting deaths were reported in EpiSurv. Less than 10% of cases notified in EpiSurv were hospitalised in 2018.

The ICD-10 code A07.2 was used to extract cryptosporidiosis hospitalisation data from the MoH NMDS database. Of the 135 hospital admissions (2.8 admissions per 100,000 population) recorded in 2018, 82 were reported with cryptosporidiosis as the principal diagnosis and 53 with cryptosporidiosis as another relevant diagnosis.

Notifiable disease data

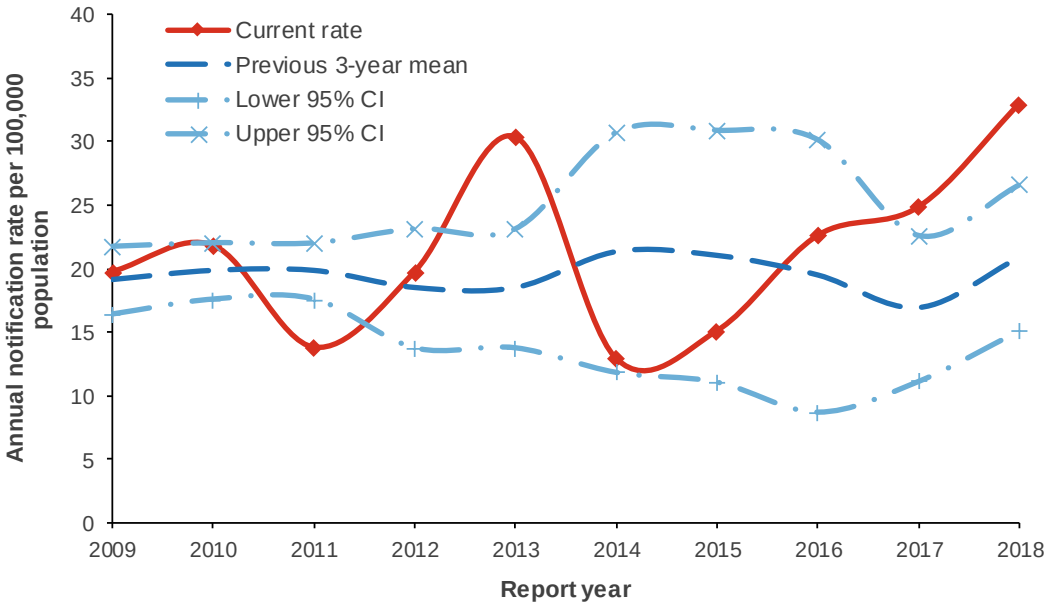
In 2018, the highest number of cryptosporidiosis notifications (1611 notifications) was recorded since cryptosporidiosis became a notifiable disease in 1996. Over the last 20 year time period there were no clear trends regarding the number of cryptosporidiosis notifications (Figure 12). Changes in laboratory testing methods since 2015 may have contributed to the recent increase in notification numbers.

Figure 12. Cryptosporidiosis notifications by year, 1997–2018



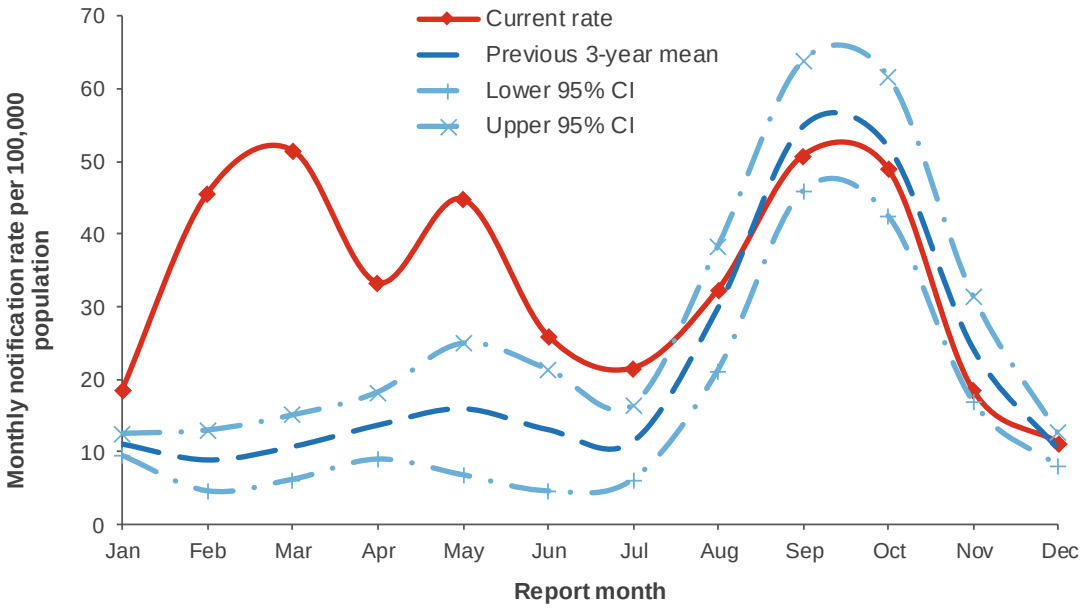
In 2018, the cryptosporidiosis notification rate was higher (33.0 cases per 100,000 population) than the previous three-year average (20.9 cases per 100,000) (Figure 13).

Figure 13. Cryptosporidiosis notification rate by year, 2009–2018



The number of notified cases of cryptosporidiosis reported per 100,000 population by month for 2018 is shown in Figure 14. The monthly number of notifications in 2018 ranged from 45 notifications (December) to 206 notifications (March). In previous years there was a distinct seasonal pattern of cryptosporidiosis cases, with the highest number of notifications generally reported during spring each year. 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), 2018



In 2018, the rate of notifications for cryptosporidiosis was higher for females (36.0 per 100,000 population) compared with males (29.8 per 100,000 population) whereas the rate of hospitalisations was similar (Table 17).

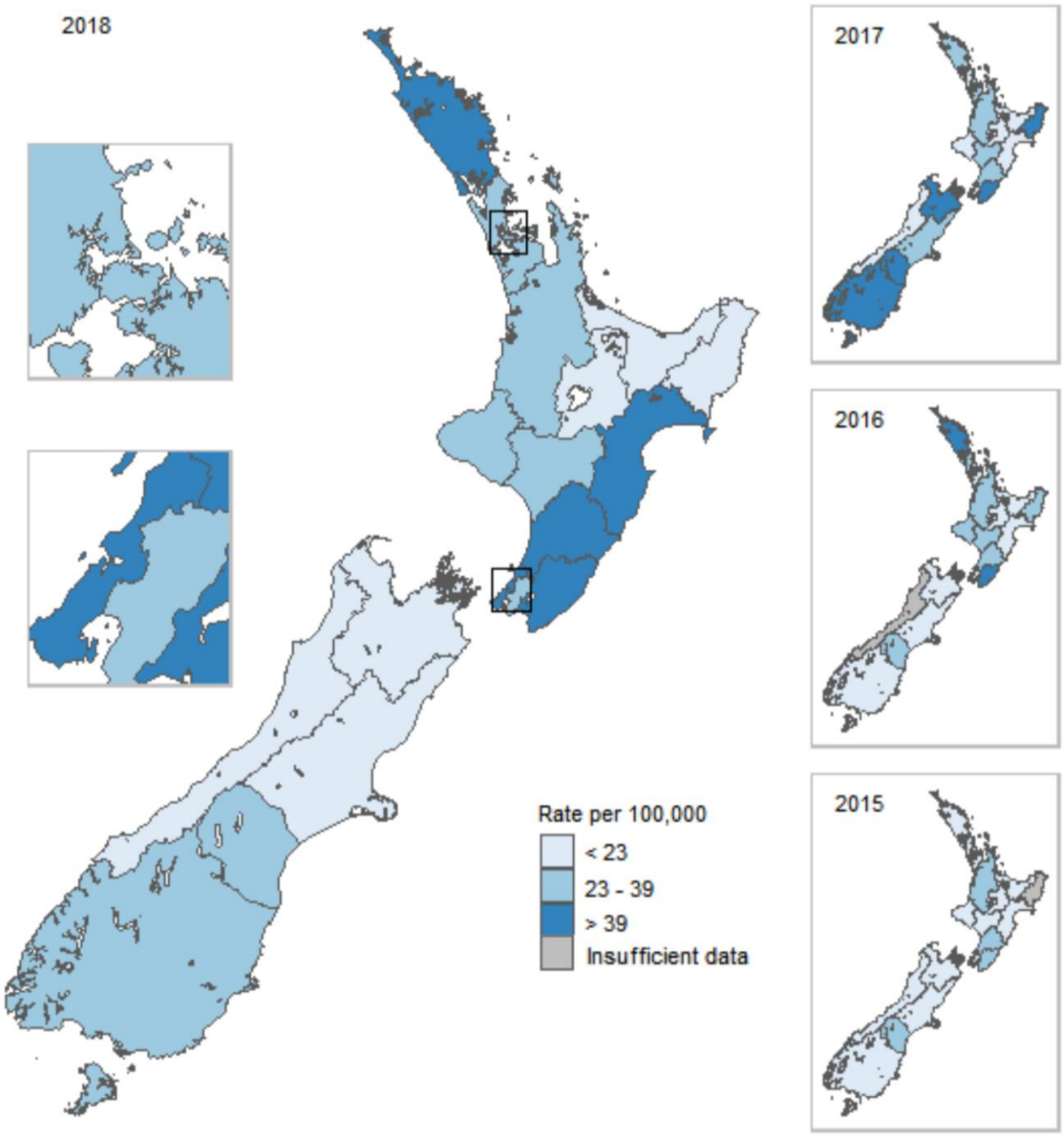
Table 17. Cryptosporidiosis cases by sex, 2018

Sex	EpiSurv notifications		Hospitalisations[a]	
	No.	Rate[b]	No.	Rate[b]
Male	718	29.8	65	2.7
Female	892	36.0	70	2.8
Total	**1611**	**33.0**	**135**	**2.8**

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

Cryptosporidiosis rates varied throughout the country in 2018 as shown in Figure 15. The highest rates of cryptosporidiosis were reported for the DHBs Capital and Coast (58.6 per 100,000, 186 cases), Hawke's Bay (46.4 per 100,000, 77 cases), MidCentral (44.6 per 100,000, 80 cases), and Wairarapa (44.0 per 100,000, 20 cases).

Figure 15. Geographic distribution of cryptosporidiosis notifications, 2015–2018



Note: Changes in laboratory methods were introduced in Northland, Waitemata, Auckland and Counties Manukau DHBs (June 2015), Southern DHB (since January 2017) and Lakes DHB (January 2017 - June 2017), Capital & Coast, Hawke's Bay, Hutt Valley, Nelson & Marlborough, Wairarapa DHBs (January 2018) and Bay of Plenty, Lakes, and Waikato DHBs (November 2018). The new, more sensitive assays may have triggered an increase in notifications for some enteric diseases. Refer to text for details.

During 2018, the highest cryptosporidiosis age-specific notification rates were for the 1 to 4 years age group (155.9 per 100,000 population, 384 cases), followed by the less than 1 year (63.1 per 100,000, 38 cases) and the 5 to 9 (59.0 per 100,000, 193 cases) age groups (Table 18). The hospitalisation rate was also highest in the 1 to 4 years age group and the less than 1 year age group.

Table 18. Cryptosporidiosis cases by age group, 2018

Age group	EpiSurv notifications		Hospitalisations[a]	
	No.	Rate[b]	No.	Rate[b]
<1	38	63.1	6	10.0
1 to 4	384	155.9	30	12.2
5 to 9	193	59.0	23	7.0
10 to 14	91	29.3	11	3.5
15 to 19	92	29.3	6	1.9
20 to 29	271	36.7	15	2.0
30 to 39	252	40.1	14	2.2
40 to 49	129	21.0	4	-
50 to 59	59	9.4	6	1.0
60 to 69	60	11.8	11	2.2
70+	42	8.2	9	1.8
Total	**1611**	**33.0**	**135**	**2.8**

[a] MoH NMDS data for hospital admissions

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

For the cases in 2018, where information on travel was provided, 7.4% (95% CI 5.7-9.4%) 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 2018. The resultant distribution has a mean of 119 cases (95% CI 85-159).

If data from the last four years are considered, the estimated proportion of cases travelling overseas within the incubation period of the organism was 9.7% (95% CI 8.7-10.8%).

Outbreaks reported as caused by *Cryptosporidium* spp.

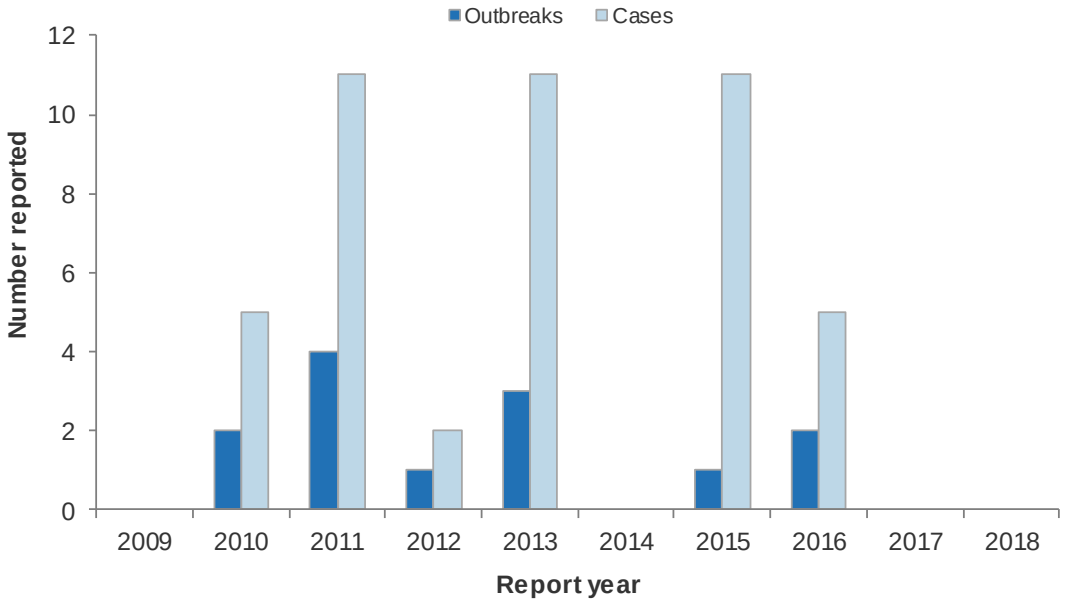
In 2018, none of the 19 *Cryptosporidium* spp. outbreaks was reported as potentially foodborne (Table 19). An outbreak is classed as foodborne in this report if food was recorded as one of the likely modes of transmission applicable to the outbreak. It is important to note that a single outbreak may have multiple pathogens, modes of transmission, settings where exposure occurred, or settings where preparation of food was conducted. Outbreaks of cryptosporidiosis accounted for 4.3% (19/446) of all enteric outbreaks and 2.9% (209/7204) of all associated cases.

Table 19. *Cryptosporidium* spp. outbreaks reported, 2018

Measure	Foodborne *Cryptosporidium* spp. outbreaks	All *Cryptosporidium* spp. outbreaks
Outbreaks	0	19
Cases	0	209
Hospitalised cases	0	1

Foodborne transmission has been rarely reported for *Cryptosporidium* spp. outbreaks, with not more than four outbreaks 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. Foodborne *Cryptosporidium* spp. outbreaks and associated cases reported by year, 2009–2018



Recent surveys

Nil.

Relevant New Zealand studies and publications

Journal papers

Molecular methods were used to detect the presence of *Cryptosporidium* spp. in commercially sourced green-lipped mussel (*Perna canaliculus*) from New Zealand [20]. *Cryptosporidium* spp. was not detected in the sampled mussel haemolymph.

Using a flexible Bayesian hierarchical framework, previously undetected space-time clusters and environmental and socio-demographic risk factors for reported cryptosporidiosis were detected at the New Zealand small area level [21]. In dairy farming areas, cryptosporidiosis outbreaks were observed in spring. Reported cryptosporidiosis was positively associated with dairy cattle density.

Relevant regulatory developments

Nil.

Giardiasis

Summary data for giardiasis in 2018 are given in Table 20.

Table 20. Summary of surveillance data for giardiasis, 2018

Parameter	Value in 2018	Source
Number of notified cases	1585	EpiSurv
Notification rate (per 100,000)	32.4	EpiSurv
Hospitalisations[a]	64	MoH NMDS
Deaths	0	EpiSurv
Estimated travel-related cases (%)[b]	375 (23.7%)	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 several laboratories across New Zealand changed the methodology for testing faecal specimens. All community faecal specimens in Northland, Waitemata, Auckland and Counties Manukau DHBs (June 2015), Southern DHB (January 2017), Lakes DHB (January 2017–June 2017), Capital & Coast, Hawke's Bay, Hutt Valley, Nelson & Marlborough, Wairarapa DHBs (January 2018) and Bay of Plenty, Lakes, and Waikato DHBs (November 2018) were screened by multiplex PCR for a range of pathogens, including *Giardia*. Prior to the change in methodology *Giardia* spp. were only screened for in those specimens where parasite screening was requested. It is unclear at this stage how laboratory changes have affected the notification rates for giardiasis as a decrease in disease rate may be masked by the increased sensitivity of the PCR methodology.

Giardiasis cases reported in 2018 by data source

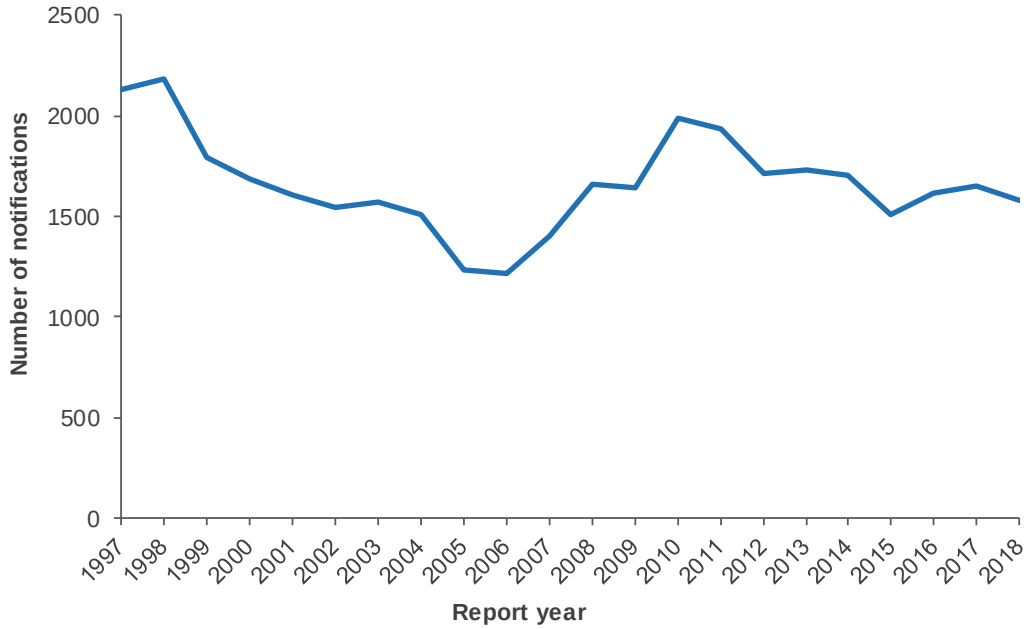
During 2018, 1585 cases (32.4 per 100,000 population) of giardiasis and no resulting deaths were reported in EpiSurv. Less than 5% of cases notified in EpiSurv were hospitalised in 2018.

The ICD-10 code A07.1 was used to extract giardiasis hospitalisation data from the MoH NMDS database. Of the 64 hospital admissions (1.3 admissions per 100,000 population) recorded in 2018, 38 were reported with giardiasis as the principal diagnosis and 26 with giardiasis as another relevant diagnosis.

Notifiable disease data

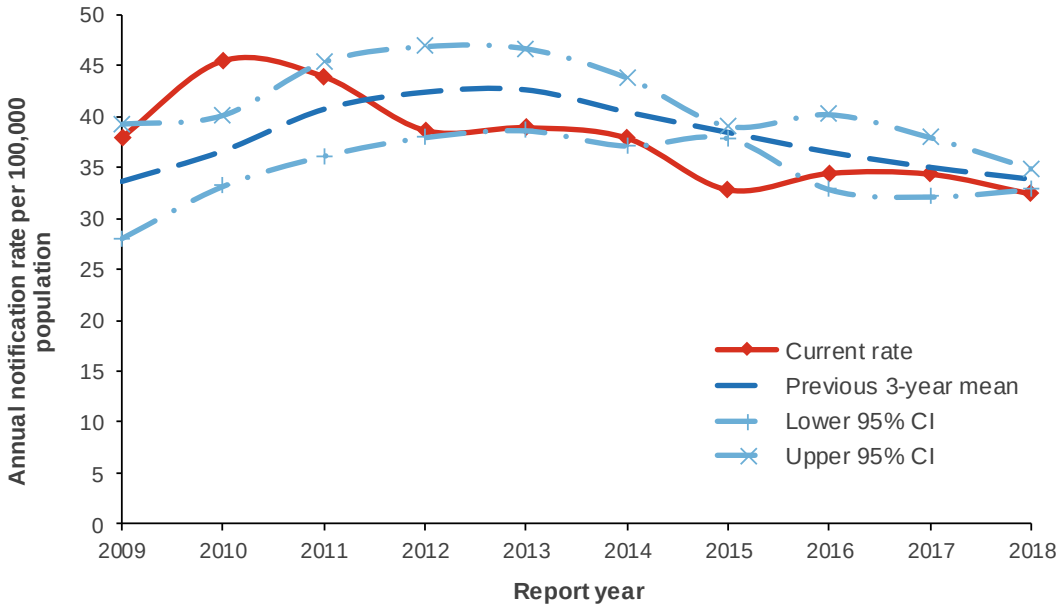
There was a steady decrease in the number of giardiasis cases reported each year from 1998 to 2006. An increasing trend in the number of notifications was observed from 2006 until 2010 followed by decreasing trend in the number of notifications. The highest number of notifications since 1999 was reported in 2010 (1985 cases), followed by 2011 (1934 cases) (Figure 17).

Figure 17. Giardiasis notifications by year, 1997–2018



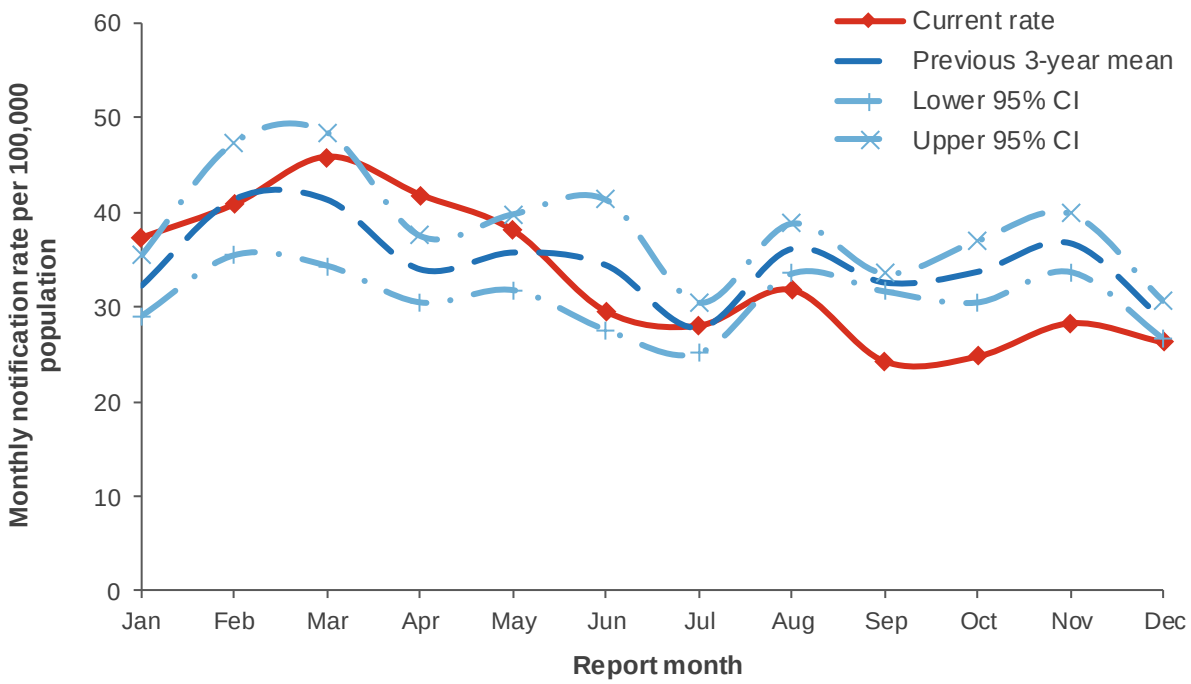
The notification rate in 2018 was slightly lower (32.4 cases per 100,000 population) than the previous three-year average (33.9 cases per 100,000), maintaining the downward trend since 2010 (Figure 18).

Figure 18. Giardiasis notification rate by year, 2009–2018



The number of notified cases of giardiasis reported per 100,000 population by month for 2018 is shown in (Figure 19). The monthly number of notifications in 2018 ranged from 97 notifications (September) to 183 notifications (March).There was no distinct seasonal pattern in the population rate of giardiasis notifications reported by month when considering the previous three years (2015–2017). In 2018, slightly lower monthly rates were observed in the second half of the year than in the previous three years.

Figure 19. Giardiasis monthly rate (annualised), 2018



In 2018, the rate of notifications for giardiasis was higher for males (35.2 notifications per 100,000 population) than females (32.8 notifications per 100,000 population). The rate of hospitalisations was somewhat higher for females than for males (1.5 and 1.1, respectively, hospitalisations per 100,000 population, Table 21).

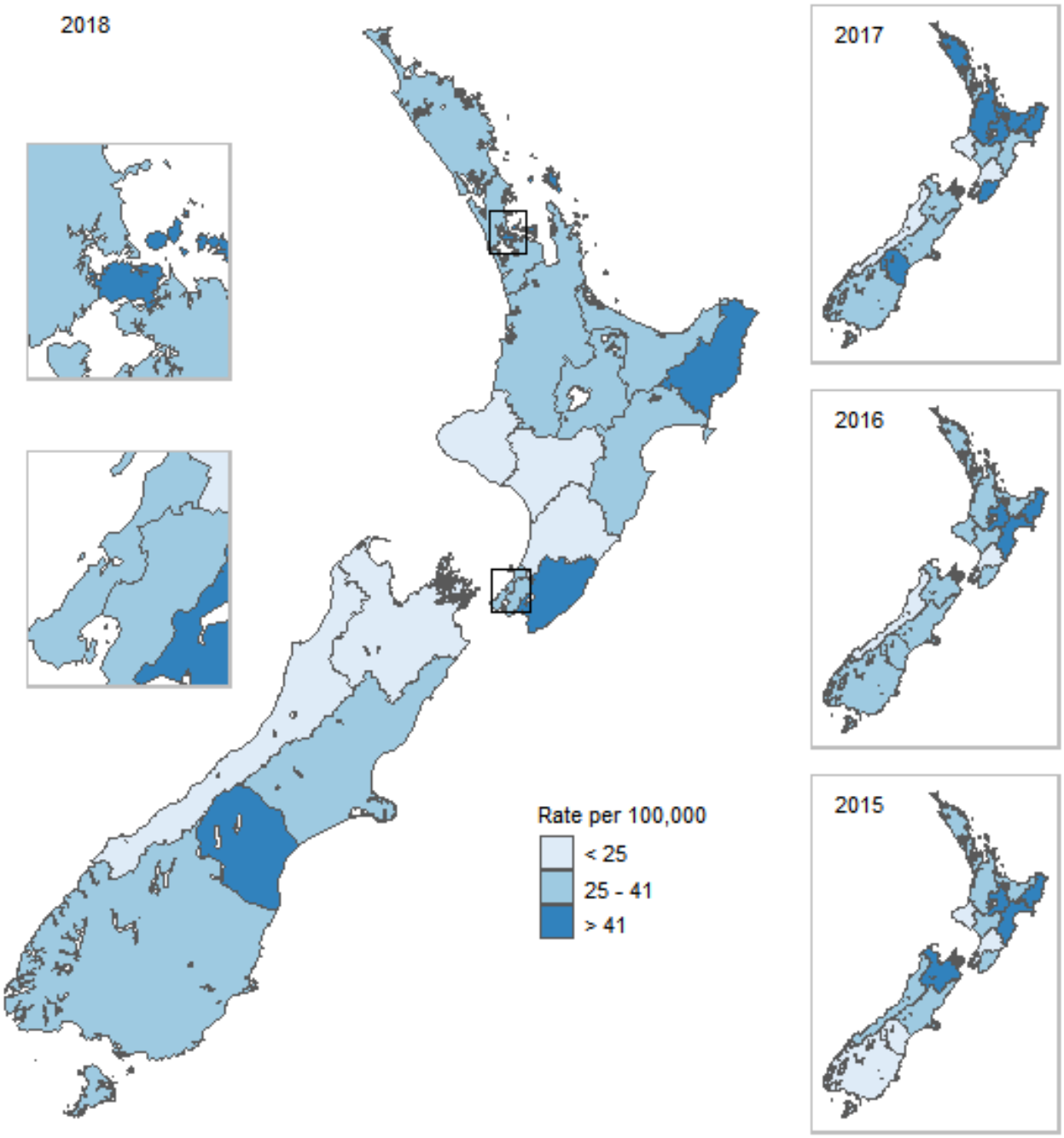
Table 21. Giardiasis cases by sex, 2018

Sex	EpiSurv notifications		Hospitalisations[a]	
	No.	Rate[b]	No.	Rate[b]
Male	848	35.2	27	1.1
Female	737	29.8	37	1.5
Total	**1585**	**32.4**	**64**	**1.3**

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

Giardiasis rates varied throughout the country during 2018 (Figure 20). The highest rate was reported for Tairawhiti (69.2 per 100,000 population, 34 cases), followed by Wairarapa (48.4 per 100,000, 22 cases). The lowest rates were reported for West Coast (18.4 per 100,000, 6 cases), Taranaki (20.9 per 100,000, 25 cases) and Whanganui (21.6 per 100,000 population, 14 cases) DHBs.

Figure 20. Geographic distribution of giardiasis notifications, 2015–2018



Note: Changes in laboratory methods were introduced in Northland, Waitemata, Auckland and Counties Manukau DHBs (June 2015), Southern DHB (since January 2017) and Lakes DHB (January 2017 - June 2017), Capital & Coast, Hawke's Bay, Hutt Valley, Nelson & Marlborough, Wairarapa DHBs (January 2018) and Bay of Plenty, Lakes, and Waikato DHBs (November 2018). The new, more sensitive assays may have triggered an increase in notifications for some enteric diseases. Refer to text for details.

In 2018, the highest notification rate was for the 1 to 4 years age group (106.0 per 100,000 population, 261 cases), followed by the 30 to 39 years age group (51.7 per 100,000, 325 cases) (Table 22). The highest hospitalisation rate was also for the 1 to 4 years age group (3.7 per 100,000 population).

Table 22. Giardiasis cases by age group, 2018

Age group (years)	EpiSurv notifications		Hospitalisations[a]	
	No.	Rate[b]	No.	Rate[b]
<1	20	33.2	2	-
1 to 4	261	106.0	9	3.7
5 to 9	98	29.9	2	-
10 to 14	46	14.8	3	-
15 to 19	32	10.2	2	-
20 to 29	217	29.4	11	1.5
30 to 39	325	51.7	10	1.6
40 to 49	186	30.2	6	1.0
50 to 59	191	30.5	6	1.0
60 to 69	144	28.3	7	1.4
70+	65	12.8	6	1.2
Total	**1585**	**32.4**	**64**	**1.3**

[a] MoH NMDS data for hospital admissions.

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

For cases where information on travel was provided in 2018, 23.7% (95% CI 20.8–26.7%) 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 2018. The resultant distribution has a mean of 375 cases (95% CI 314–442).

If data from the last four years are considered the estimated proportion of cases travelling overseas within the incubation period of the organism was 23.8% (95% CI 22.4%–25.2%).

Outbreaks reported as caused by *Giardia* spp.

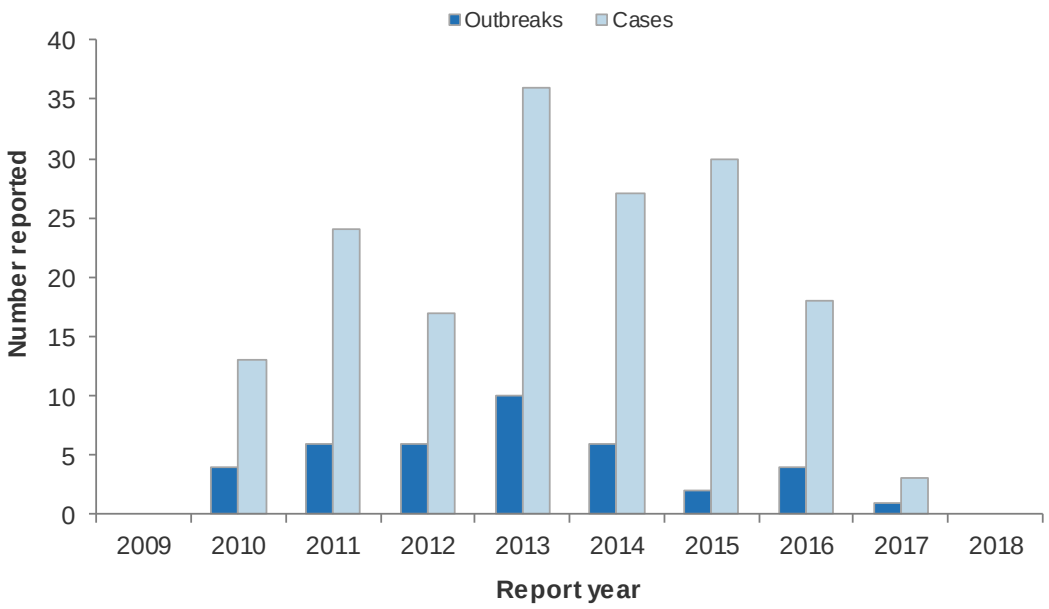
In 2018, no *Giardia* spp. outbreaks with a suspected or known foodborne source were reported (Table 23). An outbreak is classed as foodborne in this report if food was recorded as one of the likely modes of transmission applicable to the outbreak. It is important to note that a single outbreak may have multiple pathogens, modes of transmission, settings where exposure occurred, or settings where preparation of food was conducted. *Giardia* spp. outbreaks accounted for 3.6% (16/446) of all enteric outbreaks and 1.5% (106/7204) of all associated cases.

Table 23. *Giardia* spp. outbreaks reported, 2018

Measure	Foodborne *Giardia* spp. outbreaks	All *Giardia* spp. outbreaks
Outbreaks	0	16
Cases	0	106
Hospitalised cases	0	0

Between 2010 and 2017, between one and 10 foodborne *Giardia* spp. outbreaks were reported each year. No *Giardia* spp. outbreaks were reported in 2009 and 2018.(Figure 21).

Figure 21. Foodborne *Giardia* spp. outbreaks and associated cases reported by year, 2009–2018



Recent surveys

Nil.

Relevant New Zealand studies and publications

Journal papers

Molecular methods were used to detect the presence of *Giardia duodenalis* in commercially sourced green-lipped mussel (*Perna canaliculus*) from New Zealand [20]. *G. duodenalis* assemblage B, known to be pathogenic in humans, was detected in 1% of mussels tested by polymerase chain reaction.

Using a flexible Bayesian hierarchical framework, previously undetected space-time clusters and environmental and socio-demographic risk factors for reported giardiasis were detected at the New Zealand small area level [21]. For giardiasis, there was no seasonal pattern in outbreak probability and an inverse association with density of dairy cattle

Relevant regulatory developments

Nil.

Hepatitis A

Summary data for hepatitis A in 2018 are given in Table 24.

Table 24. Summary of surveillance data for hepatitis A, 2018

Parameter	Value in 2018	Source
Number of notified cases	68	EpiSurv
Notification rate (per 100,000)	1.4	EpiSurv
Hospitalisations[a]	47	MoH NMDS
Deaths	0	EpiSurv
Travel-related cases (%)[b]	44 (64.2%)	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 2018 by data source

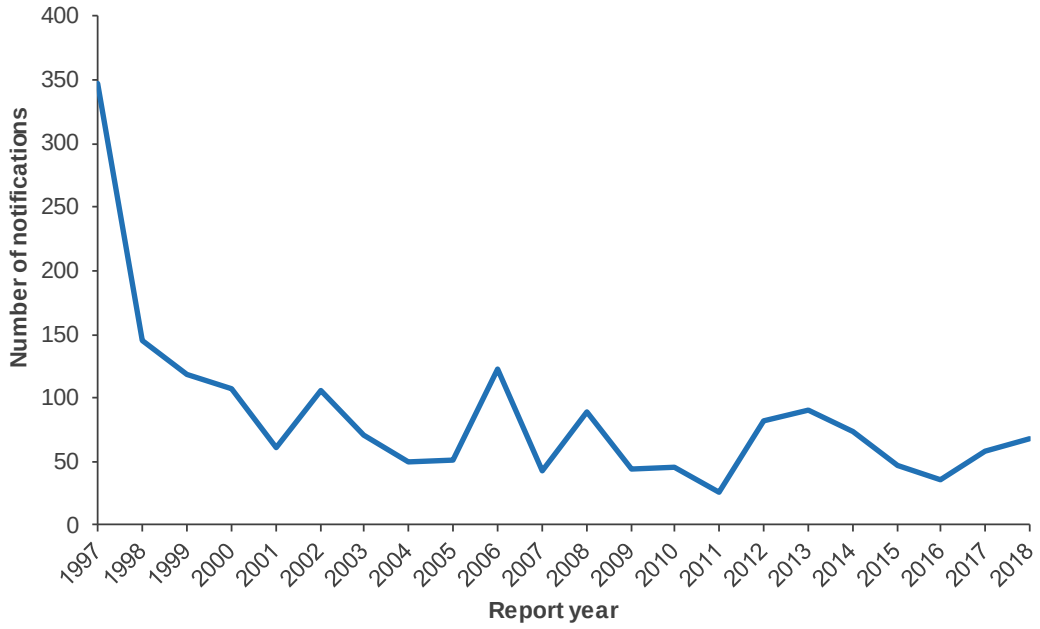
During 2018, 68 cases (1.4 per 100,000 population) of hepatitis A and no resulting deaths were reported in EpiSurv. Hospitalisation rates are usually high for hepatitis A with approximately 50% of notified cases hospitalised in 2018.

The ICD-10 code B15 was used to extract acute hepatitis A hospitalisation data from the MoH NMDS database. Of the 96 hospital admissions (2.0 admissions per 100,000 population) recorded in 2018, 47 were reported with acute hepatitis A as the principal diagnosis and 49 with acute hepatitis A as another relevant diagnosis.

Notifiable disease data

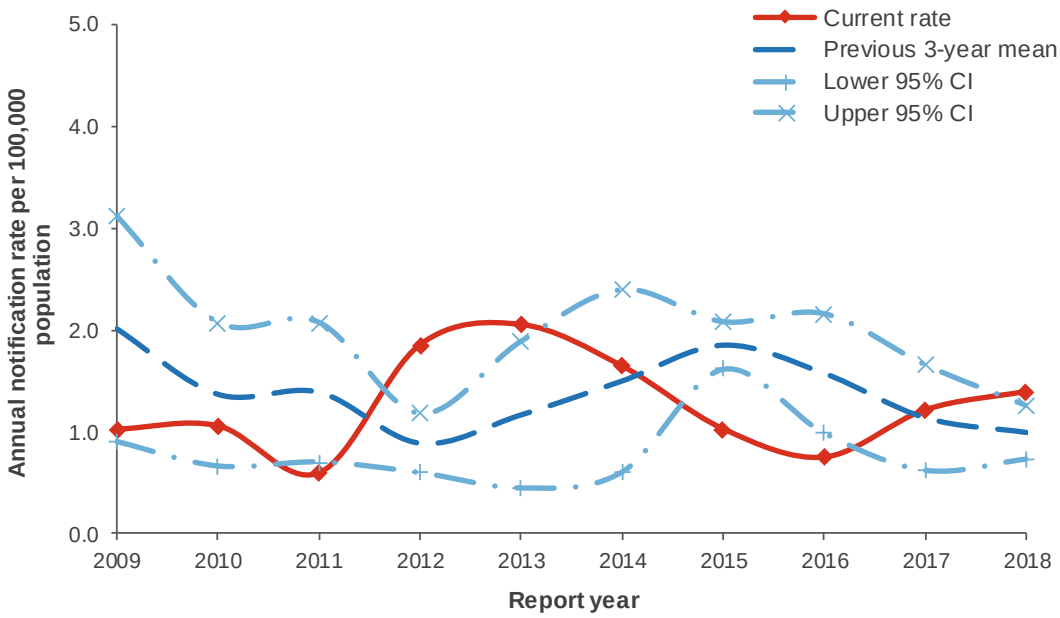
Between 2001 and 2017, the annual number of notifications has remained in the range of 26 (2011) to 123 (2006), having decreased from 347 in 1997 (Figure 22).

Figure 22. Hepatitis A notifications by year, 1997–2018



Hepatitis A notification rates have varied throughout the 10-year period 2009–2018 in the range of 0.6 to 2.0 per 100,000 population (Figure 23). In 2018, the notification rate was higher (1.4 cases per 100,000 population) than the previous three-year average (1.0 cases per 100,000).

Figure 23. Hepatitis A notification rate by year, 2009–2018



In 2018, hepatitis A notification rates were the similar for males and females, whereas hospital admissions with hepatitis A as a primary diagnosis were slightly higher for males than for females (1.2 and 0.8 hospitalisations per 100,000 population, respectively) (Table 25).

Table 25. Hepatitis A cases by sex, 2018

Sex	EpiSurv notifications		Hospitalisations[a]	
	No.	Rate[b]	No.	Rate[b]
Male	37	1.5	29	1.2
Female	31	1.3	18	0.8
Total	**68**	**1.4**	**47**	**1.0**

[a] MoH NMDS data for hospital admissions with hepatitis A as a primary diagnosis.
[b] per 100,000 of population.

In 2018, the highest notification rate was reported for the 5 to 9 years age groups (4.0 per 100,000 population, 13 cases). Hospitalisation rates with hepatitis A as a primary diagnosis were also the highest for this age group (Table 26).

Table 26. Hepatitis A cases by age group, 2018

Age group (years)	EpiSurv notifications		Hospitalisations[a]	
	No.	Rate[b]	No.	Rate[b]
<1	0	-	0	-
1 to 4	5	2.0	0	-
5 to 9	13	4.0	8	2.4
10 to 14	3	-	3	-
15 to 19	7	2.2	4	-
20 to 29	21	2.8	9	1.2
30 to 39	7	1.1	11	1.8
40 to 49	4	-	4	-
50 to 59	2	-	3	-
60 to 69	3	-	3	-
70+	3	-	2	-
Total	**68**	**1.4**	**47**	**1.0**

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

In 2018, 67 of 68 hepatitis A cases provided information on overseas travel, and 64.2% had travelled overseas during the incubation period. If data from the last four years are considered the estimated proportion of cases travelling overseas within the incubation period of the organism was 57.5% (95% CI 50.5–64.3%).

Outbreaks reported as caused by hepatitis A virus

In 2018, three of the outbreaks caused by hepatitis A virus with 8 related cases were associated with a suspected or known foodborne source (Table 27). An outbreak is classed as foodborne in this report if food was recorded as one of the likely modes of transmission applicable to the outbreak. It is important to note that a single outbreak may have multiple pathogens, modes of transmission, settings where exposure occurred, or settings where preparation of food was conducted. Outbreaks

caused by hepatitis A virus accounted for 0.9% (4/446) of all enteric outbreaks and 0.2% (17/7204) of all associated cases.

Table 27. Hepatitis A outbreaks reported, 2018

Measure	Foodborne hepatitis A outbreaks	All hepatitis A outbreaks
Outbreaks	3	4
Cases	8	17
Hospitalised cases	0	0

Table 28 contains details of the three foodborne hepatitis A outbreaks reported in 2018. The suspected vehicle of infection was shellfish for one outbreak and unknown for the other two outbreaks. The level of evidence for suspected foods was recorded as weak. No food samples related to hepatitis A outbreaks were submitted to ESR's Enteric, Environmental and Food Virology Laboratory in 2018.

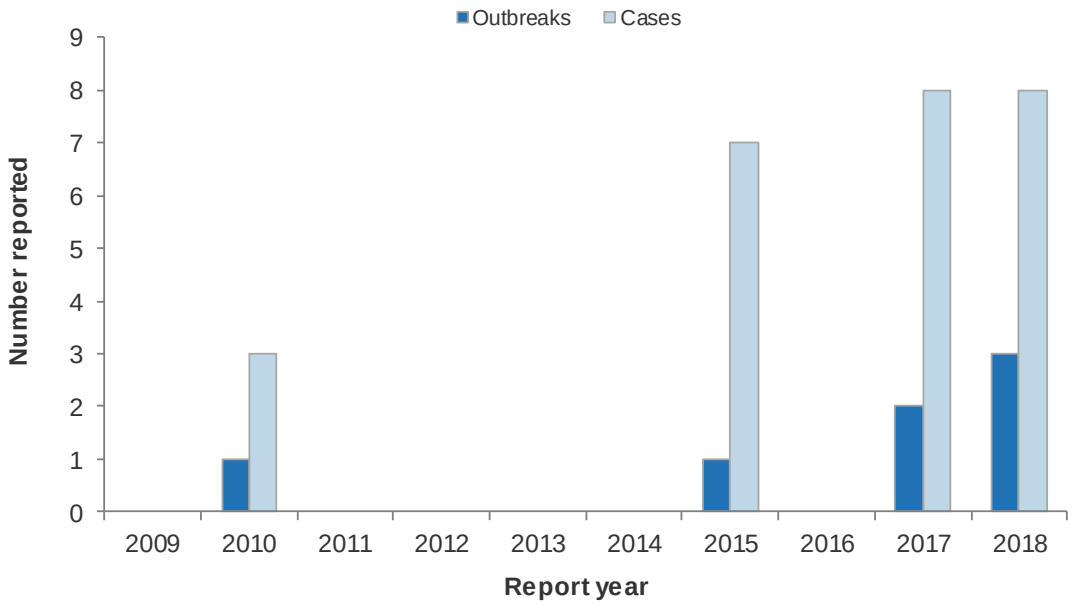
Table 28. Details of the foodborne hepatitis A virus outbreaks, 2018

PHU	Month	Suspected vehicle	Exposure setting	Preparation setting	No. ill
Auckland	Jan	Shellfish	Home	-	4C, 0P
Nelson Marlborough	Feb	Unknown	Home	-	2C, 0P
C and PH	Oct	Unknown	Other institution	-	2C, 0P

PHU: Public Health Unit, C and PH: Community and Public Health, Nelson Marlborough: Nelson Marlborough Public Health Service, Toi Te Ora: Toi Te Ora - Public Health, C: confirmed, P: probable

Foodborne hepatitis A outbreaks are rare with only seven outbreaks reported in the period 2009 to 2018 (Figure 24). Although occurring infrequently, foodborne outbreaks of hepatitis A virus infection can be associated with many cases (34 cases for an outbreak reported in 2006).

Figure 24. Foodborne hepatitis A virus outbreaks and associated cases reported by year, 2009–2018



Hepatitis A virus types 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 relates to individual notified cases where a specimen has been submitted. The data includes those cases not associated with foodborne transmission.

In 2018, hepatitis A virus positive specimens from 37 hepatitis A cases were submitted to ESR for genotyping. Hepatitis A virus IA was the most commonly identified sub-genotype, similar to 2016 and 2017. Phylogenetic analysis of hepatitis A virus genotype IA sequences indicate distinct sequence clustering associated with travel to Tonga, or contact with cases. A similar clustering was observed with hepatitis A cases associated with Samoa. There was an increase in notified cases relating to sub-genotype IIIA. Genotype IIIA is prevalent in central Asia.

Table 29. Hepatitis A subtypes identified by the Enteric, Environmental and Food Virology Laboratory, 2016–2018

Hepatitis A virus genotypes	2016	2017	2018
I.A	16	20	20
III.A	1	4	14
I.B	0	1	0
Unable to genotype	0	2	3
Total	**17**	**27**	**37**

Recent surveys

Nil.

Relevant New Zealand studies and publications

Nil.

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 2018 by data source

Nine cases of histamine (scombroid) fish poisoning were reported in EpiSurv during 2018 (0.2 cases per 100,000 population). 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 scombroid fish poisoning hospitalisation data from the MoH NMDS database. All of the five hospital admissions (0.1 admissions per 100,000 population) recorded in 2018, were reported with scombroid fish poisoning as the principal diagnosis.

Outbreaks reported as caused by histamine (scombroid) fish poisoning

Two histamine (scombroid) fish poisoning outbreaks were reported in 2018 involving five associated cases, two of whom were reported as hospitalised (Table 30). It should be noted that all histamine (scombroid) fish poisoning outbreaks will be categorised as foodborne, as consumption of contaminated fish is the only currently recognised transmission route for this disease.

Table 30. Histamine (scombroid) fish poisoning outbreaks reported, 2018

Measure	Foodborne histamine fish poisoning outbreaks	All histamine fish poisoning outbreaks
Outbreaks	2	2
Cases	5	5
Hospitalised cases	2	2

Table 31 contains details of the two foodborne histamine fish poisoning outbreaks reported in 2018. The level of evidence for suspected foods was recorded as weak in EpiSurv. No samples related to the two histamine fish poisoning outbreaks were submitted to ESR's Public Health Laboratory.

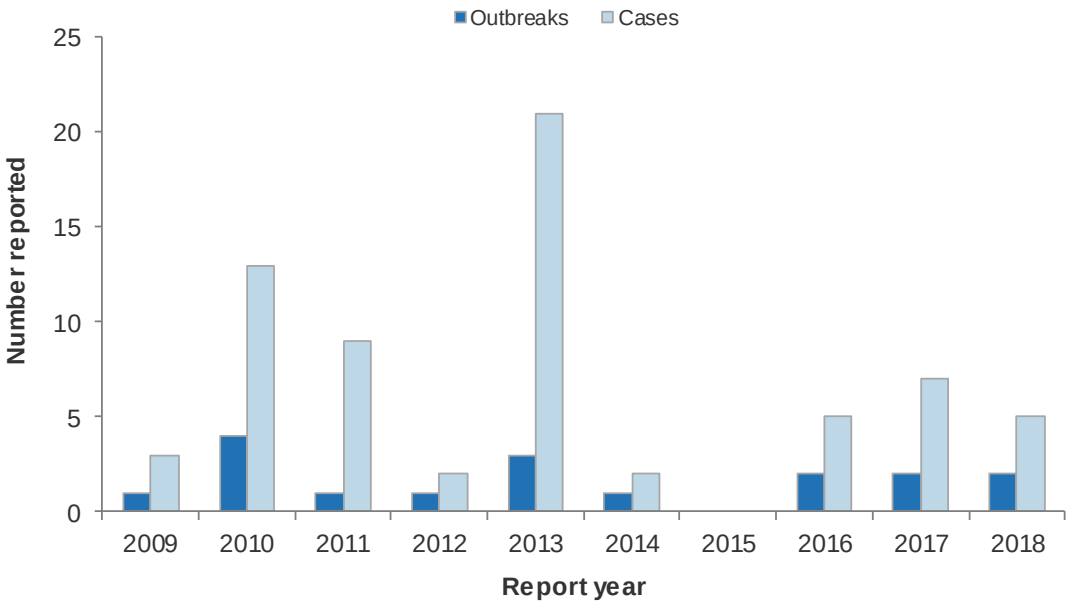
Table 31. Details of foodborne histamine fish poisoning outbreaks, 2018

PHU	Month	Suspected vehicle	Exposure setting	Preparation setting	No. ill
Nelson Marlborough	May	Tuna fish	Other food outlet	Other food outlet	0C, 3P
Regional	Oct	Unknown	Supermarket/delicatessen / Other food outlet	Supermarket/delicatessen / Other food outlet	2C, 0P

PHU: Public Health Unit, Nelson Marlborough: Nelson Marlborough Public Health Service, Regional: Regional Public Health, C: confirmed, P: probable.

Between 2009 and 2018 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 25). The highest total number of outbreak-associated cases was reported in 2013 (3 outbreaks, 21 cases).

Figure 25. Histamine (scombroid) fish poisoning outbreaks and associated cases reported by year, 2009–2018



Recent surveys

Nil.

Relevant New Zealand studies and publications

Nil.

Relevant regulatory developments

Nil.

Listeriosis

Summary data for listeriosis in 2018 are given in Table 32.

Table 32. Summary of surveillance data for listeriosis, 2018

Parameter	Value in 2018	Source
Number of notified cases[a]	30	EpiSurv
Notification rate (per 100,000)	0.6	EpiSurv
Hospitalisations [b]	41	MoH NMDS
Deaths	2	EpiSurv
Travel-related cases (%)[c]	1 (4.0%)	EpiSurv
Estimated food-related cases (%)[d]	25 (87.8%)	Expert consultation

[a] Includes non-perinatal (25) and perinatal cases (5).
[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.

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, fetus, 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 fetus or infant should be included on the case form

Listeriosis cases reported in 2018 by data source

During 2018, 30 cases (0.6 per 100,000 population) of listeriosis with 2 resulting deaths (non-perinatal) were reported in EpiSurv. Five of those cases were perinatal listeriosis with no perinatal deaths occurring in 2018. Hospitalisation rates are usually very high for listeriosis with all 30 notified cases hospitalised in 2018 (100%).

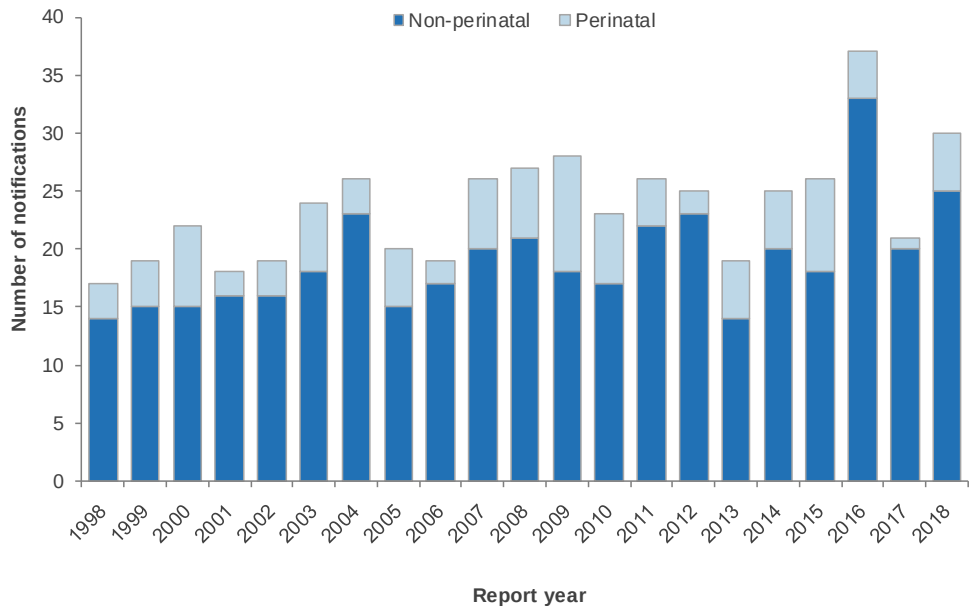
The ICD-10 code A32 was used to extract listeriosis hospitalisation data from the MoH NMDS database. Of the 41 hospital admissions (0.8 admissions per 100,000 population) recorded in 2018, 17 were reported with listeriosis as the principal diagnosis and 24 with listeriosis as another relevant diagnosis.

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 1998 and 2018, the annual number of listeriosis notifications has fluctuated between 17 (1998) and 37 (2016) (Figure 26). 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, since a peak of 0.9 per 100,000 in 1997.

Figure 26. Listeriosis non-perinatal and perinatal notifications by year, 1998–2018



In 2018, the rate and number of notifications for listeriosis was similar for females (0.6 per 100,000 population, 16 cases) and males (0.6 per 100,000, 14 cases). The number and rate of hospitalisations was also similar for males and females (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 five perinatal cases.

Table 33. Listeriosis cases by sex, 2018

Sex	EpiSurv notifications		Hospitalisations[a]	
	No.	Rate[b]	No.	Rate[b]
Male	14	0.6	21	0.9
Female	16	0.6	20	0.8
Total	**30**	**0.6**	**41**	**0.8**

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

In 2018, rates for listeriosis were highest in the 70 years and over age group for both the notifications (3.3 per 100,000 population, 17 cases) and hospitalisations (5.1 per 100,000, 26 admissions) (Table 34).

Table 34. Listeriosis cases by age group, 2018

Age group (years)	EpiSurv notifications		Hospitalisations[a]	
	No.[b]	Rate[c]	No.	Rate[c]
<1	0	-	1	-
1 to 4	0	-	0	-
5 to 9	0	-	0	-
10 to 14	0	-	0	-
15 to 19	0	-	0	-
20 to 29	1	-	3	-
30 to 39	3	-	3	-
40 to 49	2	-	1	-
50 to 59	2	-	1	-
60 to 69	5	1.0	6	1.2
70+	17	3.3	26	5.1
Total	**30**	**0.6**	**41**	**0.8**

[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 of population (rate not calculated when fewer than five cases reported)

Outbreaks reported as caused by *Listeria* spp.

There were no *Listeria* spp. outbreaks reported in 2018. Since 2006 there have been two *Listeria* spp. outbreaks reported. There was an outbreak with two associated cases in 2009 and a foodborne outbreak with six associated cases in 2012. 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.

Listeria monocytogenes types commonly reported

ESR's Special Bacteriology Laboratory reported receiving 32 isolates of *L. monocytogenes* during 2018. Table 35 shows the number of isolates and percentage of *L. monocytogenes* serotypes reported by the Special Bacteriology Laboratory at ESR between 2014 and 2018. 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, 2014–2018

Serotype	2014		2015		2016		2017		2018	
	No.	%	No.	%	No.	%	No.	%	No.	%
O1/2	12	42.9	11	42.3	17	44.7	13	65.0	12	37.5
O4	16	57.1	15	57.7	20	52.6	7	35.0	19	59.4
Untypable	0	-	0	-	1	2.6	0	-	1	3.1
Total	**28**		**26**		**38**		**20**		**32**	

Recent surveys

Nil.

Relevant New Zealand studies and publications

Nil.

Relevant regulatory developments

During 2018, New Zealand Food Safety published further guidance documents to support control of *L. monocytogenes* in the food industry. The documents published in 2018 were:

- Environment testing for *Listeria* [22]
- Fact sheet: *Listeria monocytogenes* and ready-to-eat foods [23]
- Fact sheet: Cleaning and sanitising [24]
- Fact sheet: Testing product for *Listeria monocytogenes* [25]

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 2018 by data source

During 2018, 12 cases (0.2 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 2018 there were 4280 cases associated with notified outbreaks.

The ICD-10 code A08.1 was used to extract norovirus infection hospitalisation data from the MoH NMDS database. Of the 485 hospital admissions (9.9 admissions per 100,000 population) recorded in 2018, 251 were reported with norovirus infection as the principal diagnosis and 234 with norovirus infection as another relevant diagnosis. Of the 485 hospital admissions, 204 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 2018, 8 (4.7%) of the171 norovirus outbreaks and 362 (8.5%) of the 4280 outbreak-associated cases were reported as foodborne (Table 36). 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. Norovirus outbreaks accounted for 38.3% (171/446) of all enteric outbreaks and 59.4% (4280/7204) of all outbreak-associated cases reported in 2018.

Table 36. Norovirus outbreaks reported, 2018

Measure	Foodborne norovirus infection outbreaks	All norovirus infection outbreaks
Outbreaks	8	171
Cases	362	4280
Hospitalised cases	2	40

Table 37 contains details of the eight foodborne norovirus outbreaks reported in 2018. A suspected food vehicle was not identified in seven of these outbreaks. The level of evidence for suspected foods

was recorded as weak for one outbreak related to egg sandwiches (Community and Public Health in March).

During investigation of suspected foodborne illness outbreaks by ESR's Public Health Laboratory and the Enteric, Food and Environmental Virology/Norovirus Reference Laboratory in 2018, faecal specimens relating to two of the eight foodborne outbreaks (Table 37) were received for norovirus testing. Norovirus was detected in faecal samples from both foodborne outbreaks.

During 2018 it was possible to test for norovirus in the following foods; bivalve molluscan shellfish, soft berry fruit and leafy salads.

Table 37. Details of foodborne norovirus outbreaks, 2018

PHU	Month	Suspected vehicle	Exposure setting	Preparation setting	No. ill
Auckland	Jan	Unknown	Childcare centre	Childcare centre	1C, 16P
Auckland	Jan	Unknown	Restaurant/cafe/bakery	-	17C, 4P
C and PH	Mar	Egg sandwiches	Other setting	Other setting	5C, 95P
Auckland	May	Unknown	School	-	2C, 37P
Auckland	May	Unknown	School	-	4C, 72P
Auckland	Jun	Unknown	Long term care facility	-	13C, 0P
South	Jul	Unknown	Other institution	Other institution	3C, 11P
Auckland	Aug	Unknown	Long term care facility	-	82C, 0P

PHU: Public Health Unit, Auckland: Auckland Regional Public Health Service, C and PH: Community and Public Health, South: Public Health South, C: confirmed, P: probable.

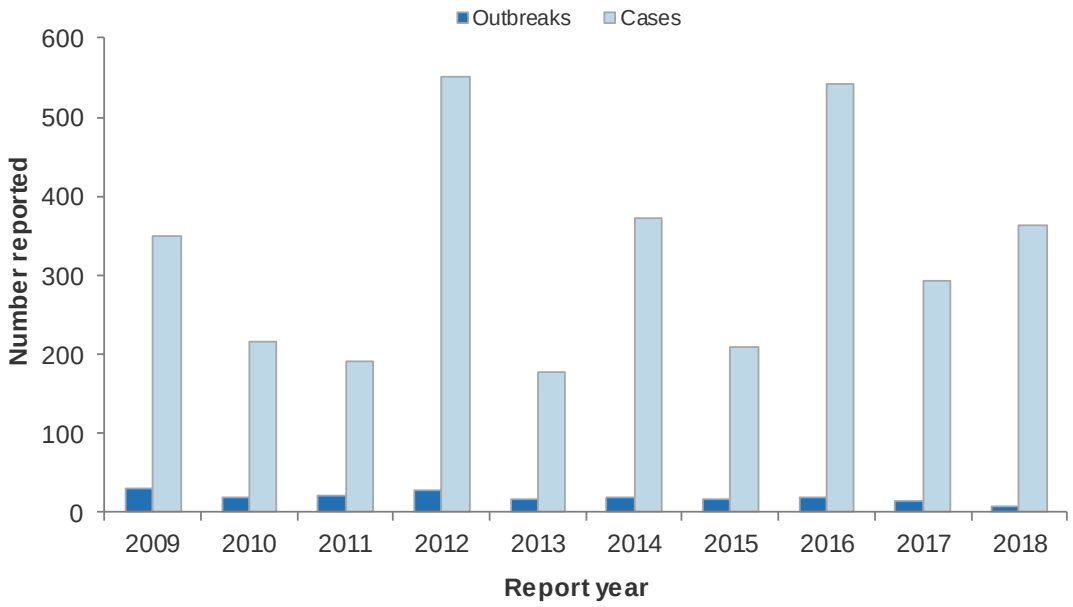
Table 38 shows the number of hospitalised cases and total cases by genotype for the eight foodborne norovirus outbreaks reported during 2018. The outbreaks are due to a variety of genotypes, with genotype GII.P16/GII.2 being more prevalent than the others. The highest number of total cases was reported for one outbreak suspected to be related to egg sandwiches at a camp due to GII.P16/GII.2 (100 cases).

Table 38. Norovirus genotypes reported in foodborne outbreaks, 2018

Norovirus genotype	Outbreaks	Total cases	Hospitalised cases
GII.P7/GII.6	1	17	0
GII.P16/GII.4	2	103	2
GII.P16/GII.2	4	228	0
GII.P17/GII.17	1	14	0
Total	**8**	**362**	**2**

Between 2009 and 2018 the annual number of foodborne norovirus outbreaks reported each year ranged from 8 (2018) to 30 (2009) (Figure 27). The total number of cases associated with these outbreaks ranged from 177 (2013) to 552 cases (2012) per year.

Figure 27. Foodborne norovirus outbreaks and associated cases reported by year, 2009–2018



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 2018, norovirus genogroup II (GII) was identified in 158/174 (90.8%) outbreaks. In the previous four years GII was identified in between 77.8% (2017) and 90.8% (2015) of outbreaks. In 2018, genogroup I (GI) was identified in 15/174 (8.6%) outbreaks. The norovirus genotype was determined for 98.6% (172/174) of ESR laboratory-confirmed norovirus outbreaks. As in previous years, GII.4 variants were the predominant norovirus genotype identified (75/174, 43.1% 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, 2014–2018

Norovirus genotypes	2014	2015	2016	2017	2018
Genogroup I	**51**	**13**	**29**	**51**	**15**
GI untyped	1	-	1	-	-
GI.1	-	-	2	2	1
GI.2	12	7	3	-	1
GI.3	17	2	15	29	6
GI.4	-	-	-	1	3
GI.5	1	2	-	1	2
GI.6	10	2	6	15	1
GI.7	1	-	-	1	-
GI.8	-	-	-	2	-
GI.9	9	-	2	-	1
Genogroup II	**253**	**167**	**159**	**186**	**158**
GII untyped	4	5	1	1	2
GII.2	2	14	1	2	-
GII.3	1	2	-	-	-
GII.Pe/GII.4 Sydney 2012[a]	200	87	30	13	3
GII.P4 New Orleans 2009/GII.4 Sydney 2012[a]	3	2	35	13	2
GII.P16/GII.4[a]	-	1	19	103	70
GII.6	22	19	2	14	10
GII.7	6	2	6	1	12
GII.8	1	1	-	2	-
GII.13	-	-	-	1	-
GII.15	-	-	-	1	-
GII.17	3	6	19	5	4
GII.20	1	-	-	-	-
GII.P7/GII.14	-	1	-	4	7
GII.P12/GII.3	-	18	19	2	8
GII.P16/GII.2	-	-	27	18	38
GII.P21/GII.3	5	8	-	1	-
Other GII recombinants	5	1	-	5	2
Mixed GI and GII	**8**	**4**	**-**	**2**	**1**
Total outbreaks[b]	**312**	**184**	**188**	**239**	**174**

[a]GII.4 variants

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

Recent surveys

Nil.

Relevant New Zealand studies and publications

Nil.

Relevant regulatory developments

Nil.

Salmonellosis

Summary data for salmonellosis in 2018 are given in Table 40. Note that in the following sections the term *Salmonella* refers to serotypes of *Salmonella enterica* subspecies *enterica*, excluding *S.* Typhi and *S.* Paratyphi.

Table 40. Summary of surveillance data for salmonellosis, 2018

Parameter	Value in 2018	Source
Number of notified cases	1100	EpiSurv
Notification rate (per 100,000)	22.5	EpiSurv
Hospitalisations[a]	227	MoH NMDS
Deaths	0	EpiSurv
Estimated travel-related cases (%)[a]	428 (38.9%)	EpiSurv
Estimated food-related cases (%)[c]	417 (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 several laboratories across New Zealand changed the methodology for testing faecal specimens. All community faecal specimens in Northland, Waitemata, Auckland and Counties Manukau DHBs (June 2015), Southern DHB (January 2017), Lakes DHB (January 2017–June 2017), Capital & Coast, Hawke's Bay, Hutt Valley, Nelson & Marlborough, Wairarapa DHBs (January 2018) and Bay of Plenty, Lakes, and Waikato DHBs (November 2018) 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 how laboratory changes have affected the notification rates for salmonellosis as a decrease in disease rate may be masked by the increased sensitivity of the PCR methodology.

Salmonellosis cases reported in 2018 by data source

The salmonellosis cases presented here exclude disease caused by the *Salmonella* serotypes Paratyphi and Typhi.

During 2018, 1100 cases (22.5 per 100,000 population) of salmonellosis and no resulting deaths were reported in EpiSurv. The Enteric Reference Laboratory at ESR reported 1127 cases infected with non-typhoidal *Salmonella* spp. (23.1 cases per 100,000) on the basis of clinical isolates received.

Seven cases had acquired mixed infections with two different *Salmonella* serotypes. Approximately 23% of cases notified in EpiSurv were hospitalised in 2018.

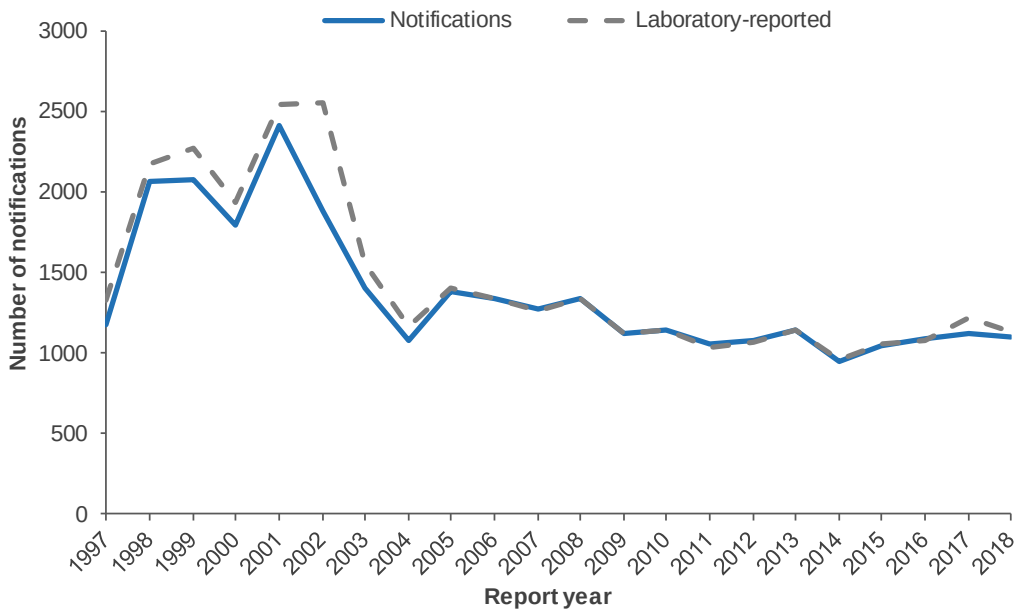
The ICD-10 code A02.0 (*Salmonella enteritis*) was used to extract salmonellosis hospitalisation data from the MoH NMDS database. Of the 227 hospital admissions (4.6 admissions per 100,000 population) recorded in 2018, 183 were reported with salmonellosis as the principal diagnosis and 44 with salmonellosis 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

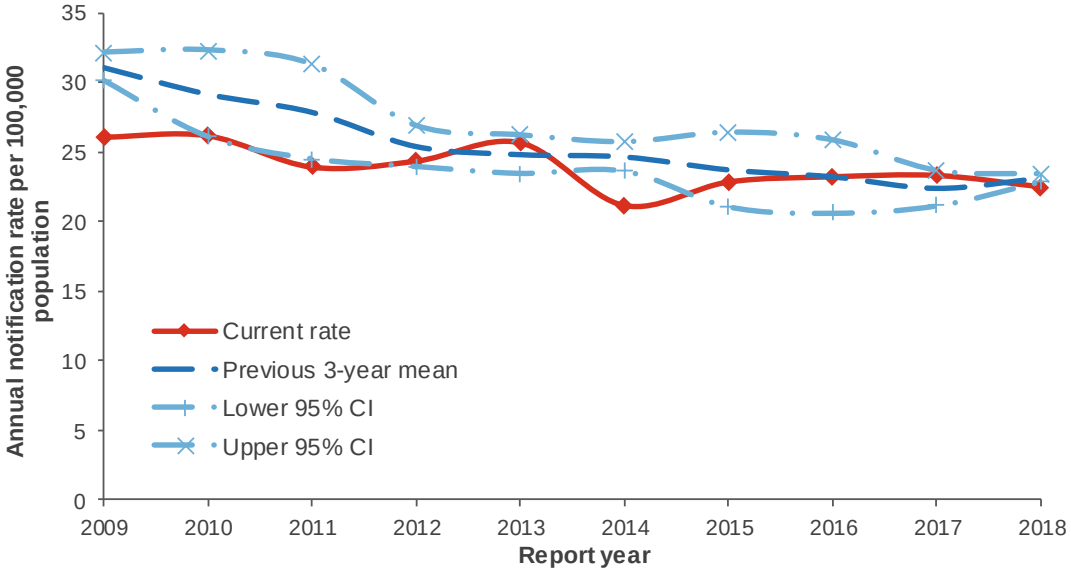
Following a generally increasing trend of salmonellosis notifications from 1997 to 2001 there was a sharp fall in notifications between 2001 and 2004. The notifications have continued to decline between 2005 and 2014 at a slower rate. The lowest number of notifications was reported in 2014 (955 cases). Since 2015, notification rates ranged between 1053 and 1216 notified cases per year (Figure 28).

Figure 28. Salmonellosis notifications and laboratory-reported cases by year, 1997–2018



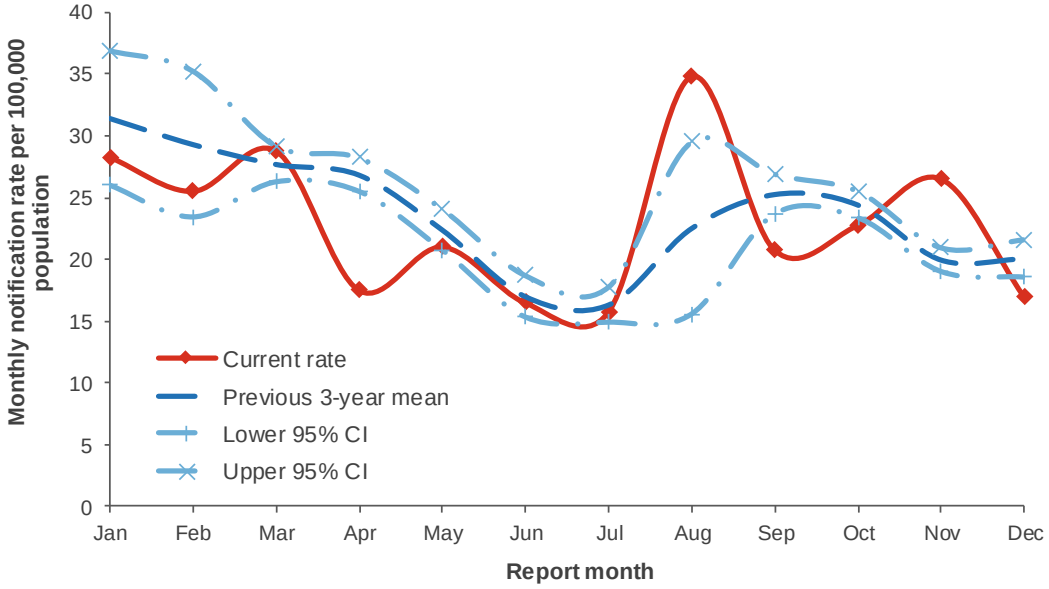
The notification rate in 2018 was similar (22.5 cases per 100,000 population) to the previous three-year average (23.2 cases per 100,000) (Figure 29).

Figure 29. Salmonellosis notification rate by year, 2009–2018



The number of notified cases of salmonellosis per 100,000 population by month for 2018 is shown in Figure 30. The overall trend for 2018 was similar to the previous three-year mean with higher rates during summer and early autumn months and lowest rates during the mid-winter months (June and July). The monthly number of notifications in 2018 ranged from 63 notifications (July) to 139 notifications (August).

Figure 30. Salmonellosis monthly rate (annualised), 2018



In 2018, the number and rate of notifications were higher for males than for females. Hospitalisation rates were similar for both genders (Table 41).

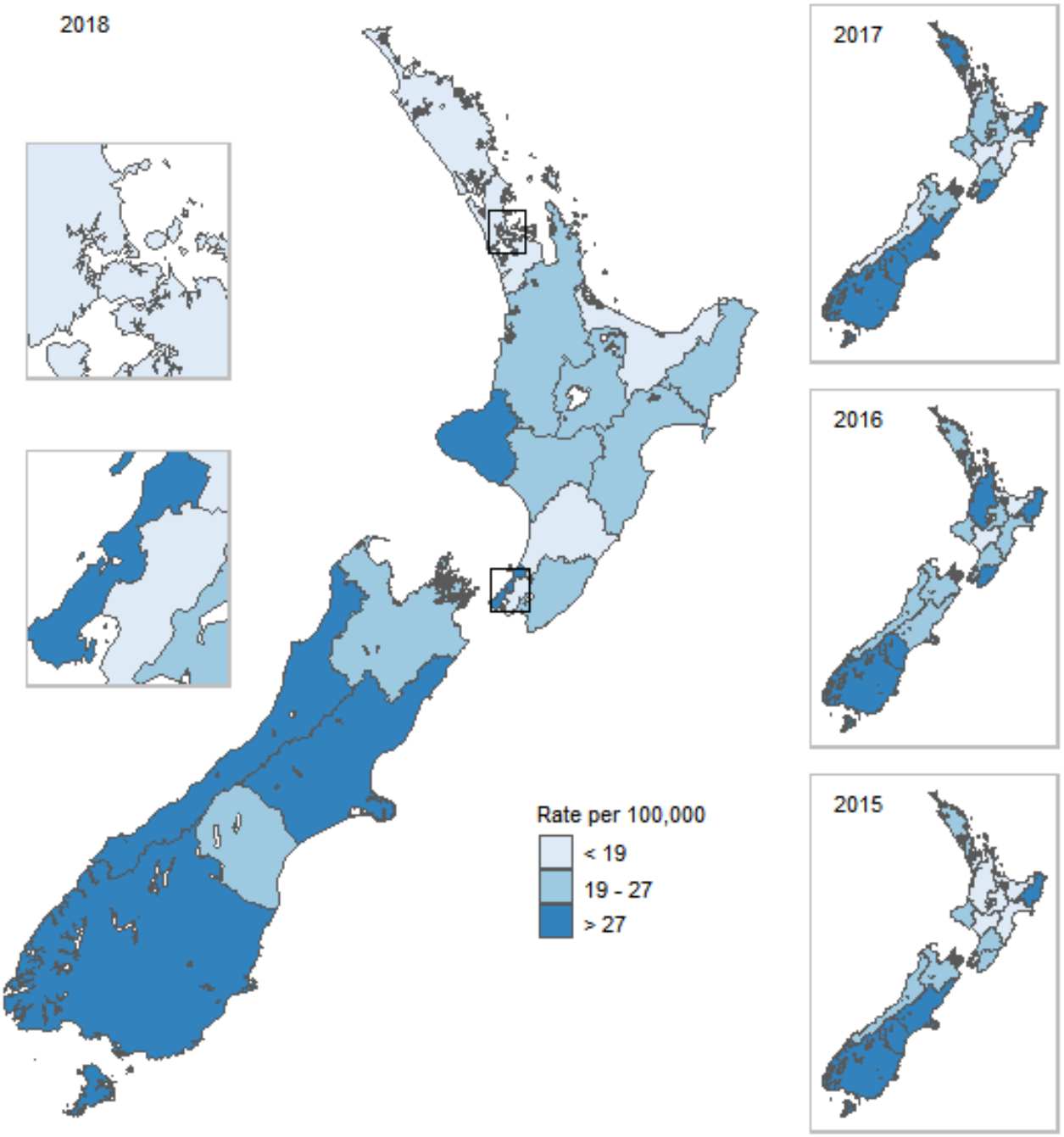
Table 41. Salmonellosis cases by sex, 2018

Sex	EpiSurv notifications		Hospitalisations[a]	
	No.	Rate[b]	No.	Rate[b]
Male	566	23.5	129	5.4
Female	533	21.5	131	5.3
Unknown	1	-	0	-
Total	**1100**	**22.5**	**260**	**5.3**

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

In 2018, rates of salmonellosis varied throughout the country as illustrated in Figure 31. The highest salmonellosis notification rate was reported for West Coast DHB (42.9 per 100,000, 14 cases), followed by Southern DHB (35.4 per 100,000, 117 cases), Taranaki (30.1 per 100,000 population, 36 cases), and Canterbury DHB (29.7 per 100,000 population, 167 cases). Southern DHB had consistently high salmonellosis notification rates between 2015 and 2018 compared to the rest of the country.

Figure 31. Geographic distribution of salmonellosis notifications, 2015–2018



Note: Changes in laboratory methods were introduced in Northland, Waitemata, Auckland and Counties Manukau DHBs (June 2015), Southern DHB (since January 2017) and Lakes DHB (January 2017 - June 2017), Capital & Coast, Hawke's Bay, Hutt Valley, Nelson & Marlborough, Wairarapa DHBs (January 2018) and Bay of Plenty, Lakes, and Waikato DHBs (November 2018). The new, more sensitive assays may have triggered an increase in notifications for some enteric diseases. Refer to text for details.

In 2018, notification rates and hospitalisation rates of salmonellosis were highest for infants aged less than 1 year (88.0 cases and 29.9 admissions per 100,000 population) (Table 42).

Table 42. Salmonellosis cases by age group, 2018

Age group	EpiSurv notifications		Hospitalisations[a]	
	No.	Rate[b]	No.	Rate[b]
<1	53	88.0	18	29.9
1 to 4	134	54.4	20	8.1
5 to 9	71	21.7	17	5.2
10 to 14	29	9.3	11	3.5
15 to 19	65	20.7	17	5.4
20 to 29	160	21.7	23	3.1
30 to 39	120	19.1	22	3.5
40 to 49	126	20.5	28	4.6
50 to 59	147	23.5	33	5.3
60 to 69	109	21.4	30	5.9
70+	86	16.9	41	8.1
Total	**1100**	**22.5**	**260**	**5.3**

[a] MoH NMDS data for hospital admissions.

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

For cases where information on travel was provided in 2018, 38.9% (95% CI 35.8–42.2%) 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 2018. The resultant distribution has a mean of 428 cases (95% CI 370–489).

If data from the last four years are considered the estimated proportion of cases travelling overseas within the incubation period of the organism is 34.0% (95% CI 32.5–35.6%).

Outbreaks reported as caused by *Salmonella*

In 2018, there were 14 *Salmonella* outbreaks reported, five of which (35.7%) with 17 associated cases were reported as foodborne (Table 43). 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.

Table 43. *Salmonella* outbreaks reported, 2018

Measure	Foodborne *Salmonella* spp. outbreaks	All *Salmonella* spp. outbreaks
Outbreaks	5	14
Cases	17	75
Hospitalised cases	1	4

Table 44 contains details of the five foodborne *Salmonella* outbreaks reported in 2018. For all outbreaks the evidence linking the outbreak to a suspected food vehicle was weak. No food samples relating to the outbreaks of salmonellosis in Table 44 were submitted to ESR's Public Health Laboratory.

Table 44. Details of foodborne *Salmonella* outbreaks, 2018

PHU	Month	Suspected vehicle	Exposure setting	Preparation setting	No. ill	Serotype[b]
Auckland	Jan	Unknown	-	-	8C, 0P	*S.* Typhimurium phage type RDNC
Toi Te Ora	Feb	Undercooked supermarket-purchased chicken prepared at home	Home	Home	1C, 1P	*S.* Bovismorbificans
South	Mar	Raw sea cucumber from Samoa	Home	Other setting	1C, 1P[a]	*S.* Weltevreden
Auckland	Jun	Unknown	Restaurant/cafe/ bakery	Restaurant/cafe/ bakery	2C, 0P	*S.* Typhimurium phage type 23
Auckland	Nov	Supermarket roast leg ham	Supermarket/ delicatessen	Supermarket/ delicatessen	2C, 1P	*S.* Typhimurium 195

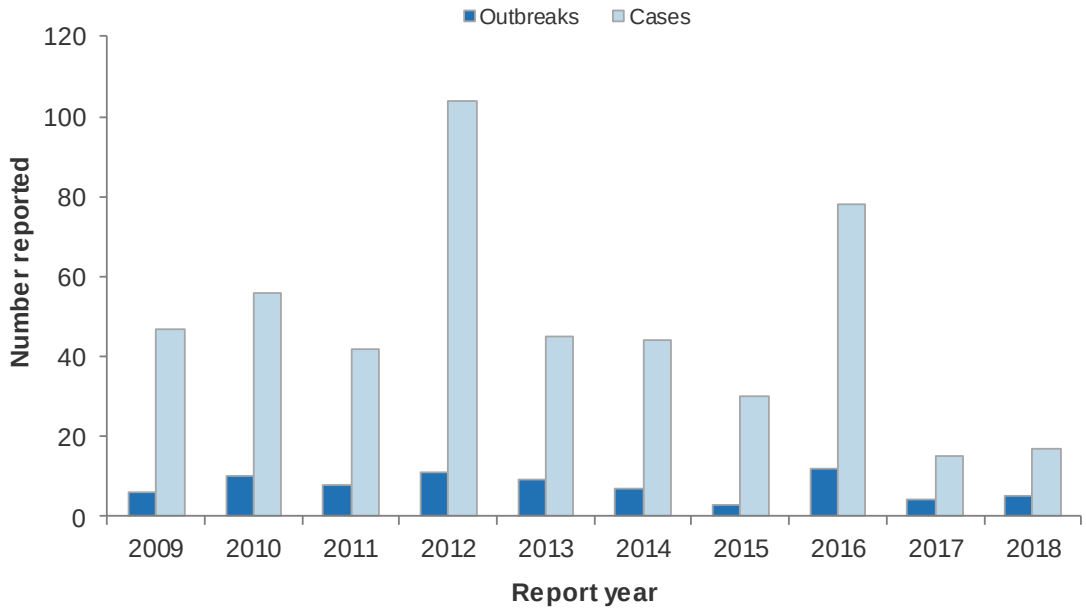
PHU: Public Health Unit, Auckland: Auckland Regional Public Health Service, South: Public Health South, Toi Te Ora: Toi Te Ora - Public Health, C: confirmed, P: probable.

[a] One case associated with this outbreak was hospitalised.

[b] Serotypes were identified in clinical samples from outbreak cases.

The number of foodborne *Salmonella* outbreaks reported between 2009 and 2018 ranged from three (2015) to 12 (2016) (Figure 32). The total number of cases associated with the outbreaks over the same period ranged between 15 (2017) and 104 (2012).

Figure 32. Foodborne *Salmonella* outbreaks and associated cases reported by year, 2009–2018



Salmonella types commonly reported

Human isolates

Isolates from 1134 cases infected with non-typhoidal *Salmonella* were typed by the ESR Enteric Reference Laboratory during 2018. Of these isolates, 345 (30.4%) were *Salmonella* serotype Typhimurium.

Table 45 shows the number of cases by *Salmonella* serotype reported by the Enteric Reference Laboratory at ESR. *S.* Typhimurium and *S.* Enteritidis were the most common serotypes identified in 2018, of which *S.* Typhimurium phage type 56 variant (prior to 2012 known as RDNC-May 06 (70 cases)), *S.* Typhimurium phage type 101 (61 cases) and *S.* Enteritidis phage type 11 (30 cases) were most commonly detected. Other serotypes most commonly reported were *S.* Bovismorbificans (83 cases) and *S.* Brandenburg (45 cases), with an annually increasing number of cases reported for *S.* Bovismorbificans since 2015.

Table 45. *Salmonella* case serotypes and subtypes identified by the Enteric Reference Laboratory, 2015–2018

Serotype[a]	2015	2016	2017	2018	% of cases with overseas travel history, 2018[b]	% of cases with unknown travel history, 2018[c]
S. Typhimurium	**447**	**389**	**429**	**345**	**11.9**	**22.1**
1	38	34	22	16	0.0	31.3
9	27	42	14	21	42.9	33.3
12a	18	6	7	7	0.0	42.9
42	24	12	27	13	0.0	15.4
56 variant	96	64	115	70	0.0	21.4
101	56	47	65	61	2.3	29.5
135	64	30	34	39	5.6	7.7
156	27	12	4	11	0.0	0.0
160	9	6	5	7	0.0	0.0
Other or unknown	88	136	136	100	29.5	22.8
S. Enteritidis	**110**	**114**	**151**	**130**	**57.4**	**16.9**
1b	4	8	7	14	91.7	14.3
11	45	46	55	30	0.0	26.7
Other or unknown	61	60	89	86	68.9	14.0
Other serotypes	**496**	**570**	**523**	**575**	**49.6**	**16.1**
S. Agona	12	18	16	27	75.0	11.1
S. Bovismorbificans	23	39	52	83	4.7	22.9
S. Brandenburg	52	67	54	45	5.1	13.3
S. Infantis	52	14	18	16	33.3	25.0
S. Mississippi	16	21	15	15	9.1	26.7
S. Montevideo	3	2	2	5	100.0	20.0
S. Saintpaul	37	35	27	39	39.4	15.4
S. Stanley	25	60	39	35	78.6	20.0
S. Thompson	32	13	12	10	14.3	30.0
S. Virchow	16	10	7	7	66.7	14.3
S. Weltevreden	18	18	21	21	63.2	9.5
S. enterica (I) ser. 4,[5],12 : i : -	22	23	28	26	78.3	11.5
Other or unknown	188	250	232	246	64.5	13.7
Total	**1053**	**1073**	**1103**	**1050**	**38.8**	**18.2**

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.

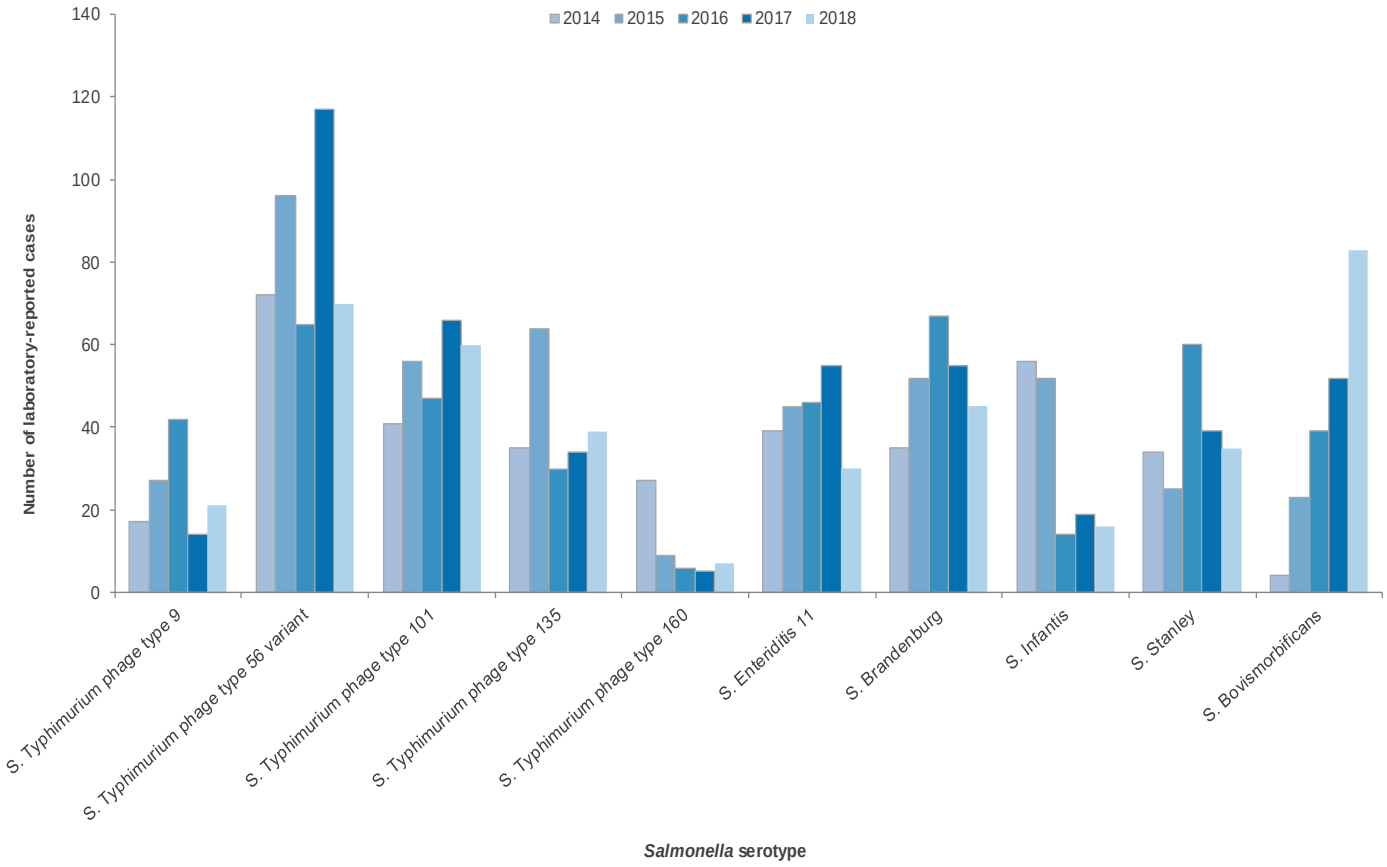
[b] Percentage refers to the number of cases that answered "yes" for overseas travelling during the incubation period out of the total number of cases for which travel information was recorded.

Note: Some of these cases might be travel-associated. 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.

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

Figure 33 shows the annual trend for selected *Salmonella* serotypes in recent years. The number of laboratory-reported cases of *S.* Typhimurium phage type 56 infection fluctuated between 2014 and 2018, with numbers remaining high relative to the other serotypes shown. There is an increasing number of cases serotyped as *S*. Bovismorbificans moving from 2014 to 2018.

Figure 33. Number of laboratory-reported cases for selected *Salmonella* serotypes by year, 2014–2018



Non-human isolates

A total of 848 non-human *Salmonella* isolates were typed by the Enteric Reference Laboratory during 2018. *S.* Typhimurium and *S.* Bovismorbificans were the most commonly isolated serotypes in non-human samples in 2018. *Salmonella* Typhimurium phage type 101 (62 isolates), phage type 56 variant (36 isolates) and phage type RDNC (35 isolates) were the most commonly detected phage types. The most common of the other serotypes were *S.* Bovismorbificans and *S.* Brandenburg with 297 and 106 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, 2014–2018

Serotype	2014	2015	2016	2017	2018	Major sources, 2018
S. Typhimurium	**220**	**258**	**249**	**372**	**282**	
1	13	16	14	19	9	Bovine (8)
9	9	9	12	20	28	Bovine (20), ovine (6)
12a	12	19	1	8	9	Bovine (8)
23	2	3	7	17	19	Bovine (19)
42	5	6	17	8	18	Bovine (12), equine (1), poultry environmental (3), poultry miscellaneous (2)
56 variant[a]	38	56	43	59	36	Feline (10), bovine (7), equine (5)
101	48	32	45	92	62	Bovine (49), canine (5)
108/170	10	3	21	34	3	Bovine (2)
135	12	18	10	11	25	Bovine (21)
RDNC	16	41	31	42	35	Bovine (30)
Unknown or other	65	58	69	62	38	
Other serotypes	**509**	**379**	**435**	**600**	**566**	
S. Agona	17	22	10	17	18	Bovine (13)
S. Anatum	23	6	9	12	5	Bovine (2), poultry environmental (2)
S. Bovismorbificans	13	71	135	292	297	Bovine (271), canine (7), feline (6)
S. Brandenburg	129	102	127	137	106	Bovine (80), ovine (15), food[b] (5)
S. Hindmarsh	77	49	48	27	26	Ovine (24), bovine (1)
S. Infantis	27	14	20	26	8	Bovine (2), canine (2), food[b] (2)
S. Mbandaka	20	10	6	9	4	Bovine (2)
S. Ruiru	8	3	1	8	16	Bovine (9), environmental (5), meat/bone meal (2)
S. Saintpaul	22	12	9	12	12	Avian (5), bovine (4)
S. Senftenberg	19	15	4	9	8	Bovine (3)
S. Stanley	-	-	2	4	14	Bovine (12), equine (1), poultry environmental (1)
Other or unknown serotypes	154	75	64	36	52	
Total	**729**	**637**	**684**	**972**	**848**	

[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

Recent surveys

Nil.

Relevant New Zealand studies and publications

Nil.

Relevant regulatory developments

New Zealand Food Safety published an Animal Products Notice entitled *Specifications for National Microbiological Database Programme* in February 2018 [19]. The Notice includes details of sampling, analysis and assessment for *Salmonella* in meat chickens and red meat species, including bobby calf, bovine, caprine and ratite species.

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 2018 by data source

In 2018, two individual cases of sapovirus infection were reported in EpiSurv (0.04 per 100,000 population). It should be noted that not every case of sapovirus infection is 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 2018, none of the three sapovirus outbreaks was reported as potentially foodborne (Table 47). 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.

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.

Table 47. Sapovirus outbreaks reported, 2018

Measure	Foodborne sapovirus outbreaks	All sapovirus outbreaks
Outbreaks	0	3
Cases	0	44
Hospitalised cases	0	0

There have been no foodborne outbreaks due to sapovirus infection in the last two 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 2018 are given in Table 48.

Table 48. Summary of surveillance data for shigellosis, 2018

Parameter	Value in 2018	Source
Number of notified cases	219	EpiSurv
Notification rate (per 100,000)	4.5	EpiSurv
Hospitalisations[a]	59	MoH NMDS
Deaths	0	EpiSurv
Estimated travel-related cases (%)[b]	145 (66.3%)	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 screeing 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 several laboratories across New Zealand changed the methodology for testing faecal specimens. All community faecal specimens in Northland, Waitemata, Auckland and Counties Manukau DHBs (June 2015), Southern DHB (January 2017), Lakes DHB (January 2017–June 2017), Capital & Coast, Hawke's Bay, Hutt Valley, Nelson & Marlborough, Wairarapa DHBs (January 2018) and Bay of Plenty, Lakes, and Waikato DHBs (November 2018) 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 as there are marked differences between the sensitivity of CIDT compared with traditional culture-based methodology.

Shigellosis cases reported in 2018 by data source

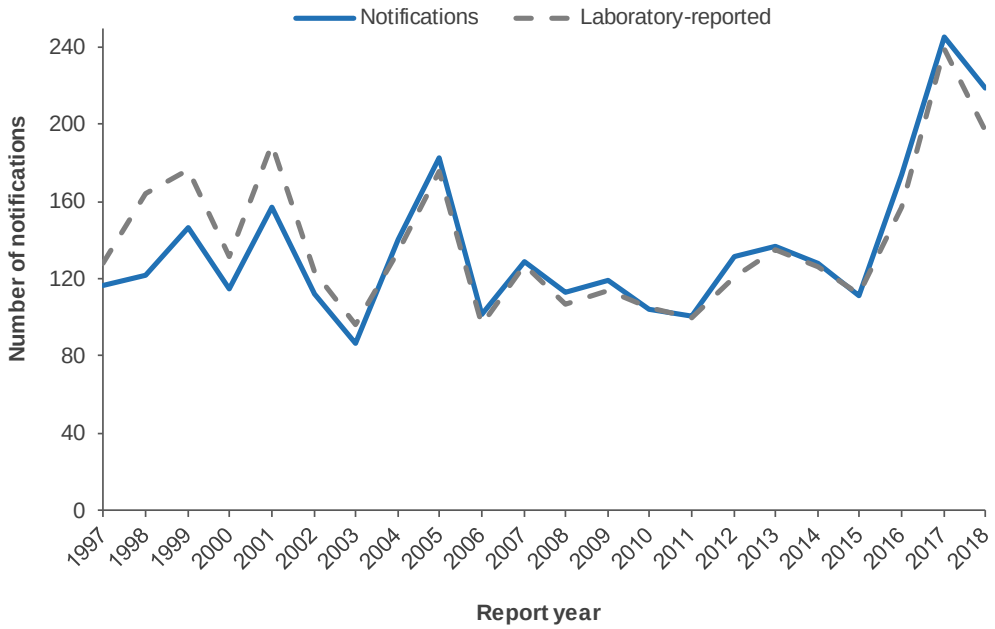
In 2018, 219 cases (4.5 per 100,000 population) of shigellosis and no resulting deaths were reported in EpiSurv. Approximately 24% of cases notified in EpiSurv were hospitalised in 2018. The Enteric Reference Laboratory at ESR reported 197 cases (4.0 per 100,000 population) infected with *Shigella* in 2018.

The ICD-10 code A03 was used to extract shigellosis hospitalisation data from the MoH NMDS database. Of the 59 hospital admissions (1.2 admissions per 100,000 population) recorded in 2018, 37 were reported with shigellosis as the principal diagnosis and 22 with shigellosis as another relevant diagnosis.

Notifiable disease data

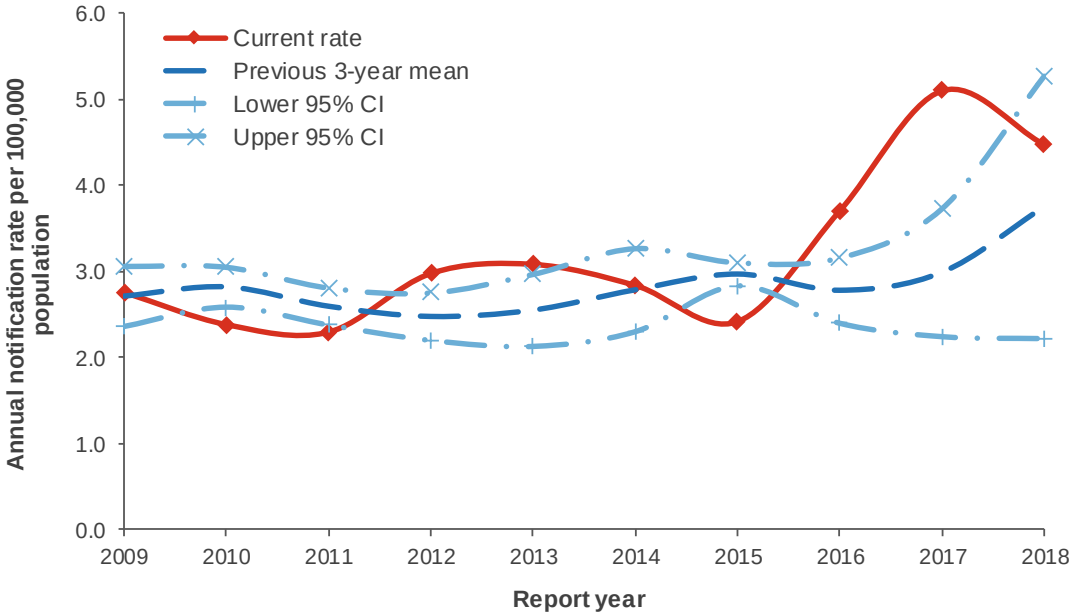
The number of notifications and laboratory reported cases of shigellosis was variable from year to year with the highest number of notifications in 2017 (245), followed by the the second highest number of notifications in 2018 (219 cases). Between 2006 and 2015 the number of notifications has been in the range of 101 to 137 cases (Figure 34).

Figure 34. Shigellosis notifications and laboratory-reported cases by year, 1997–2018



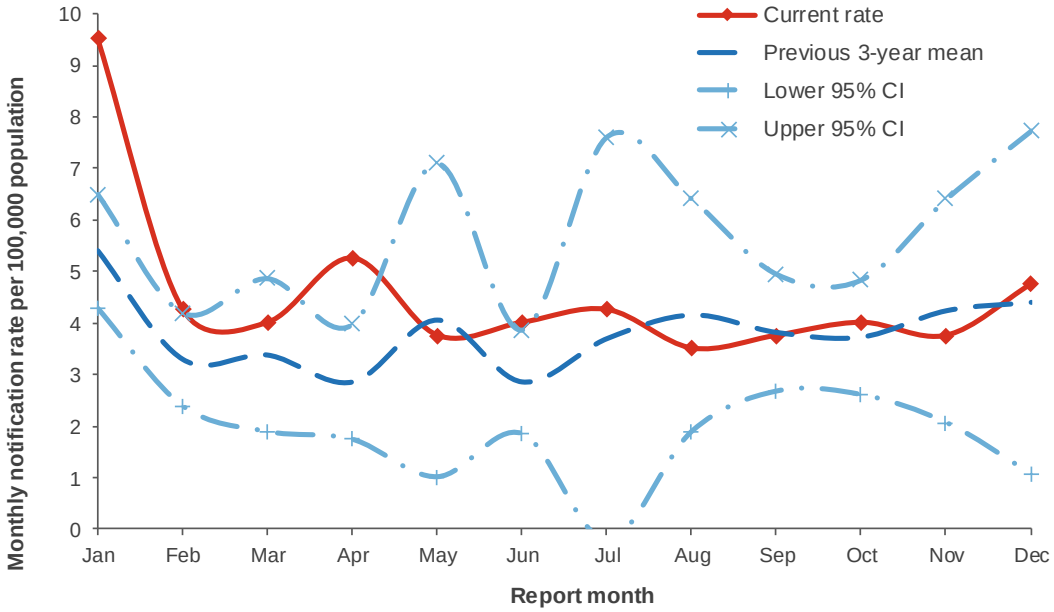
Between 2009 and 2015, the shigellosis notification rate has consistently been in the range of 2.3 to 3.1 notifications per 100,000 population (Figure 35). Higher rates have been noted in 2016 (3.7 per 100,000 population), 2017 (5.1 per 100,000 population) and 2018 (4.5 per 100,000 population). The notification rate in 2018 was higher than the previous three-year average (3.7 cases per 100,000).

Figure 35. Shigellosis notification rate by year, 2009–2018



The number of notified cases of shigellosis per 100,000 population by month for 2018 is shown in Figure 36. In 2018, the shigellosis notification rate peaked in January compared to the following months and the three previous years January rates. However, the number of notifications per month was small, ranging from 14 in August and June to 38 in January

Figure 36. Shigellosis monthly rate (annualised), 2018



In 2018, the rates for notification and hospitalisation were higher for males (4.8 and 1.4 per 100,000 population, respectively) compared to females (4.2 and 1.1 per 100,000, respectively) (Table 49).

Table 49. Shigellosis cases by sex, 2018

Sex	EpiSurv notifications		Hospitalisations[a]	
	No.	Rate[b]	No.	Rate[b]
Male	115	4.8	33	1.4
Female	104	4.2	26	1.1
Total	**219**	**4.5**	**59**	**1.2**

[a] MoH NMDS data for hospital admissions.

[b] per 100,000 of population.

Shigellosis notification rates were highest for those in the 1 to 4 years of age-group (9.34 per 100,000 population, 23 cases). The number of hospitalisations was highest in the 60 to 69 years and 70+ years age groups (Table 50).

Table 50. Shigellosis cases by age group, 2018

Age group	EpiSurv notifications		Hospitalisations[a]	
	No.	Rate[b]	No.	Rate[b]
<1	1	-	1	-
1 to 4	23	9.3	4	-
5 to 9	12	3.7	5	1.5
10 to 14	7	2.3	0	-
15 to 19	8	2.5	3	-
20 to 29	39	5.3	2	-
30 to 39	28	4.5	7	1.1
40 to 49	25	4.1	4	-
50 to 59	29	4.6	7	1.1
60 to 69	26	5.1	12	2.4
70+	21	4.1	14	2.7
Total	**219**	**4.5**	**59**	**1.2**

[a] MoH NMDS data for hospital admissions.

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

For cases where information on travel was provided in 2018, 66.3% (95% CI 59.4–72.8%) 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 2018. The resultant distribution has a mean of 145 cases (95% CI 112–181).

If data from the last four years are considered the estimated proportion of cases travelling overseas within the incubation period of the organism is 60.6% (95% CI 56.9–64.2%).

Outbreaks reported as caused by *Shigella* spp.

In 2018, there were seven *Shigella* spp. outbreaks, one of which was reported to be foodborne (Table 51). 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. There was no hospitalisation due to a foodborne *Shigella* spp. associated outbreak.

Table 51. *Shigella* spp. outbreaks reported, 2018

Measure	Foodborne *Shigella* spp. outbreaks	All *Shigella* spp. outbreaks
Outbreaks	1	7
Cases	3	36
Hospitalised cases	0	5

Table 52 contains details of the single foodborne *Shigella* spp. outbreak reported in 2018. The suspected food vehicle was unknown, but was suspected to be from food eaten overseas. No clinical or food samples relating to this outbreak were submitted to ESR's Public Health Laboratory.

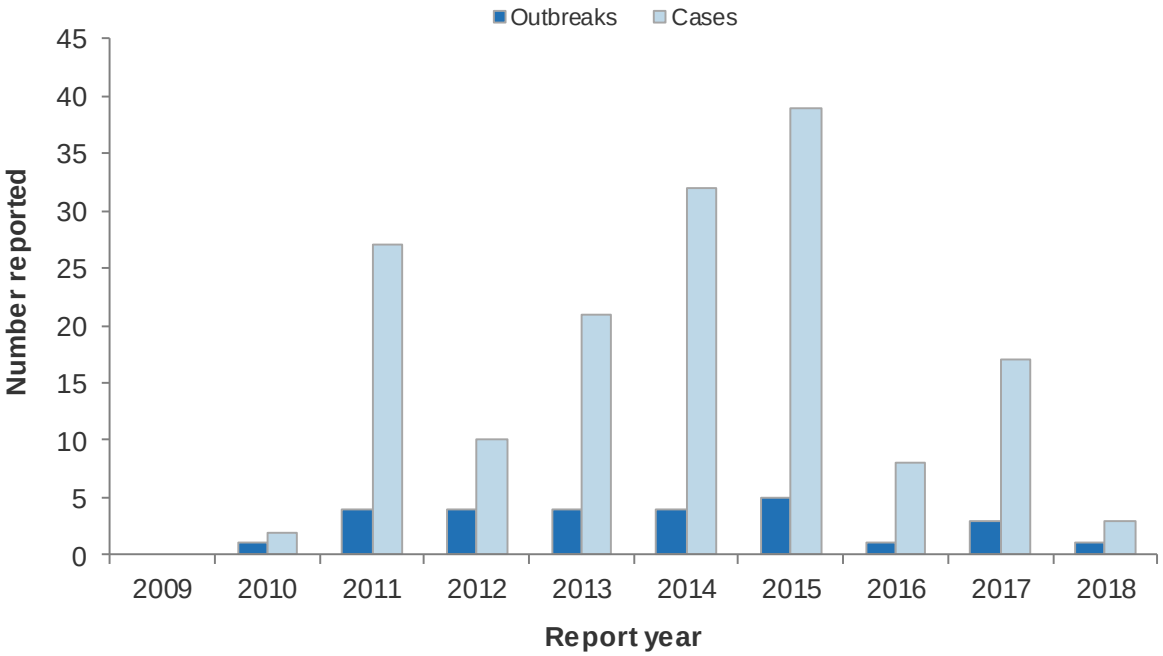
Table 52. Details of foodborne *Shigella* spp. outbreaks, 2018

PHU	Month	Suspected vehicle	Exposure setting	Preparation setting	No. ill
Auckland	Nov	unknown	Other setting (overseas - Tonga)	Unknown	3C, 0P

PHU: Public Health Unit, Auckland: Auckland Regional Public Health Service, C: confirmed, P: probable.

The number of foodborne shigellosis outbreaks has ranged between zero and five outbreaks each year in the ten year period 2009–2018, with between two and 39 associated cases (Figure 37).

Figure 37. Foodborne *Shigella* spp. outbreaks and associated cases reported by year, 2009–2018



Shigella types commonly reported

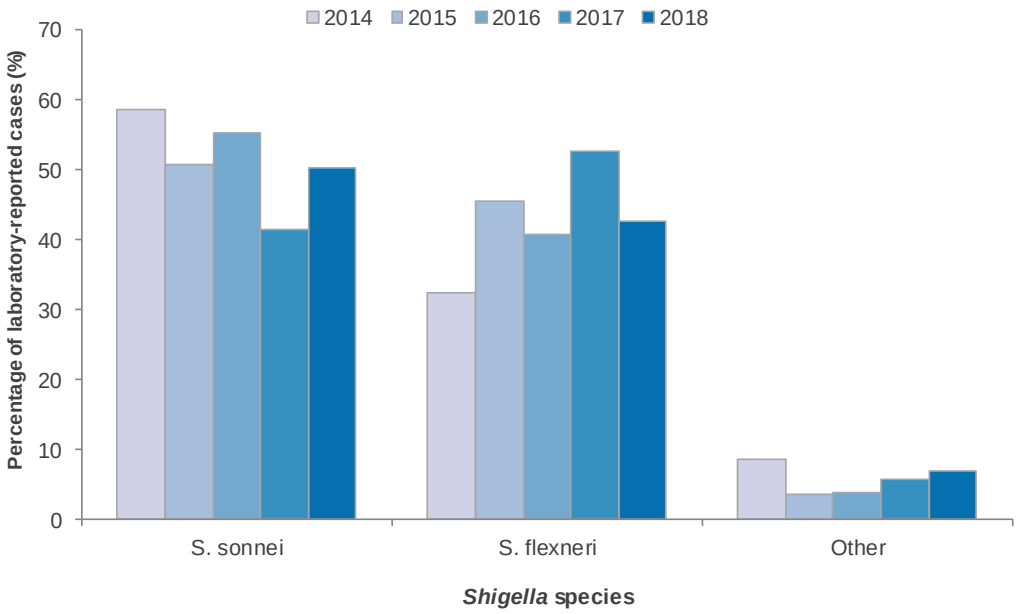
In 2018, isolates from 197 cases infected with *Shigella* spp. were typed by the Enteric Reference Laboratory at ESR. *S. sonnei* and *S. flexneri* were the species most often identified. Of these, *S. sonnei* biotype g was most common in 2018 (Table 53).

Table 53. *Shigella* species and subtypes identified by the Enteric Reference Laboratory, 2014–2018

Species	2014	2015	2016	2017	2018
S. sonnei	**74**	**57**	**87**	**99**	**99**
biotype a	32	20	31	30	37
biotype f	6	0	1	1	1
biotype g	36	37	55	68	61
S. flexneri	**41**	**51**	**64**	**126**	**84**
1	7	8	21	42	45
2a	11	14	18	18	15
2b	6	6	4	7	1
3a	4	7	1	5	3
Other	13	16	20	57	20
Other	**11**	**4**	**6**	**14**	**14**
S. boydii	9	4	3	13	10
S. dysenteriae	1	0	2	1	4
Shigella species not identified	1	0	1	0	0
Total	**126**	**112**	**157**	**239**	**197**

The percentage of shigellosis cases infected with *S. sonnei* in 2018 (50.3%) was within the range of values observed between 2014 and 2017 (between 41.4% and 58.7%). The percentage of shigellosis cases with *S. flexneri* in 2018 (42.6%) was also within the range of values observed between 2014 and 2017 (between 32.5% and 52.7%) (Figure 38).

Figure 38. Percentage of laboratory-reported cases by *Shigella* species and year, 2014–2018



Recent surveys

Nil.

Relevant New Zealand studies and publications

Nil.

Relevant regulatory developments

Nil.

Staphylococcus aureus intoxication

Case definition

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

Staphylococcus aureus intoxication cases reported in 2018 by data source

During 2018, there were no notifications of *S. aureus* intoxication 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. In 2018, there was one hospital admission recorded with *S. aureus* intoxication recorded as the principal diagnosis, which was female.

Outbreaks reported as caused by *Staphylococcus aureus*

In 2018, one foodborne *S. aureus* outbreak was reported with nine associated cases (Table 54). 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.

Table 54. *S. aureus* outbreaks reported, 2018

Measure	Foodborne *S. aureus* outbreaks	All *S. aureus* outbreaks
Outbreaks	1	1
Cases	9	9
Hospitalised cases	0	0

Table 55 contains details of the foodborne *S. aureus* outbreak reported in 2018. The specific food vehicle was unknown. No clinical or food samples relating to this outbreak were submitted to ESR's Public Health Laboratory.

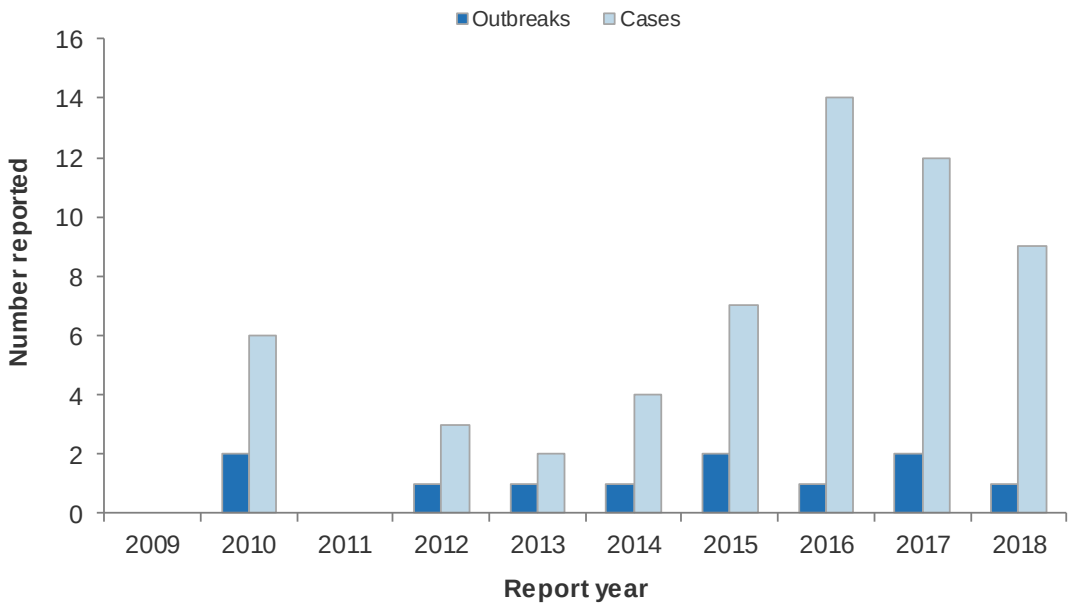
Table 55. Details of foodborne *S. aureus* outbreak, 2018

PHU	Month	Suspected vehicle	Exposure setting	Preparation setting	No. ill
C and PH	Jun	Unknown	Restaurant/cafe/bakery	Restaurant/cafe/bakery	8C, 1P

PHU: Public Health Unit, C and PH: Community and Public Health, C: confirmed, P: probable.

The number of foodborne outbreaks associated with *S. aureus* reported each year between 2009 and 2018 ranged from zero to two (Figure 39), with between two and 14 associated cases.

Figure 39. Foodborne *S. aureus* outbreaks and associated cases reported by year, 2009–2018



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 2018

During 2018, three cases (0.06 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.

All three cases were adults aged between 20 and 49 years and had eaten recreationally collected seafood. Two cases were male and one female. Cases were reported from Waikato, Bay of Plenty and Nelson Marlborough DHBs. Two cases were of Māori ethnicity and one was European or Other. In EpiSurv, two cases were 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. A total of 12 hospital admissions (0.2 admissions per 100,000 population) were reported in 2018, eight of which were reported with 'other fish and shellfish poisoning' as the primary diagnosis and four as another relevant diagnosis. Note that this ICD-10 code includes shellfish and other fish. It should be noted that EpiSurv and the MoH NMDS database are separate systems and hospital admission can occur without cases being notified.

Outbreaks reported as caused by toxic shellfish poisoning

In 2018, no toxic shellfish poisoning outbreaks were reported in which cases had symptoms consistent with PSP. It should be noted that all toxic shellfish poisoning outbreaks are categorised as foodborne, as consumption of contaminated shellfish is the only currently recognised transmission route for this disease.

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

Recent surveys

Nil.

Relevant New Zealand studies and publications

Nil.

Relevant regulatory developments

Nil

VTEC/STEC infection

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

Summary data for STEC infection in 2018 are given in Table 56.

Table 56. Summary of surveillance data for STEC infection, 2018

Parameter	Value in 2018	Source
Number of notified cases	925	EpiSurv
Notification rate (per 100,000)	18.9	EpiSurv
Hospitalisations[a]	41	MoH NMDS
Deaths	2	EpiSurv
Estimated travel-related cases (%)[b]	135 (14.6%)	EpiSurv
Estimated food-related cases (%)[c]	236 (29.9%)	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 O157 STEC, the dominant serotype, has been used to estimate the number of food-related cases.

Case definition

Clinical description: Diarrhoea resulting from infection with STEC may range from mild, watery and non-bloody to almost pure bloody diarrhoea with abdominal cramping. The disease is distinguishable from other causes of gastroenteritis by its high incidence of bloody diarrhoea (profuse rectal bleeding without fever sometimes clouds the diagnosis), severity (approximately 40% of cases are hospitalised) and frequency of complications. Haemolytic uraemic syndrome (HUS) complicates 8–10% of STEC infections in children; this syndrome includes haemolytic anaemia, thrombocytopenia and acute renal failure. Of children with HUS, 12–30% will have severe sequelae, including renal and cerebral impairment. Elderly patients with STEC infections may suffer thrombotic thrombocytopenic purpura (TTP), which is similar to HUS but with greater neurological involvement.

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.

Confirmed A clinically compatible illness that is laboratory confirmed.

Terminology

In 2016, a joint FAO/WHO consultation on STEC reviewed 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" [26].

Changes to laboratory methods since 2015

Since 2015 several laboratories across New Zealand changed the methodology for testing faecal specimens. All community faecal specimens in Northland, Waitemata, Auckland and Counties Manukau DHBs (June 2015), Southern DHB (January 2017), Lakes DHB (January 2017–June 2017), Capital & Coast, Hawke's Bay, Hutt Valley, Nelson & Marlborough, Wairarapa DHBs (January 2018) and Bay of Plenty, Lakes, and Waikato DHBs (November 2018) were screened by multiplex PCR for a range of pathogens, including STEC. Prior to the change in methodology only faecal samples with blood, or those from under 5-year-olds were tested for STEC infection. It is likely that laboratory changes have affected the notification rates for STEC infection.

STEC infection cases reported in 2018 by data source

During 2018, 925 cases (18.9 per 100,000 population) of STEC infection and 2 resulting deaths were reported in EpiSurv. Approximately 20% of cases notified in EpiSurv were hospitalised in 2018. The Enteric Reference Laboratory at ESR reported 632 cases (12.9 per 100,000) infected with STEC in 2018.

The ICD-10 code A04.3 was used to extract enterohaemorrhagic *E. coli* infection hospitalisation data from the MoH NMDS database. Of the 41 hospital admissions (0.8 admissions per 100,000 population) recorded in 2018, 19 were reported with enterohaemorrhagic *E. coli* infection as the principal diagnosis and 22 with enterohaemorrhagic *E. coli* infection as another relevant diagnosis.

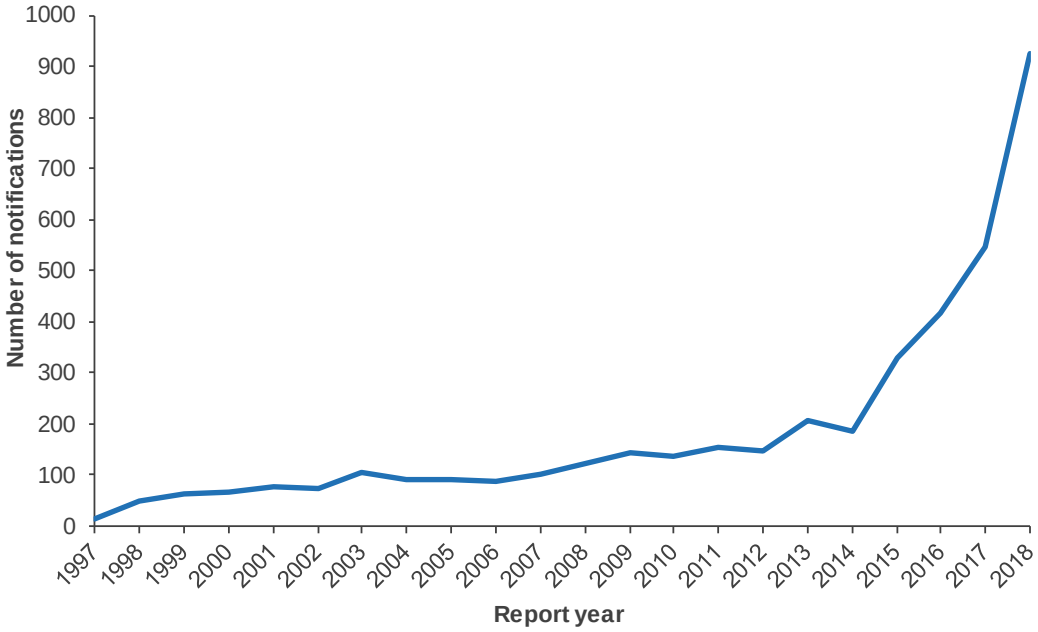
It has been estimated by expert consultation that 29.9% (95th percentile credible interval; 3.5% to 60.7%) of O157 STEC incidence and 34.0% (95th percentile credible interval: 3.5% to 63.5%) of non-O157 incidence is due to foodborne transmission. The expert consultation also estimated that approximately 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 increase since 2015 (Figure 40).

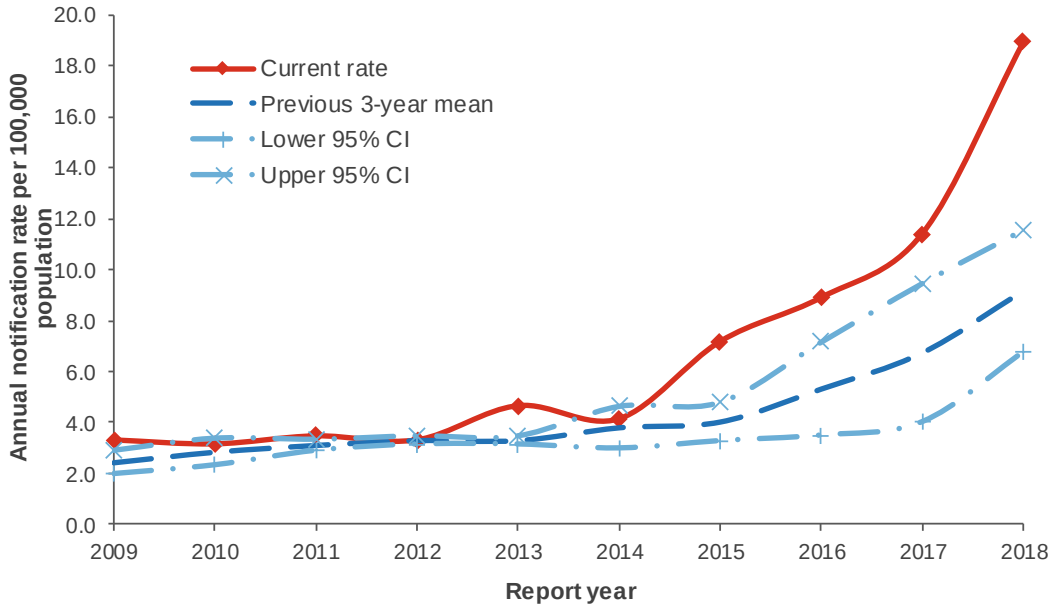
[*] In NZ, however, no outbreaks of STEC have been conclusively linked to consumption of red meat.

Figure 40. STEC infection notifications by year, 1997–2018



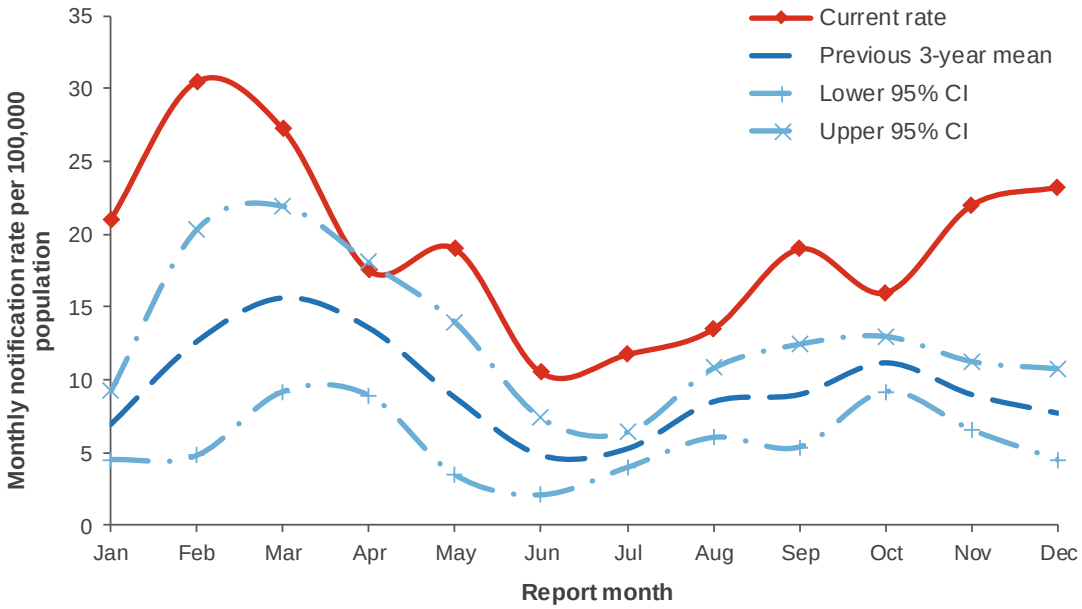
Between 2009 and 2014, the notification rate of STEC infection has been in the range of 3.2 to 4.7 notifications per 100,000 population (Figure 41), with increasing rates noted every year since 2015. The notification rate in 2018 (18.9 cases per 100,000 population) was about twice as high as the previous three-year average (9.2 cases per 100,000).

Figure 41. STEC infection notification rate by year, 2009–2018



The number of notified cases of STEC infection per 100,000 population by month for 2018 are shown in Figure 42. In 2018, monthly notification rates were generally higher compared to the previous three-year mean monthly rates. The monthly number of notifications in 2018 ranged from 42 notifications (June) to 122 notifications (February). The trend in monthly notification rates in 2018 was similar to recent years (2015-2017) with a small increase in spring, and a high peak from January to March.

Figure 42. STEC infection monthly rate (annualised), 2018



In 2018 notification rates were slightly higher for females than males (19.7 and 18.1 notifications per 100,000 population, respectively), however, hospitalisations were slightly higher for males (1.0 admissions per 100,000) compared to females (0.6 admissions per 100,000) (Table 57).

Table 57. STEC infection cases by sex, 2018

Sex	EpiSurv notifications		Hospitalisations[a]	
	No.	Rate[b]	No.	Rate[b]
Male	437	18.1	25	1.0
Female	488	19.7	16	0.6
Total	**925**	**18.9**	**41**	**0.8**

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

In 2018, the STEC infection notification rate was highest for the less than 1 year age group (69.7 per 100,000 population, 42 cases) and the 1 to 4 years age group (54.4 per 100,000, 134 cases). The number of hospitalisations was highest in the 70+ age group and ranged between zero and six in all other age groups (Table 58).

Table 58. STEC infection cases by age group, 2018

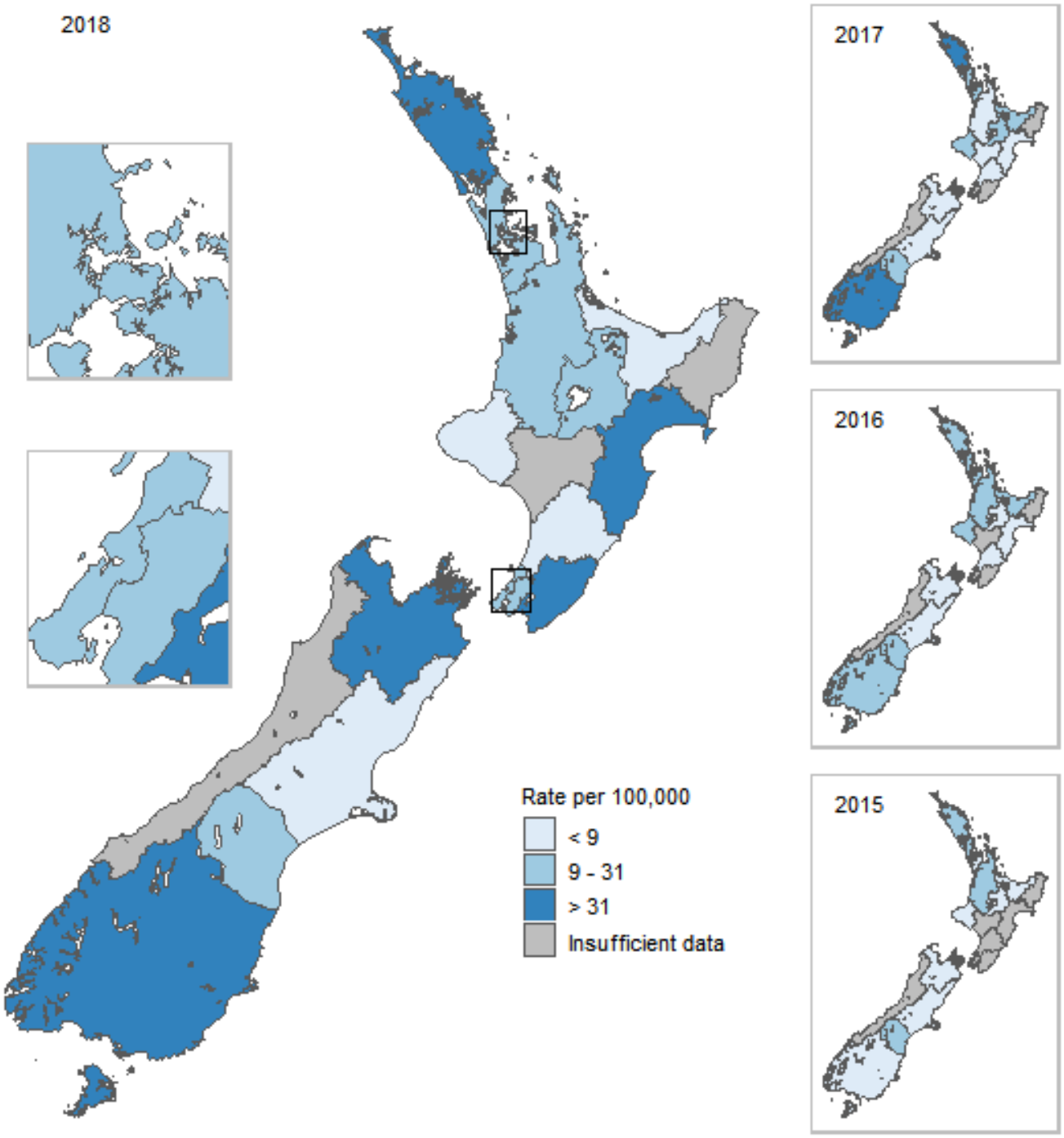
Age group (years)	EpiSurv notifications		Hospitalisations[a]	
	No.	Rate[b]	No.	Rate[b]
<1	42	69.7	0	-
1 to 4	134	54.4	6	2.4
5 to 9	49	15.0	2	-
10 to 14	42	13.5	4	-
15 to 19	47	15.0	1	-
20 to 29	103	14.0	1	-
30 to 39	79	12.6	1	-
40 to 49	78	12.7	2	-
50 to 59	89	14.2	3	-
60 to 69	110	21.6	6	1.2
70+	152	29.8	15	2.9
Total	**925**	**18.9**	**41**	**0.8**

[a] MoH NMDS data for hospital admissions (IDC-10 Code: A04.3).

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

Rates of STEC infection varied throughout the country as illustrated in Figure 43. In 2018, the highest rates of STEC infection were reported for the DHBs Southern (65.1 per 100,000, 215 cases) and Wairarapa (61.5 per 100,000, 28 cases), followed by Nelson Marlborough DHB (43.8 per 100,000, 66 cases) and Northland DHB (38.0 per 100,000, 68 cases). Note that rates were not calculated for three DHBs where there were insufficient (less than five) cases notified in 2018.

Figure 43. Geographic distribution of STEC infection notifications, 2015–2018



Note: Changes in laboratory methods were introduced in Northland, Waitemata, Auckland and Counties Manukau DHBs (June 2015), Southern DHB (since January 2017) and Lakes DHB (January 2017 - June 2017), Capital & Coast, Hawke's Bay, Hutt Valley, Nelson & Marlborough, Wairarapa DHBs (January 2018) and Bay of Plenty, Lakes, and Waikato DHBs (November 2018). The new, more sensitive assays may have triggered an increase in notifications for some enteric diseases. Refer to text for details.

For cases where information on travel was provided in 2018, 14.6% (95% CI 12.2–17.2%) had travelled overseas during the incubation period. Assuming that the cases for which travel information was provided were representative of all STEC infection cases, a Poisson distribution can be used to estimate the total number of potentially travel-related cases of STEC infection in 2018. The resultant distribution has a mean of 135 cases (95% CI 104–170).

If data from the last four years are considered the estimated proportion of cases travelling overseas within the incubation period of the organism is 11.5% (95% CI 10.1–13.0%).

Outbreaks reported as caused by STEC

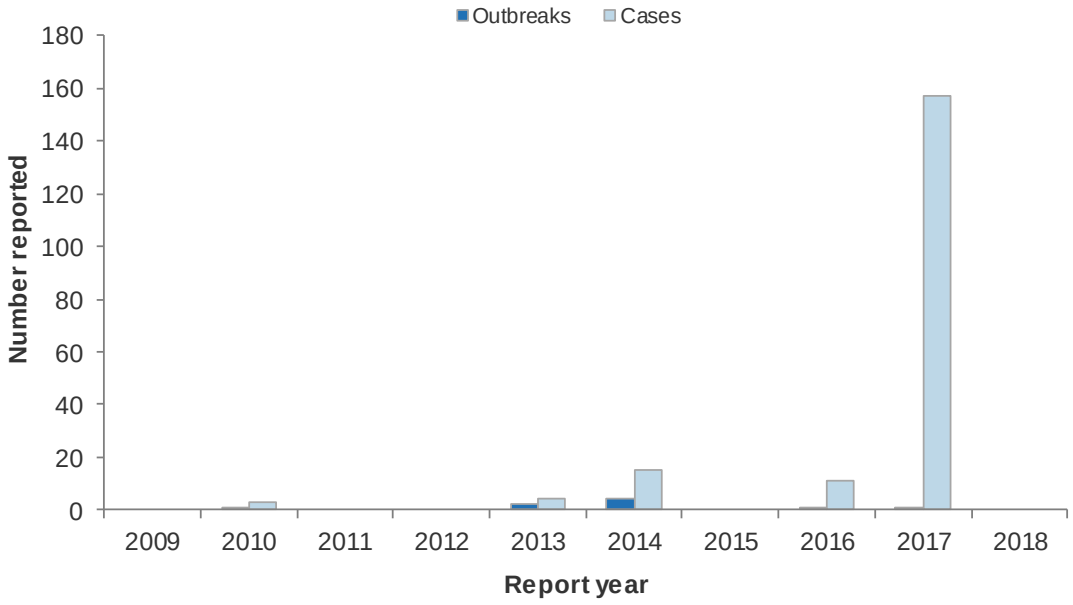
Of the 15 outbreaks (57 cases) of STEC infection during 2018, no outbreak was classed as foodborne (Table 59). An outbreak is classed as foodborne in this report if food was recorded as one of the likely modes of transmission applicable to the outbreak. It is important to note that a single outbreak may have multiple pathogens, modes of transmission, settings where exposure occurred, or settings where preparation of food was conducted.

Table 59. STEC outbreaks reported, 2018

Measure	Foodborne STEC outbreaks	All STEC outbreaks
Outbreaks	0	15
Cases	0	57
Hospitalised cases	0	1

The number of foodborne STEC outbreaks reported between 2009 and 2018 ranged from one to four per year, with no outbreaks reported for five of the ten years (Figure 44). 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 44. Foodborne STEC outbreaks and associated cases reported by year, 2009–2018



STEC types commonly reported

In 2018, a total of 632 cases infected with STEC were reported by the ESR Enteric Reference Laboratory in 2018. Of these, 194 (30.7%) isolates were identified as *E. coli* O157:H7, 376 (59.5%) as non-O157 and for 62 (9.8%) isolates the serotype was not identified.

Of the 376 non-O157 isolates, 76 were typed as O26:H11, 27 as ONT:HNM and 22 as O128:H2 (Table 60). The percentage of non-O157 STEC cases has been increasing every year since 2014 (10.9%, 2015: 29.5%, 2016: 36.9%, 2017: 42.8%, 2018: 59.5%) possibly due to changes in laboratory methods and the screening of all submitted faecal samples for STEC infection (Figure 45).

Figure 45. Number of *E. coli* O157 and non-O157 laboratory-reported cases by year, 2014–2018

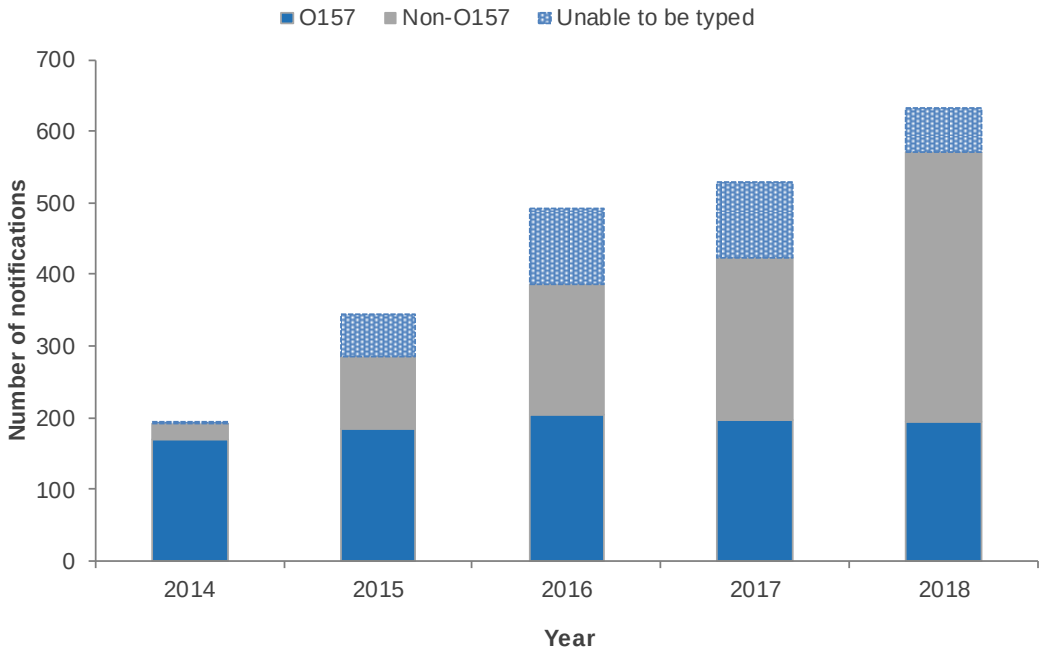


Table 60. STEC subtypes identified by the Enteric Reference Laboratory, 2014–2018

Serotype	2014	2015	2016	2017	2018
O157	**170**	**183**	**205**	**196**	**194**
O157:H7	170	183	205	196	194
Non-O157	**21**	**101**	**181**	**226**	**376**
O103:H2	-	2	2	3	7
O103:H25	-	2	1	1	4
O111:HNM	-	-	1	2	3
O123/O186:HNM	-	-	-	1	13
O128:H2	-	4	25	6	22
O128:HNM	-	1	5	1	6
O146:H21	1	2	4	13	17
O146:HNM	-	-	-	3	2
O153:H2	-	4	2	-	3
O174:H8	-	1	-	1	4
O174:HNM	-	1	1	-	3
O176:HNM	3	10	2	4	9
O186:HNM	-	-	-	4	-
O188:H14	-	-	-	-	5
O26:H11	1	14	46	44	76
O26:HNM	-	-	5	4	1
O38:H26	2	5	10	7	19
O5:HNM	-	-	4	1	4
O64:H20	-	-	3	2	4
O84:HNM	-	-	2	6	2
O91:HNM	-	5	2	2	5
ONT:H2	1	9	3	22	17
ONT:H21	-	-	1	4	4
ONT:H26	-	-	-	4	-
ONT:H7	-	-	3	7	6
ONT:HNM	2	10	6	9	27
ONT:HNT	-	1	2	4	3
ORough:H2	-	1	6	4	7
ORough:HNM	-	3	2	8	10
ORough:HNT	-	-	-	1	3
Other types[a]	11	26	43	58	90
Unable to be typed	**2**	**59**	**105**	**106**	**62**
Total	**193**	**343**	**491**	**528**	**632**

a Case isolates not listed in table, single isolates unless indicated otherwise. NM: Non-Motile, NT: Non-Typable

2014: O108:H25, O182:HNM (two cases), O6:H7, O26:HNM (two cases), O68:HNM (two cases), O84:H2, ONT:H6, ONT:H21

2015: O112:H8, O117:H7 (two cases), O130:H11, O145:HNM, O149:H18, O163:H19, O177:HNM, O178:H7, O179:H8, O183:H18, O186:H10, O38:HNM, O55:HNT, O8:H28, O80:HNM, O84:H2, O91:H21, ONT:H8 (two cases), ONT:H11 (two cases), ONT:H26, ONT:H49, ORough:H16, ORough:H7

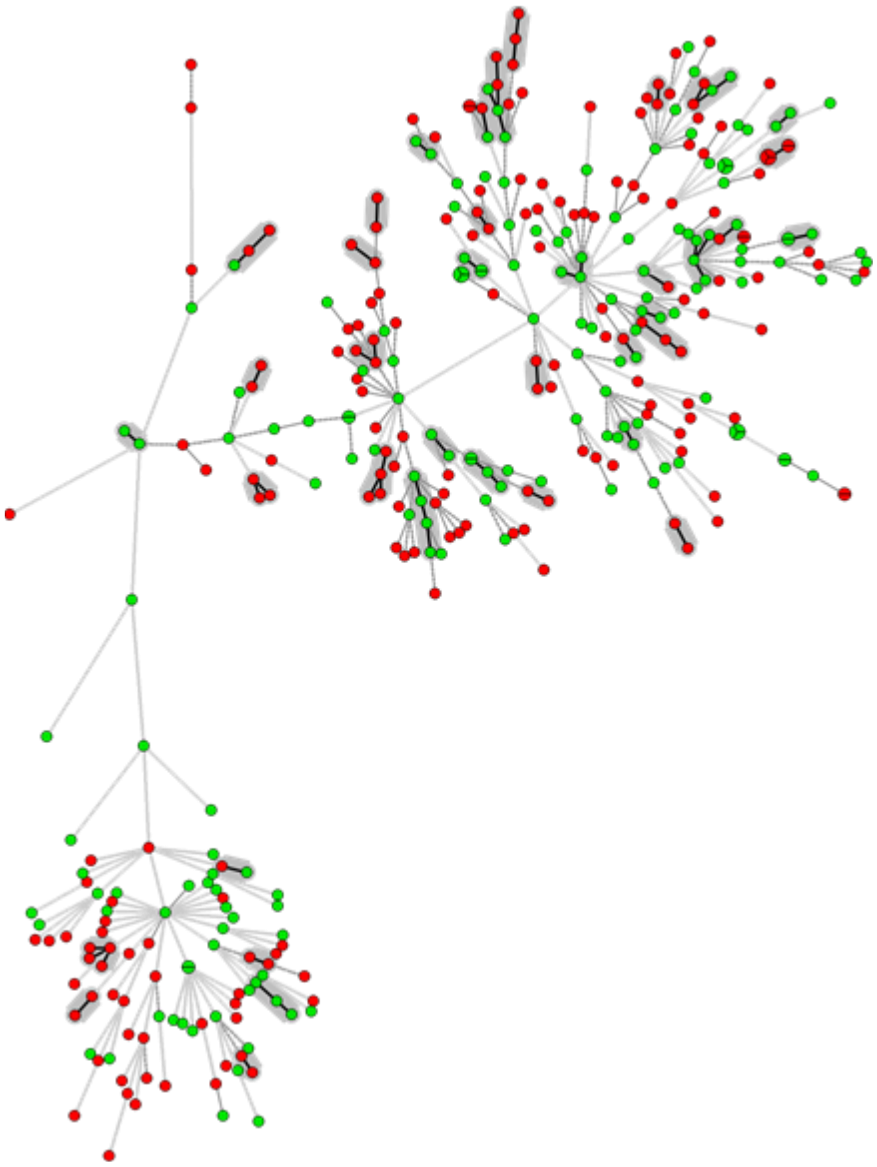
2016: O101:H2, O101:HNM, O104:H7, O113:H4, O130:H11 (two cases), O145:H2 (three cases), O146:H8, O149:H2 (two cases), O15:H2, O162:H7, O172:HNM, O178:H7, O182:HNM, O183:H18 (three cases), O183:HNM, O38:HNM, O55:H12, O63:H6, O65:H2, O75:H7, O76:H19 (two cases), O76:H20, O8:HNM, O80:H2, O81:H6, O91:H21 (two cases), O95:H16, O96:H5, ONT:H10, ONT:H13, ONT:H14, ONT:H28, ONT:H5, ORough:H21, ORough:H7

2017: O107:H7, O113:H21 (two cases), O117:H7, O123:H2, O128:HNT, O130:H11, O130:H23, O145:H2, O145:HNM, O146:H11, O146:HNT, O148:H21, O15:H14, O15:H21, O153:HNT (two cases), O156:H19, O165:HNM (three cases), O176:HRough, O177:HNM, O179:H8 (two cases), O18:H7, O182:HNM (two cases), O186:H10 (two cases), O20:HNM, O22:H16, O23:H39, O26:HNT (two cases), O38:HNT, 60:HNM, O75:H8 (two cases), O76:H19, O78:HNT, O8:H7, O8:HNM, O80:H2, O88:HNM, O88:HNT, O9:H2, ONT:H11, ONT:H14 (two cases), ONT:H19 (two cases), ONT:H27, ONT:H3, ONT:H45, ONT:H8, ONT:H9, ORough:H25

2018: O101:H19, O103:HNT, O103:HRough, O104:H7, O108:H25, O111:H21, O112:HNM (two cases), O117:H4 (two cases), O117:H7 (two cases), O117:HNM, O119:H4, O123/O186:H2 (two cases), O123/O186:H10 (two cases), O128:H45, O128:HNT, O130:H11, O136:H16, O145:H2, O149:H2 (two cases), O15:H2, O152:H10, O152:H38, O158:HNM, O162:H10, O163:H19, O171:H2, O174:H21, O174:HNT (two cases), O177:HNM, O178:H7, O181:H16, O182:HNM, O187:H7, O188:H7, O26:HNT, O29:H4, O45:H2, O6:HNM, O65:H2, O75:H8, O75:HNT, O76:H21, O77:HNM, O8:H9, O8:HNM, O80:HNM, O81:H21, O84:HNM, O87:H2, O88:HNM (two cases), O88:HNT (two cases), O91:H21 (two cases), O91:HNT, ONT:H10, ONT:H11 (two cases), ONT:H12, ONT:H14, ONT:H15, ONT:H19, ONT:H20 (two cases), ONT:H27, ONT:H30, ONT:H31, ONT:H4 (two cases), ONT:H8 (two cases), ONT:H9 (two cases), ONT:HRough, ORough:H10, ORough:H19 (two cases), ORough:H21, ORough:H26, ORough:H45, ORough:H5, ORough:HRough

Since 2017, pulsed field gel electrophoresis (PFGE) is no longer routinely performed on *E. coli* O157:H7 isolates with whole genome sequencing (WGS) now replacing this methodology. Figure 46 shows a minimum spanning tree of human O157:H7 isolates from 2017 and 2018 using the BioNumerics whole genome MLST (wgMLST) scheme. Consistent with previous PFGE analysis there is a wide diversity of genotypes present, with most of the isolates quite distinct from any other. There are, however, a number of small clusters of indistinguishable or very similar isolates, with less than 5 differences by wgMLST. These are analogous to SNP clusters with less than five differences.

Figure 46. Minimum spanning tree of human *E. coli* O157:H7 isolates, 2017 and 2018



Note: Each circle is a different genotype of *E. coli* O157, with indistinguishable isolates indicated by divisions within each circle. Shading and solid black lines connecting isolates indicates five or less wgMLST differences. Green circles: 2017. Red circles: 2018.

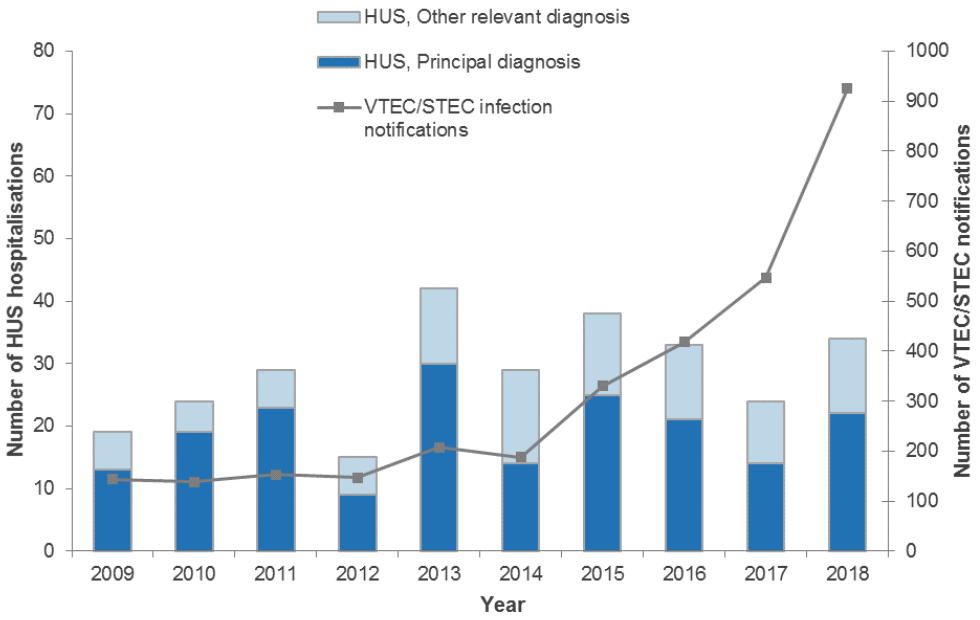
Disease sequelae – haemolytic uraemic syndrome (HUS)

HUS is a serious sequela that may result from a STEC infection. HUS is usually preceded by a STEC infection [27]. While most HUS cases are associated with *E. coli* O157 infections, non-O157 genotypes differ markedly in their virulence with respect to HUS causation [28].

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 2018 year were considered, rather than all cases that were hospitalised in that year. That is, if a HUS cases hospitalised in 2018 had been hospitalised with HUS in a previous year, the 2018 admission was considered to be a readmission, rather than an incident case. Of the 34 incident hospital admissions recorded in 2018 (0.7 per 100,000 population), 22 were reported with HUS as the primary diagnosis and 12 with HUS as another relevant diagnosis.

Between 2009 and 2018, the number of incident hospitalised cases (any diagnosis code) of HUS each year ranged from 15 to 42 (Figure 47). In 2018, the number of incident hospitalised cases increased to 34 from 24 in 2017, but was almost the same as the number in 2016 (33). STEC notifications have increased steadily over this period (Figure 46).

Figure 47. Haemolytic-uraemic syndrome (HUS) hospitalised cases, 2009–2018



In 2018, the number of female incident hospitalised cases due to HUS was greater than the number of male cases (Table 61). This is a reversal of the pattern seen in 2017, when more males were hospitalised with HUS than females, but is similar to the pattern seen in 2016.

Table 61. Haemolytic uraemic syndrome hospitalised cases by sex, 2018

Sex	Hospitalised cases[a]	
	No.	Rate[b]
Male	13	0.5
Female	21	0.8
Total	**34**	**0.7**

[a] MoH NMDS data for hospital admissions.

[b] per 100,000 of population.

In 2018, the highest age-specific rates of incident hospitalised cases due to HUS were in the less than 5 years age group (Table 62).

Table 62. Haemolytic uraemic syndrome hospitalised cases by age group, 2018

Age group (years)	Hospitalised cases [a]	
	No.	Rate[b]
<5	13	4.2
5 to 9	5	1.5
10 to 14	4	-
15 to 19	3	-
20 to 29	1	-
30 to 39	0	-
40 to 49	0	-
50 to 59	0	-
60 to 69	3	-
70+	5	1.0
Total	**34**	**0.7**

[a] MoH NMDS data for hospital admissions.

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

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

During 2018, 14 cases of HUS were reported to the NZPSU, of which 13 had a diarrhoeal prodrome. The median age of cases was 6.0 years. Twelve of the 13 diarrhoea-associated cases had *E. coli* O157:H7 isolated from their stools. Eight of these cases were from the North Island.

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

During the 2014 spring calving season, a random, stratified, cross-sectional study of dairy farms (*n* = 102) in six regions across New Zealand assessed the prevalence of the “Top 7” STEC bacteria (serogroups O157, O26, O45, O103, O111, O121, and O145) in young calves (*n* = 1,508), using a culture-independent diagnostic test (PCR/MALDI-TOF) [29]. Twenty percent (306/1,508) of calves on 75% (76/102) of dairy farms were positive for at least one of the “Top 7” STEC bacteria. STEC carriage by calves was associated with environmental factors, increased calf age, region, and increased number of calves in a shared calf pen.

The effect of transportation and lairage on the faecal shedding and post-slaughter contamination of carcasses with *Escherichia coli* O157 and O26 in young calves (4–7-day-old) was assessed in a cohort study at a regional calf-processing plant in the North Island of New Zealand, following 60 calves as cohorts from six dairy farms to slaughter [30]. Genotype analysis of *E. coli* O157 and O26 isolates provided little evidence of faecal-oral transmission of infection between calves during transportation and lairage.

Relevant regulatory developments

Nil.

Yersiniosis

Summary data for yersiniosis in 2018 are given in Table 63.

Table 63. Summary of surveillance data for yersiniosis, 2018

Parameter	Value in 2018	Source
Number of notified cases	1202	EpiSurv
Notification rate (per 100,000)	24.6	EpiSurv
Hospitalisations[a]	152	MoH NMDS
Deaths	0	EpiSurv
Estimated travel-related cases (%)[b]	67 (5.5%)	EpiSurv
Estimated food-related cases (%)[c]	718 (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 2017

Since June 2017 all community faecal specimens in Northland, Waitemata, Auckland and Counties Manukau DHBs were screened by multiplex PCR for *Y. enterocolitica,* in addition to a range of other pathogens. The introduction of these more sensitive assays may have triggered an increase in notifications. It is unclear at this stage how laboratory changes have affected the notification rates for yersiniosis.

Yersiniosis cases reported in 2018 by data source

During 2018, 1202 cases (24.6 per 100,000 population) of yersiniosis and no resulting deaths were reported in EpiSurv. Less than 15% of cases notified in EpiSurv were hospitalised in 2018.

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 152 hospital admissions (3.1 admissions

[*] 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 [12].

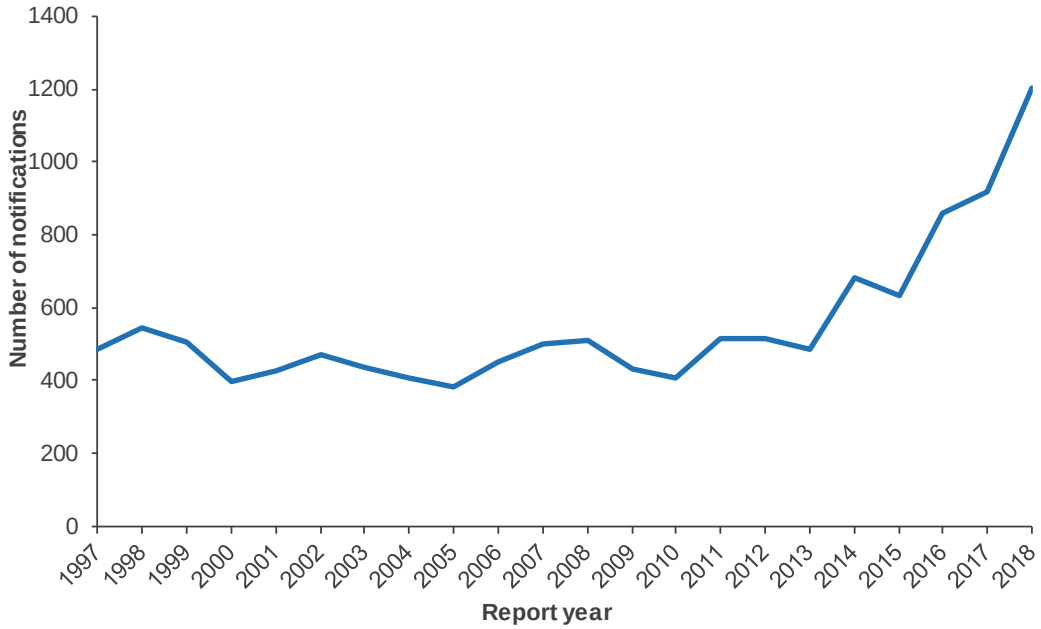
per 100,000 population) recorded in 2018, 85 were reported with yersiniosis as the principal diagnosis and 67 with yersiniosis as another relevant diagnosis.

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

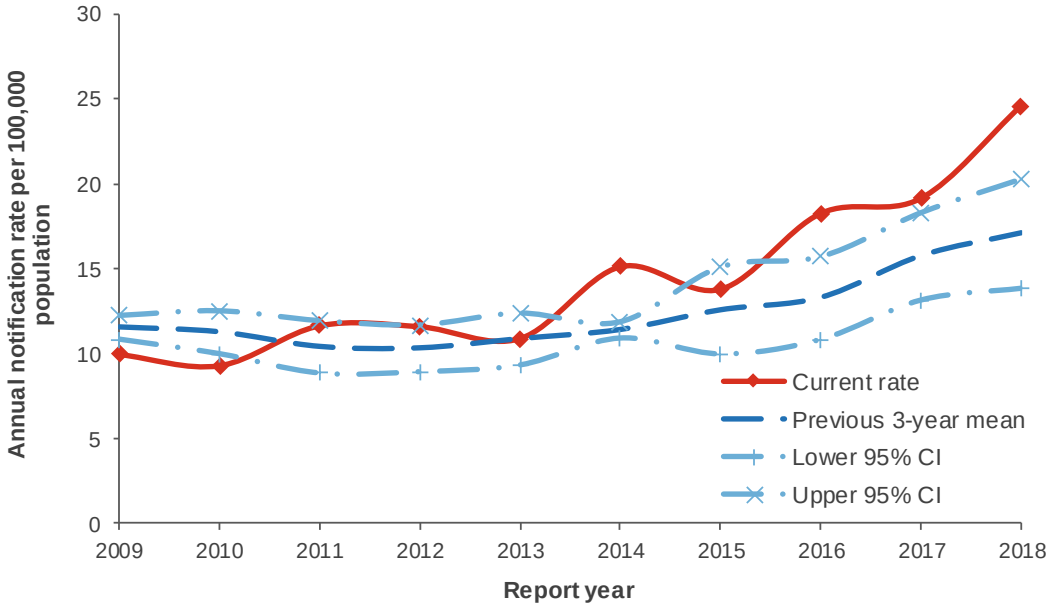
Yersiniosis became notifiable in 1996. Between 1998 and 2013 the annual number of notifications reported ranged between 383 and 546. Since 2010, the number of notifications for yersiniosis has been steadily increasing, with the highest number of cases reported in 2017 (918 cases) and 2018 (1202 cases) (Figure 48).

Figure 48. Yersiniosis notifications by year, 1997–2018



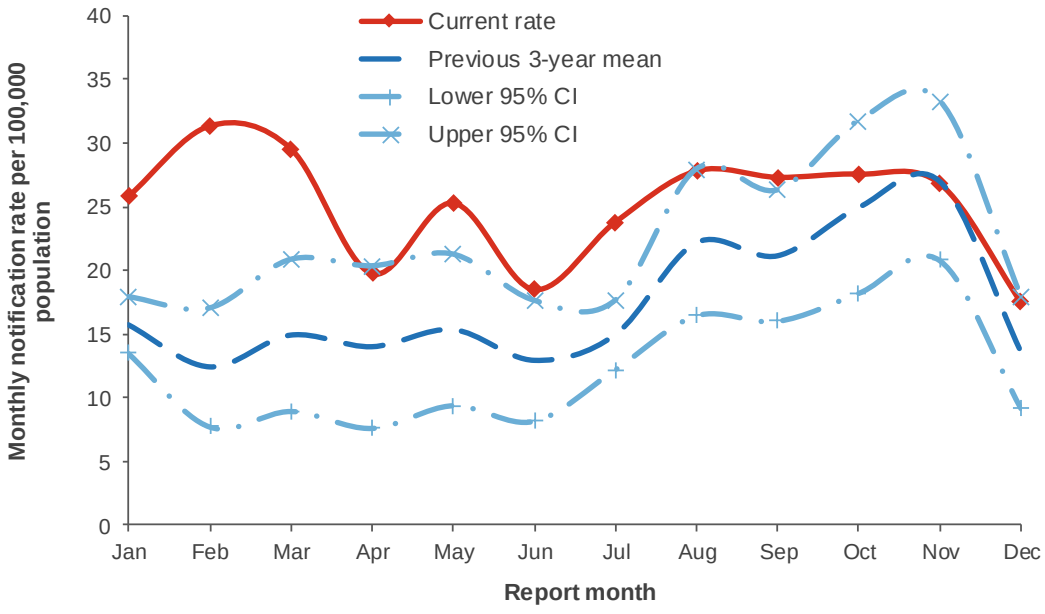
The yersiniosis annual notification rate remained stable between 2008 and 2013 (ranging from 9.3 to 11.9 per 100,000) and has increased steadily since then (Figure 49). In 2018, the rate has increased to 24.6 per 100,000 population from 19.2 per 100,000 population in 2017. The 2018 notification rate was higher than the previous three-year average (17.1 cases per 100,000).

Figure 49. Yersiniosis notification rate by year, 2009–2018



The number of notified cases of yersiniosis per 100,000 population by month for 2018 is shown in Figure 50. In 2018, monthly notification rates were generally higher compared to the previous three-year mean monthly rates. The monthly number of notifications ranged from 70 notifications (December) to 125 notifications (February). In contrast to previous years (2015–2017), where increased rates were observed in October and November, in 2018 no seasonal trend in monthly notification rates was apparent.

Figure 50. Yersiniosis monthly rate (annualised), 2018



In 2018, the yersiniosis notification and hospitalisation rates were similar for males and females (Table 64).

Table 64. Yersiniosis cases by sex, 2018

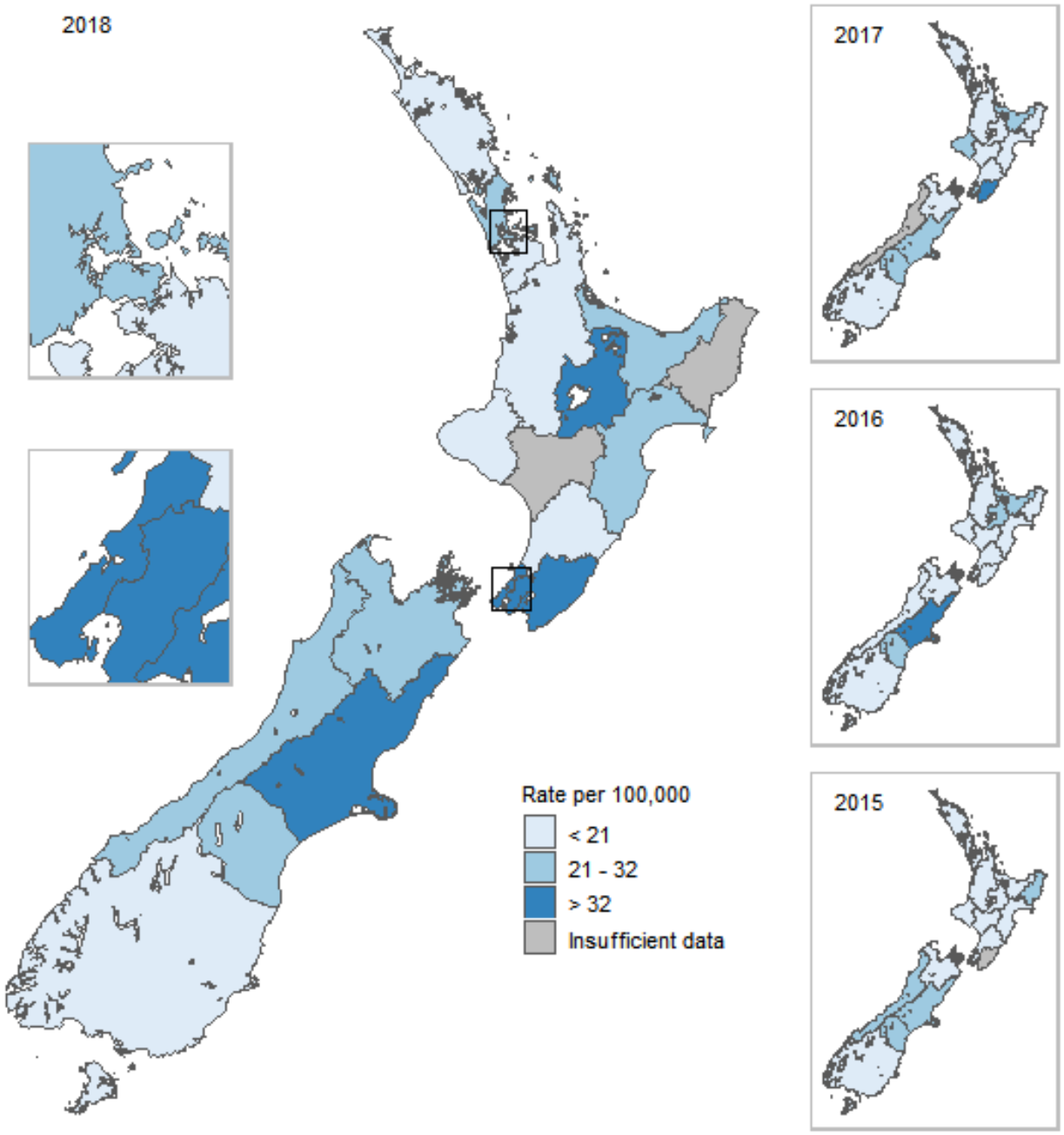
Sex	EpiSurv notifications		Hospitalisations[a]	
	No.	Rate[b]	No.	Rate[b]
Male	623	25.9	81	3.4
Female	579	23.4	71	2.9
Total	**1202**	**24.6**	**152**	**3.1**

[a] MoH NMDS data for hospital admissions.

[b] per 100,000 of population.

Yersiniosis notification rates have varied spatially and temporally throughout New Zealand over the last four years as illustrated in Figure 51. In 2018, the highest rates were reported for the DHBs Lakes (46.5 per 100,000 population, 51 cases), Wairarapa (44.0 per 100,000 population, 20 cases) and Hutt Valley (42.8 per 100,000 population, 64 cases). South Canterbury and Canterbury DHBs had consistently high yersiniosis notification rates between 2015 and 2018 compared to the rest of the country. Note that rates were not calculated for DHB year combinations where there were insufficient (less than five) cases notified.

Figure 51. Geographic distribution of yersiniosis notifications, 2015–2018



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 triggered an increase in notifications for yersiniosis. Refer to text for details.

In 2018, the highest yersiniosis notification rates were for the less than 1 year (132.8 per 100,000 population, 80 cases) and 1 to 4 years (80.0 per 100,000, 197 cases) age groups (Table 65). The highest hospitalisation rate was reported for the under 1 year age group (18.3 per 100,000 population, 11 cases).

Table 65. Yersiniosis cases by age group, 2018

Age group (years)	EpiSurv notifications		Hospitalisations[a]	
	No.	Rate[b]	No.	Rate[b]
<1	80	132.8	11	18.3
1 to 4	197	80.0	12	4.9
5 to 9	48	14.7	4	-
10 to 14	53	17.0	9	2.9
15 to 19	55	17.5	7	2.2
20 to 29	152	20.6	16	2.2
30 to 39	141	22.4	11	1.7
40 to 49	110	17.9	14	2.3
50 to 59	147	23.5	22	3.5
60 to 69	106	20.8	11	2.2
70+	113	22.2	35	6.9
Total	**1202**	**24.6**	**152**	**3.1**

[a] MoH NMDS data for hospital admissions (IDC-10 Code: A04.6).

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

For cases where information on travel was provided in 2018, 5.6% (95% CI 3.9–7.6%) 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 2018. The resultant distribution has a mean of 67 cases (95% CI 42–96).

If data from the last four years are considered, the estimated proportion of cases travelling overseas within the incubation period of the organism was 7.5% (95% CI 6.4–8.7%).

Outbreaks reported as caused by *Yersinia* spp.

In 2018, there were two *Yersinia* spp. outbreaks, one of which was reported to be foodborne (2 cases), in EpiSurv. 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.

Table 66. *Yersinia* spp. outbreaks reported, 2018

Measure	Foodborne *Yersinia* spp. outbreaks	All *Yersinia* spp. outbreaks
Outbreaks	1	2
Cases	2	8
Hospitalised cases	0	0

Table 67 contains details of the single foodborne *Yersinia* spp. outbreak reported in 2018. The level of evidence for the suspected food vehicle (pork brawn) was weak. No clinical or food samples relating to this outbreak were submitted to ESR's Public Health Laboratory.

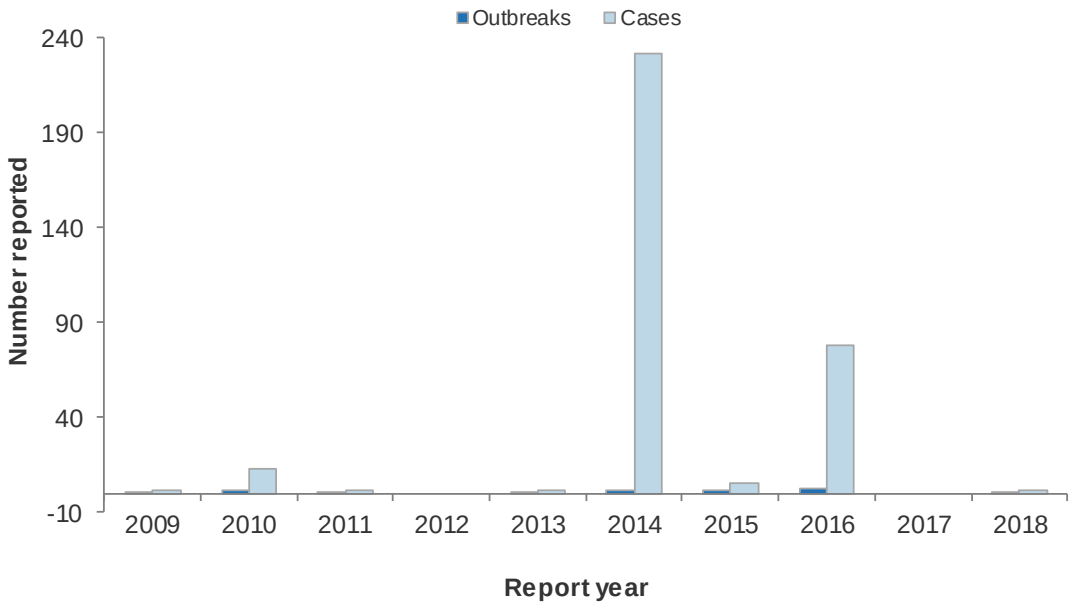
Table 67. Details of foodborne *Yersinis* spp. outbreaks, 2018

PHU	Month	Suspected vehicle	Exposure setting	Preparation setting	No. ill
PH Waikato	Dec	Pork brawn	Other food outlet	Other food outlet	2C, 0P

PHU: Public Health Unit, PH Waikato: Population Health Service Waikato, C: confirmed, P: probable.

Between 2009 and 2018 very few foodborne *Yersinia* spp. outbreaks were reported in EpiSurv (three or less each year, with a total number of associated cases ranging from two to 232. The number of foodborne 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 (Figure 52).

Figure 52. Foodborne *Yersinia* spp. outbreaks and associated cases reported by year, 2008–2018



Yersinia types commonly reported

In 2018, clinical laboratories submitted 1122 isolates for *Yersinia* spp. confirmation and typing to the Enteric Reference Laboratory (ERL) at ESR. Notifiable *Yersinia* spp. (i.e. *Y. enterocolitica* (YE) and *Y. pseudotuberculosis* (YTB)) cases were identified in 1064 (94.8%) of these isolates. The remaining 58 isolates were for either; duplicate samples from the same case, isolates not confirmed as *Yersinia* species or *Yersinia* species that are not notifiable.

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 53. The table and figure need to be interpreted with some caution as;

a) not all clinical laboratories forward isolates to ERL for confirmation and biotyping,
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 laboratories.

Between 2014 and 2018, each year the largest proportion of cases was due to *Y. enterocolitica*. A spike in 2014 of *Y. pseudotuberculosis* cases was predominantly associated with a single large outbreak of yersiniosis.

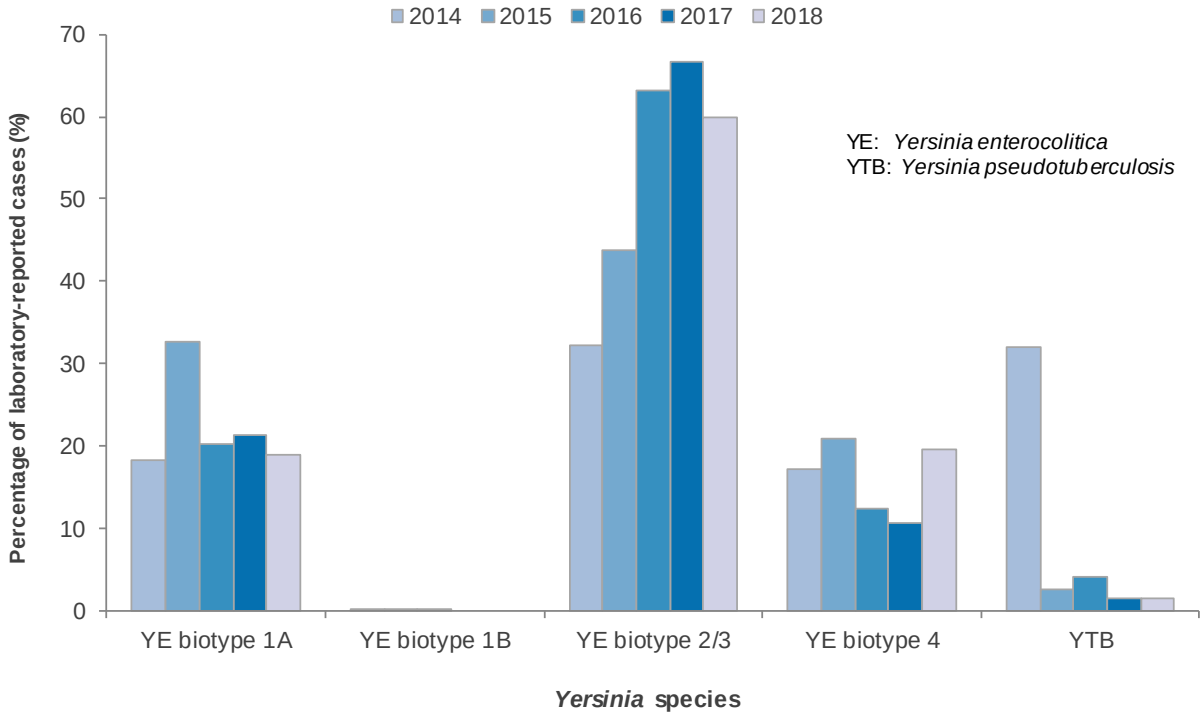
Since 2014 the number of cases reported with *Y. enterocolitica* biotypes 2/3 has continued to increase, however the percentage of cases reported with *Y. enterocolitica* biotypes 2/3 compared to all typed cases was similar across 2016 to 2018. In 2018, an increase in the number of cases with *Y. enterocolitica* biotype 4 was observed compared to the years 2014 to 2017, however the percentage of cases with *Y. enterocolitica* biotype 4 is similar to that observed in 2014 and 2015

Table 68. Notifiable *Yersinia* spp. identified by the Enteric Reference Laboratory, 2014–2018

Species	2014	2015	2016	2017	2018
Yersinia enterocolitica	**384**	**521**	**748**	**822**	**1049**
biotype 1A	103	173	157	178	201
biotype 1B	1	1	1	0	0
biotype 2/3[a]	182	232	493	556	637
biotype 4	97	111	96	88	207
biotype not identified	1	4	1	0	4
Yersinia pseudotuberculosis	**181**	**13**	**32**	**12**	**15**
Total	**565**	**534**	**780**	**834**	**1064**

[a]*Yersinia enterocolytica* biotypes 2 and 3 were shown to be genetically very similar and should not be separated (2017 ESR study, personal communication Jackie Wright). The discriminating biochemical test, a delayed weak indole reaction, can be subjective [31]. 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 53. Percentage of laboratory-reported cases of notifiable *Yersinia* spp. by species and year, 2014–2018



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 2018* [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 includes repeated admissions for patients with chronic notifiable diseases or diseases which have long-term health impacts (e.g. GBS). For some diseases, the criteria for notification (clinical and laboratory or epidemiological evidence) do not match those required for diagnostic coding. For these reasons hospitalisation numbers and notifications may differ.

In this report 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.

A new outbreak report form was introduced in October 2010. As a result, some variables reported previously are no longer available for analysis. For example, coding indicating the strength of evidence for concluding that an outbreak is foodborne was changed.

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 Annual Summary of Outbreaks in New Zealand 2018 [32].

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.

This report only includes reports 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 sub type 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 vehicle or 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 23 February 2019. Outbreak data contained in this report are based on information recorded as an outbreak in EpiSurv as at 10 May 2019. 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.

Data used for calculating rates of disease

All population rates use Statistics New Zealand 2018 mid-year population estimates and are crude rates unless otherwise stated. At 30 June 2018, the New Zealand population was estimated to be 4,885,530. 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).

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 year's data (2015−2017).

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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, 2017–2018

Disease	2017		2018		Change [b,c]
	Cases	Rates	Cases	Rates	
Campylobacteriosis	6482	135.2	6957	142.4	→
Cryptosporidiosis	1192	24.9	1611	33	→
Gastroenteritis[a]	324	6.8	234	4.8	←
Giardiasis	1648	34.4	1585	32.4	←
Hepatitis A	58	1.2	68	1.4	→
Listeriosis	21	0.4	30	0.6	→
Salmonellosis	1127	23.5	1100	22.5	←
Shigellosis	244	5.1	219	4.5	←
STEC infection	547	11.4	925	18.9	→
Yersiniosis	917	19.1	1202	24.6	→

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

[b] ←= Significant decrease, → = Significant increase, ▫ = No change, ← = Not significant decrease, → = Not significant increase

[c] Fisher's exact tests were used to determine statistical significance. Results are considered statistically significant when the *P* value is less than or equal to 0.05.

Table 70. Deaths due to selected notifiable diseases recorded in EpiSurv, 1997–2018

Disease	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018
Campylobacteriosis	2	2	1	3	1	1	0	0	1	1	1	0	0	0	0	0	1	0	0	0	0	0
Gastroenteritis	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	2	0	1	0	0
Giardiasis	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Listeriosis - non perinatal	2	0	1	2	1	0	2	3	1	0	2	3	2	3	1	4	2	3	1	0	0	2
Listeriosis - perinatal	6	0	2	4	1	3	2	2	4	1	2	2	2	4	0	2	3	2	3	2	0	0
Salmonellosis	2	2	1	7	2	1	0	0	1	1	1	1	1	0	0	0	0	0	0	0	1	0
Shigellosis	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0
STEC infection	1	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0	2
Yersiniosis	0	2	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0

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, 2016–2018

Disease	ICD 10 Codes	2016		2017		2018	
		Principal diagnosis	Other relevant diagnosis	Principal diagnosis	Other relevant diagnosis	Principal diagnosis	Other relevant diagnosis
Campylobacteriosis	A04.5	609	124	591	142	630	150
Cryptosporidiosis	A07.2	39	11	46	21	82	53
Giardiasis	A07.1	29	22	38	33	38	26
Hepatitis A	B15	19	65	40	42	47	49
Listeriosis	A32	21	22	7	12	17	24
Salmonellosis[a]	A02.0	137	34	144	26	183	44
Shigellosis	A03	21	10	33	12	37	22
STEC infection[b]	A04.3	10	6	11	9	19	22
Yersiniosis	A04.6	41	26	54	37	85	67

[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, 2018

Disease	Ethnic group											
	Māori		Pacific peoples		Asian		MELAA[a]		European or Other		Total[b]	
	Cases	Rate	Cases	Rate	Cases	Rate	Cases	Rate	Cases	Rate	Cases	Rate
Campylobacteriosis	577	79.9	142	47.5	367	65.2	44	80.5	4977	153.3	6957	142.4
Cryptosporidiosis	205	28.4	72	24.1	86	15.3	13	23.8	1078	33.2	1611	33.0
Gastroenteritis[c]	22	3.0	10	3.3	15	2.7	2	-	167	5.2	234	4.8
Giardiasis	144	20.0	23	7.7	98	17.4	27	49.4	1132	34.9	1585	32.4
Hepatitis A	5	0.7	21	7.0	18	3.2	5	9.2	17	0.5	68	1.4
Listeriosis	1	-	3	-	3	-	0	-	23	0.7	30	0.6
Salmonellosis	122	16.9	65	21.7	107	19.0	10	18.3	767	23.6	1100	22.5
Shigellosis	16	2.2	64	21.4	30	5.3	5	9.2	97	3.0	219	4.5
STEC infection	96	13.3	27	9.0	57	10.1	11	20.1	709	21.8	925	18.9
Yersiniosis	102	14.1	49	16.4	229	40.7	13	23.8	702	21.6	1202	24.6

[a] Middle Eastern/Latin American/African.

[b] Total includes cases where ethnicity was unknown.

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

Note: Denominator data used to determine disease rates for ethnic groups is based on the proportion of people in each ethnic group from the estimated resident 2013 census population applied to the 2018 mid-year population estimates from Statistics New Zealand. Ethnicity is prioritised in the following order: Māori, Pacific peoples, Asian, MELAA and European or Other Ethnicity (including New Zealander). Where fewer than five cases have been notified, a rate has not been calculated and the cell marked NC (-).

Table 73. Number of cases and rates of selected notifiable diseases per 100,000 population by sex, 2018

Disease	Sex					
	Male		Female		Total[a]	
	Cases	Rate	Cases	Rate	Cases	Rate
Campylobacteriosis	3871	160.7	3085	124.6	6957	142.4
Cryptosporidiosis	718	29.8	892	36.0	1611	33.0
Gastroenteritis[b]	101	4.2	131	5.3	234	4.8
Giardiasis	848	35.2	737	29.8	1585	32.4
Hepatitis A	37	1.5	31	1.3	68	1.4
Listeriosis[c]	14	0.6	16	0.6	30	0.6
Salmonellosis	566	23.5	533	21.5	1100	22.5
Shigellosis	115	4.8	104	4.2	219	4.5
STEC infection	437	18.1	488	19.7	925	18.9
Yersiniosis	623	25.9	579	23.4	1202	24.6

[a] Total includes cases where sex was unknown.

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

[c] It should be noted that notification case details for perinatal cases are those for the mother, so the female cases will include all five perinatal cases.

Table 74. Number of cases and rates of selected notifiable diseases per 100,000 population by age group, 2018

	<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**	
Disease	Cases	Rate	Cases	Rate	Cases	Rate	Cases	Rate	Cases	Rate	Cases	Rate	Cases	Rate	Cases	Rate	Cases	Rate	Cases	Rate	Cases	Rate	**Cases**	**Rate**
Campylobacteriosis	138	229.2	746	302.9	300	91.7	232	74.6	391	124.5	1,057	143.2	761	121.1	775	125.9	877	140.2	799	156.9	880	172.6	**6,957**	**142.4**
Cryptosporidiosis	38	63.1	384	155.9	193	59.0	91	29.3	92	29.3	271	36.7	252	40.1	129	21.0	59	9.4	60	11.8	42	8.2	**1611**	**33.0**
Gastroenteritis	6	10.0	21	8.5	6	1.8	4		14	4.5	30	4.1	39	6.2	33	5.4	31	5.0	24	4.7	17	3.3	**234**	**4.7**
Giardiasis	20	33.2	261	106.0	98	29.9	46	14.8	32	10.2	217	29.4	325	51.7	186	30.2	191	30.5	144	28.3	65	12.8	**1585**	**32.4**
Hepatitis A			5	2.0	13	4.0	3		7	2.2	21	2.8	7	1.1	4		2		3		3		**68**	**1.4**
Listeriosis											1		3		2		2		5	1.0	17	3.3	**30**	**0.6**
Salmonellosis	53	88.0	134	54.4	71	21.7	29	9.3	65	20.7	160	21.7	120	19.1	126	20.5	147	23.5	109	21.4	86	16.9	**1100**	**22.5**
Shigellosis	1		23	9.3	12	3.7	7	2.3	8	2.5	39	5.3	28	4.5	25	4.1	29	4.6	26	5.1	21	4.1	**219**	**4.5**
VTEC/STEC infection	42	69.7	134	54.4	49	15.0	42	13.5	47	15.0	103	14.0	79	12.6	78	12.7	89	14.2	110	21.6	152	29.8	**925**	**18.9**
Yersiniosis	80	132.8	197	80.0	48	14.7	53	17.0	55	17.5	152	20.6	141	22.4	110	17.9	147	23.5	106	20.8	113	22.2	**1202**	**24.6**

[a] Cases of acute gastroenteritis from a common source or foodborne intoxication e.g. staphylococcal intoxication.
[b] Total may include cases where age was unknown.

Note: Where fewer than five cases have been notified a rate has not been calculated.
Rates for each disease have been divided into three bands and shaded to indicate the age groups with highest, medium and lowest rates of disease. Shadings used are:

Fewer than 5 cases in a cell or less than a national total of 50 cases for the year

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

Second (middle) band

Third (highest) band (above 75th percentile)

Table 75. Number of cases of selected notifiable diseases by District Health Board, 2018

Disease	District Health Board																				
	Northland	Waitemata	Auckland	Counties Manukau	Waikato	Lakes	Bay of Plenty	Tairawhiti	Taranaki	Hawke's Bay	Whanganui	MidCentral	Hutt Valley	Capital & Coast	Wairarapa	Nelson Marlborough	West Coast	Canterbury	South Canterbury	Southern	Total
Campylobacteriosis	244	903	586	577	675	154	242	54	222	294	81	297	195	432	79	239	50	762	150	721	6957
Cryptosporidiosis	72	198	170	206	132	25	54	10	35	77	15	80	58	186	20	34	6	99	21	113	1611
Gastroenteritis[a]	41	9	5	3	17	10	15	0	2	0	3	1	17	41	4	9	4	47	0	6	234
Giardiasis	56	177	233	150	151	32	82	34	25	68	14	43	51	130	22	35	6	167	25	84	1585
Hepatitis A	2	11	16	8	6	0	0	0	0	3	2	2	0	1	0	3	0	4	0	10	68
Listeriosis	2	4	3	4	1	0	2	0	0	0	1	1	1	4	1	1	0	3	0	2	30
Salmonellosis	33	107	92	87	112	22	45	12	36	36	15	27	28	86	10	40	14	167	14	117	1100
Shigellosis	2	39	49	34	17	2	8	1	4	9	1	0	8	12	0	12	0	14	1	6	219
STEC infection	68	78	75	66	56	10	18	3	9	52	4	8	41	77	28	66	1	39	11	215	925
Yersiniosis	25	133	147	90	85	51	69	3	22	41	4	15	64	110	20	45	8	184	17	69	1202

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

Table 76. Rate per 100,000 population of selected notifiable diseases by District Health Board, 2018

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	136.2	145.6	109.2	103.4	162.1	140.4	102.1	110.0	185.3	177.3	124.8	165.6	130.4	136.1	173.6	158.7	153.4	135.3	250.4	218.4	**142.4**
Cryptosporidiosis	40.2	31.9	31.7	36.9	31.7	22.8	22.8	20.4	29.2	46.4	23.1	44.6	38.8	58.6	44.0	22.6	18.4	17.6	35.1	34.2	**33.0**
Gastroenteritis	22.9	1.5	0.9		4.1	9.1	6.3						11.4	12.9		6.0		8.3		1.8	**4.7**
Giardiasis	31.3	28.5	43.4	26.9	36.3	29.2	34.6	69.2	20.9	41.0	21.6	24.0	34.1	40.9	48.4	23.2	18.4	29.7	41.7	25.4	**32.4**
Hepatitis A		1.8	3.0	1.4	1.4															3.0	**1.4**
Listeriosis																					**0.6**
Salmonellosis	18.4	17.2	17.1	15.6	26.9	20.1	19.0	24.4	30.1	21.7	23.1	15.1	18.7	27.1	22.0	26.6	42.9	29.7	23.4	35.4	**22.5**
Shigellosis		6.3	9.1	6.1	4.1		3.4			5.4			5.4	3.8		8.0		2.5		1.8	**4.5**
VTEC/STEC infection	38.0	12.6	14.0	11.8	13.4	9.1	7.6		7.5	31.4		4.5	27.4	24.3	61.5	43.8		6.9	18.4	65.1	**18.9**
Yersiniosis	14.0	21.4	27.4	16.1	20.4	46.5	29.1		18.4	24.7		8.4	42.8	34.6	44.0	29.9	24.5	32.7	28.4	20.9	**24.6**

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

Note: Where fewer than five cases have been notified a rate has not been calculated.
Rates for each disease have been divided into three bands and shaded to indicate DHBs with the highest, middle and lowest rates of disease. Shadings used are:

Fewer than 5 cases in a cell or less than a national total of 50 cases for the year

First band (lower than 25th percentile)

Second (middle) band

Third band (above 75th percentile)

Table 77. Number of cases of selected notifiable diseases by year, 1988–2002

Disease	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002
Campylobacteriosis	2796	4187	3850	4148	5144	8101	7714	7442	7635	8924	11 572	8161	8418	10 146	12 493
Cryptosporidiosis[a]	-	-	-	-	-	-	-	-	119	357	866	977	775	1208	975
Gastroenteritis[a b]	-	-	-	-	-	-	-	-	555	310	492	601	727	940	1087
Giardiasis[a]	-	-	-	-	-	-	-	-	1235	2127	2183	1793	1688	1604	1547
Hepatitis A	176	134	150	224	288	257	179	338	311	347	145	119	107	61	106
Listeriosis	7	10	16	26	16	11	8	13	10	35	17	19	22	18	19
Salmonellosis	1128	1860	1619	1244	1239	1340	1522	1334	1141	1177	2069	2077	1795	2417	1880
Shigellosis	145	137	197	152	124	128	185	191	167	117	122	147	115	157	112
STEC infection[c]	-	-	-	-	-	3	3	6	7	13	48	64	67	76	73
Yersiniosis[a]	-	-	-	-	-	-	-	-	330	488	546	503	396	429	472

[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 [33]. Note: cell is blank where data are unavailable.

Table 78. Number of cases of selected notifiable diseases by year, 2003–2018

Disease	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018
Campylobacteriosis	14 788	12 215	13 836	15 873	12 778	6694	7177	7346	6686	7016	6837	6782	6218	7456	6482	6957
Cryptosporidiosis	817	611	888	737	924	764	854	954	610	877	1348	584	696	1062	1192	1611
Gastroenteritis[a]	1030	1363	560	938	625	687	713	493	570	765	559	756	500	510	327	234
Giardiasis	1570	1514	1231	1214	1402	1660	1639	1985	1934	1714	1729	1709	1510	1616	1648	1585
Hepatitis A	70	49	51	123	42	89	44	46	26	82	91	74	47	35	58	68
Listeriosis	24	26	20	19	26	27	28	23	26	25	19	25	26	36	21	30
Salmonellosis	1401	1081	1382	1335	1275	1339	1128	1146	1055	1081	1143	955	1051	1091	1119	1100
Shigellosis	87	140	183	102	129	113	119	104	101	131	137	128	111	174	245	219
STEC infection	104	89	92	87	100	124	143	138	153	147	205	187	330	418	547	925
Yersiniosis	436	407	383	453	502	508	430	406	513	514	483	680	634	858	918	1202

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

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 (2018)	Australia[a] (2018)	USA[b] (2018)	Canada[d] (2016)	UK (2017)	EU Total (2017)	Other high	
Campylobacteriosis	142.4	130.5	19.5	27.2	96.2[e]	64.8[e]	230.0 (Czech Republic)[e]	127.8 (Slovakia)[e]
Cryptosporidiosis	33.0	12.2	3.5[c]	2.7	10.3[f]	3.8[f]	11.8 (Ireland)[f]	11.0 (Belgium)[f]
Giardiasis	32.4	NN	5.9[c]	10.5	7.2[f]	5.8[f]	19.1 (Bulgaria)[f]	17.7 (Belgium)[f]
Hepatitis A	1.4	1.8	1.0[c]	0.7	0.8[f]	2.4[f]	25.0 (Slovakia)[f]	22.7 (Bulgaria)[f]
Listeriosis	0.6	0.3	0.3	0.53	0.24[e]	0.48[e]	1.77 (Iceland)[e]	1.62 (Finalnad)[e]
Salmonellosis	22.5	57.6	18.3	21.0	15.5[e]	19.7[e]	108.5 (Czech Republic)[e]	106.5 (Slovakia)[e]
Shigellosis	4.5	10.1	4.9	2.4	2.8[f]	1.5[f]	4.1 (Bulgaria)[f]	3.7 (Denmark)[f]
STEC infection	18.9	2.3	5.9	2.0	1.5[e]	1.7[e]	16.6 (Ireland)[e]	5.0 (Sweden)[e]
Yersiniosis	24.6	NN	0.9	NN	0.2[e]	1.8[e]	7.7 (Finland)[e]	6.1 (Lithuania)[e]

NN: Not notifiable

[a] National Notifiable Diseases Surveillance System (NNDSS) http://www9.health.gov.au/cda/source/CDA-index.cfm (data downloaded on 7 June 2019)

[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 2017 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 Summary Report on Trends and Sources of Zoonoses, Zoonotic Agents and Food-borne Outbreaks in 2017 https://efsa.onlinelibrary.wiley.com/doi/epdf/10.2903/j.efsa.2018.5500

[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 2016 year).

Table 80. Foodborne outbreaks and associated cases by pathogen/condition, 2018

Pathogen/Condition	Outbreaks (n = 43)[d]		Cases (n = 580)[d]	
	No.	%[a]	No.	%[b]
Norovirus	8	18.6	362	62.4
Campylobacter	7	16.3	24	4.1
Salmonella	5	11.6	17	2.9
Hepatitis A	3	7.0	8	1.4
Histamine (scombroid) fish poisoning	2	4.7	5	0.9
Clostridium perfringens	1	2.3	21	3.6
Shigella	1	2.3	3	0.5
Staphylococcus aureus	1	2.3	9	1.6
Yersinia	1	2.3	2	0.3
Pathogen not identified[c]	14	32.6	129	22.2

[a] Percentage of outbreaks for each pathogen/condition, calculated using the total number of foodborne outbreaks (43). 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 (580).

[c] All enteric outbreaks with no pathogen identified in 2018 were recorded as gastroenteritis.

Table 81. Foodborne outbreaks and associated cases by exposure setting, 2018

Exposure setting	Outbreaks (n = 43)[c]		Cases (n = 580)[c]	
	No.	%[a]	No.	%[b]
Commercial food operators	**19**	**44.2**	**98**	**16.9**
Restaurant/café/bakery	9	20.9	58	10.0
Other food outlet	5	11.6	13	2.2
Supermarket/delicatessen	3	7.0	9	1.6
Takeaway	2	4.7	5	0.9
Caterers	1	2.3	15	2.6
Institutions	**13**	**30.2**	**350**	**60.3**
School	4	9.3	170	29.3
Long-term care facility	3	7.0	114	19.7
Childcare centre	2	4.7	27	4.7
Hotel/motel	1	2.3	2	0.3
Other institution	3	7.0	37	6.4
Other	**11**	25.6	**139**	24.0
Private home	6	14.0	15	2.6
Farm	2	4.7	5	0.9
Workplace	1	2.3	4	0.7
Other setting[d]	3	7.0	118	20.3
Unknown exposure setting	**1**	**2.3**	**8**	**1.4**

[a] Percentage of outbreaks for each exposure setting, calculated using the total number of foodborne outbreaks (43). 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 (580).

[c] Three outbreaks had two or more exposure settings (20 cases).

[d] One outbreak with other setting had an overseas exposure location.

Table 82. Foodborne outbreaks and associated cases by preparation setting, 2018

Preparation setting	Outbreaks (n = 43)[c]		Cases (n = 580) [c]	
	No.	%[a]	No.	%[b]
Commercial food operators	**17**	**39.5**	**75**	**12.9**
Restaurant/café/bakery	7	16.3	34	5.9
Other food outlet	5	11.6	13	2.2
Supermarket/delicatessen	3	7.0	9	1.6
Takeaway	2	4.7	6	1.0
Caterers	1	2.3	15	2.6
Institutions	**6**	**14.0**	**81**	**14.0**
Childcare centre	2	4.7	27	4.7
Hotel/motel	1	2.3	2	0.3
Long term care facility	1	2.3	19	3.3
School	1	2.3	19	3.3
Other institution	1	2.3	14	2.4
Other	**8**	**18.6**	**149**	**25.7**
Private home	2	4.7	23	4.0
Farm	2	4.7	5	0.9
Workplace	1	2.3	4	0.7
Other setting	3	7.0	117	20.2
Unknown exposure setting	**13**	**30.2**	**290**	**50.0**

[a] Percentage of outbreaks for each preparation setting, calculated using the total number of foodborne outbreaks (43). 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 (580).

[C] Two outbreaks had two or more preparation settings (17 cases).

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